STUDIES ON COMBINING ABILITY, GENE ACTION AND STABILITY ANALYSES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN WHEAT *(Triticum aestivum* L.)

Thesis Submitted for the Award of the Degree of

DOCTOR OF PHILOSOPHY

in

Genetics and Plant Breeding

By

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DECLARATION

I, Tukur Bubuche Sani, hereby solemnly declare that the thesis entitled “Studies on Combining Ability, Gene Action, and Stability Analyses for Yield and Yield-Contributing Traits in Wheat (*Triticum aestivum* L.)” is a true and original record of the research work carried out by me at Lovely Professional University. This work was undertaken as part of the requirements for the award of the degree of **Doctor of Philosophy (Ph.D.)** in Genetics and Plant Breeding, under the guidance and supervision of Dr. Shiv Prakash Shrivastav (Assistant Professor), Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University Punjab, India. I further affirm that this thesis has not been submitted, either in part or in full, for the award of any other degree or diploma elsewhere. All the sources of information used and referenced in this thesis have been duly acknowledged. This declaration is made with full knowledge of the academic and ethical responsibilities regarding the originality of the work presented.

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DEDICATION

This research work is dedicated to my beloved parents, whose unwavering love, sacrifices, and encouragement have been the foundation of all my achievements. Their constant support and belief in me have been my greatest source of strength, and I am forever grateful for their sacrifices that have made this journey possible.

CERTIFICATE-I

This is to certify that the thesis entitled “Studies on Combining Ability, Gene Action, and Stability Analyses for Yield and Yield-Contributing Traits in Wheat (*Triticum aestivum* L.)” submitted in fulfillment of the requirement for the award of degree of **Doctor of Philosophy (Ph.D.)** in the Genetics and Plant Breeding, School of Agriculture, is a research work carried out by Mr. Tukur Bubuche Sani (Registration No. 12201269), is bonafide record of his original work carried out under my supervision and that no part of thesis has been submitted for any other degree, diploma or equivalent course.

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CERTIFICATE-II

This is to certify that the thesis entitled "Studies on Combining Ability, Gene Action, and Stability Analyses for Yield and Yield-Contributing Traits in Wheat (*Triticum aestivum* L.)" submitted by **Mr. Tukur Bubuche Sani (Registration No. 12201269)** for partial fulfillment of the requirements for the award of the degree of **Doctor of Philosophy** (Ph.D.) in Genetics and Plant Breeding, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab, has been thoroughly reviewed and approved by the Advisory Committee. The work presented in the thesis has been evaluated following an oral examination of the student, conducted in collaboration with an external examiner. This certification affirms that the thesis has met the necessary academic standards for the award of the Ph.D. degree.

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Place: Phagwara **Tukur Sani Bubuche**

Date: 22/08/2025

ABSTRACT

Present investigation entitled "Studies on combining ability, gene action and stability analyses for yield and yield contributing traits in wheat (*Triticum aestivum* L.)" designed to (i) study the combining ability variances and their effects (ii) to find out gene actions involved in the inheritance of various characters (iii) to estimate heterosis over better-parent and standard varieties and (iv) to work out stability analysis of parents involves in hybridization programme and their offrings.

Wheat belong to family poaceae and second most important staple food crop next to rice and contributed immensely to world's economy and human nutrition to meet the growing global demand. It is considered as allohexaploid species consisting of 21 chromosome pairs, organized into three subgenomes; A, B, and D, with AABBDD genome composition and chromosome number of $2n = 6x = 42$. Wheat is a self-pollinating plant, characterized by segmented culm and blade-like leaves with three anthers connected to the base by slender filaments, enclosed within bract-like structures called lemma and palea.

In an attempt to improve yield in wheat, commercial hybrid seed production was attempted several to many times through various sterility induction techniques, encompasses genetic male sterility, cytoplasmic genetic male sterility and through chemical hybridizing agents to improve yield in wheat, but all efforts have little or no practical relevance owing to polyploidy nature of wheat and technical intricacies involved in hybrid seed production at commercial scale. Most existing and previous studies on stability analysis were carried out in either India or Nigeria but not both, leaving a serious gap between the two diverse agro ecological zones for stability analysis. Wheat production faces several challenges that affect its yield and quality like heat stress, insufficient breeding information such as genetic variances, GCA, SCA, stability analysis and exploitation of heterosis that involves different agro-ecological zones. Nigeria previously listed among world's wheat-producing countries, but Nigeria is no longer considered as one of the major world wheat producer due to the use of low yielding varieties and insufficient breeding information.

Present investigation provides potential solutions to the aforementioned problems by providing sufficient, eco-friendly and non-transgenic breeding techniques that will underpin the development of advanced breeding techniques viz.; heterosis breeding; stability analysis and selection of superior genotype aimed at improvement of wheat production to ensure resilience against environmental stresses that ultimately contributes to sustainable agricultural practices and the ability to meet the demand of growing population. Study of heterosis is no longer optional but imperative for wheat improvement due to challenges associated with the development of commercial hybrid seeds in wheat, the economic exploitation of heterosis in self-pollinated crops like wheat is highly essential. Data from India and Nigeria unlocked the breeding information on wheat performance across South Asia (India) and West Africa (Nigeria). The assessment of potential genotypes across different environmental conditions (stability analysis) is vital and last step in most applied plant breeding programme.

The experiment conducted during 2022-23 and 2023-24 *Rabi* seasons at three locations. Line x tester mating design was used to generate forty five F_1s hybrids by the cross of fifteen lines with three testers. Randomized Complete Block Design (RCBD) with three replications was used during 2024 *Rabi* season (multilocational trial). Observations were recorded on sixteen

quantitative and qualitative parameters such as days to 50% heading (DH); number of productive tiller (NPT); grain filling period (GFP); flag leaf area (FLA) (cm^2); days to maturity (DM); spike length (SL) (cm); chlorophyll content (CLC) (SPAD-meter value); harvest index (HI) (%); number of spikelets/spike (NS/S); number of grain/spike (NG/S); grain weight/spike (GW/S) (g); thousand grains weight (1000 GW) (g); plant height (PH) (cm); biological yield (BY) (g); protein content (PC) (%); (GYP) (g). Data subjected to statistical analysis through the procedures outlined by Panse and Sukhatme 1967 (ANOVA), Kempthorne (combining ability), Fonseca and Patterson (heterosis) and Eberhart and Russell (stability analysis).

Analysis of variance (ANOVA) recorded significant ($p < 0.001$) from grain yield per plant observed in line (11.53) and line x tester (5.43) were significant at 1% level, indicating that genetic differences among lines and their interaction with testers were crucial in determining grain yield per plant.

Four out of eighteen parents considered as best general combiners for yield and yield components which hierarchically mentioned below; PBW ZN1 (GCA for GYP 0.532642 (ranked 1), HI 0.007111 (ranked 2), and SL 0.11336 (ranked 3)); PBW-757 (GCA for GYP 1.473681 (ranked 2), HI 1.814672 (ranked 3), and SL 0.220864 (ranked 3)); PBW-822 (GCA for GYP 1.143581 (ranked 3), HI 1.16343 (ranked 4) and SL 0.03543 (ranked 9)), DBW-173 (GCA for GYP 0.606278 (ranked 5), HI 2.326054 (ranked 1), and SL 0.36247 (ranked 15)). Thus, best general combiners could serve as potential candidates for future breeding programme like early generation selection or good potential for grain yield improvement.

Six out of forty five crosses recorded significant positive SCA effects for yield and yield components viz.; PBW-822X PBW ZN1 (GYP 3.795527 ranked 1), DBW-222X PBW ZN1 (GYP 3.400949 ranked 2), DH-3086XPBWZN1 (GYP 3.159307 ranked 3), PBW-677XPBW-343 (GYP 2.812548 ranked 5), HD-3721X HD-3326 (GYP 1.133811 ranked 12), and CRD GEHNU1XPBW ZN1 (GYP 0.680626 ranked 16). The aforementioned crosses indicated the present of non-additive gene effects and could be used for later generation selection and for further breeding program like heterosis breeding for yield improvement in wheat.

Mode of gene expression observed that additive gene action recorded the highest contributions to the total genetic variation for yield and yield components for almost all the studied traits (indicates the preponderance of additive effects) in wheat. However, non-additive gene action also recorded significant contributions to the total genetic variation in some traits (indicates the presence of non-additive effects in such traits that will appear in next generation). Therefore, both the pure line selection and heterosis breeding could be applicable for yield improvement in wheat. Example, additive contribution for harvest index was 2.83%, non-additive contribution was 1.34%; and the relative contributions of additive gene effect for grain yield per plant was 5.51% while non-additive contribution was 1.43% and an additive contribution of biological yield was 1.76% while non-additive contribution was 1.34%. However, non-additive contribution of protein content was 8.8%; but additive contribution was 0.0%. With regard to number of spikelet per spike, the relative contributions of non-additive was 1.78%; whereas additive contribution was 0.74%. Furthermore, number of productive tillers per plant, non-additive was 2.17% whereas additive contribution was 1.78%

The magnitude of heterosis over better parent (BP) and standard varieties (SV) considered four crosses as the best for grain yield per plant and other yield parameters such as BHU-31 X PBWZN1 (BP 19.85 and for all SV1-SV4); HD-3721 X PBW-343 (BP 24.84; and for all SV1-SV4); PBW-822 X PBW ZN1 (BP 47.15 and for all SV1-SV4); and PBW-822 X

PBWZN1 (51.51 and for all SV1-SV4).Same being for chlorophyll content, the high BP and SV heterosis recorded in PBW-822 X PBW ZN1 (BP heterosis (22.52%) and standard variety (30.14% in SV2) indicating high hybrid vigor and PBW-757 X PBW ZN1 (BP heterosis of 18.42%, with SV4 heterosis (25.78%) showed better performance). Thus, present investigation provides valuable breeding information on inheritance patterns of yield-related traits for exploitation of heterosis that underpin the development of advanced breeding techniques (like heterosis breeding).

Stability analysis observed no single genotype recorded high stability for all studied traits. However, some genotypes like NORMAN (bi -0.03) and BHU-31 X PBW-343 (bi 0.13) recorded higher stability estimate for number of productive tillers (under favorable and unfavorable conditions). However, for biological yield good stability observed in genotypes DBW-173X HD-3326 (mean 65.61, bi 1.36, S^2di 1.68 (under favorable condition only) and harvest index results revealed that, genotype DH-3086X PBW-343 (S^2di -1.29) and PBW-822X PBW ZN1 (S^2di -1.33) showed best level of stability estimate making them strong candidates for cultivation in diverse environments. For grain yield per plant, highly stable with moderate yield recorded in HD-3326, DBW-173, BHU-25, BHU-25 X HD-3326, indicating stability across environments, while the least stability was recorded in BHU-25 X HD-3326 (S^2di 20.80). With regard to some quality parameters like protein content the best and stable genotype was PBW-757X PBW-343 with mean yield of 53.67, bi (2.01 and S^2di (-2.15).. While genotype DBW-173 with mean yield of 41.46, bi 0.59 (average stability), indicating the preponderance of additive gene action. Conclusively, grain yield per plant and other yield contributing traits recorded high yield with moderate stability in genotypes DH-3086 X PBW-343 and DBW-222 X PBW ZN1 in contrast for genotypes DBW-173 and PBW ZN1 with highest stability but moderate yielding ability. Therefore, for further wheat improvement genotype DH-3086 X PBW-343 could be cross with DBW-173, same being DBW-222 X PBW ZN1 could be cross with PBW ZN1 to develop ideal genotype (high yielding and stable genotype). This approach allows breeders to develop wheat varieties that meet the demands of the consumers and can support sustainable agriculture.

(Dr. Shiv Prakash Shrivastav) **(Tukur Sani Bubuche)**

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CHAPTER ONE

INTRODUCTION

1.1 Background of the study

Wheat (*Triticum aestivum* L.) belong to family poaceae and second most important staple food crop next to rice and contributed immensely to the world's economy and human nutrition (AbdEl-Hady *et at.,* 2018). Wheat is an allohexaploid species consisting of 21 chromosome pairs, organized into three subgenomes; A, B, and D, with AABBDD genome composition and chromosome number of 2n = 6x = 42 (Bajaniya *et al*., 2019). It was developed through natural hybridization between Emmer wheat (AABB) (*Triticum dicoccon*) and Goat grass (DD) (*Aegilops tauschii*) commonly called hard grass (Kumar *et al.*, 2020). Wheat is a self-pollinating plant with three anthers connected to the base by slender filaments, enclosed within bract-like structures called the lemma and palea (Dhiwar *et al.,* 2020). The optimal tSSSemperatures is 20-25^0C for germination, 16-20^0C for tillering, and 20-23^0C for grain formation (Gami *et al.*, 2010).

Sprague and Tatum (1942) proposed the concepts of combining ability (general combining ability (GCA) and specific combining ability (SCA). GCA considered to be the average performance of line in a series of various cross combinations, while SCA refers to the deviation from GCA (perform better or worse). It was noted that genes with additive effects play more significant role in GCA, whereas SCA is influenced by dominance genes and epistatic effects (inter-allelic interactions) (Dholariya *et al.,* 2014).

Combining ability serves as effective tool for selecting desirable parents capable of producing crosses with high genetic value (Dhadhal *et al.,* 2008) and Ahma & Gupta (2024). The level of hybrid vigor depends on the combining ability of the genotypes used (Bhutto *et al.,* 2015). The genotype capable of transmitting favorable traits or hybrid vigor to their offspring are considered to have high combining ability (good combiners) (Bergale *et al.,* 2002).

Combining ability helps in identifying parental lines that contribute favorable traits to their offspring (Bergale *et al.,* 2002). This allows plant breeders to select the best combinations of wheat genotypes, leading to the development of high-yielding and stress-tolerant varieties (Gupta *et al.,* 2017). For developing countries, where resources for extensive breeding programs may be limited, combining ability approach can be used to maximize the chances of success with fewer inputs (Fellahi *et al.,* 2018).

According to Koumber and El-Gammaal (2012) the term "gene action" encompasses additive, non-additive and epistatic types of inheritance, gene action refers to how different genes control phenotypic traits, whether they work independently, interact with each other (epistasis), or show dominant-recessive relationships. In wheat, traits like yield and yield components are influenced by both additive and non-additive gene actions. Additive effects, in particular, are the keys for predicting genetic gains through selection, while non-additive effects (dominance and epistasis) play a vital role in hybrid vigor or heterosis Hajer *et al*. (2021). Genetic improvement largely depend on the suitable method of selection applied (Kumar *et al.,* 2015). Therefore, any breeding programme that aimed at altering the genetic makeup of genotype a breeder must be conversant with type of gene action involves in the expression of various characters (Madan *et al.,* 2014). This involves a comprehensive understanding of the nature, type, and impact of gene action, as well as the influence of yield components on grain yield (Kempthorne, 1957). The purpose of selection is to identify genetically superior genotypes, if superiority is genetics in nature the genotypes can reproduce their yield faithfully across different environments, however, if their performance is not genetic in nature, the genotype will not reproduce its values across different environmental conditions (Hajer *et al.,* 2021). As yield per hectare, is a factor that determine commercially acceptability of wheat variety in most developing countries like India and Nigeria (Kumar *et al.,* 2018)

Study of heterosis is no longer optional but imperative due to challenges associated with the development of commercial hybrid seeds in wheat, the economic exploitation of heterosis in self-pollinated crops like wheat is highly essential (Kumar *et al.,* 2018). Reif *et al.* (2012) reported that, the degree of heterosis depends on the strength of non-additive gene action and the parents' high genetic variability. According to Mohammed *et al.* (2019) heterosis is more prevalent in cross-pollinated crops than in self-pollinated like wheat. Conversely, inbreeding depression, is the opposite of heterosis, results in a decline in hybrid vigor due to an increase in recessive alleles (Hajer *et al.,* 2021). To restore plant's vigor, it is necessary to study heterosis extensively (additive, non-additive and epistatic kinds of gene effects) and mitigate the adverse effects of recessive genes (Hajer *et al.,* 2021).

According to Kshatri *et al.* (2021) the assessment of stability involves estimation the effects of genotypes, environments, and their interactions, and various statistical methods are available for this purpose viz.; regression models, AMMI model, and multivariate analysis. A genotype is deemed stable if it exhibits a high mean yield with minimal variation across multiple environmental conditions, as indicated by the widely used regression statistics proposed by Eberhart and Russell (1966). The assessment of potential genotypes across different environmental conditions (stability analysis) is vital and last step in the majority of applied plant breeding programme (Kabir *et al.,* 2009). Grain yields are quantitative character that may has been influenced by environments, thus, phenotype is the function of genotype and environment as well as their interaction (genotype × environment (G x E)) that can significantly affects selection (Siddhi et al., 2018). One of the challenges in breeding high-yielding wheat varieties is ensuring that they perform well across diverse environmental conditions, thus, stability analysis is a method used to assess the consistency of a genotype's performance across different environments (Kumar *et al.,* 2019). Yield stability is of great importance, particularly in regions where environmental fluctuations are common (Gulzar *et al.,* 2015).

1.2 Scenario of wheat in India and Nigeria

Data from Ministry of Agriculture and Farmers Welfare, Government of India and Federal Ministry of Agriculture and Rural Development of Nigeria, reveals a significant difference in wheat productivity per hectare between India's and Nigeria's top wheat-producing states. In India, states like Punjab and Haryana achieve much higher productivity, with yields ranging from 4.8–5.2 tons/ha and 4.5–4.9 tons/ha, respectively. Other Indian states, like Western Uttar Pradesh and Gujarat, also produce more than 3 tons/ha (MAFW, 2023). While Nigeria’s leading wheat-producing states, such as Borno and Kano, have considerably lower productivity, with yields ranging from 1–1.2 tons/ha (FMARD, 2023).

Table 1.0 Area, Production and Productivity of Wheat

	World	**India**	**Nigeria**
Area	228 million ha	31.8 million ha	0.07 million ha
Total production	797 million t	110 million t.	0.08 million t.
Productivity	3.5 t/ha	4.7 (varies by region) t/ha	1.2 t /ha

Source: FAO, 2022

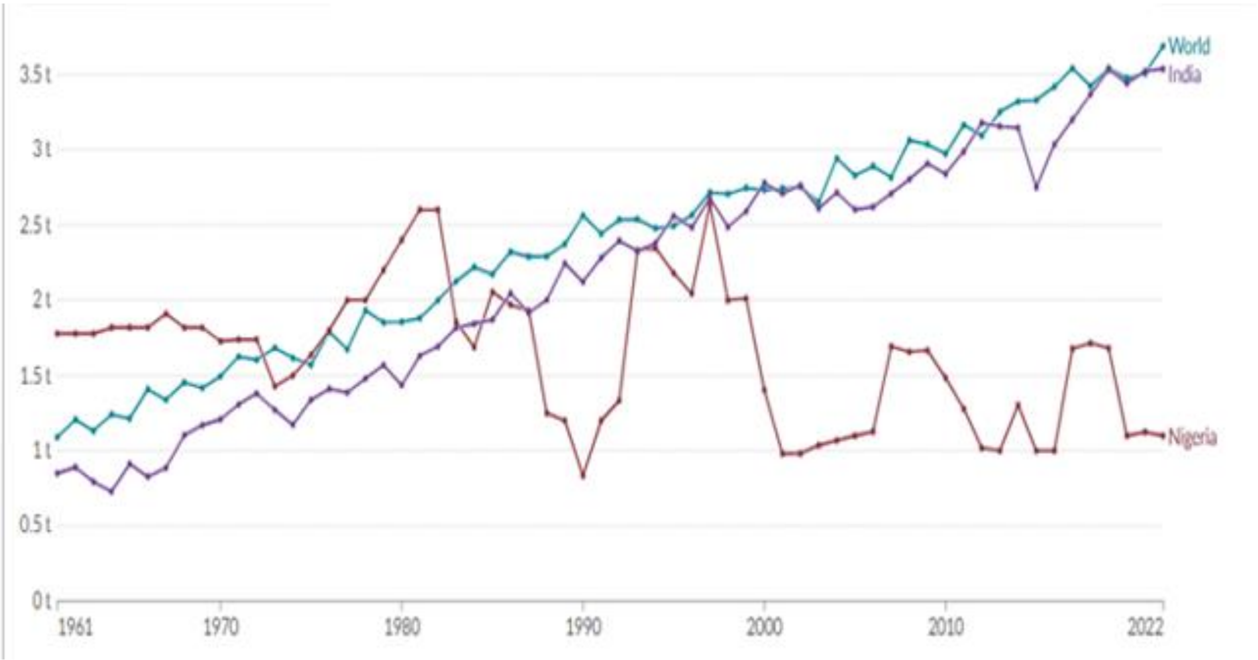


Fig. 1 Wheat production graph based on yield/ha (y=yield & x=production period) from 1961 to 2022 (FAOSTAT, 2022)

Line x tester is a powerful mating design used to study GCA and SCA for crop improvement (Abinasa *et al.*, 2011). Heterosis (hybrid vigor) is the phenomenon where the progeny of cross between genetically distinct parents of a species or between different species exhibit enhanced traits, such as greater biomass, faster development, disease resistant and higher fertility compared to their parents (Samier and Ismail, 2015), (Bouchareb and Guendouz, 2022 and Kumar *et al.,* 2018) and (Abinasa *et al.,* 2011). Stability analysis is a method used to assess the consistency and reliability of a genotype's performance across different conditions (Ahmad *et al.*, 2011). It can be assess by the use of three parameters viz.; average performance of genotype (mean yield), regression coefficient (bi) and deviation from the regression (S^2di) (Kumar *et al.*, 2018 and Adhikari *et al.,* 2019) and (Hajer *et al*., 2021).

1.3 Research gap

In an attempt to improve yield in wheat, commercial hybrid seed production was attempted several to many times through various sterility induction techniques, encompasses genetic male sterility, cytoplasmic genetic male sterility and chemical hybridizing agents to improve yield in wheat, but all efforts have little or no practical relevance owing to polyploidy nature of wheat and technical intricacies involved in hybrid seed production at commercial scale (Koumber *et al.*, 2012). Thus, study seeks to optimize wheat breeding strategies within the limitations imposed by the crop's biology, offering a more realistic and effective route to yield improvement than hybrid seed production alone. This research is therefore highly relevant and timely, providing insights into how targeted conventional breeding and genetic analysis can help overcome the practical hurdles of hybrid wheat development and contribute meaningfully to crop improvement programs.

Most existing and previous studies on stability analysis were carried out in either India or Nigeria but not both, leaving a serious gap between the two diverse agro ecological zones for stability analysis. Wheat production faces several challenges that affect its yield and quality like heat stress and insufficient breeding information such as genetic variances, GCA, SCA, stability analysis and exploitation of heterosis that involves different agro-ecological zones (Adel and Ali, 2013). Nigeria previously listed among world's wheat-producing countries before the advent of new breeding techniques, but Nigeria is no longer considered as one of the major world wheat producer due to the use of low yielding varieties (FAO, 2022).

Present investigation provides potential solutions to the aforementioned problems by providing sufficient, eco-friendly and non-transgenic breeding techniques that will underpin the development of advanced breeding techniques viz.; heterosis breeding; stability analysis and selection of superior genotype aimed at improvement of wheat production to ensure resilience against environmental stresses that ultimately contributes to sustainable agricultural practices and the ability to meet the demand of growing population. Data from India and Nigeria unlocked the breeding information on wheat performance across South Asia (India) and West Africa (Nigeria). The assessment of potential genotypes across different environmental conditions (stability analysis) is vital and last step in the majority of applied plant breeding programme.

1.4 Objectives of the Study

Keeping these points in view, the present investigation has been planned to fulfil the following objectives:

1. To study the combining ability variances and their effects
2. To find out gene actions involved in the inheritance of various characters
3. To estimate heterosis over better-parent and standard varieties
4. To workout Stability analysis in 18 parents involves in hybridization programme and their offerings

CHAPTER TWO
REVIEW OF LITERATURE

A concise review of the literature related to various aspects of the current investigation in wheat, along with relevant compiled works directly or indirectly associated with the study, is presented in chronological order under the following headings:

2.1 Combining ability variance and their effects

2.2 Gene actions in wheat

2.3 Nature and magnitude of heterosis and its components

2.4 Stability analysis

2.1 Combining ability variance and their effects

Sprague and Tatum (1942), proposed the concepts of combining ability (general combining ability (GCA) and specific combining ability (SCA)). GCA considered to be the average performance of line in a series of various cross combinations, while SCA refers to the deviation from GCA (perform better or worse).

Kant *et al.* (2011) found that both the GCA and SCA significantly influenced all the traits studied, indicating that additive and non-additive genetic effects are equally important.

Samier and Ismail (2015) the findings highlighted the potential of some genotypes for using selection-based breeding techniques to exploit additive genetic effects for improving the studied traits.

Talukder *et al.* (2016) and Nivedha *et al.* (2024). observed significant variances in grain yield and its associated traits, with both general and specific combining abilities showing substantial influence.

Schwarzwälder *et al.* (2016) the findings suggest that hybrid breeding techniques can use non-additive gene actions compared to pure-line selection.

Gupta *et al.* (2017) the results underscore the utility of combining ability analysis in identifying suitable parental lines and effective hybrid combinations for wheat improvement.

Rajput and Kandalkar (2018) research findings indicated highly significant differences for most traits in both F_1 and F_2 generations, except for days to maturity, number of effective tillers per plant, and harvest index in F_1.

Bajaniya *et al.* (2019) results indicates that, non-additive gene action plays a dominant role in the inheritance of all the tested traits.

Salam *et al.* (2019) reported that, the mean square values for testers were significant for most traits, except for the number of spikelets per main spike, grain filling period, and 100-grain weight.

Kumar *et al.* (2020) found that traits such as plant height, number of effective tillers, main spike length, grain yield per plant, and grain yield per spike exhibited highly significant GCA and SCA, however, GCA for spike length was not significant.

Patel *et al.* (2020) reported that, most crosses showed high GCA/SCA ratios greater than unity, indicating that additive genetic effects and additive × additive interactions were the primary contributors to the inheritance of tested traits.

Hajer *et al.* (2021) highlighted the critical role of line × tester interactions, which contributed more to trait variation than either lines or testers individually.

Hammadi and Fayyad (2021) emphasized the importance of combining ability analysis for evaluating newly developed cultivars. This approach serves is a valuable tool for identifying suitable parental lines to create promising hybrid combinations, thereby enhancing breeding efficiency.

Tariq *et al.* (2023) reported that, combining ability was not considered for selection in early generations if GCA is low but can be used for later generation selection if for SCA.

Ahmed *et al.* (2023) the findings suggest exploitation of GCA for higher grain yield is important due to the presence of additive gene action and selection in the filial generations will be effective and fixable with improved rust resistance.

Prakash *et al.* (2024) recorded that, the lines PBW 725 and tester PBW 343 were a good donor for biological yield/plant, number of spikelets / spikes and grain yield per plant.

Mohamed *et al.* (2024) observed that, plant height, kernels number per spike and 100-kernel weight along with grain yield in F_2 tend to be determined by additive gene effect through partial dominance.

Afsar *et al.* (2024) recorded that, crosses like UP 2748 x HD 3059, UP2565 x HD3086 and WH 1105 x UP 2526 were identified as good specific combiners for higher grain yield and associated traits.

Ponaganti *et al.* (2024) revealed that while several traits show positive associations with grain yield in wheat, biomass per meter stands out as both a direct determinant and an amplifier of the effects of other yield-related traits. Therefore, breeding programs should prioritize increasing biomass to achieve more impactful yield gains.

Kiranakumara *et al.* (2024) the findings shows that all traits related to crop yield were positively linked, except for canopy temperature at different growth stages.

Mahmood (2024) reported that, additive gene action (GCA) was more important for most traits (plant height, spike length, grains per spike, etc.). Non-additive gene action (SCA) also played a significant role, especially for traits like grains per spike and grain yield.

Mohamed *et al.* (2024) stated that, half-diallel mating design, involving 10 parent genotypes and 45 F2 segregating hybrids (crosses between parent genotypes) for three consecutive seasons. The study emphasizes the role of additive gene effects in improving yield traits, which is critical for developing new bread wheat varieties with improved yield potential under changing climate and limited agricultural land.

Table 2.1 Review of literature for combining ability variance and their effects

Reference	**Mating Design**	**GCA (General Combining Ability)**	**SCA (Specific Combining Ability)**	**Gene Action**	**Major Findings on Combining Variances and Effects**
Jinks and Jones (1958)	Diallel Cross	GCA is related to overall performance, with additive gene effects	SCA reflects interactions between specific parents	Additive and dominance	The study underlined the dominance of GCA in the inheritance of traits like plant height and yield.
Baker (1978)	Diallel Cross	GCA explains a large proportion of the total variance in most traits	SCA contributes less to the variance in simple traits, but is significant for complex traits	Additive-dominant and epistatic interaction	The importance of GCA for yield traits suggests additive gene action predominates. SCA effects are more important for complex traits.
Eagles *et al*. (2006)	North Carolina Design II (NC II)	High GCA values for grain quality traits indicate additive effects	SCA effects are important for disease resistance traits	Additive and dominance	GCA is important for quality traits, while SCA plays a key role in disease resistance and stress tolerance.
Sharma *et al*. (2009)	Diallel Cross	GCA effects were highly significant for grain yield and flowering time	SCA contributes to variability in hybrid performance for yield and resistance traits	Additive, dominance, epistasis	Both GCA and SCA variances are crucial for yield improvement, but SCA has a more prominent role in disease resistance.
Duarte *et al*. (2010)	Diallel Cross	GCA significantly impacts kernel size and plant height	SCA affects hybrid vigor for kernel size and resistance to pests	Additive-dominant	GCA for size-related traits is predominant, but SCA is essential for hybrid vigor and pest resistance.
Parveen *et al*. (2013)	Line × Tester Design	High GCA observed for drought tolerance and growth traits	SCA plays an important role in hybrid vigor for stress tolerance traits	Additive-dominant	GCA plays a major role in drought tolerance, while SCA is crucial for heterosis under stress conditions.
Srinivas and Reddy (2014)	Top Cross and Diallel Cross	GCA effects significantly influence yield and	SCA is highly significant in heterosis expression for yield.	Additive, dominance, and epistasis	Found that SCA plays a significant role in heterosis expression, particularly for yield and plant height.

		plant height			
Singh *et al.* (2015)	Diallel Cross	GCA is significant for yield and traits; indicates additive gene action	SCA is significant for yield; indicates dominance and epistasis	Additive-dominant model	GCA and SCA variances play crucial roles in selecting parents for hybrid development. SCA significantly affects yield.
Sosa *et al.* (2019)	North Carolina Design III (NC III)	GCA effects are important for yield, leaf area, and disease resistance	SCA has a significant role in yield components such as ear length and weight	Additive, dominance, and epistasis	GCA is essential for yield, while SCA is more significant for secondary traits such as ear length.
Fatima *et al.* (2020)	Diallel Cross	GCA for plant height, leaf size, and yield components	SCA plays a major role in heterosis expression for biomass production	Additive-dominant and epistatic	Found that combining ability variances are essential in selecting parents for biomass production. GCA affects height, while SCA influences biomass.
Mahmood R. (2024).	Line × Tester	Additive gene action (GCA) was more important for most traits.	Non-additive gene action (SCA) also played a significant role in grains per spike and grain yield.	GCA was greater than SCA for most attributes.	GCA variance was greater than SCA variance for most attributes, indicating that additive gene action played a predominant role.
Mohamed A. *et al.*(2024)	Half-diallel mating design	GCA showed significant differences for most of the traits under study.	SCA also showed significant differences.	Additive gene effects (GCA) were more significant than dominance effects (SCA).	Additive gene effects with partial dominance, as confirmed by GCA effects and graphical analysis (Wr/Vr).

2.2 Gene actions

Sprague and Tatum (1942) described gene action as mode of gene expression (additive, dominance, and epistatic). Additive gene action refers to the cumulative effects of individual alleles, while dominance gene action occurs when one allele suppresses or masks the expression of another at the same locus and epistatic gene action involves interactions between alleles at different loci.

Kempthorne (1957) reported that, successful breeding program must consider the genetic makeup of the population and the type of gene action involved in expressing target traits to optimize improvement. Fahard *et al.* (2011) revealed that, both additive (D) and dominant (H) gene effects were significant for traits such as days to heading, productive tillers per plant, number of grains per spike, grain yield per plant, and 1000-grain weight across three different planting environments.

Dholariya *et al.* (2014) study' highlighted that additive gene action with partial dominance governed days to heading and 1000-grain weight under early and normal planting period.

Aslam *et al.* (2014) revealed that, non-additive effects (dominance, over dominance and epistasis) were significant under late planting conditions for traits like days to heading and 1000-grain weight.

Barot *et al.* (2014 study' highlighted that both additive (d) and dominance (h) effects significantly influenced the expression of key traits, including grain yield per plant, tillers per plant, number of grains per spike, 1000-grain weight, number of spikelets per spike, and spike length in wheat.

Kumar *et al.* (2015) observed over-dominance for the trait grains per spike, indicating a strong non-additive genetic influence. However, parental genotypes, "Unnat" and "Halna" were found to carry predominantly recessive genes.

Kumar *et al.* (2017) identified parents with heat tolerance genes (K 0307 and K 0911) highlights their potential in developing wheat varieties resilient to late sowing and high temperatures during the reproductive phase.

Jat *et al.* (2017) reported significant differences among genotypes across two environments (E1 and E2), indicating substantial genetic variability. The ratio of σ^2gca to σ^2sca indicated non-additive gene action for all traits studied in both environments.

Tabassum *et al.* (2017) results identified several parents with strong general combining ability (GCA), including DBW 88, WH 1126, UP 2425, UP 2696, and UP 2845, and suggesting their ability to transmit desirable additive genes to their progeny.

Jatav *et al.* (2017) analysis revealed the presence of both additive and non-additive genetic components influencing grain yield and its related traits across the two conditions (under water stress and non-stress conditions), except for spike length under stress conditions.

Fellahi *et al.* (2018) reported that, additive effects can be fixed through selection in advanced generations, while non-additive effects can be exploited for heterosis in hybrid development.

Kumar *et al.* (2018) confirmed the involvement of both additive and non-additive gene actions on length of the main spike, the number of spikelets per spike and amount of grain produced per spike except the amount of grain produced per plant which was more affected by additive gene action

Kumar *at el.* (2020) revealed that every other cross had significant GCA/SCA ratios, showing that additive and additive by additive kinds of gene activity were crucial in the inheritance of every characteristic under investigation.

Patel *et al.* (2020) noted that yield is a determining the commercial acceptability of wheat varieties, particularly in developing countries, however, it is a complex trait influenced by multiple yield components.

Adel *et al.* (2021) said" the sca/gca variance ratio indicated a predominance of additive gene action in the inheritance of yield and its contributing traits, highlighting the importance of selecting parents with strong additive effects for achieving genetic improvements.

Fayyad *et al.* (2022) findings suggested the use of reciprocal recurrent selection method to improve traits with presence of both additive and non-additive gene actions in an equal proportion.

Rubby *et al.* (2023) results showed that traits in all crosses had highly significant estimated mean effects (m), showing the quantitative inheritance of the selected traits.

Divya *et al.* (2023) the results demonstrated that tillers per plant and biological yield per plant are important components for improving grain yield in both irrigated and rainfed conditions, thus, selection can be done based on these traits in both environments (irrigated and rainfed).

Raza *et al.* (2023) revealed that in both normal and heat stress conditions, Khirman and SKD-1 proved to be better general combiners for various characters. Kwame *et al.* (2023) confirmed that, early generation selection using plant height, spike biomass, plant biomass and grain yield will improve drought tolerance by exploiting additive gene action under drought conditions.

Ashish *et al.* (2024) recorded that, the ratio of variances was observed to be less than unity indicating the presence of non-additive genetic effects in these cross combinations.

Santhiya *et al*. (2024) observed that the ratio of dominant genetic variance to additive genetic variance exceeded unity, indicating the prevalence of non-additive gene action in governing the inheritance of all examined traits.

Baiumy (2024) observed that, the magnitudes of the GCA/SCA ratios showed that additive and additive by additive gene action types might account for the majority of the total genetic variability linked to the traits under study characters.

Table 2.2 Review of literature on gene actions in wheat

Reference	Mating Design	GCA (General Combining Ability)	SCA (Specific Combining Ability)	Gene Action	Major Findings on Gene Action and Their Effects
Sprague and Tatum (1942)	Line × Tester	GCA reflects the additive effects of alleles	SCA reflects dominance and epistasis effects	Additive, Dominance, Epistasis	Described modes of gene expression: additive, dominance, and epistatic interactions. Emphasized the need to understand these in breeding.
Kempthorne (1957)	Full Diallel	GCA is key for predicting the inheritance of target traits	SCA affects hybrid performance under different conditions	Additive, Dominance, Epistasis	Successful breeding programs must consider genetic makeup and gene action types to optimize trait improvement.
Fahard *et al.* (2011)	NCII (North Carolina Design II)	Both additive (D) and dominant (H) gene effects were significant for traits like yield and heading time	SCA was significant for traits like grains per spike and weight	Additive and Dominance	Both additive and dominance gene actions affect wheat traits under different environmental conditions, with dominant effects on yield components.
Dholariya *et al.* (2014)	Diallel Cross	Additive gene action governed days to heading and 1000-grain weight	Partial dominance observed for days to heading and 1000-grain weight	Additive with Partial Dominance	Additive gene action dominated early sowing traits, suggesting potential for selection of early heading and high weight genotypes.
Aslam *et al.* (2014)	Line × Tester (Multiple crosses)	Non-additive effects (dominance, over-dominance, epistasis) were significant for heading and 1000-	Dominance and epistasis played a key role in late planting conditions	Non-additive effects (dominance, over-dominance, epistasis)	Non-additive gene effects were significant for late planting conditions, impacting key traits like heading time and grain weight.

		grain weight			
Barot *et al.* (2014)	Diallel Cross Design	Both additive and dominance effects influenced grain yield and other key traits	SCA influenced traits like tillers per plant and grains per spike	Additive and Dominance	Both additive and dominance effects were found to be significant for grain yield and key agronomic traits.
Kumar *et al.* (2015)	NCII Design	Over-dominance for grains per spike	Recessive gene action in parental genotypes ("Unnat" and "Halna")	Over-dominance, Recessive effects	Over-dominance was observed for grains per spike, while recessive genes were present in certain parent genotypes.
Kumar *et al.* (2017)	Top Cross Design	Parents K 0307 and K 0911 have heat tolerance genes	SCA effects were significant for heat tolerance-related traits	Additive and Dominance	Heat tolerance genes in certain parents can help develop wheat varieties resilient to high temperatures and late sowing.
Jat *et al.* (2017)	Lattice Design	GCA effects significant for all traits	SCA showed non-additive gene action in both environments	Non-additive (SCA)	Non-additive gene action predominated for traits studied across different environments, showing substantial genetic variability.
Tabassum *et al*. (2017)	Line × Tester Design	Strong GCA observed in genotypes DBW 88, WH 1126, and others	GCA is important for transmitting desirable additive genes	Additive	Strong GCA identified in key parents, suggesting they are good candidates for improving additive traits in wheat breeding.
Jatav *et al.* (2017)	NCII Design	Both additive and non-additive components influenced yield traits	SCA effects were observed in both stress and non-stress conditions	Additive and Non-additive	Both additive and non-additive genetic components influenced grain yield under water stress and non-stress conditions.
Fellahi *et al.* (2018)	Diallel Cross	Additive effects can be fixed	Non-additive effects are	Additive and	Additive effects are useful for improving traits through selection, while non-additive effects

		through selection	important for hybrid vigor	Non-additive	contribute to hybrid vigor.
Kumar *et al.* (2018)	Diallel Cross	Both additive and non-additive gene actions influenced spike length and grain production	Additive effects were more important for grain production per plant	Additive and Non-additive	Additive gene action was important for grain production per plant, while both additive and non-additive effects influenced other traits.
Kumar *et al.* (2020)	North Carolina Design II (NC II)	GCA/SCA ratios showed significant effects of both additive and additive-by-additive gene actions	Both additive and additive-by-additive gene actions were important	Additive and Additive-by-additive	Both additive and additive-by-additive gene actions played crucial roles in the inheritance of all traits studied.
Patel *et al.* (2020)	Diallel Cross	Additive gene action important for yield	Non-additive gene actions are critical for hybrid performance	Additive and Non-additive	Yield is complex and influenced by both additive and non-additive gene actions; selection should target both types of effects.
Adel *et al.* (2021)	Top Cross and Diallel Cross	Additive gene action predominates for yield traits	GCA/SCA variance ratios indicated dominance of additive effects	Additive	Additive gene action was found to be key in the inheritance of yield and related traits, highlighting the importance of selecting parents with strong additive effects.
Fayyad *et al.* (2022)	Diallel Cross	Both additive and non-additive gene actions were important	Reciprocal recurrent selection should be used for trait improvement	Additive and Non-additive	A balanced approach utilizing both additive and non-additive gene actions through reciprocal recurrent selection can improve wheat traits.
Rubby *et al.* (2023)	North Carolina Design III (NC III)	All crosses showed significant mean effects	Traits exhibited quantitative inheritance	Quantitative inheritance	Quantitative inheritance was observed for all traits, indicating the role of both additive and non-additive genetic effects.

Divya *et al.* (2023)	Line × Tester Design	TPP and BYP are key for improving grain yield	Non-additive gene action influenced yield components	Non-additive (SCA)	TPP and BYP are important components for improving grain yield across environments, with non-additive gene action playing a significant role.
Raza *et al.* (2023)	Diallel Cross	Khirman and SKD-1 identified as good general combiners	SCA played a role in heat tolerance and yield traits	Additive and Non-additive	Khirman and SKD-1 exhibited good general combining ability for traits under heat stress, highlighting their potential for improving heat tolerance.
Kwame *et al.* (2023)	Diallel Cross	Additive gene action important for drought tolerance traits	SCA effects contributed to drought tolerance	Additive and Non-additive	Additive gene action is crucial for improving drought tolerance, and early generation selection can exploit this for better wheat varieties.
Ashish *et al.* (2024)	Diallel Cross	Variance ratios less than unity, indicating non-additive effects	SCA effects predominate for most traits studied	Non-additive (SCA)	Non-additive genetic effects were dominant, suggesting the importance of SCA in the inheritance of traits under study.
Santhiya *et al.* (2024)	Line × Tester Design	Dominant genetic variance exceeded additive variance	Non-additive gene action was prevalent in trait inheritance	Non-additive (Dominance)	Dominant genetic variance dominated the inheritance of all traits, indicating the importance of non-additive gene action.
Baiumy (2024)	NDC III	GCA/SCA ratios showed additive and additive-by-additive gene actions	Additive and additive-by-additive gene actions explained most genetic variability	Additive and Additive-by-additive	Additive and additive-by-additive gene actions were crucial in explaining the genetic variability for the studied traits.

2.3 Nature and magnitude of heterosis and its components

The term heterosis (hybrid vigor) was introduced by Shull (1914) as the phenomenon where the progeny of crosses between genetically diverse varieties of a species or between different species exhibit enhanced traits, such as greater biomass, faster development, disease resistant and higher fertility compared to their parents. Later, in 1948, Shull refined the definition to describe it as observable phenomenon resulting from the combination of genetically distinct gametes to produce a hybrid, equating heterosis with hybrid vigor. Fonseca and Patterson (1968) described the analysis of variance (ANOVA) to workout heterosis.

Titan and Meglic (2011) progeny expressing predominantly additive effects often fail to exhibit significant heterosis, underlining the critical role of dominance in maximizing hybrid vigor.

Reif *et al*. (2012) highlighted that, the extent of heterosis depends on the magnitude of non-additive gene action and the genetic diversity between the parents.

Jernej *et al.* (2013) reported that, heterosis breeding has demonstrated potential way to boost agricultural yields both at national and international levels.

Samier and Ismail (2015) found that the mean squares for genotypes, parents, and crosses were significant for all studied traits, indicating substantial genetic diversity among the parental genotypes as both positive and negative heterosis over the better parent and standard varieties were observed.

AbdEl-Hady *et al.* (2018) and Rezgar, and Hussain (2024) their findings implied that dominance gene action plays a more prominent role than additive gene action in the inheritance of the studied traits.

Kumar *et al.* (2018) identified significant potential use of heterosis in breeding programs to enhance agricultural productivity at both national and international levels.

Anil *et al.* (2019) reported that, high genetic variability among parents enhances the potential for heterotic responses, making parent selection a crucial step in designing high-yielding hybrids.

Kumar *et al.* (2019) the findings suggest that achieving high levels of heterosis requires careful selection of genetically diverse parents with significant non-additive gene interactions.

Salam *et al.* (2019) reported that, maternal effects in reciprocal cross analysis identified in some hybrids. The observed maternal effects highlight the importance of considering parental lineage in breeding programs.

Kaur *et al.* (2020) confirmed the exploitation of heterosis in wheat breeding offers a promising approach to achieve substantial gains in yield and other agronomic traits.

AL-Mafarji & AL-Jubouri (2023) reported that all the traits analyzed exhibited negative and significant heterosis, suggesting a lower contribution of additive genetic variance compared to dominant genetic variance in trait expression.

KamboJ *et al.* (2021) reported that, the observed negative heterosis indicates that hybrids underperformed relative to their mid-parent values, potentially due to unfavorable genetic interactions.

Mohan *et al.* (2022) the observed negative heterosis for plant height may be advantageous in breeding programs where reduced plant height is desirable for improving lodging resistance.

Ramakrishna *et al.* (2023) revealed that, three of the 32 hybrids under study had considerable standard heterosis for grain yield viz., JMS 13A x MTU 1153, CMS 59A x RNR 26015 and CMS 64A x MTU 1153, which outperformed the best checks JKRH 3333 and MTU 1001.

Hussain *et al.* (2024) identified genotypes with superior traits emerge as promising candidates for further investigation and integration into breeding initiatives for enhanced drought tolerance in spring wheat.

Nageshwar *et al.* (2024) reported that, the outcome of better parent heterosis revealed that the cross combinations, namely, HD3086 x HD-2733, HD3086 x K0307, HD3086 x HD2967, HD3086 x K1601, and HD2967 x K0402 exhibited positive and high heterosis for grain yield.

Nivedha *et al.* (2024) observed, most of the superior hybrids were derived from crossing between parents with low x high gca effects.

Table 2.3 Summary of nature and magnitude of heterosis and its components

Reference	**Effects of heterosis**	**Major findings**
Shull (1914)	Hybrid vigor (heterosis) leads to enhanced traits like biomass, faster development, and higher fertility	Introduced the concept of heterosis, where progeny exhibit superior traits compared to parents.
Shull (1948)	Observable hybrid vigor from the combination of genetically distinct gametes	Refined the definition of heterosis as the phenomenon from combining genetically distinct gametes.
Fonseca & Patterson (1968)	Non-specific heterosis based on analysis of variance (ANOVA)	Described the use of ANOVA to measure heterosis, indicating its importance in hybrid performance.
Titan & Meglic (2011)	Limited or no significant heterosis when additive effects are predominant	Emphasized the role of dominance over additive effects in achieving significant heterosis.
Reif *et al.* (2012)	High heterosis depends on non-additive gene actions and genetic diversity	Highlighted the importance of non-additive gene action and genetic diversity for heterosis.
Jernej *et al.* (2013)	General increase in agricultural yields at national and international levels	Identified heterosis breeding as a promising strategy to improve agricultural yields.
Samier & Ismail (2015)	Positive and negative heterosis for various traits	Found significant genetic diversity among parental genotypes, with both positive and negative heterosis observed.
AbdEl-Hady *et al.* (2018) and Rezgar, & Hussain (2024).	Dominance gene action is more influential than additive effects	Dominance gene action plays a more critical role than additive effects in the inheritance of key traits.
Kumar *et al.* (2018)	Significant potential for heterosis in breeding programs	Identified heterosis as a potential strategy to boost agricultural productivity at both national and international levels.
Anil *et al.* (2019)	High genetic variability enhances heterosis potential	Reported that high genetic variability in parents enhances the potential for heterotic responses.
Kumar *et al.* (2019)	High heterosis through careful selection of genetically diverse parents	Achieving high heterosis requires selecting parents with significant non-additive gene interactions.
Salam *et al.* (2019)	Identified maternal effects in certain hybrids	Found that maternal effects are significant in reciprocal crosses and should be considered in breeding programs.
Kaur *et al*. (2020)	Positive heterosis for yield and agronomic traits	Demonstrated that exploiting heterosis in wheat breeding is a promising approach for substantial yield gains.
AL-Mafarji & AL-Jubouri (2023).	Negative and significant heterosis, with dominance effects contributing more than additive variance	Reported negative heterosis for all traits, with dominance gene action being more influential than additive variance in trait expression.

KamboJ *et al.* (2021)	Negative heterosis for certain traits	Negative heterosis observed, suggesting underperformance in hybrids compared to mid-parent values, possibly due to unfavorable genetic interactions.
Mohan *et al.* (2022)	Negative heterosis for plant height	Negative heterosis for plant height could be beneficial in breeding programs aimed at reducing plant height for lodging resistance.
Ramakrishna *et al.* (2023)	Standard heterosis for grain yield in some hybrids	Three hybrids outperformed best checks for grain yield, demonstrating positive standard heterosis.
Hussain *et al.* (2024)	Identification of superior drought-tolerant genotypes	Identified promising genotypes for drought tolerance, which can be integrated into breeding programs for spring wheat.
Nageshwar *et al.* (2024)	Positive and high heterosis for grain yield	Several cross combinations exhibited positive heterosis for grain yield, suggesting good breeding potential.
Nivedha *et al.* (2024)	Superior hybrids from low x high GCA crosses	Most superior hybrids came from crosses between parents with low and high General Combining Ability (GCA) effects.

2.4 Stability analysis

Eberhart and Russell (1966) reported three parameters that helps to measure stability among population, namely; average yield performance, regression coefficient (bi) and deviation from the regression (S^2di). The model also described, bi value around 1 indicates average stability, bi < 1 indicates stability (under both the favorable and unfavorable environmental conditions) and bi > 1 indicates stability (under favorable environmental conditions only) and deviation from the regression (S^2di), lower S^2di values indicates higher stability (very little variation across different locations).

Ranjana and Kumar (2013) the genotype-by-environment (G × E) interaction mean squares were highly significant for most traits, except for spikelets per spike, harvest index, and protein content.

Adjabi *et al.* (2014) concluded that, genotypes CMT 1162, CMT 198, CMT 1006, CMT 125, and CMT 1193 were identified as having average stability, indicating consistent performance across diverse environmental conditions.

Sabaghnia *et al.* (2014) reported significant environmental variation for most traits, except for grains per spike and protein content, indicating that the performance of genotypes was largely influenced by the environments in which they were grown.

Meena *et al.* (2014) reported that two out of seven advanced generation selections lines, indicated better stability for grain yield per plant when all the three stability parameters were considered at a time.

Gulzar *et al*. (2015) the study observed significant variations in mean performance for these traits across the tested environments. Mean performance for plant height, effective tillers, and phenological traits (days to 50% heading and maturity) differed significantly among environments.

Saleem *et al,* (2015) said" genotype with least AMMI stability Value (ASV) score is the most stable. The high interaction of genotypes with environments was also confirmed by high ASV and rank, suggesting unstable yield across environments.

Siddhi *et al.* (2018) said” regression coefficients in different attributes were recorded in parental material which included cultivars and advanced generation selection lines exhibiting different degree of environmental responses.

Dhiwar *et al.* (2020) revealed significant differences across 11 agronomic traits and recorded that, genotypes “Ratan” and CG 1029 as the most stable across environments for the assessed traits.

Kshatri *et al.* (2021) reported significant variability in grain yield among wheat genotypes; however, the analysis of variance indicated no substantial differences in stability across the genotypes evaluated.

Bayisa *et al.* (2022) revealed that the environment was the predominant factor with 74% of the total variability observed in grain yield compared with genotypic effects contributed 21.6%, and genotype-by-environment interaction (G×E) accounted for 3.8% of the variation.

Bouchareb and Guendouz (2022) stability analysis revealed that the linear component of genotypes x locations was found to be significant for all the 16 attributes reflecting significant differences. The non-liner component (pooled deviation) indicated significant differences in six traits and predominance in nine indicating considerable diversity in component and quality traits in spring wheat.

Ismail *et al.* (2023) recorded genotypes Sk5001/42 × SC.120 and Sk5003/53 × SC.120 (hybrids) could be subjected to further multi-location evaluation to assess the yield stability for commercial exploitation.

Sadhu *et al.* (2024) and Destaw *et al.* (2024) reported that, AMMI ANOVA showed that genotype and environment accounted for 11.46% and 47.50% of the variation respectively, where GEI captured 36.57% of the variation for seed yield.

Sujitha *et al.* (2024) GGE biplots revealed two mega-environments, from which Kharif seasons (mega environment 2) provided more informative assessments of genotype stability compared to summer seasons.

Jayalakshmi *et al.* (2024) found that among three locations, Gulbarga was the most favourable environment for expression of the traits.

Yendluri *et al.* (2024) recorded genotypes NEST-17-04 and NEST-17-37 were found to be promising for optimum yield over varying environments.

Zelalem *et al.* (2024) revealed that, G7 was identified as the most stable and high-yielding genotype and Environment ree (E3) selected as the most suitable environment for screening the genotypes.

Table 2.4 Review of literature on stability analysis

References	**Parameter and findings**	**Report on stability**
Eberhart & Russell (1966)	bi ≈ 1 indicates average stability; bi < 1 indicates stability under both favorable and unfavorable conditions and bi > 1 indicates stability under favorable conditions only	Stability assessed using bi (regression coefficient) and S2di (deviation from regression) and- Lower S2di indicates better stability (less variation across locations).
Ranjana & Kumar (2013)	Significant G × E interaction for most traits, except spikelets per spike, harvest index, and protein content.	G × E interactions are significant for most traits, showing varying degrees of environmental influence.
Adjabi *et al.* (2014)	Genotypes CMT 1162, CMT 198, CMT 1006, CMT 125, and CMT 1193 were identified as having average stability.	Genotypes with average stability show consistent performance across environments.
Sabaghnia *et al.* (2014)	Significant environmental variation for most traits, except for grains per spike and protein content.	Environmental factors play a dominant role in influencing genotype performance, particularly for most traits.
Meena *et al.* (2014)	Two out of seven advanced generation selection lines showed better stability for grain yield per plant.	Stability in grain yield was assessed using all three parameters, with two lines showing better stability across environments.
Gulzar *et al.* (2015)	Significant differences observed in plant height, effective tillers, and phenological traits across environments.	Environmental differences significantly affect performance for key traits such as plant height and phenology.
Saleem *et al.* (2015)	Genotypes with the least AMMI stability value are the most stable. High ASV indicates instability.	AMMI model is used to assess genotype stability; the lowest ASV indicates the most stable genotypes, while high ASV suggests unstable yield.
Siddhi *et al.* (2018)	Regression coefficients for parental material and selection lines showed varying degrees of environmental response.	Genotypes exhibit different stability responses based on environmental factors, with varying degrees of stability.
Dhiwar *et al.* (2020)	Genotypes "Ratan" and CG 1029 were identified as the most stable across environments for the	"Ratan" and CG 1029 displayed stable performance for key

	assessed traits.	agronomic traits across different environments.
Kshatri *et al.* (2021)	No significant differences in stability across genotypes, despite variability in grain yield.	Despite variability in yield, no significant difference was found in stability across the genotypes evaluated.
Bayisa *et al.* (2022)	Environmental effects contributed 74% of variability in grain yield, while genotypic effects contributed 21.6%, and G × E interaction accounted for 3.8%.	Environmental factors are the primary influence on grain yield variability, with genotype effects having a smaller role.
Bouchareb & Guendouz (2022)	Linear G × E interaction significant for all traits, non-linear interaction significant for six traits, showing considerable diversity in wheat quality traits.	Both linear and non-linear G × E interactions contribute to trait variability, with environmental factors influencing wheat quality.
Ismail *et al.* (2023)	Genotypes Sk5001/42 × SC.120 and Sk5003/53 × SC.120 (hybrids) require further evaluation across multiple locations for stability.	Hybrids Sk5001/42 × SC.120 and Sk5003/53 × SC.120 should undergo multi-location trials for stability assessment.
Sadhu *et al.* (2024)	Genotype and environment accounted for 11.46% and 47.50% of variation, with G × E interaction capturing 36.57% for seed yield.	Genotype and environment factors play significant roles in seed yield, with a large proportion of variability due to G × E interaction.
Sujitha *et al.* (2024)	Two mega-environments identified, with Kharif season (mega-environment 2) providing more informative assessments of genotype stability.	Mega-environment analysis indicates that Kharif season provides better genotype stability assessments than the summer season.
Jayalakshmi *et al.* (2024)	Gulbarga was the most favorable environment for expression of traits among three locations.	Gulbarga environment is more favorable for trait expression in the studied genotypes.
Yendluri *et al.* (2024)	NEST-17-04 and NEST-17-37 were identified as promising for optimum yield across different environments.	NEST-17-04 and NEST-17-37 genotypes show potential for stable yield across varying environments.
Zelalem *et al.* (2024)	G7 identified as the most stable and high-yielding genotype, and Environment 3 was selected as the most suitable environment for genotype screening.	G7 genotype is the most stable and high-yielding, with Environment 3 being optimal for screening genotypes for stability.

Destaw *et al.* (2024)	G7 was identified as the most stable and high-yielding genotype with minimal GEI.	E3 was identified as the ideal environment for grain yield production. G6 was high-yielding but unstable, ranking third in stability.

CHAPTER THREE

MATERIAL AND METHODS

The present investigation entitled "Studies on combining ability, gene action and stability analyses for yield and yield contributing traits in wheat (*Triticum aestivum* L.)" was conducted at three locations viz.; (i) Lovely Professional University, Phagwara Punjab India (ii) Kebbi State University of Science and Technology Aliero (KSUSTA), Kebbi State Nigeria and (iii) Lake Chad Research Institute, Borno State Nigeria during the Rabi seasons of 2022-23 and 2023-24. The edaphic and climatic conditions under which present study was carried along with techniques applied and materials used have been described in this chapter.

3.1 Experimental Materials

Eexperimental materials comprises sixty seven genotypes of wheat (fifteen line, three testers, four checks and forty five F_1's) that were derived by the cross of fifteen lines (females) with three testers (males) to workout stability analyses for yield and yield components. The planting material used were fifteen lines namely BHU 25, WB-02, BHU 31, HD 3721, PBW 725, CRD GEHNU1, PBW 550, PBW 677, PBW 822, HD 3117, DBW 173, HD 3086, DBW 222, CSW 18, and PBW 757. Three testers (PBW ZN1, PBW 343 and HD 3326) and four checks such as HD 2967, DBW 187, Norman and Borlaug-100. Non plant materials used includes; Breeders kit; SPAD (Soil Plant Analysis Development) handheld meter, meter rule, electric balance (Compax- Cx-600), seed counting machine, digestion apparatus, sodium hydroxide, hydrochloric acid etc.

Table 3.2 Pedigree of parents and four checks

SN	Genotype	Pedigree of genotypes
1	BHU 25	-
2	WB-02	T.DICOCCONC19309/AE.SQUARROSA(409)/3/MILAN/S87230//BAV92/4/2* MILAN/S8732/ 0//BAV92
3	BHU 31	-
4	HD 3721	ND/VG 9144//KALYANSONA/BLUEBIRD/3/YACO/4/VEE#5
5	PBW 725 CRD	PBW621//GLUPR 0/3* PBW 568/3/ PBW 621
6	GEHNU1	-
7	PBW 550	WH 594/RAJ 3856//W 485
8	PBW 677	PFAU/MILAN/5/CHEN/Ae, squarrosa// BCN/32/VEE#7 /BOW/4/PASTOR
9	PBW 822	-
10	HD 3117	HD 2733/ HD 2824 // DW 1278
11	DBW 173	KAUZ/AA//KAUZ/P BW602
12	HD 3086	DBW14/HD2733//HUW468
13	DBW 222	KACHU/SAUAL/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW /C ROW// BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR
14	CSW 18	-
15	PBW 757	PBW550/YR15/6* AVOCET/3/2*PBW550/4/PBW568+YR36/3* PBW550
16	PBW ZN1	T. dicoccon C19309/Ae. sauarrosa (409)/3/ MILAN/S87230//BAV92/4/2*MILAN/S87230/BAV92
17	PBW 343	ND/VG 144//KAL/BB/3/YACO’S’/4/VEE#5’S
18	HD 3326	-
19	HD 2967	ALONDRA/CUCKOO//URES81/HD-2160-M/ HD-2278
20	DBW 187	NAC/THAC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/ KACHU
21	Norman	- -
22	Borlaug-100	BABAX/Lr//BABAX

Table 3.3 Salient feature of Selected Parents (parents and four checks)

SN	Genotype	Source	Duration (Days)	Eco-system	Salient Features
1	BHU 25	Banaras Hindu University (BHU)	~140-150	Irrigated	High yield, resistance to lodging.
2	WB-02	Private Breeder (West Bengal)	~130-140	Irrigated	Early maturity, disease resistance.
3	BHU 31	Banaras Hindu University (BHU)	~140-150	Irrigated	Adaptable variety with moderate rust resistance.
4	HD 3721	ICAR-IIWBR	~145	Irrigated	High grain quality, rust resistance.
5	PBW 725	Punjab Agricultural University (PAU)	~140-145	Irrigated	Rust resistance, higher protein content.
6	CRDGEHNU1	ICAR-IIWBR	~140-150	Conservation Agriculture	Suitable for zero tillage, high yield.
7	PBW 550	Punjab Agricultural University (PAU)	~140-145	Irrigated	Suitable for chapati, rust resistant.
8	PBW 677	Punjab Agricultural University (PAU)	~140	Irrigated	Early sowing, rust resistance.
9	PBW 822	Punjab Agricultural University (PAU)	~140	Irrigated	High yielding, suitable for timely sowing.
10	HD 3117	ICAR-IIWBR	~135-145	Irrigated	High tillering ability, rust resistant.
11	DBW 173	ICAR-IIWBR	~140	Irrigated	High yield potential, suitable for timely sowing.
12	HD 3086	ICAR-IIWBR	~135-140	Irrigated	High yielding, rust and Karnal bunt resistance.
13	DBW 222	ICAR-IIWBR	~140-145	Irrigated	Excellent chapati quality, rust resistant.
14	CSW 18	ICAR-IIWBR	~140	Conservation Agriculture	Early sowing, suitable for zero tillage, rust resistant.
15	PBW 757	Punjab Agricultural University (PAU)	~135-140	Advanced Line	Testing phase for high yield and adaptability.
16	PBW ZN1	Punjab Agricultural University (PAU)	~140-145	Advanced Line	Testing phase with improved disease resistance.
17	PBW 343	Punjab Agricultural University (PAU)	~135-140	Irrigated	High yield, widely adopted.
18	HD 3326	ICAR-IIWBR	~140-145	Irrigated	Resistant to rust and foot rot, suitable for bread and chapati.
19	HD 2967	ICAR-IIWBR	~140	Irrigated	High yield, resistant to stripe and leaf rust.
20	DBW 187	ICAR-IIWBR	~140-145	Irrigated	High protein content, rust resistant.
21	Norman	CIMMYT/ICAR Collaborations	~135-140	Irrigated	High yield, rust resistant, good for bread quality.
22	Borlaug-100	CIMMYT/ICAR Collaborations	~140-140	Irrigated	High yield, rust resistant, good for bread quality

3.2 Experimental Site

The present investigation was conducted at three locations viz.; (i) Lovely Professional University, Phagwara Punjab India (ii) Kebbi State University of Science and Technology Aliero (KSUSTA), Kebbi State Nigeria and (iii) Lake Chad Research Institute, Borno State Nigeria during the *Rabi* seasons of 2022-23 and 2023-24. The edaphic and climatic conditions under which present study viz.; location one was teaching and research farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara Punjab India, located between latitude 31.2245° N and longitude 75.7711° E on an altitude of about 243 m above the sea level with annual rainfall of 527.1 mm. Location two was teaching and research farm of Kebbi State University of Science and Technology Aliero, Kebbi State (KSUSTA), Nigeria, located in the Sudan Savanna agro-ecological zone of Nigeria between latitude 13^0 08 N and longitude 5^0 15 E on an altitude of about 250 m above sea level with annual rainfall ranges from 1500-1700 mm. While lake chard wheat research Institute, Borno State Nigeria, located between latitude 11.8467° N and longitude 13.1571° E, on an altitude of about 325 m above sea level with annual rainfall ranges from 900-1500 mm. Punjab State, India, high temperatures ranged from 19°C (January) to 36°C (April) with low temperatures ranged from 8°C (January) to 21°C (April). Kebbi State, Nigeria, temperatures ranged from 17.1°C (January) to 27°C (April) and Borno State, Nigeria, temperatures ranged from 14°C (January) to 24°C (April). For location one (India) has a climate with cooler winters during the two *Rabi* seasons, while Kebbi and Borno States (location II and III respectively) have a dry climate compared to India, however, Borno State was dryer than India and Kebbi State during two *Rabi* seasons. With regards to soil types and soil's inherent nutrients content, India location (location I) has fertile, alluvial soils with low organic matter content. While Kebbi State (location II) soils were generally sandy or loamy with lower organic matter content and Borno States (location III) has sandy or loamy, (entisols or aridisols) and nutrient-depleted soils.

Table 3.4 Weather report 2023-2024 seasons across three locations

	Borno state Nigeria 2023				**Kebbi state Nigeria 2023**				**Punjab state India**			
Month	High Temp (°C)	Low Temp (°C)	Rainfall (mm)	R. H. (%)	High Temp (°C)	Low Temp (°C)	Rainfall (mm)	R. H. (%)	High Temp (°C)	Low Temp (°C)	R. H. (%)	Rainfall (mm)
Oct.	36	23	15	45	37.4	25.5	36.3	58	32	20	54	14
Nov.	34	18	0	25	37.1	22.4	0	29	27	15	52	30
Dec.	31	15	0	20	34.4	18.1	0	20	21	10	58	25
					***Rabi* season 2024**							
Jan.	31	14	0	15	34.7	17.1	0	20	19	8	60	75
Feb.	34	17	0.2	14	37.8	19.8	0.53	18	23	10	57	61
Mar.	38	20	1	17	40.8	23.3	4.9	24	29	15	52	51
Apr.	41	24	3	21	42.3	27	24.2	36	36	21	45	39
May	40	27	13.5	35	41.3	29.8	75.5	49	40	26	38	27
June	37	26	63	50	38.8	28.8	94.9	58	41	29	50	50
July	33	24	115	65	35.4	26.3	170.2	70	36	28	73	211
Aug.	31	23	198	75	32.8	24.4	179.1	79	34	26	67	150
Sept.	33	24	80	68	34.7	24.9	151.1	76	34	24	60	101

Source: Nigerian Meteorological Agency (Nimet) report for the two State **Source:** Punjab Agricultural University

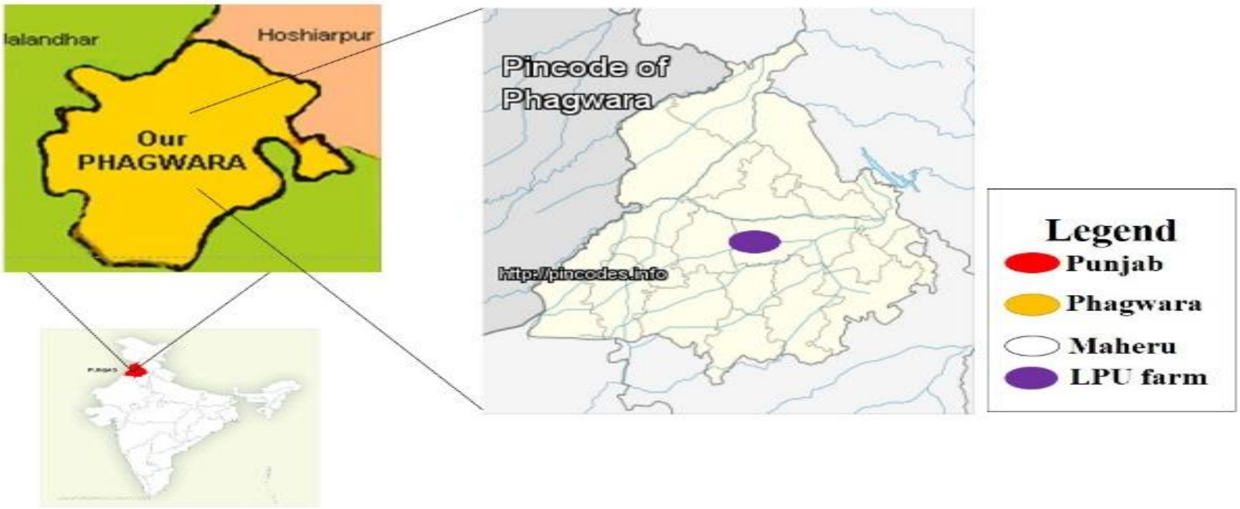


Fig. 2: shows the experimental site in Lovely Professional University, Phagwara (LPU), India (Location I)

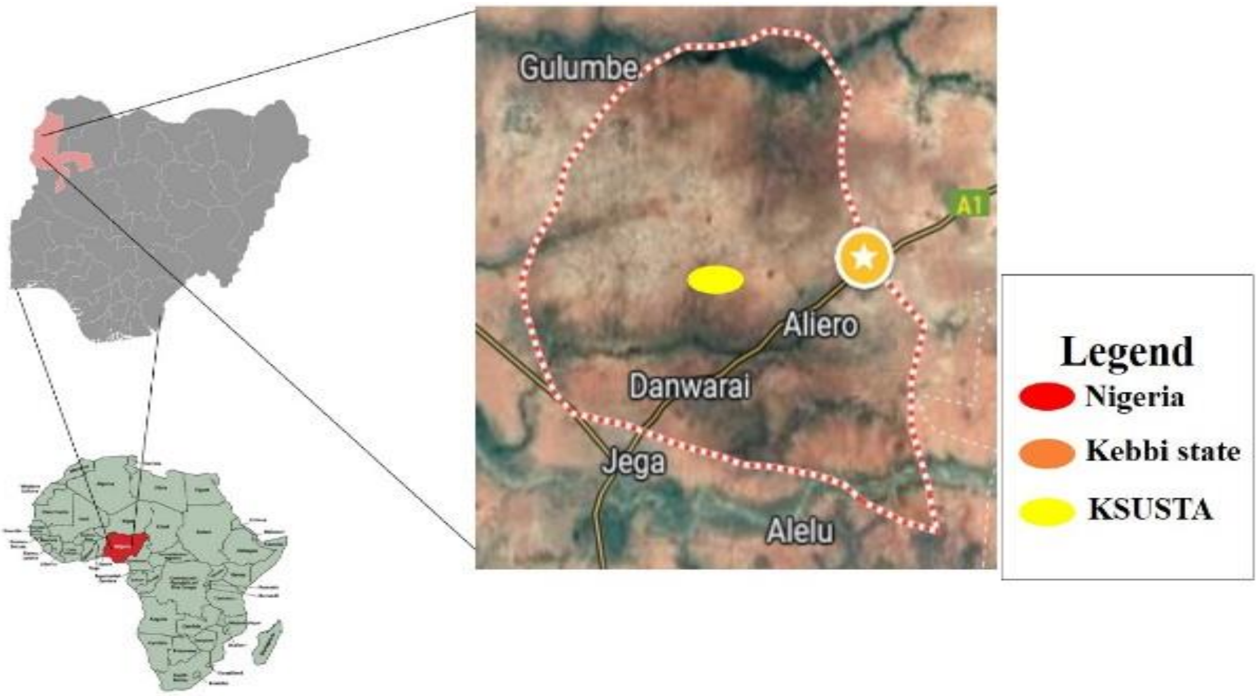


Fig. 3: shows the experimental site in Kebbi State University of Science and Technology Aliero (KSUSTA), Nigeria (Location II)

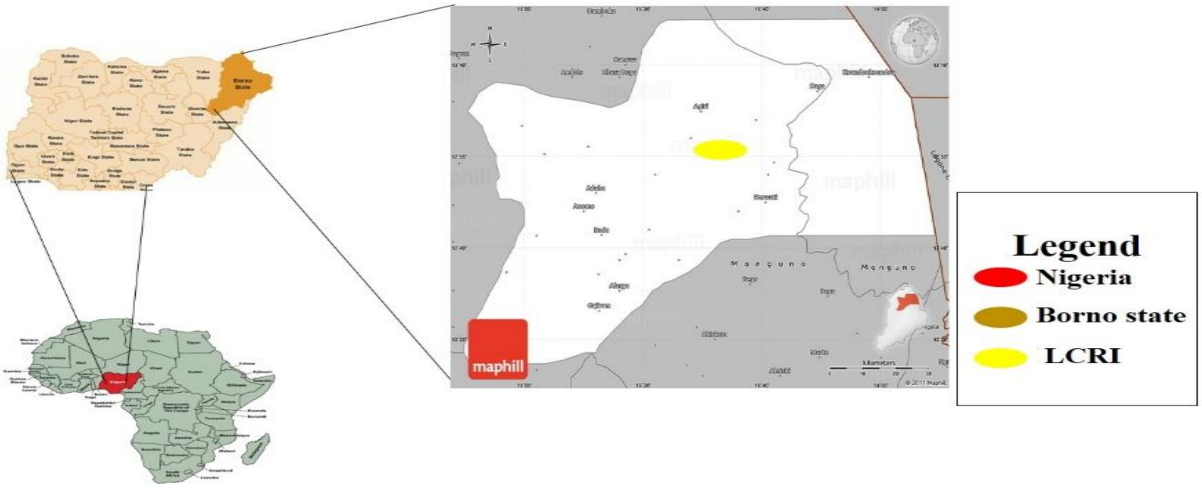


Fig. 4: shows the experimental site Lake Chad Research Institute (LCRI) in Kukawa, Borno State Nigeria (Location III)

3.3 Experimental details

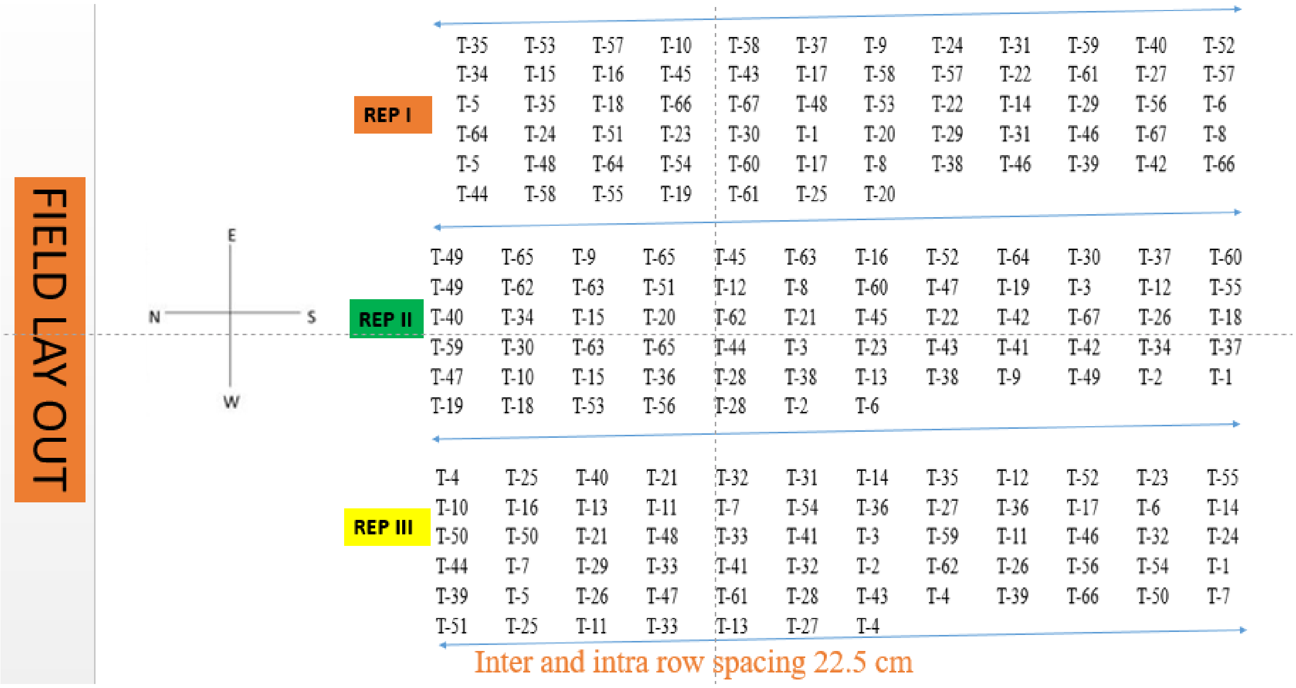
The present study was based on line x tester mating Design (L x T) as explained below:

A line x tester was used to generate a set of 45 hybrids (F_1’s) by crossing of fifteen lines (females) with three testers (males) during *Rabi* 2022-23. The parent along with their hybrids and four local checks were evaluated in during *Rabi* 2023-24 using Randomized Complete Block Design with three replications at three locations. Each plot consist of three rows of 3m length, where inter and intra row spacing was 22.5 cm. The package of practices for cultivation will be followed as per agronomical recommendations. Other materials used includes Breeder's kit; SPAD (Soil Plant Analysis Development) handheld meter; meter rule; electric weighing balance (Compax-Cx-600); seed counting machine; digestion apparatus; sodium hydroxide, hydrochloric acid etc.

Procedures for emasculation and pollination where hand emasculation or anther removal was used and plants were chosen at the right stage; the development of wheat flowers begins in the center and moves both upward and downward. When the spike of the line's (female) flag leaf is just about to emerge, it were emasculated (at booting stage). Glumes were cut in one third within a floret using scissors, and all three anthers were removed using pointed forceps without damage of the stigma. For protection against contamination with foreign pollens, the emasculated spikes were bagged. Spikes from pollen parents (tester) were removed in the morning, and spikelets were trimmed in the manner previously indicated. Anthers were burst after few minutes in the sun, releasing sufficient pollen grains that were sprinkled/dusted over emasculated females (lines). Also were re-bagged and careful labelled the pollinated plants as described by Uresh and Bishnoi (2020).

Table 3.5 Experimental details

Location(s)	3 (1 in India and 2 in Nigeria)
Seasons	Rabi (2023-2024)
Design	Randomized Block Design
Plot size	3.0 m^2 (3 m x 1 m)
Number of rows	3 per plot
Spacing between the row	22.5 cm
Number of lines	15
Number of testers	3
Number of crosses	45 hybrids (F1s)
No. of checks	4



REP I

T-35	T-53	T-57	T-10	T-58	T-37	T-9	T-24	T-31	T-59	T-40	T-52
T-34	T-15	T-16	T-45	T-43	T-17	T-58	T-57	T-22	T-61	T-27	T-57
T-5	T-35	T-18	T-66	T-67	T-48	T-53	T-22	T-14	T-29	T-56	T-6
T-64	T-24	T-51	T-23	T-30	T-1	T-20	T-29	T-31	T-46	T-67	T-8
T-5	T-48	T-64	T-54	T-60	T-17	T-8	T-38	T-46	T-39	T-42	T-66
T-44	T-58	T-55	T-19	T-61	T-25	T-20					

REP II

T-49	T-65	T-9	T-65	T-45	T-63	T-16	T-52	T-64	T-30	T-37	T-60
T-49	T-62	T-63	T-51	T-12	T-8	T-60	T-47	T-19	T-3	T-12	T-55
T-40	T-34	T-15	T-20	T-62	T-21	T-45	T-22	T-42	T-67	T-26	T-18
T-59	T-30	T-63	T-65	T-44	T-3	T-23	T-43	T-41	T-42	T-34	T-37
T-47	T-10	T-15	T-36	T-28	T-38	T-13	T-38	T-9	T-49	T-2	T-1
T-19	T-18	T-53	T-56	T-28	T-2	T-6					

REP III

T-4	T-25	T-40	T-21	T-32	T-31	T-14	T-35	T-12	T-52	T-23	T-55
T-10	T-16	T-13	T-11	T-7	T-54	T-36	T-27	T-36	T-17	T-6	T-14
T-50	T-50	T-21	T-48	T-33	T-41	T-3	T-59	T-11	T-46	T-32	T-24
T-44	T-7	T-29	T-33	T-41	T-32	T-2	T-62	T-26	T-56	T-54	T-1
T-39	T-5	T-26	T-47	T-61	T-28	T-43	T-4	T-39	T-66	T-50	T-7
T-51	T-25	T-11	T-33	T-13	T-27	T-4					

Inter and intra row spacing 22.5 cm

Fig. 5 RBD for second year experiment comprises 67 of wheat genotypes

3.4 Observations recorded

Sixteen parameters/observations were recorded which involves; growth, yield and quality parameters. Five plants were randomly selected, tagged and the average value per plant were computed for various traits as shown below:

Table 3.6 List of traits/parameters recorded from each experimental site

S/N	Traits	S/N	Traits
1	Days to 50% heading (DH)	9	Chlorophyll content (SPAD value) mg/cm²
2	Plant height (cm) (PH)	10	Number of grains/spike (NG/S)
3	Days to maturity (DM)	11	Grain weight/spike (GW/S)
4	Grain filling period (GFP)	12	1000-grain weight (g) (1000-GW)
5	Number of productive tiller (NPT)	13	Biological yield (BY) (g)
6	Number of spikelets/spike (NS/S)	14	Harvest index (%)
7	Spike length (cm) (SL)	15	Protein content per 5g
8	Flag leaf area (FLA) (cm^2)	16	Grain yield/plant (GY/P) (g)

3.5.0 Detail of data collected

Observations were recorded, where 5 plants were randomly selected and tagged and the average value per plant was computed for various traits which involves16 parameters briefly discussed as per below:

3.5.1 Days to 50% heading: The number of days to 50% heading in wheat, refers to the number of days it takes to reach the stage where half of the heads (spikes) in a field have emerged.

3.5.2 Days to maturity: Number of days taken from the date of sowing to the time when more than 75 percent of the spikes turned golden yellow was recorded.

3.5.3 Plant height (cm): Plant height of a plant was recorded in centimeters from ground level to the tip of the main spike excluding awns at maturity.

3.5.4 Number of productive tillers per plant: The number of grain bearing tillers in randomly selected plants was counted and averaged.

3.5.5 Flag leaf area (cm2): The area of primary flag leaf was calculated at maturity by measuring and multiplying the length and width of primary flag leaf and further multiplying the value by factor 0.75.

3.5.6 Spike length (cm): The length of spike was measured in centimeters from the base to the tip of the spike excluding awns.

3.5.7 Grain-filling period: Grain-filling period is the time between milk stage and maturity period (soft to hard dough stage).

3.5.8 Number of spikelets per spike: Wheat's spike consists of smaller units called spikelets which bear 3-5 florets. Total numbers of spikelets on main spike of ten selected plants were counted at the time of maturity and average was recorded.

3.5.9 Number of grains per spike: Total number of grains in the main spike of selected plants were counted at the time of harvest and averaged.

3.5.10 1000-grain weight (g): Total of 1000 grains were dried in each entry, was taken and weighed in gram with the help of an electric balance (Compax- Cx-600).

3.5.11 Grain weight/spike: Weight of grains per spike was measured with the help of an electric balance (Compax- Cx-600).

3.5.12 Harvest Index (%) The ratio of grain yield (g) to biological yield (g) of a plant was considered as harvest-index and expressed in percentage. The value was calculated as:

$$\text{Harvest index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.5.13 Biological yield (g): The total biomass excluding roots of a plant was sun-dried and dry matter was weighed in grams with the help of an electric balance (Compax- Cx-600) before threshing for obtaining their biological yield and their average was calculated.

3.5.14 Grain yield per plant (g): The grains of each selected plant were hand threshed and sun-dried. The weight of the grains obtained from each plant was taken on an electronic balance (Compax- Cx-600) in gram and averaged for each genotype in each replication were recorded

3.5.15 Chlorophyll content (mg/cm^2**):** SPAD (Soil Plant Analysis Development) handheld meter was used to the relative chlorophyll content of the leaf and average was recorded.

3.5.16 Protein content: Protein content was taken by micro-Kjeldahl method to determine the total nitrogen content, from which protein content was calculated by multiplying the nitrogen content by a conversion factor (usually 6.25 for wheat). The process as follows; 1 Sample preparation is to grind the wheat sample into a fine powder. 2 Digestion is to digest the sample in concentrated sulfuric acid using digestion apparatus. This breaks down proteins into their constituent amino acids. 3 Distillation where sodium hydroxide was added to the digested sample to release ammonia and distilled the ammonia from the sample. 4 Titration is to collect the distilled ammonia in an acidic solution and then titrate it with a standardized solution of hydrochloric acid. 5 The nitrogen content obtained was used to calculate the protein content by multiplying it with conversion factor (usually 6.25 for wheat).

3.6 Statistical Analysis

3.6.1. Analysis of Variance (Panse and Sukhatme, 1967)

3.6.2. Line x tester analysis (Kempthorne, 1957)

3.6.3. Analysis of Variance for Combining Ability (Kempthorne, 1957)

3.6.4. Estimation of Heterosis (Fonseca and Patterson, 1968)

3.6.5. Stability analysis (Eberhart and Russell, 1966).

3.6.1 Analysis of Variance for the Design of Experiment

The analysis of variance for the design of experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967).

Table 3.7 Analysis of Variance for the Design of Experiment

Source of variation	d.f.	S.S	M.S.	F ratio
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Error	(r-1) (t-1)	SSE	MSE	-
Total	(rt-1)	TSS	-	-

Where,

r = Number of replications

t = Number of treatments

MSR = Mean squares due to replications

MST = Mean squares due to treatments

MSE = Mean squares due to error

d.f. = Degrees of freedom

The standard error and critical difference were calculated as follows:

$$\text{SE of mean} = \sqrt{\text{MSE/r}}$$

Critical difference $(\text{CD}) = \sqrt{2\text{MSE/r}}$ x 't' value at 5% or 1% level of Significance at error degree of freedom.

The analysis of variance was further extended to partition the variance due to treatments (genotypes) in to various components such as parents, crosses, parent's vs crosses, females, males and females' vs males as outlined below:

Table 3.8 Analysis of variance for further partition due to treatments

Source of variation	**d.f.**	**S.S.**	**M.S.**	**F-ratio**
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Parents	(p-1)	SSP	MSP	MSP/MSE
Females	(f-1)	FSS	MSF	MSF/MSE
Males	(m-1)	MSS	MSM	MSM/MSE
Females vs Males	1	FSS vs MSS	MSF vs MSM	MSF vs MSM/MSE
Crosses	(F_1-1)	F_1SS	MSF$_1$	MSF$_1$/MSE
Parents vs Crosses	1	PSS vs F_1SS	MSP vs MSF$_1$	MSP vs MSF$_1$/MSE
Error	(r-1) (t-1)	SSE	MSE	-

Where,

r = number of replications

t = number of treatments

p = number of parents

f = number of females

m = number of males

F_1 = number of hybrids

S.S. = Sum of squares

M.S. = Mean sum of squares

d.f. = Degree of freedom

The significance among treatment was tested by 'F' test. To test the hypothesis H_0: $t_1 = t_2 =$ ------------ t_y, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$Y_{ij} = \mu + t_i + b_j + e_{ij}$

Where,

Yij = yield of i^{th} entry in the j^{th} replication

μ = general mean

t_i = effect of the i^{th} entry (i = 1, 2, ---------, v.)

b_j = effect of the jth replicate (j = 1, 2, ----------, r.)

e_{ij} = environmental effect

Table 3.9 ANOVA for parents and crosses

Source of variation	DF	SS	MS	F ratio
Replication	(r-1)	SSR	SSR	MSR/MSE
Treatments	(t-1)	SST	SST	MST/MSE
Parents	(P-1)	SSP	SSP	MSP/MSE
Crosses	(C-1)	SSC	SSC	MSC/MSE
Parents *vs* crosses	1	SSP vs SSC	MSP vs MSC	MSP vs MSC/MSE
Error	(r-1) (t-1)	SSE	MSE	

Where,

r = Number of replications

t = Number of treatments

P = Number of parents

C = Number of crosses

The standard error, critical difference and coefficient of variation were calculate as follows:

S. E. of mean = $\sqrt{\frac{MSE}{r}}$

Critical difference = $\sqrt{\frac{2MSE}{r} \times t\ value}$

Where,

Table value of t distribution at error df and $P \leq 0.05$

Coefficient of variation (CV) = $\sqrt{\frac{MSE}{Gm} \times 100}$

Analysis of variance for randomized complete block design:

The analysis of variance for randomized complete block design was carried out following Panse and Sukhatme (1967) as follows:

Table 3.10 ANOVA for line x tester analysis as outlined by Kempthorne (1957)

Source of variation	**df**	**SS**	**MS**
Replication	(r-1)	$\Sigma\frac{x^2..K}{mt} - \cdots \frac{x^2}{mtr}$	
Treatments (Hybrids)	(mf-1)	$\Sigma\frac{X^2 ij}{r} - \frac{x^2\ldots}{mfr}$	
Males	(m-1)	$\Sigma\frac{X^2 i\ldots}{fr} - \frac{x^2\ldots}{mfr}$	Mm
Females	(f-1)	$\Sigma\frac{X^2 j}{mr} - \frac{x^2\ldots}{mfr}$	Mf
Males x Females	(m-1) (f-1)	$\Sigma\frac{X^2 ij}{r} - \Sigma\frac{x^2 i..}{fr} - \Sigma\frac{x^2 j..}{mr} + \frac{x^2..}{Mfr}$	
Error	(mf-1) (r-1)	by difference	
Total	(nfr-1)	$\Sigma\frac{X^2}{ijk} - \frac{x^2\ldots}{mfr}$	

Where,

x..k = Sum of all the mf hybrids in the k^{th} replication,

X_{ij} = Sum of ij^{th} hybrid combination over all replications,

x_i = Sum of j^{th} male parent over all the females and replications,

x^2.j. = Sum of female parent over all the males and replications,

x… = Sum of all the mf hybrids over all the replications,

$\sigma^2 e$ = Error variance,

r = Number of replications

m = Number of males,

f = Number of females,

m = M.S. due to males,

f = M.S. due to females,

mf = M.S. due to males x females,

Me = Error M. S.

3.6.2 Combining ability analysis

The combining ability analysis was carried out following line × tester mating design outlined by Kempthorne (1957) and further elaborated by Arunachalam (1974). Line × tester analysis was used to estimate general combining ability (gca) and specific combining ability (sca) variances and their effects using the observations taken on F_1 generation of the line × tester sets of crosses. In this mating system, a random sample of 'l' lines is taken and each line is mated to each of the't' testers (Singh and Chaudhary, 1977).

The model underlying this analysis is as follows:

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

μ = General mean

g_i = gca effect of the i^{th} male (tester), i = 1,2,…m.

g_j = gca effect of j^{th} female (line), j = 1,2,…f.

s_{ij} = sca effect of the i^{th} tester and j^{th} line cross combination

e_{ijk} = Error associated with ijk^{th} observation, k = 1,2,…r.

The individual effects were estimated as follows:

(i) $\mu = \frac{X...}{mfr}$

Where,

X... = total of all hybrid combinations

(ii) $g_i = \frac{X_{i}..}{fr} - \frac{X...}{mfr}$

Where,

$X_i..$ = total of i^{th} male over all the females and replications.

(iii) $g_j = \frac{X._{j}.}{mr} - \frac{X...}{mfr}$

Where,

$X._j.$ = total of j^{th} female over all males and replications.

(iv) $s_{ij} = \frac{X_{ij}.}{r} - \frac{X_{i}..}{fr} - \frac{X._{j}.}{mr} + \frac{X...}{mfr}$

Where,

$X_{ij.}$ = total of ij^{th} combination over all replications.

Standard errors for combining ability estimates were calculated as given below:

SE (gca for line) = $(Me/rm)^{1/2}$

SE (gca for tester) = $(Me/rf)^{1/2}$

SE (sca effect) = $(Me/r)^{1/2}$

SE (g_i-g_j) line = $(2Me/rm)^{1/2}$

SE (g_i-g_j) tester = $(2Me/rf)^{1/2}$

SE (S_{ij}-S_{kl}) = $(2Me/r)^{1/2}$

Where,

Me = Error MS

Critical differences (CD) were calculated as:

CD = SEd × t at 5% and 1% probability levels at error d.f.

Table 3.11 The Analysis of variance for combining ability

Source of variation	**d.f.**	**S.S.**	**M.S.**	**Expected MS**
Replications	(r-1)	-	-	-
Lines (females)	(l-1)	SS (l)	MS (l)	$\sigma^2 e$ + r (Cov. F.S.-2 Cov. H.S.) + rt Cov. H.S.
Testers (males)	(t-1)	SS (t)	MS (t)	$\sigma^2 e$ + r (Cov. F.S.-2 Cov. H.S.) + rl Cov. H.S.
Lines × Testers	(l-1) (t-1)	SS (l × t)	MS (l × t)	$\sigma^2 e$ + r (Cov. F.S.-2 Cov. H.S.)
Error	(rlt-1)	SS (e)	MS (e)	$\sigma^2 e$

Where,

r = number of replications

l = number of lines

t = number of testers

$\sigma^2 e$ = variance due to error

Genetic components:

$$\text{Cov. Half sib (line)} = \frac{M_f - M_{fm}}{rm}$$

$$\text{Cov. Half sib (tester)} = \frac{M_m - M_{fm}}{rf}$$

$$\text{Cov. Half sib (average)} = \frac{1}{r(2fm - f - m)}\left[\frac{(f-1)\,M_f + (m-1)\,M_m}{f+m-2} - M_{fm}\right]$$

$$\text{Cov. F.S. (average)} = \frac{(M_f - M_e) + (M_m - M_e) + (M_{fm} - M_e)}{3r} + \frac{6r\ \text{Cov. H.S. (average)} - r\,(f+m)\ \text{Cov. H.S. (average)}}{3r}$$

Where,

M_f = Mean squares due to lines (females)

M_m = Mean squares due to testers (males)

M_{fm} = Mean squares due to line × tester interactions

M_e = Mean squares due to error

r = number of replications

f = number of lines

m = number of testers

gca variance (σ^2gca) = Cov. H.S. (average) = $\left[\frac{1+F}{4}\right] \sigma^2 A$

Therefore,

Additive genetic variance (σ^2A) = 2 Cov. H.S. (average), if F = 1 and

(σ^2A) = 4 Cov. H.S. (average), If F = 0

sca variance (σ^2sca) $= \frac{(M_{fm} - M_e)}{r}$

$$\sigma^2 sca = \left[\frac{1+F}{2}\right]^2 \sigma^2 D$$

Therefore,

Dominance variance (σ^2D) = σ^2 sca with F = 1, and

σ^2D = 4σ^2sca, if F = 0

Where,

F = Inbreeding coefficient

Average degree of dominance

It was calculated using formula given by Kempthorne and Curnow (1961).

$$\text{Average degree of dominance} = \sqrt{(\sigma^2 sca)/(2\sigma^2 gca)} \text{ or } \sqrt{(\sigma^2 D)/(\sigma^2 A)}$$

Where, σ^2sca = Estimated variance due to sca.

σ^2gca = Estimated variance due to gca

Predictability ratio:

It was suggested by Baker (1978) and was calculated as follows:

$$\text{Predictability ratio} = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s}$$

Heritability in narrow sense:

Heritability in narrow sense ($h^2{}_{(ns)}$) was calculated as suggested by Kempthorne (1957).

$$h^2 n\,(\%) = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s + \sigma^2 e} \times 100$$

Where,

$\sigma^2 g$ = variance due to gca

$\sigma^2 s$ = variance due to sca

$\sigma^2 e$ = variance due to error

Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines (\%)} = \frac{\text{S.S. (lines)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of testers (\%)} = \frac{\text{S.S. (testers)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of lines} \times \text{testers} = \frac{\text{S.S. (lines x testers)}}{\text{S.S. (crosses)}} \times 100$$

3.6.3 Estimation of heterosis over better parent (Heterobeltiosis) and standard variety

The heterosis was computed as per cent increase or decrease of the mean values of crosses (F_1's) over better parent (Heterobeltiosis) and standard variety (Standard Heterosis).

Estimation of heterosis over better-parent (Heterobeltiosis) and standard variety (standard heterosis) (Fonseca and Patterson, 1968).

1. Heterosis over better parent (Heterobeltiosis) $= \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$
2. Heterosis over standard variety (Standard heterosis) $= \frac{\overline{F}_1 - \overline{SV}}{\overline{SV}} \times 100$

Where,

F_1 = Mean of F_1

$\overline{\text{BP}}$ = Mean of better - parent

$\overline{\text{SV}}$ = Mean of standard variety or check vari ety

The test of significance was applied to determine the significance of heterosis by using the following formula:

$$\text{'t' (Heterobeltiosis)} = \frac{\overline{F}_1 - \text{BP}}{\text{S.E.}}$$

$$\text{'t' (Standard heterosis)} = \frac{\overline{F}_1 - \overline{\text{SV}}}{\text{S.E.}}$$

$$\text{S.E. of heterosis over better parent and standard variety} = \sqrt{2\text{Me}/\text{r}}$$

Where,

Me = Mean error variance

r = Number of replications.

Thus, C.D. = SE ×'t' value at error d.f. and 5% or 1% probability level. Critical difference was used to test the significance of difference mean value of F_1 over better parent and standard variety which signified significance of the respective heterosis.

3.6.4 Stability analysis (Eberhart and Russell, 1966).

The statistical technique proposed by Eberhart and Russell (1966) was utilized to estimate the stability parameters with respect to different characters.

Table 3.12 The ANOVA for stability analysis (Eberhart and Russell, 1966)

Source of variation	**d.f.**	**S.S.**	**M.S**
Total	(nv-1)	$\sum_{i=1}^{v} \sum_{j=1}^{n} Yij - CF = TSS$	
Genotypes (G)	(v-1)	$^1/_n \sum_{i=1}^{v}$ Y^2i-CF = GSS	MS_1
Environment (E)	n-1	$^1/_n \sum_{i=1}^{v}$ Y^2i-CF = GSS	
E x G	(n-1)(v-1)	TSS (GSS + ESS)	MS_2
E + (GxE)	V(n-1)	$\sum_{i=1}^{v} \sum_{j-1}^{n}$ Y^2_{ij}-$^1/_n$ Y^2_i	
E (Linear)	1	$^1/_v (\sum_{j=1}^{n} YjIj)^2 / \sum_{j=1}^{n} I^2$j	
G x E (Linear)	v-1	$\sum_{i=1}^{n}(\sum_{j=1}^{n} YijIj)^2 /(\sum_{j=1}^{n} I^2$j-E (Lin.)	MS_3

Polled deviation	V (n-2)	$\sum_{i=1}^{v} \sum_{j=1}^{v} \sigma^2_{ij}$	MS_4
Genotype I	n-2	$\sum_{j=1}^{n} Y^2_{ij} - ({}^1/_n) (Y_1)^2 - (\sum_{j=1}^{n} Y_{ij} I_j)^2 / \sum_{j=1}^{n} I^2_j$	
Genotype v	n-2	$\sum_{j=1}^{n} Y^2_{vj} - ({}^1/_n) (Y_v)^2 - (\sum_{j=1}^{n} Y_{vj} I_j)^2 / \sum_{j=1}^{n} I^2_j$	
Pooled error	N(r-1)	${}^1/_n \sum_{j=1}^{n} \sigma^2_e$ = TSS-Grand SS (GXE)	MS_5

Where;

$Y_{ij} = \mu_{ij} + \beta_i I_j + \sigma_{ij}$

Y_{ij} = mean performance of i^{th} genotype in j^{th} environment ($i = 1, 2, 3, 4 \ldots\ldots\ldots V$; $j = 1, 2, 3, 4 \ldots\ldots\ldots n$)

v = number of genotypes,

n = number of environments,

μ = mean performance of i^{th} genotype over all the environments,

B_i = regression co-efficient of i^{th} individual mean performance on environmental index Ij,

Ij = jth environmental index, and

σ_{ij} = deviation from regression of the i^{th} genotype at j^{th} environment I_j is estimated as:

$$Ij = \sum_{i=j}^{v} {}^{Yij}/_{V} - \sum_{i=j}^{v} \sum_{j=i}^{n} {}^{Yij}/_{Vn}$$

Where, $\sum_{j=i}^{n} Ij = 0$

The first stability parameter regression coefficient (b_i) was estimated using the following formula:

$$bi = [\sum_{j=i}^{n} Yij\ Ij)/[\sum_{j=i}^{n} r2]$$

The second stability parameter (S^2di) was estimated using the following formula:

$$S^2di = ({}^1/_{n} - 2) = [\sum_{j=i}^{n} \sigma 2ij) - Pooled\ error$$

Where,

$$\sum_{j=1}^{n} \sigma 2\ ij = (\sum_{j=i}^{n} Y2 - Y2 \quad /_{n}\ (\Sigma Yij\ Ij)^{2}$$

$$[\sum_{j=i}^{n} I\,2j\; j = 1$$

The average of error squares over all the environments was considered as the estimates of the pooled error.

The Eberhart and Russell (1966) model enables the partitioning of the genotype x environment interaction of each variety into two part (i) the variation due to response of variety to varying environmental indices (sum of squares due to regression) and (ii) the explaining deviation from the regression on environmental index.

The following tests of significance were applied:

(i) The test of mean performance of genotypes using ‘F’ test.

$F = {}^{MS1}/_{MS4}$

The test of mean performance of genotypes using‘t’ test.

$t = {}^{(\mu i - \mu)}/_{SE(x)}$

$$SE\ (x) = \sqrt{\frac{Pooled\ deviation\ MS}{Number\ of\ environments - 1}}$$

μi = mean performance of the genotype over all environment and

μ = general mean

(iii) Genotype x environment interaction was tested using the ‘F’ test

$F = {}^{MS2}/_{MS4}$

(ii) The genotypic differences among the genotypes for their regression on the environmental index were tested using ‘F’ test.

$F = {}^{MS3}/_{MS4}$

(iii) The deviation of bi value from unity was tested using‘t’ test.

t = (bi – 1) and SE (b) at v (n-2) d. f.

Where,

$$SE\ (b) = \sqrt{\frac{Pooled\ deviation\ MS}{\sum_{j=1}^{n} I2j}}$$

Deviation from regression for each genotype was tested using the ‘F’ test.

$F = {}^{1}/_{(n-1)} \sum_{j=1}^{n} \quad \sigma^2_{ij}/\ MSS$

CHAPTER FOUR

RESULTS

The experimental findings of the present investigation entitled "Studies on combining ability, gene action and stability analyses for yield and yield contributing traits in wheat (*Triticum aestivum* L.)" have been set out in the following sub-heads:

4.1 Analysis of variance
4.2 Components of genetic variances and their magnitudes
4.3.1 Combining ability analysis effects for combined locations
4.3.2 Combining ability analysis across three locations
4.4 Estimates of heterosis over better parent and standard variety
4.5 Estimation of stability analysis

4.1 Analysis of variance

This table represents an analysis of variance (ANOVA) for various characters (traits) measured in a set of treatments, using three sources of variation such as replications, treatments, and error.

It is therefore recommended that wheat breeders capitalize on the dual nature of gene action by employing complementary breeding strategies pure line selection for additive traits and heterosis breeding for traits governed by dominance and epistasis. The identified parents and hybrids should be further evaluated and advanced in breeding pipelines targeting region-specific and climate-resilient wheat varieties. Additionally, the incorporation of physiological traits into breeding programs should be strengthened to enhance selection efficiency and trait pyramiding. The comprehensive methodology and cross-continental design employed in this study should serve as a model for future collaborative wheat improvement initiatives aimed at ensuring global food security.

Each character has its own set of degrees of freedom (d.f.) and the values indicate the variation attributed to each source for that particular character.

4.1.1 Days to 50% heading

Results on variance due replications revealed that, replications effect recorded 1.70 which is relatively low. While treatments recorded 176.73 (highly significant), this shows that treatment effects contributed a lot to the variation in this trait and error variance 3.40 indicating a small amount of unexplained variation. The treatments (such as different varieties or environmental factors) significantly influence the number of days it takes for 50% of plants to head.

4.1.2 Days to maturity

Effect of replications observed as 0.39 (low variation from replications). While treatments recorded 88.619 (highly significant), meaning treatments have a strong impact on this trait. Error 0.80 (minimal error, a low amount of unexplained variation). Therefore, treatments significantly affect the number of days it takes for plants to mature.

4.1.3 Flag leaf area (cm²)

Results on flag leaf area revealed that, replications effect recorded 6.71 (small contribution to variation). Treatments effect observed as 226.05 (highly significant), suggesting treatment differences are important. While as error 13.40 (moderate variation due to error). Therefore, flag leaf area is strongly influenced by the treatments, with a reasonable amount of error variation.

4.1.4 Grain filling period

Replications recorded 9.507 (moderate variation from replications). While treatments revealed 205.14 (highly significant), indicating a strong effect of treatments on this trait. Whereas error variance recorded 19.03 (moderate error variation). Thus, grain filling period is strongly affected by treatments, though there's a noticeable level of error variation.

4.1.5 Plant height (cm)

Results on plant height for replications recorded 107.76 (substantial variation due to replications). Whereas treatments effect revealed 93.10 (highly significant), showing that treatments significantly impact plant height. Error variances recorded 15.60 (small amount of unexplained variation). There by implication the plant height is significantly influenced by treatments, although replications contribute a noticeable amount of variation.

4.1.6 Number of productive tillers

Results revealed that, replications effect recorded 0.90 (low variation). While treatments 11.04 (significant), indicating treatments have an impact, though smaller than other traits. With regards to error variance it observed that 1.81 (low error). The number of productive tillers is moderately influenced by the treatments, with a relatively low amount of unexplained variation.

4.1.7 Chlorophyll content

The results for analysis of variance revealed that, effect of replications observed as 12.63 (low contribution from replications). Treatments effect recorded 189.43 (highly significant), suggesting that treatments have a significant effect on chlorophyll content. Error variance recorded 25.30 (a moderate level of error variation). Chlorophyll content is significantly impacted by the treatments, although there is some level of error.

4.1.8 Number of spikelets/spike

The effect of replications recorded 0.21 (very low variation). Whereas, treatments effect was 15.47 (significant), indicating treatment effects are relevant but less influential than in other traits. Error observed as 0.44 (minimal unexplained variation). The number of spikelets per spike is moderately influenced by treatments, with minimal error.

4.1.9 Spike length (cm)

Replications effect recorded 2.34 (low variation from replications**).** Treatments effects revealed 2.49 (significant), meaning treatments affect spike length but the effect is not large. Error was 4.69 (moderate error variation). Treatments moderately affect spike length, with some error involved.

4.1.10 Number of grains/spike

Results of replications recorded 8.16 (moderate variation). While treatments variance observed as 149.66 (highly significant), indicating that treatments have a strong influence. Error 16.30 (moderate level of error). The number of grains per spike is strongly influenced by treatments, although there is some variation due to error.

4.1.11 Grain weight/spike (g)

Replications observed as 0.17 (negligible variation). Treatments was 0.86 (no significant treatment effect), suggesting that the treatment does not significantly affect grain weight per spike. However, error variance was 0.34 (minimal error variation). Grain weight per spike is not significantly affected by treatments in this experiment.

4.1.12 1000 grain weight (g)

Results revealed that, treatments effect recorded 73.58 (highly significant), showing treatments significantly influence the 1000 grain weight. While replications effects recorded as 0.47 (small variation from replications). Error variances was 1.07 (minimal error variation). The 1000 grain weight is highly significantly influenced by treatments.

4.1.13 Biological yield (g)

Results on effect of replications revealed as 1.30 (low variation). Treatments variances recorded as 188.94 (highly significant), indicating a strong treatment effect on biological yield. Error variance 2.60 (small unexplained variation). Biological yield is highly influenced by the treatments applied in this experiment.

4.1.14 Harvest index (%)

Effect of replications revealed 4.13 (moderate contribution from replications). Treatments: 22.42 (highly significant), suggesting treatments have a significant effect on harvest index. Error variance was 2.42 (small amount of error variation). Harvest index is significantly affected by the treatments, with a relatively small amount of unexplained variation.

4.1.15 Protein (%)

Results on effect of replications recorded 1.22 (low variation). Whereas treatments effect observed as 2.516 (significant), showing that treatments have some effect on protein content but the effect is weaker than for other traits. Error observed as 2.44 (moderate error variation). Protein content is moderately influenced by treatments, with a moderate level of unexplained variation.

4.1.16 Grain yield/plant (g)

Replications variances observed as 8.51 (moderate variation from replications). While treatments effect as 17.07 (highly significant), indicating treatments have a significant effect on grain yield per plant. Error variance was 11.12 (moderate error variation). Grain yield per plant is highly influenced by the treatments, but there is some variation due to error.

4.1.2 Analysis of variance for L x T

The analysis of variance (ANOVA) provided detailed breakdown of the contributions of line, tester, and line x tester interactions for sixteen different characters in wheat using line x tester mating design. This table described the genetic variances and the effects of the different sources of variation on each character

4.1.2.1 Days to 50% heading (DH)

Line (5.87) and line x tester (5.92) were highly significant at 1% level, indicating that both lines and line x tester plays critical role in the days to 50% heading. Tester (0.58) was not significant, suggesting that tester differences have little impact on this trait. Parent vs Crosses 33.02 (highly significant).

4.1.2.2 Plant height (cm)

Both line (2.85) and line x tester (3.66) have significant effects at the 1% level, while tester (1.38) was not significant. This means the lines and their interaction with tester significantly affect plant height, while the testers themselves had smaller role. Parent vs crosses 10.35 (highly significant).

4.1.2.3 Days to maturity (DM)

The line (7.85) and tester (32.03) were significant at 1% level, with line x tester (7.95) also significant. Both the genetic differences in lines and testers, as well as their interaction, significantly influenced the maturity period.

4.1.2.4 Grain-filling period (GFP)

Tester (8.23) was significant at 1% level, suggesting testers were crucial in determining the grain-filling period. However, line (4.01) and line x tester (1.67) were not significant. Parent vs Crosses 29.45 (highly significant)

4.1.2.5 Number of productive tillers (NPT)

Line (3.83) was significant at 5% level, indicating that line variation has a moderate effect on the number of productive tillers. However, tester (1.76) and line x tester (1.54) was not significant. Parent vs crosses 73.22 (highly significant).

4.1.2.6 Number of spikelets per spike (NS/S)

Both Line (3.55) and line x tester (2.23) were significant at the 1% and 5% levels, respectively, showing that both genetic differences between lines and their interaction with testers play a significant role in determining this trait. Tester (1.16) was not significant.

4.1.2.7 Spike length (cm)

Tester (5.64) was significant at 5% level, and tine x tester (2.89) significant at the 1% level, showing that both the testers and their interaction with lines affect spike length, with line differences playing a smaller role (line 2.41, was not significant).

4.1.2.8 Flag leaf area (cm^2)

Both line (180.45) and tester (210.07) were highly significant (1% level), showing that both the genetic variation among lines and testers were crucial in determining flag leaf area. The line x tester (79.13) interaction also was significant, emphasizing the importance of the interaction between lines and testers.

4.1.2.9 Chlorophyll content

Line (4.04) was significant at 1% level, while tester (1.18) and line x tester (0.81) were not significant. This indicates that lines differences were the main contributors to chlorophyll content.

4.1.2.10 Number of grains per spike (NG/S)

Line (4.03) was significant at 1% level, while tester (0.52) and line x tester (1.59) were not. This suggests that genetic differences among lines primarily influenced the number of grains per spike.

4.1.2.11 Grain weight per spike (g)

None of the sources of variation were significant, meaning that the variation in grain weight per spike was likely due to random or unaccounted factors.

4.1.2.12 1000-grain weight (g)

Tester (5.33) was significant at 5% level, indicating that tester variation has moderate impact on this trait. Line (1.25) and line x tester (1.31) were not significant. Parent vs crosses 3.26 (Not significant).

4.1.2.13 Biological yield (g)

Line (2.31) was significant at 5% level, suggesting that line differences play a significant role in biological yield. Tester (1.08) and line x tester (0.94) were not significant.

4.1.2.14 Harvest index (%)

Line (6.22) was significant at 1% level, indicating that the line variation was the primary contributor to harvest index, with tester (0.75) and line x tester (1.43) being non-significant.

4.1.2.15 Protein content

Line (1.46) and tester (0.978) were significant at 5% level, indicating both factors contribute to the variation in protein content, although their effects were smaller compared to other traits. Line x tester (3.94) was not significant. Parent vs crosses 20.45 (highly significant).

4.1.2.16 Grain yield per plant (g)

Line (11.53) and line x tester (5.43) were significant at 1% level, indicating that both genetic differences among lines and their interaction with testers were crucial in determining grain yield per plant. Tester (4.31) was significant at 5% level. Parent vs crosses 17.33 (highly significant)

4.1.3 Analysis of variance (ANOVA) for combining ability variances

Analysis of variance of combining ability for 16 characters in L x T mating design. The ANOVA recorded significant different ($p < 0.001$) among line, tester and line x tester reported that, no single genotype was significant for all traits across three locations.

4.1.3.1 Days to 50% heading (DH)

GCA was high and significant (5.87), indicating additive gene effects are important for this trait. SCA was moderate but significant (5.92), showing some non-additive effects also contribute to DH. Mean square (MS) is relatively high (61.82), meaning this trait has considerable variability.

4.1.3.2 Plant height (cm)

GCA was significant (2.85), showing that PH was influenced by additive genetic effects. SCA also significant (3.66), indicating role for non-additive effects in specific crosses. Mean square was moderate (63.97), showing variability in PH that could be exploited through both additive and non-additive effects.

4.1.3.3 Days to maturity (DM)

For GCA and SCA it was revealed that both GCA and SCA were highly significant (7.85 and 7.95, respectively), implying that both additive and non-additive effects control this trait. MS was also moderate (42.52), indicating considerable genetic variability.

4.1.3.4 Grain-filling period (GFP)

GCA was not significant (4.01), but SCA was highly significant (8.23), showing GFP was mostly controlled by non-additive effects and specific parental combinations. Therefore, mean square was moderate (51.8), indicating variation that could be leveraged in specific crosses.

4.1.3.5 Number of productive tillers (NPT)

GCA recorded moderately significant (3.83), while SCA was not significant, indicating that NPT is mostly influenced by additive genetic effects. While mean square showed low (1.61), indicated very limited variation.

4.1.3.6 Number of spikelets per spike (NS/S)

Number of spikelets per spike (NS/S), the line was highly significant (3.55), indicating genetic differences among lines. Tester was not significant (1.16), reflecting limited impact by testers in the cross. Line × Tester was highly significant (2.23), suggesting interactions between lines and testers. While error variance was low (0.84), indicating reliable data.

4.1.3.7 Spike length (cm)

Both GCA and SCA were highly significant, with GCA (2.41) and SCA (2.89) values, showing almost equal contribution of additive and non-additive gene action. But mean square was very low (0.63), indicating minimal variation in SL.

4.1.3.8 Flag leaf area (cm^2)

Results revealed that GCA and SCA both were very high and significant, with GCA at 180.45 and SCA at 79.13, meaning both additive and non-additive effects play strong roles. Mean square was very low (3.82), which suggests specific crosses could optimize this trait.

4.1.3.9 Chlorophyll content (mg)

GCA was significant (4.04), indicating additive effects are important. SCA was not significant, suggesting little contribution of non-additive influence. However, mean square value was moderate (37.32), indicating a relatively high variance due to additive effects.

4.1.3.10 Number of grains per spike (NG/S)

Number of grains per spike (NG/S) for line indicated high significant different (4.03), reflecting genetic variability. Tester recorded no significant variation (0.52), indicating minimal tester impact. Line × tester not significant (1.59), suggesting weak interaction effects. While error variance has moderate effect (14.55).

4.1.3.11 Grain weight per spike (g)

Grain weight per Spike (GW/S) line was not significant (1.16), indicating weak genetic variability. Tester not significant (1.21), suggesting testers have little effect. Line × Tester not significant (0.93), showing weak interaction effects. Error was very low error (0.17), indicating precise data.

4.1.3.12 1000-grain weight (g)

1000-Grain weight (1000-GW) for line was not significant (1.25), indicating limited genetic differences for the trait. But tester significant (5.33), reflecting notable tester influence. While Line × Tester was not significant (1.31), showing minimal interaction effects. Error variance was low (3.52).

4.1.3.13 Biological yield (g)

Biomass yield for line was highly significant (2.31), indicating genetic variability. Tester was not significant (1.08), showing limited tester effect. While Line × Tester was not significant (0.94), suggesting weak interaction effects. However, error variance was moderate (32.39).

4.1.3.14 Harvest index (%/ 5g)

Harvest Index (%) for line was highly significant (6.22), reflecting strong genetic differences. The tester was not significant (0.75), showing minimal tester impact. Similarly Line × Tester was not significant (1.43), indicating weak interaction effects. While error variance was low (15.23).

4.1.3.15 Protein content

Protein content for line was highly significant (1.46), showing high genetic variability among genotypes under study. Tester was also highly significant (0.978), reflecting some effect by testers. However, line × tester was not significant (3.94), showing weak interaction effects. While error variance was very low (0.37).

4.1.3.16 Grain yield per plant (g)

The results revealed that GCA and SCA were significant, with GCA (11.53) and SCA (5.43), indicating that GY/P was influenced by both additive and non-additive effects. While mean square was moderate (10.47), making this trait suitable for selection through a combination of general and specific combining ability.

4.2.4 Estimates of components of genetic variance and their magnitudes

This ratio determines the extent to which a trait's performance is determined by additive genetic effects (GCA). A higher ratio (closer to 1) indicates that the trait is predominantly influenced by additive genetic variance, making it predictable and easier to improve through selection. Heritability (h^2n) % measures how much of the phenotypic variance is due to genetic factors. A higher value indicates that genetic factors explain a larger portion of the trait's variation, making the trait easier to improve through selection. Genetic advance in percent of mean, this indicates the expected genetic gain from selection in a breeding program. It is influenced by heritability and the amount of genetic variance. A high value suggests that the trait is responsive to selection and can be genetically improved.

4.2.4.1 Days to 50% heading

Days to 50% heading revealed GCA variance (σ^2g) 0.72; SCA variance (σ^2s) 0.00; average degree of dominance 1.00 (complete dominance); predictability ratio 1.00 (high); heritability (h^2n) % 46% (moderate) and genetic advance was 27.90%. This trait is highly influenced by additive genetic effects (GCA), with no influence of SCA. The high predictability ratio (1.00) indicates that selection for this trait is very predictable and can result in a significant genetic advance, though its heritability is moderate.

4.2.4.2 Plant height (cm)

Plant height was observed in GCA variance (σ^2g) 0.13; SCA variance (σ^2s) 0.02; average degree of dominance 0.15; predictability ratio 0.86 (high); heritability (h^2n) 25% (low) and genetic advance was 0.32%. The trait has low GCA and SCA variance, indicating that it is poorly controlled by genetic factors. The predictability ratio is high, but the low heritability means environmental effects dominate, and genetic improvement will be slow.

4.2.4.3 Days to maturity

Days to maturity recorded that GCA variance (σ^2g) 0.00; SCA variance (σ^2s) 0.00; average degree of dominance 0.00; predictability ratio 0.00 (none); heritability (h^2n) 42% (moderate) and genetic advance was 65.39%. Both additive and non-additive genetic effects are negligible, and the trait is primarily under environmental control. The genetic advance is moderate, and improvement via selection may be difficult.

4.2.4.4 Grain filling period

Grain filling period recorded GCA variance (σ^2g) 4.48; SCA variance (σ^2s) 2.51; average degree of dominance 0.56; predictability ratio 0.64 (moderate); heritability (h^2n) 54% (moderate) and genetic advance recorded 39.55%. Both GCA and SCA play roles in this trait, and there is a moderate predictability ratio. It means additive genetic effects contribute significantly, but non-additive effects also influence the trait. This trait is amenable to improvement via both selection and hybridization.

4.2.4.5 Number of productive tillers

Number of productive tillers was revealed in GCA variance (σ^2g) 0.04; SCA variance (σ^2s) 0.00; average degree of dominance 0.00; predictability ratio 1.00 (high); heritability (h^2n) 10% (low) and genetic advance 0.08%. This trait is highly influenced by SCA, and non-additive genetic effects dominate. The predictability ratio is high, but its low heritability means that improvement will be slow, and environmental factors will have a major impact.

4.2.4.6 Number of spikelets per spike

Number of spikelets per spike recorded in GCA variance (σ^2g) 14.33; SCA variance (σ^2s) 3.73; average degree of dominance 0.26; predictability ratio 0.79; heritability (h^2n) 59% (moderate) and genetic advance was 97.40%. The high GCA variance (14.33) indicates that additive genetic effects play a significant role in determining the number of spikelets per spike. The moderate SCA variance (3.73) shows that non-additive effects are also present but less influential than additive genetic effects. The average degree of dominance (0.26) suggests partial dominance, where the dominant allele does not completely overshadow the recessive allele. The predictability ratio of 0.79 indicates a good degree of predictability for this trait. The moderate heritability value of 59% suggests that this trait can be improved through selection. The genetic advance of 97.40% is high, meaning substantial progress can be made through breeding programs focusing on additive genetic effects.

4.2.4.7 Spike length (cm)

Spike length GCA variance (σ^2g) 4.45; SCA variance (σ^2s) 0.10; average degree of dominance 0.02; predictability ratio 0.97; heritability (h^2n) 45% (moderate) and genetic advance 10.57%. The high GCA variance (4.45) indicates that additive genetic effects play a significant role in determining spike length. The low SCA variance (0.10) suggests that non-additive genetic effects have minimal influence. The average degree of dominance (0.02) is very low, indicating that this trait exhibits little to no dominance and that the expression is mainly controlled by additive genetic factors. The high predictability ratio (0.97) further supports that additive effects are dominant. Moderate heritability (45%) suggests that genetic improvement is feasible, and the genetic advance (10.57%) indicates potential for substantial progress through selection.

4.2.4.8 Flag leaf area (cm^2)

Flag leaf area observed that, GCA variance (σ^2g) 0.00; SCA variance (σ^2s) 7.58; average degree of dominance 0.00; predictability ratio 0.00 (none); heritability (h^2n) 51% (moderate) and genetic advance scored 51.30%. This trait is highly influenced by SCA, suggesting that hybrid vigor will be important. Despite the moderate heritability, genetic improvement would be most effective through crossing different parent combinations rather than direct selection.

4.2.4.9 Chlorophyll content (SPAD meter-value)

Chlorophyll content revealed GCA variance (σ^2g) 0.00, SCA variance (σ^2s) 0.01; average degree of dominance 0.00; predictability ratio 0.00; heritability (h^2n) 42% (moderate) and genetic advance was 0.50%. The GCA variance is low (0.00), indicating that additive genetic effects contribute minimally to the chlorophyll content. The SCA variance is also low, showing that non-additive effects (such as dominance) have little influence. The average degree of dominance is 0.00, suggesting no significant dominance effect. Despite the low GCA and SCA variances, the moderate heritability indicates that genetic factors still have an impact on this trait, but environmental influences may be significant. The genetic advance is also low, indicating that improvement through selection may be limited. However, moderate progress can still be made under ideal conditions.

4.2.4.10 Number of grains per spike

Number of grains per spike recorded as GCA variance (σ^2g) 1.31; SCA variance (σ^2s) 0.00; predictability ratio 1.00; heritability (h^2n) 2.88%; and genetic advance was 3.82%. With no SCA variance and high predictability, this trait is largely influenced by additive genetic effects, but the very low heritability suggests that environmental factors might play a larger role, limiting potential for improvement.

4.2.4.11 Grain weight per spike (g)

Grain weight per spike recorded GCA variance (σ^2g) as 0.01; SCA variance (σ^2s) 0.03; average; degree of dominance 3.00; predictability ratio was 0.25; heritability (h^2n) 6% (low) and genetic advance as 0.04%. This trait has a low GCA variance, indicating that additive genetic effects are minimal. It also has a high SCA variance, suggesting that non-additive effects (likely dominance) play a significant role. The high average degree of dominance (3.00) implies over dominance, and improvement is likely to come from hybridization rather than selection. The low heritability and genetic advance values indicate that genetic improvement through selection will be limited.

4.2.4.12 1000-Grain weight (g)

1000-Grain weight observed in GCA variance (σ^2g) 1.63; SCA variance (σ^2s) 0.10**;** average degree of dominance 0.06**;** **p**redictability ratio 0.94**;** **h**eritability (h^2n) 8% (low) and genetic advance 0.15%. The high GCA variance suggests that the trait is mainly influenced by additive genetic effects, which makes it relatively easy to improve through selection. The low average degree of dominance (0.06) indicates under dominance, and additive effects will dominate over dominance effects. Despite the high predictability ratio, the low heritability suggests that environmental factors have a significant influence on this trait, limiting the genetic advance from selection.

4.2.4.13 Biological yield (g)

Biological yield was observed in GCA Variance (σ^2g) 2.70; SCA variance (σ^2s) 0.03; average degree of dominance 0.01; predictability ratio 0.98; heritability (h^2n) 26% (low) and genetic advance 3.87%. The high GCA variance indicates that additive genetic effects play a significant role in determining biological yield, making it a predictable trait for genetic improvement. The low average degree of dominance (0.01) further suggests that dominance does not play a major role in this trait. Despite the high predictability ratio, the low heritability indicates that environmental factors may influence the trait strongly, meaning improvement through selection could be slow. The genetic advance is also relatively moderate, indicating potential for some improvement with careful selection. Non-additive contribution was 1.43% and the additive contribution of biological yield (1.76%) while non-additive contribution was 1.34%.

4.2.4.14 Harvest index (%)

Harvest index revealed GCA variance (σ^2g) 2.35; SCA variance (σ^2s) 0.00; average degree of dominance 1.00; predictability ratio 1.00; heritability (h^2n) 43% (moderate) and was genetic advance 6.18%. The high GCA variance suggests that additive genetic effects are the main contributor to harvest index and that this trait is highly predictable. The average degree of dominance being 1.00 indicates complete dominance, and the trait can be improved through selection. With moderate heritability and high genetic advance, this trait shows strong potential for improvement through breeding programs focused on additive effects. Additive contribution for harvest index was 2.83%, non-additive contribution was 1.34%;

4.2.4.15 Protein content (%)

Protein content was observed in GCA variance (σ^2g) 0.00; SCA variance (σ^2s) 0.00; average degree of dominance 0.00; predictability ratio 0.00; predictability (h^2n) 0% (negligible) and genetic advance was 0.00%. The negligible GCA and SCA variances suggest that genetic factors have minimal impact on protein content. This trait is primarily influenced by environmental factors. The low heritability indicates that genetic improvement through selection is not feasible, and there is no significant genetic advance to be gained from breeding. Non-additive contribution of protein content was 8.8%; but additive contribution was 0.0%

4.2.4.16 Grain yield per plant (g)

Grain yield per plant was recorded in GCA variance ($\sigma^{2}g$) 2.35; SCA variance ($\sigma^{2}s$) 0.00; average degree of dominance 1.00; predictability ratio 1.00; heritability ($h^{2}n$) 18% (low) and genetic advance was 5.35%. The high GCA variance suggests that additive genetic effects contribute significantly to grain yield per plant and that this trait can be predicted with a high degree of accuracy. The average degree of dominance being 1.00 suggests complete dominance, and selection can improve this trait effectively. Grain yield per plant additive effect was 5.51% while non-additive contribution was 1.43%. However, the low heritability indicates that environmental factors may have a large influence, limiting the potential genetic improvement from selection.

Table 4.1.1 Analysis of variance for randomized complete block design of sixteen characters in wheat

Characters	Source of variation		
	Replications	**Treatments**	**Error**
d.f.	**2**	**66**	**132**
	F_1s	F_1s	F_1s
Days to 50% heading	1.70	176.73*	3.40
Days to maturity	0.39	88.619*	0.80
Flag Leaf Area (cm^2)	2.71*	226.05*	13.40
Grain filling period	1.507*	205.14*	19.03
Plant height (cm)	2.76*	93.10*	15.60
No. of productive tiller	0.90	11.04*	1.81
Chlorophyll content (SPAD meter-value)	2.63*	189.43**	25.30
No. of spikelet/spike	0.21	15.47*	0.44
Spike length (cm)	2.34	2.49*	4.69
No. of grain /spike	1.16	149.66**	16.30
Grain weight /spike (g)	0.17	0.86	0.34
1000 grain weight (g)	0.47	73.58**	1.07
Biological yield (g)	1.30	188.94**	2.60
Harvest index (%)	2.13	22.42**	2.42
Protein (%)	1.22	2.516*	2.44
Grain yield /plant (g)	2.51	17.07**	11.12

“*” and “” significant at 5% and 1% probability levels respectively**

Table 4.1.2 Analysis of variance for sixteen characters of L x T set of crosses (F_1s) and their parents in wheat.

Character	**Source of variation**	**Rep.**	**Treatment**	**Parent**	**Line**	**Tester**	**Line vs Tester**	**Parent vs Crosses**	**Crosses**	**Line effect**	**Tester effect**	**Line vs Tester effect**	**error**
	d.f.	**2**	**66**	**17**	**14**	**2**	**1**	**1**	**44**	**14**	**2**	**28**	**132**
Days-50% heading		11.21**	24.99	44.22	33.02	222.94	23.11	306.24	22.64	13.22**	19.33**	6.73	9.65
Plant height (cm)		12.32**	20.12**	34.12**	10.35**	213.11**	9.10*	2.22	63.43**	26.67**	12.51	23.64*	14.23**
Days to maturity		14.11**	28.44	78.23	92.99	86.17	2.99	256.23	25.23	27.71**	19.37	8.18	8.46
Grain filling period		21.94**	47.11**	76.24**	29.45**	39.12**	49.36**	25.24**	19.34**	16.94**	11.83**	53.01**	3.46
No. of productive tiller		12.37**	124.32**	281.10**	299.53**	73.22**	19.91**	356.20**	345.75**	23.21**	7.23	2.24	7.07
No. of spikelet/spike		6.68**	211.81**	205.22**	301.01**	44.25**	213.24**	66.10**	135.45**	8.45**	6.45	3.65	1.02
Spike length (cm)		4.77	8.27**	5.68**	9.31**	1.01	2.25	24.22**	6.22**	11.67	3.77	11.32	2.18
Flag leaf area (cm^2)		8.68	1.34**	5.56**	0.92**	2.28	2.14	0.94	9.66**	2.83	2.37	18.10	4.99
Chlorophyll content (SPAD meter-value)		9.24	9.36	3.68**	9.37**	0.36	2.77	340.12	2.24**	2.38	6.35	0.44	1.45
No. of grains/spike		21.25**	8.92**	23.27**	3.99**	0.24	9.77**	0.10	7.34**	1.98**	47.74	9.11	2.67**
Grain weight/spike (g)		9.23**	73.81**	20.09**	31.34**	9.31	20.44	263.63**	17.11**	2.66**	7.32	0.94	2.64
1000-grain weight (g)		6.87	17.15**	9.23**	12.11**	3.26	2.42	3.02	28.03**	5.23	23.02**	9.74	0.02*
Biological yield (g)		12.33	51.04**	19.99**	41.33**	1.99	2.65	3.66**	29.94**	15.92	5.46	20.33*	1.31
Harvest index (%)		4.34	12.01**	9.09**	19.99**	1.17	3.71	0.10	31.10**	2.34	6.17	3.9	12.04**
Protein content (%)		6.54	122.37**	23.10**	32.01**	20.45	1.44	262.41**	23.36**	23.20	3.16	1.14	3.14
Grain yield/plant (g)		2.33*	33.33**	27.23**	19.33**	17.33**	1.16	18.22	28.03**	7.09*	22.13*	11.17	11.12**

“*” and “” significant at 5% and 1% probability levels respectively**

Table 4.1.3: Estimates of components of genetic variance, average degree of dominance, predictability ratio, heritability in narrow sense, and genetic advance in per cent of mean for sixteen characters in wheat.

Components of genetic variance	**gca variance ($\sigma^2 g$)**	**sca variance ($\sigma^2 s$)**	**Average degree of dominance** $\sqrt{(\sigma^2 sca)/(2\sigma^2 gca)}$	**Predictability ratio** $2\sigma^2 g/(2\sigma^2 g + \sigma^2 s)$	$\sigma^2 A$	$\sigma^2 D$	**Heritability ($h^2 n$) %**	**Genetic advance in per cent of mean**
Characters	**F_1s**	**F_1s**	**F_1s**	**F_1s**	**F_1s**	**F_1s**	**F_1s**	**F_1s**
Days to 50% heading	0.72	0.00	0.00	1.00	127.90	125.13	46	27.90
Days to maturity	0.00	0.00	0.00	0.00	65.39	65.39	42	65.39
Flag Leaf Area (cm^2)	0.00	7.58	0.00	0.00	151.30	130.60	51	51.30
Grain filling period	4.48	2.51	0.56	0.64	39.55	15.58	54	39.55
Plant height (cm)	0.13	0.02	0.15	0.86	0.32	0.39	25	0.32
No. of productive tiller	0.04	0.00	0.00	1.00	0.08	0.46	10	0.08
Chlorophyll content (SPAD meter-value)	0.00	0.01	0.00	0.00	0.50	0.46	42	0.50
No. of spikelet/spike	14.33	3.73	0.26	0.79	197.40	132.60	59	97.40
Spike length (cm)	4.45	0.10	0.02	0.97	10.57	0.00	45	10.57
No. of grain /spike	1.31	0.00	0.00	1.00	2.88	3.82	24	2.88
Grain weight /spike (g)	0.01	0.03	3.00	0.25	0.04	0.00	6	0.04
1000 grain weight (g)	1.63	0.10	0.06	0.94	0.15	0.49	8	0.15
Biological yield (g)	2.70	0.03	0.01	0.98	3.87	0.00	26	3.87
Harvest index (%)	2.35	0.00	0.00	1.00	6.18	2.93	43	6.18
Protein (%)	0.00	0.00	0.00	0.00	0.00	0.49	0	0.00
Grain yield /plant (g)	2.35	0.00	0.00	1.00	5.35	2063	18	5.35

4.3.1 Estimates of general combining ability (GCA) effects for combined locations

4.3.1.1 Days to 50% heading (DH)

The earliest DH (shorter heading duration) is observed in WB-02 with -0.30136 (Rank 15). BHU-31 and DBW-173 with similar negative values and ranks of 14 and 12, respectively. The latest DH (longer heading duration) is observed in DBW-222 with 0.301763 (Rank 1). HD-3117 (line10) and PBW-757 with positive DH values and ranks of 2 and 3. Rank Consistency lines like BHU-25 (line1) and PBW-550 maintain moderate DH values, indicating relatively stable heading times across environments. DBW-222 consistently ranks high in heading duration, suggesting a later heading genotype, potentially beneficial in environments with longer growing seasons. Tester effects reported that all testers (PBW ZN1, PBW-343, HD-3326) exhibit consistent DH values (83.38519) without significant variation. This consistency implies that tester choice might not heavily influence DH under the given conditions.

4.3.1.2 Plant height (PH) (cm)

The tallest genotypes was HD-3721 which has the highest PH value (4.605716), ranking 1st, followed by BHU-31 and WB-02. Taller plants can have advantages in biomass production but may be more prone to lodging. While shortest genotypes was DBW-222 has the lowest PH (-4.89947), ranking 15th, followed by PBW-757 and CSW-18. Shorter plants are generally more resistant to lodging.

4.3.1.3 Days to maturity (DM)

Present investigation revealed that, the earliest maturing genotype was BHU-25 matures the earliest with DM value of 7.07407, ranking 1st. Early-maturing varieties are beneficial in regions with shorter growing seasons. Whereas the latest maturing genotype was HD-3721 with DM of -4.37037, ranking 15th. Late-maturing varieties may benefit from extended grain-filling, potentially improving yield.

4.3.1.4 Grain filling period (GFP)

The finding revealed that, the longest grain filling period recorded in genotype WB-02 has the longest GFP (2.336642), ranking 1st, indicating it may have a higher grain weight and better quality. HD-3721 and PWB-725 also have high GFP values. However, shortest grain Filling

Period recorded in DBW-222 has the shortest GFP (-2.23317), ranking 15th, which may reduce grain development.

4.3.1.5 Number of productive tillers (NPT)

Results on NPT revealed that genotype PBW-82 has the highest NPT (0.325522), ranked 1st, indicating a greater yield potential as it produces more productive tillers. While minimum NPT recorded in BHU-25 (-0.71235), ranking 15th, which may limit its yield potential.

4.3.1.6 Number of spikelet per spike (NSS)

PBW-757 genotype has the highest NSS (0.279104), ranking 1st, suggesting a high grain-bearing capacity. Whereas lowest NSS recorded in PWB-725 has the lowest NSS (-0.18575), ranking 15th, which may limit the number of grains per spike and affect yield.

4.3.1.7 Spike length (cm)

The highest GCA effect for SL is observed in CSW-18 with a value of 5.980954 and a rank of 1, indicating a strong positive contribution to this trait. PBW-757 follows with a GCA effect of 2.83065, ranked 2, also suggesting significant positive influence. The lowest GCA effect for SL is seen in BHU-31 with a value of 0.084198, ranked 7, indicating a minimal positive contribution. Negative contributions to SL are noted in DBW-173 (-0.36247), WB-02 (-0.30395), and HD-3721 (-0.27395). Among the testers, PBW-343 exhibits the highest GCA effect of 1.569494, ranked 1, which suggests it contributes positively to increasing SL. PBW ZN1 has a moderate GCA effect of -0.10511, ranked 2. HD-3326 shows the lowest effect with -1.46438, ranked 3, indicating it negatively impacts the SL trait.

4.3.1.8 Flag leaf area (cm^2)

With regards to flag leaf area the genotype CSW-18 has the largest FLA (5.980954), ranking 1st. A larger FLA enhances photosynthetic efficiency, supporting grain development. However, the smallest flag leaf area recorded in BHU-31 has the smallest FLA (-7.26192), ranking 15th, which may restrict photosynthetic potential and affect yield.

4.3.1.9 Chlorophyll content (CLC)

The highest CLC was found in genotype DH-3086 (4.760765), ranking 1st, indicating high photosynthetic efficiency which could support better biomass and grain production but the lowest CLC was recorded in BHU-25 (-4.4696), ranking 15th, which may indicate a limitation in photosynthetic potential and, consequently, a reduced yield capacity.

4.3.1.10 Number of grains per spike

Genotype DBW-222 shows the highest NGS value (1.606142, Rank 1), suggesting its potential for producing more grains per spike. CSW-18 ranks second with 1.367705, followed by WB-02 at 1.161813 (Rank 3). Poor performers recorded in PBW-822 has the lowest NGS (-1.30612, Rank 15), followed by BHU-31 (-1.06561, Rank 14). These lines may have limitations in grain production under the given environmental conditions. Lines with lower NGS values (PBW-822 and BHU-31) also exhibit poor performance in related traits, indicating overall lower productivity. Tester effects for all testers (PBW ZN1, PBW-343, HD-3326) exhibit consistent NGS values (46.51096), indicating minimal variation in their contribution to NGS.

4.3.1.11 Grain Weight per Spike (g)

It has been revealed that genotype PWB-725 ranks 1st with GWS of 0.18398, which is beneficial for grain yield potential as it implies higher individual spike productivity however, lowest GWS recorded in CSW-18 ranks 15th with a GWS of -0.1464, indicating less productive spikes which may impact overall grain yield.

4.3.1. 12 1000-grain weight (g)

Results on 1000GW indicated that genotype PBW-757 ranks 1st with 1000GW of -0.64711, indicating it has relatively heavier grains, which is generally favorable for grain quality. Whereas the lowest 1000GW recorded in HD-3721 ranks 15th with a 1000GW of -0.64304, suggesting a lower grain weight, which might impact market value and yield.

4.3.1.13 Biological yield (BY)

PWB-725 has the highest BY (3.779852), ranking 1st, which points to a high overall biomass production and potentially higher grain yield while lowest reported in PBW-822 ranks 15th with a BY of -4.40015, indicating it has a low biomass yield, which could negatively impact the overall grain yield.

4.3.1.14 Harvest index (%)

Results revealed that genotype DBW-173 has the highest HI (2.326054), ranking 1st, which is advantageous as it indicates a high proportion of the biomass is allocated to grain, improving yield efficiency. Lowest HI reported in BHU-25 ranks 15th with an HI of -3.02, indicating a lower efficiency in converting biomass to grain yield.

4.3.1.15 Protein content (PC)

DBW-173 has the highest PC (0.221605), ranking 1st, which is valuable for nutritional quality and marketability and lowest PC recorded in CSW-18 (line14) ranks 15th with a PC of 0.020124, which may reduce its market appeal for nutritional quality.

4.3.1.16 Grain yield per plant (g)

Results reported highest GYP in DH-3086 (1.968039), ranking 1st, suggesting that it has the highest yield potential among the genotypes. Lowest GYP found in BHU-25 ranks 15th with a GYP of -2.15445, indicating a low yield potential, which may limit its usefulness for grain production.

Table 4.2.1: Estimates of general combining ability (GCA) effects of 15 lines and three tester of different characters for combined locations

GENOTYPES	DH	RANK	PH	RANK	DM	RANK	GFP	RANK	NPT	RANK	NSS	RANK	SL	RANK	FLA	RANK
BHU-25 (LINE1)	-0.10	10	-2.23	14	7.07	1	2.27	2	-0.71	15	-0.08	10	-0.20	12	-0.02	8
WB-02 (LINE2)	-0.30	15	3.50	3	2.67	5	2.34	1	-0.43	14	-0.08	11	-0.30	14	-0.92	13
BHU-31 (LINE3)	-0.26	14	3.83	2	-1.78	9	0.98	5	-0.10	12	-0.15	14	0.08	7	-7.26	15
HD-3721 (LINE4)	-0.03	7	4.61	1	-4.37	15	2.12	4	-0.10	11	-0.07	9	-0.27	13	-0.36	10
PWB-725 (LINE5)	0.11	6	-0.35	7	-2.04	11	2.25	3	-0.01	10	-0.19	15	-0.18	11	0.88	5
CRD GEHNU1 (LINE6)	-0.06	8	1.76	4	-2.70	12	-0.85	11	0.18	4	-0.11	13	0.14	5	-3.16	14
PBW-550 (LINE7)	-0.17	13	1.70	5	-1.26	8	-0.85	10	0.13	7	-0.03	8	0.10	6	0.14	7
PBW-677 (LINE8)	-0.10	9	0.03	6	-0.41	7	-1.85	14	0.17	5	0.09	4	-0.01	8	1.04	4
PBW-822 (LINE9)	0.17	5	-1.49	11	4.41	2	-0.40	8	0.33	1	0.10	3	-0.04	9	0.30	6
HD-3117 (LINE10)	0.28	2	-0.59	8	4.30	3	-1.61	13	0.16	6	-0.10	12	0.15	4	1.66	3
DBW-173 (LINE11)	-0.15	12	-1.35	10	3.37	4	0.31	6	0.28	2	-0.02	7	-0.36	15	-0.49	12
DH-3086 (LINE12)	-0.12	11	-1.08	9	-0.04	6	-0.27	7	-0.25	13	0.09	5	0.45	1	-0.22	9
DBW-222 (LINE13)	0.30	1	-4.90	15	-1.82	10	-2.23	15	0.27	3	0.19	2	0.28	2	-0.41	11
CSW-18 (LINE14)	0.19	4	-1.73	13	-3.22	13	-0.81	9	0.08	8	0.06	6	-0.06	10	5.98	1
PBW-757 (LINE15)	0.24	3	-1.70	12	-4.19	14	-1.39	12	0.01	9	0.28	1	0.22	3	2.83	2
SE(gca for line)	3.72		13.97		13.78		2.46		6.37		4.72		1.78		8.42	
SE(gi-gj) for line)	2.68		19.75		19.49		3.48		9.01		6.68		2.51		11.91	
Tester																
PBW ZN1 (TESTER 1)	83.39	2	0.56	1	-0.04	2	0.28	2	0.02	1	0.07	1	-0.11	3	-0.11	2
PBW-343 (TESTER 2)	83.39	2	-0.93	3	-3.16	3	-1.53	3	-0.01	2	0.03	2	0.18	1	1.57	1

HD-3326 (TESTER 3)	83.39	2	0.37	2	3.19	1	1.26	1	-0.01	3	-0.10	3	-0.07	2	-1.46	3
SE(gca for tester)	4.77		6.25		6.16		1.10		2.85		2.11		0.79		3.77	
SE(gi-gj) for tester	8.33		8.83		8.72		1.56		4.03		2.99		1.12		5.33	
SE(sij-skl) for tester	29.63		34.21		33.76		6.03		15.60		11.57		-0.20		20.63	

Note: Ranking is in ascending order (i.e. 1 is the best followed by 2 on and on). Days to heading (DH), Plant height (PH), Days to maturity (DM), Grain-filling period (GFP), Number of productive tiller (NPT), Number of spikelet/spike (NS/S), Spike length (cm) (SL), and Flag leaf area (FLA)

Table 4.2.1: contd.

GENOTYPES	CLC	RANK	NGS	RANK	GWS	RANK	1000GW	RANK	BY	RANK	HI	RANK	PC	RANK	GYP	RANK
BHU-25 (LINE1)	-4.47	15	0.90	4	8.07	10	0.13	6	-2.07	13	-3.02	15	-0.17	12	-2.15	15
WB-02 (LINE2)	0.69	6	1.16	3	-0.13	14	0.39	7	0.07	8	-1.30	13	0.14	6	-1.09	14
BHU-31 (LINE3)	-2.34	14	-1.07	14	-0.08	13	0.05	9	2.78	2	-0.51	10	0.10	8	-1.07	13
HD-3721 (LINE4)	0.49	7	-0.29	10	0.09	2	-0.64	15	1.98	4	-1.70	14	0.11	7	-0.60	11
PWB-725 (LINE5)	2.06	4	-0.20	7	0.18	1	0.26	11	3.78	1	-0.56	11	-0.15	1	-0.60	10
CRD GEHNU1 (LINE6)	2.60	2	-1.02	13	0.03	6	0.27	2	0.09	7	-0.19	8	-0.24	9	-0.45	8
PBW-550 (LINE7)	-0.78	9	-0.26	9	0.03	5	0.59	12	-0.42	10	-0.18	7	-0.19	13	0.45	6
PBW-677 (LINE8)	-1.62	12	-0.52	11	0.03	7	0.09	10	-1.40	12	0.58	5	0.08	10	-0.66	12
PBW-822 (LINE9)	-2.22	13	-1.31	15	0.05	4	-0.01	14	-4.40	15	1.16	4	0.05	4	1.14	3
HD-3117 (LINE10)	-1.06	10	0.13	6	0.02	9	-0.68	3	1.44	5	-0.58	12	0.08	2	-0.51	9
DBW-173 (LINE11)	-0.78	8	-0.76	12	-0.05	11	-0.12	8	-1.40	11	2.33	1	0.22	5	0.61	5
DH-3086 (LINE12)	4.76	1	-0.22	8	-0.06	12	0.55	13	-0.22	9	-0.39	9	0.02	3	1.97	1
DBW-222 (LINE13)	1.51	5	1.61	1	0.02	8	-0.14	5	1.34	6	0.50	6	-0.17	11	1.09	4
CSW-18 (LINE14)	-1.08	11	1.37	2	-0.15	15	-0.06	4	-3.96	14	2.06	2	0.02	15	0.39	7

PBW-757 (LINE15)	2.24	3	0.47	5	0.08	3	-0.65	1	2.39	3	1.82	3	0.10	14	1.47	2
SE(gca for line)	13.85		2.33		6.80		2.61		9.41		1.33		0.32		1.06	
SE(gi-gj)for line)	19.59		0.64		9.62		3.69		13.31		0.84		0.45		1.50	
Tester																
PBW ZN1 (TESTER 1)	-0.21	3	46.51	2	-0.04	2	0.04	1	0.56	1	0.14	3	-0.59	3	0.40	1
PBW-343 (TESTER 2)	0.32	1	46.51	2	-3.16	3	0.00	2	-0.93	3	0.20	1	0.56	1	-0.33	3
HD-3326 (TESTER 3)	-0.11	2	46.51	2	3.19	1	-0.04	3	0.37	2	0.79	2	0.03	2	-0.07	2
SE(gca for tester)	1.17		3.21		6.16		3.04		6.25		-3.02		6.20		4.21	
SE(gi-gj)tester	1.65		6.95		8.72		4.30		8.83		-1.30		8.76		5.95	
SE(sij-skl)tester	6.38		20.05		33.76		16.66		34.21		-0.51		33.93		23.05	

Note: Ranking is in ascending order (i.e. 1 is the best followed by 2 on and on). Chlorophyll content (CLC), number of grains per spike (NGS), Grain weight/spike (GW/S), 1000-grain weight (g) (1000-GW), Biomass yield (BY), Harvest index (HI %), Protein content (PC), and Grain yield/plant (GY/P)

4.3.2 Estimates of general combining ability effects for GCA across three locations (E1, E2, & E3)

The Standard Errors (SE) values for each parameter indicate that some traits such as BY, GWS, and HI show higher SE values, suggesting more variability among genotypes for these traits. However, the lower SE values for CLC and PC suggest more consistency in these measurements.

4.3.2.1 Days to 50% heading

The results found that the genotype PBW-822 shows the earliest heading in E1 (-4.400) and is ranked 15, suggesting it is well-suited for environments where early flowering is advantageous. CSW-18 has early heading values in E1 (-3.954) and E2 (-3.972), ranking 14th in both environments. Late heading genotypes DH-3086 has the latest heading in E2 with a value of 6.143, ranking 1st in E2, indicating late flowering in that specific environment. BHU-25 is consistently late across all locations, with values of 4.946 in E2 and -4.7 in E3 (rank 15 in both E2 and E3). The top genotypes by ranking in each location such as E1 PWB-725 (rank 1, 3.779), PBW-757 (rank3, 2.388) while E2 DH-3086 (rank 1, 6.143), CRD GEHNU1 (line6) (rank 2, 3.98763) and E3 DBW-173 (rank1, 2.852), PBW-677 (rank2, 2.742).

4.3.2.2 Plant height (cm)

The tall genotypes was PBW-550 shows the highest plant height across all environments, with values of 1.833926 in E1, 2.468963 in E2, and 2.703556 in E3. While genotypes CRD GEHNU1 ranks high across all environments (rank 2 in E1, rank 3 in E2, rank 2 in E3), with significant values, suggesting a strong potential for growth across different locations. However, short genotypes were recorded in BHU-25 is among the shortest genotypes across all environments, with values of -3.30163 in E1, -7.05437 in E2, and -1.30422 in E3, ranking it among the shortest plants, which may help in environments prone to lodging. HD-3117 also ranks low across locations, especially in E3 where it ranks 15th with a height of -3.45422. Consistent and stable height genotypes was found in genotype PBW-757 ranks consistently high with heights of 2.065037 in E1, 4.066741 in E2, and -1.63978 in E3, indicating a balanced height across varying environments. But the top genotypes by ranking in each location such as E1 PBW-757 (rank 1, 2.065037), CRD

GEHNU1 (rank 2, 1.931704), E2 BHU-31 (line4) (rank 1, 4.917852), PBW-757 (rank 2, 4.066741) and E3 PBW-550 (line7) (rank 1, 2.703556), CRD GEHNU1 (rank 2, 2.518).

4.3.2.3 Days to 50% maturity

Early maturing genotypes such as WB-02 is one of the earliest maturing genotypes across locations, ranking 1st in E3 (4.8) and showing relatively early maturity in E1 (2.851852, rank 4) and PBW-757 ranks consistently low in terms of days to maturity, especially in E1 (-3.81481, rank 13) and E3 (-2.86667, rank14), indicating a tendency to mature early. However, late maturing genotypes like BHU-25 is among the latest maturing genotypes, ranking 1st in E1 (9.962963) and 2nd in E2 (8.237037). This suggests adaptability in terms of reaching maturity across different environmental conditions and DH-3086 shows relatively moderate values, ranking 5th in E1 (2.740741) and 8th in E3 (-1.53333), indicating a moderate maturity rate. But top maturity genotypes by ranking in each location recorded that E1 the genotype BHU-25 (rank 1, 9.962963), DBW-173 (rank 2, 6.407407) while at E2 genotype HD-3117 (rank 1, 9.903704), BHU-25 (rank 2, 8.237037) and at E3 genotype WB-02 (rank 1, 4.8), PBW-822 (rank 2, 3.577).

4.3.2.4 Grain filling period

Long grain filling period genotypes BHU-25 has one of the longest grain filling periods across environments, ranking 1st in E1 (5.407407) and 2nd in E2 (4.325926). While short grain filling period genotypes CSW-18 has a very short grain filling period across all environments, ranking 15th in E1 (-7.48148), 11th in E2 (-1.11852), and 9th in E3 (-0.91111). BHU-31 also has a shorter grain filling period, with values of -7.03704 in E1 and 4.755556 in E3 (rank 3). Stable grain filling period genotypes was recorded in DBW-173 shows stable rankings, 2nd in E1 (4.296296), 5th in E2 (3.548148), and 4th in E3 (3.755556), suggesting a consistent grain filling period across locations. PBW-822 also demonstrates a relatively stable grain filling period, ranking 6th in E1 (-3.92593), 1st in E2 (1.437037), and 7th in E3 (7.533333). Top grain filling genotypes by ranking in each location revealed that E1 BHU-25 (rank1, 5.407407), DBW-173 (rank 2, 4.296296) while E2 HD-3117 (rank 1, 5.548148), BHU-25 (rank 2, 4.325926) and E3 PBW-677 (line8) (rank1, 8.755556), PBW-822 (rank 2, 7.333).

4.3.2.5 Number of productive tillers per plant

Productive tillers are essential for wheat yield as each tiller potentially contributes to spike production revealed that genotype DBW-222 ranks 1st in E1 with a high tiller count of 1.130074, followed by stable middle-ranking performances in E2 and E3, indicating strong productivity at E1 but moderate adaptability elsewhere and WB-02 ranks 1st in E2 with a value of 0.889259, showing an environment-specific boost in productive tillers, though it falls to moderate positions in E1 and E3. Also genotype CSW-18 is a standout in E3, ranking 1st (0.576304), and also shows a good performance across E2 (4th), suggesting a general adaptability across environments for tiller production. Lower performers was recorded in genotype BHU-25 remains the lowest across all locations (ranking 15th with negative values), indicating poor tiller production and adaptability. PBW-677 also consistently ranks low in tiller count, especially at E1 and E2, suggesting limited potential for productive tillering across tested environments. Genotype performance variability, several genotypes, such as PBW-757, show environment-specific responses. Ranking 2nd in E1 (1.027852) but dropping to 9th in E3, PBW-757 highlights the influence of environment on tiller productivity.

4.3.2.6 Number of spikelets per spike

Results for number of spikelet per spike recorded that, PBW-550 shows the highest values at E1 and E2, ranking 1st in both locations (values 1.050519). However, at E3, it drops to 8th position with a much lower value of 0.039778, suggesting that its productivity in terms of spikelets is environment-dependent. CSW-18 ranks 1st at E3 with a value of 0.908667, indicating that it is well-suited to the conditions at E3. It maintains a relatively stable rank across E1 and E2, placing around 9th. PWB-725 performs consistently well across E1 and E2, ranking 2nd in both locations with values of 0.672741, although it falls to 7th place in E3. BHU-25 ranks last (15th) across all three locations, with values dropping significantly at E3 (-1.03689), suggesting limited adaptability and poor spikelet productivity. PBW-822 also ranks low at E1 and E2, showing poor adaptability across environments.

4.3.2. 7 Spike length (cm)

The highest SL values across locations were observed in DH-3086 at E3 with 0.640963 (Rank 1) and E2 with 0.721704 (Rank 1). PBW-757 at E1 with 0.628815 (Rank 1). The lowest SL values are observed for BHU-25 at E1 with -0.71452 (Rank 15). HD-3721 at E3 with -0.72904 (Rank 15). WB-02 at E2 with -0.51274 (Rank 14). Stability across locations in DH-3086 shows consistent performance across all locations with high SL values, ranking 1st or close in each. BHU-25 and HD-3721 consistently show low SL values across locations, indicating poor performance for this trait. Tester SL effects, the best tester for SL is PBW-343, showing a positive GCA effect at E2 (0.329037, Rank 1) and E3 (0.270519, Rank 1). PBW ZN1 performs well at E1 (0.10437, Rank 1) but negatively at other locations. HD-3326 (tester 3) has negative contributions at E1 (-0.05185) and E3 (-0.13681), suggesting it is less effective for improving SL.

4.3.2. 8 Number of grain per spike

The highest NG/S values across locations are observed for PBW-822 (line9) at E1 with 1.690519 (Rank 1). PWB-725 (LINE1) at E2 with 2.312444 (Rank 1). PBW-677 at E3 with 6.754148 (Rank 1). The lowest NG/S values are observed for: DBW-173 at E1 with -1.35059 (Rank 15). PBW-822 (line9) at E3 with -4.03919 (Rank 15). DH-3086 at E2 with -2.072 (Rank 14). Stability across locations for CRD GEHNU1 and PBW-550 demonstrate consistent performance across locations, ranking in the top five in most environments. This indicates their stability and adaptability for NG/S. PBW-822 (line9) and DH-3086 show highly variable performance, with strong values in one location but poor values in others. Tester NG/S effects for HD-3326 ranks 1st at E1 with the highest NG/S value of 44.36111, indicating its strong ability to improve NG/S in this environment. PBW ZN1 has consistent performance across environments but lower NG/S values than HD-3326 (tester 3) and PBW-343. PBW-343 shows the best performance at E2 and E3, with NG/S values of -0.67748 and 0.466148, respectively.

4.3.2.9 Flag leaf area (cm^2)

Flag leaf area was highest in DBW-173 ranks 1st in E3 (0.469556) and 2nd in E1 (0.211778), indicating strong adaptability and a consistent capacity to maintain larger flag leaf areas across environments followed by PBW-757 performs exceptionally well in E2, ranking 1st with a value of 0.229037, and remains competitive across other environments with 4th in E1 and 9th in E3. Its performance in E2 makes it a promising genotype for maximizing flag leaf area under those conditions and WB-02 ranks 3rd in E2 and E3, with a relatively high flag leaf area, indicating that it maintains a productive leaf area in these environments. While low performing genotype was CRD GEHNU1 consistently ranks among the lowest across all three locations (ranking 15th in E1, 14th in

E2, and 12th in E3), with a notably negative flag leaf area value (-0.39489 in E3), showing limited potential for flag leaf area maintenance followed by PBW-550 ranks last in E3 with -0.52044, also showing a decline across locations, which indicates that its flag leaf area is highly susceptible to environmental conditions.

4.3.2.10 Chlorophyll content

Revealed that, PBW-757 ranks highest in E1 and performs consistently well in E2 (ranking 6th) with chlorophyll content values of 4.131 at E1 and 3.077 at E2. DH-3086 has the highest chlorophyll content at E2 and E3 (values: 10.36044 and 5.235185, respectively), making it the top-performing genotype in these two environments. However, it ranks moderately (10th) at E1, suggesting that while it excels in certain conditions, it may be sensitive to specific environmental factors at E1. CRD GEHNU1 ranks among the top three in both E1 (3.008889) and E2 (5.349333), indicating robust chlorophyll content in these locations but a notable decrease at E3 (ranking 9th). Whereas low performance were recorded in BHU-25 ranks lowest across all three locations, particularly at E3, with a chlorophyll content value of -6.58815.

4.3.2.11 Grain weight per spike (g)

Grain weight per spike is a measure of the yield of each spike, directly related to the plant's productivity. Higher values indicate more grain weight per spike, suggesting better yield potential. PBW-725 ranks highest in E3 (0.342519) and consistently performs well across other locations (ranked 4th in E1 and 3rd in E2). This consistent high performance demonstrates its potential to maintain good productivity across different environments followed by DBW-222 ranks 2nd in E3 with a value of 0.27363, although it performs lower in other environments. This performance suggests it may be better suited for environments similar to E3 and PBW-757 achieves the highest ranking in E1 with 0.236741, indicating strong productivity in this specific location, even though it experiences fluctuations across other environments. While BHU-31 ranks last in E3 (-0.26748) and has inconsistent performance in other locations, indicating a lack of adaptability and potential difficulty in producing high yields and WB-02 ranks lowest in E1, suggesting that this genotype is less capable of maximizing yield per spike under E1 conditions.

4.3.2.12 1000-grain weight (g)

Results recorded that genotype DH-3086 ranks high across all three locations, with a maximum value of 0.891037 in E3 and consistently ranks within the top three at E1 (2nd) and E2 (3rd). This indicates its stable grain weight production across diverse environments, which is beneficial for consistent yield. CRD GEHNU1 (line6) has the highest value in E1 (0.431778), ranking 1st, and maintains moderate to high values in E3 (ranked 7th). However, it drops in rank at E2 (10th), suggesting that while it performs well in some locations, it may be sensitive to specific environmental factors at E2. PBW-550 shows high performance across locations, ranking 1st in E2 (0.786963) and maintaining top 6 positions in E1 and E3. This consistency indicates a strong ability to produce larger grains in varied conditions. However, DBW-173 ranks last in E1 and performs poorly in E3, with values indicating limited potential for producing larger grains followed by PBW-757 experiences a drastic drop in performance at E3, ranking last (-2.13674) despite a higher performance at E1 (5th rank).

4.3.2.13 Biological yield (g)

Biological yield for PWB-725 ranks 1st in E1 with a high yield value of 3.779852. It also performs well in E3, ranking 6th with 0.702222, though it drops significantly in E2 (13th). This indicates that PWB-725 may thrive better under the environmental conditions at E1 and E3. DH-3086 ranks 1st in E2 with a biological yield value of 6.143185, showing exceptional performance in this location. However, it ranks much lower in E1 and E3, suggesting its yield might be highly environment-dependent, thriving specifically in E2 conditions. PBW-757 shows high biological yield across multiple locations, ranking 3rd in E1 and 4th in E3. This indicates its ability to maintain substantial biomass production across diverse environments, making it a strong candidate for consistent growth. Whereas PBW-822 ranks last in E1 and shows poor performance across all locations, indicating limited adaptability and low biomass production potential followed by BHU-25 performs poorly, ranking among the bottom genotypes across locations, especially in E2 and E3, which suggests it may not be suitable for achieving high biomass production in these environments.

4.3.2.14 Harvest index (%)

Results revealed that, PBW-757 achieves the highest Harvest Index in E1 (2.065037) and also performs well in E2, ranking 2nd. This indicates that PBW-757 effectively allocates biomass to grain yield, especially under E1 conditions. CRD GEHNU1 ranks 2nd in E1 and performs consistently across all locations (ranked 3rd in E3), suggesting a stable ability to convert biomass into grain yield in different environments. PBW-550 ranks 1st in E3 with the highest Harvest Index value (2.703556) and performs well in other locations, ranking within the top 6, which indicates both efficiency and adaptability in resource allocation. However, HD-3117 (line10) shows very low values and ranks last in E3, indicating poor efficiency in grain production. This trend across locations suggests limited potential for this genotype in terms of yield efficiency. WB-02 ranks low in both E1 and E3 for harvest index, although it performs moderately well in E2 (5th).

4.3.2.15 Protein content

HD-3117 shows the highest protein content in E1 (0.585111) and performs moderately across other locations. This consistent performance makes it a strong candidate for breeding focused on protein content, particularly in environments similar to E1. PBW-757 ranks first in E2 (0.229037) and 4th in E1, though its protein content is lower in E3. It performs well for both yield and protein content, especially in E1 and E2. DBW-173 has the highest protein content in E3 (0.469556) and ranks 2nd in E1. PBW-550 ranks low in all locations, with the lowest protein content in E3 (-0.52044). Despite its good yield, PBW-550 may not be ideal if protein content is a primary breeding goal. Statistical error (SE) analysis for GCA across three locations (E1, E2, & E3). SE (gca) and SE (gi-gj) values for both traits indicate the relative stability and variability of the genotypes across locations. Lower SE values, such as 0.29004 for yield in E2, suggest less variability, making it easier to identify stable performers. The higher SE (sij-skl) values, like 1.394098 for yield in E1, imply greater genotype-environment interaction, particularly in E1 for yield. For protein content, SE (sij-skl) values like 0.435927 in E1 reveal high environmental influence, meaning genotype performance in protein content may vary significantly depending on environmental factors.

4.3.2.16 Grain yield per plant (g)

Grain yield for PBW-757 ranks 1st in E1 with the highest yield (4.303259) and also performs well in E3 (5th). Although it ranks 8th in E2, PBW-757’s high yield in E1 and E3 suggests it is a strong performer under certain environmental conditions. HD-3721 (line5) consistently ranks high, with the highest yield in E2 (4.760667) and the second-highest in E3 (3.853333). Its stability across locations makes it an attractive candidate for environments similar to E2. PBW-550 ranks 2nd in E1 and 3rd in E3, indicating it has reliable productivity across different conditions. While low performance were recorded in BHU-25 ranks among the lowest in all locations (15th in both E1 and E3). This low yield across different environments suggests that BHU-25 may not be suitable for environments similar to those of E1, E2, or E3. PBW-677 also performs poorly, with ranks of 9th, 14th, and 11th across E1, E2, and E3, respectively. Its low values indicate low yield potential, especially under the conditions at E2. Results on grain yield revealed that PBW ZN1 shows the highest yield in E3 and performs consistently across all locations, making it a reliable standard for yield.PBW-343 ranks 2nd in E3, providing a good balance in yield performance across different locations. HD-3326 ranks lower in E1 and E3 for yield, suggesting it may be less suitable as a high-yield benchmark under those conditions. Protein Content PBW-343 ranks highest in E3, while PBW ZN1 is the highest in E1. These testers show location-specific advantages, helping validate protein content variability across genotypes. HD-3326 shows moderate protein content across locations, which could serve as a stable benchmark for protein quality assessment.

Table 4.2.2: Estimates of general combining ability effects on different traits in wheat across three (E1-E3) locations

	Days to 50% heading (DH) across locations (E1, E2 & E3)						**Plant height (PH) across locations (E1, E2 & E3)**					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	-2.07	13	4.95	15	-4.70	15	-3.30	15	0.83	15	-1.30	10
WB-02 (LINE2)	0.07	8	1.60	4	-0.25	10	-2.50	13	0.83	5	-2.23	14
BHU-31 (LINE3)	2.78	2	-1.84	12	-0.77	12	1.65	4	0.83	1	2.41	4
HD-3721 (LINE4)	1.98	4	2.19	3	0.12	9	0.98	6	0.83	12	0.27	7
PWB-725 (LINE5)	3.78	1	-2.21	13	0.70	6	0.26	7	0.83	4	-1.72	13
CRD GEHNU1 (LINE6)	0.09	7	3.99	2	0.68	7	1.93	2	0.83	3	2.52	2
PBW-550 (LINE7)	-0.42	10	-0.16	9	-0.28	11	1.83	3	0.83	6	2.70	1
PBW-677 (LINE8)	-1.40	12	1.39	5	2.74	2	-2.60	14	0.83	13	0.33	6
PBW-822 (LINE9)	-4.40	15	-1.46	10	-2.48	13	-0.02	10	0.83	11	0.20	8
HD-3117 (LINE10)	1.44	5	-1.70	11	0.58	8	-0.01	9	0.83	14	-3.45	15

DBW-173 (LINE11)	-1.40	11	0.52	6	2.85	1	-0.97	11	0.83	8	-0.69	9
DH-3086 (LINE12)	-0.22	9	6.14	1	-3.30	14	-1.17	12	0.83	10	1.81	5
DBW-222 (LINE13)	1.34	6	0.18	8	1.59	3	1.59	5	0.83	9	-1.66	12
CSW-18 (LINE14)	-3.96	14	-3.97	14	0.97	5	0.26	8	0.83	7	2.45	3
PBW-757 (LINE15)	2.39	3	0.26	7	1.53	4	2.07	1	0.83	2	-1.64	11
SE(gca for line)	1.23		0.49		0.18		1.03		0.83		0.50	
SE(gi-gj)for line)	1.74		0.70		0.25		1.45		0.83		0.71	
Tester												
PBW ZN1 (TESTER 1)	0.40	1	-0.15	2	0.10	2	-0.06	2	0.83	3	1.00	1
PBW-343 (TESTER 2)	-0.33	3	-0.68	3	-0.66	3	0.54	1	0.83	1	-0.21	2
HD-3326 (TESTER 3)	-0.07	2	0.83	1	0.56	1	-0.49	3	0.83	2	-0.79	3
SE(gca for tester)	0.55		0.22		0.08		0.46		0.83		0.22	
SE(gi-gj) for tester	0.78		0.31		0.11		0.65		0.83		0.32	
SE(sij-skl) for tester	3.02		1.21		0.44		2.52		0.83		1.22	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

	Grain filling period (GFP) across 3 locations (E1, E2 & E3)						Days to 50% maturity DM across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	5.41	1	4.33	2	1.98	6	9.96	1	8.24	2	3.02	3
WB-02 (LINE2)	3.63	3	-8.23	15	-3.69	12	2.85	4	0.35	6	4.80	1
BHU-31 (LINE3)	-7.04	14	3.88	4	4.76	3	-2.48	8.5	-2.54	10.5	-0.31	8
HD-3721 (LINE4)	-2.48	12	0.22	7	0.87	7	-6.48	15	-7.21	15	0.58	5

PWB-725 (LINE5)	3.19	4.5	-3.67	13	-11.02	15	-2.48	8.5	-2.54	10.5	-1.09	10
CRD GEHNU1 (LINE6)	0.85	8	-0.67	9	-4.36	13	-3.82	12	-1.65	9	-2.64	13
PBW-550 (LINE7)	2.07	6	-2.79	12	-6.47	14	-2.82	10	0.02	7	-0.98	9
PBW-677 (LINE8)	-0.59	9	3.88	3	8.76	1	-4.48	14	3.13	4	0.13	7
PBW-822 (LINE9)	-3.93	13	1.44	6	7.53	2	6.19	3	3.46	3	3.58	2
HD-3117 (LINE10)	3.19	4.5	5.55	1	2.20	5	0.85	6	9.90	1	2.13	4
DBW-173 (LINE11)	4.30	2	3.55	5	3.76	4	6.41	2	3.13	5	0.58	6
DH-3086 (LINE12)	-0.70	10	-1.12	10	-2.58	11	2.74	5	-1.32	8	-1.53	11.5
DBW-222 (LINE13)	1.41	7	-4.79	14	-1.02	10	0.41	7	-4.32	13	-1.53	11.5
CSW-18 (LINE14)	-7.48	15	-1.12	11	-0.91	9	-3.04	11	-2.76	12	-3.87	15
PBW-757 (LINE15)	-1.82	11	-0.45	8	0.20	8	-3.82	13	-5.87	14	-2.87	14
SE(gca for line)	0.36		0.23		0.31		0.20		0.91		0.18	
SE(gi-gj) for line)	0.50		0.33		0.44		0.29		1.28		0.26	
Tester												
PBW ZN1 (TESTER 1)	-0.26	3	0.59	2	0.71	2	-1.55	2	-0.54	2	1.98	1
PBW-343 (TESTER 2)	0.34	1	-1.25	3	-4.87	3	-2.33	3	-3.34	3	-3.80	3
HD-3326 (TESTER 3)	-0.08	2	0.66	1	4.16	1	3.87	1	3.88	1	1.82	2
SE(gca for tester)	0.16		0.10		0.14		0.09		0.41		0.08	
SE(gi-gj) for tester	0.23		0.15		0.20		0.13		0.57		0.12	
SE(sij-skl) for tester	0.87		0.57		0.76		0.50		2.22		0.45	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

Number of spikelet/Spike (NSS) across 3 locations (E1, E2 & E3)							Number of productive tiller/plant across locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	0.22	4	0.22	4	-1.04	15	-1.41	15	-1.09	15	-1.09	15
WB-02 (LINE2)	-0.14	10	-0.14	10	-0.46	12	-0.30	11	0.89	1	0.21	8
BHU-31 (LINE3)	-0.27	11	-0.27	11	0.40	3	0.73	4	0.22	6	0.46	2
HD-3721 (LINE4)	-0.12	8	-0.12	8	0.90	2	-0.11	7	-0.67	12	-0.45	12
PWB-725 (LINE5)	0.67	2	0.67	2	0.12	7	0.87	3	0.21	7	0.25	6
CRD GEHNU1 (LINE6)	0.06	5	0.06	5	0.36	4	0.31	6	-0.09	11	0.17	10
PBW-550 (LINE7)	1.05	1	1.05	1	0.04	8	0.67	5	0.32	5	-0.93	14
PBW-677 (LINE8)	-0.38	12	-0.38	12	0.14	6	-1.16	14	-0.96	14	-0.03	11
PBW-822 (LINE9)	-0.65	15	-0.65	15	0.17	5	-0.72	13	-0.06	10	0.26	5
HD-3117 (LINE10)	-0.05	7	-0.05	7	-0.42	11	-0.19	9	-0.73	13	0.41	3
DBW-173 (LINE11)	-0.48	14	-0.48	14	-0.46	13	-0.49	12	0.07	9	0.38	4
DH-3086 (LINE12)	-0.44	13	-0.44	13	0.04	9	-0.20	10	0.88	2	0.23	7
DBW-222 (LINE13)	-0.01	6	-0.01	6	-0.19	10	1.13	1	0.14	8	-0.61	13
CSW-18 (LINE14)	-0.12	9	-0.12	9	0.91	1	-0.17	8	0.43	4	0.58	1
PBW-757 (LINE15)	0.64	3	0.64	3	-0.50	14	1.03	2	0.44	3	0.18	9
SE(gca for line)	0.26		0.37		0.24		0.25		0.18		0.15	
SE(gi-gj) for line)	0.36		0.52		0.15		0.36		0.25		0.21	

Tester

PBW ZN1 (TESTER 1)	0.05	1	0.05	1	0.10	1	0.17	1	0.20	1	0.13	1
PBW-343 (TESTER 2)	0.01	2	0.01	2	0.07	2	0.09	2	-0.14	3	-0.18	3
HD-3326 (TESTER 3)	-0.06	3	-0.06	3	-0.18	3	-0.27	3	-0.07	2	0.06	2
SE(gca for tester)	0.12		0.17		0.11		0.11		0.08		0.07	
SE(gi-gj) for tester	0.16		0.23		0.15		0.16		0.11		0.10	
SE(sij-skl) for tester	0.63		0.91		0.59		0.62		0.44		0.37	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

Number of grain per spike (NG/S) across locations (E1, E2 & E3)							**Spike length (SL) across 3 locations (E1, E2 & E3)**					
GENOTYPES	E1	RANK	E2	RANK	E3	RANK	E1	RANK	E2	RANK	E3	RANK
BHU-25 (LINE1)	-0.97	12	0.44	8	4.85	3	-0.72	15	-0.06	9	0.19	4
WB-02 (LINE2)	-0.14	9	1.49	4	-0.72	8	-0.10	13	-0.51	14	-0.31	14
BHU-31 (LINE3)	-0.58	11	0.64	6	-3.73	14	0.36	4	-0.07	10	-0.04	9
HD-3721 (LINE4)	1.10	3	-0.50	10	-1.65	10	0.56	6	-0.65	15	-0.73	15
PWB-725 (LINE5)	-0.19	10	2.31	1	5.61	2	-0.14	7	-0.21	11	-0.18	12
CRD GEHNU1 (LINE6)	1.12	2	2.18	2	3.29	4	-0.12	2	0.28	4	0.26	3
PBW-550 (LINE7)	0.15	8	1.63	3	0.49	5	0.14	3	0.03	7	0.14	5
PBW-677 (LINE8)	0.27	6	-1.43	11	6.75	1	-0.87	14	0.51	2	0.32	2
PBW-822 (LINE9)	1.69	1	-2.78	15	-4.04	15	0.39	10	-0.26	12	-0.23	13
HD-3117 (LINE10)	0.55	4	-1.73	12	-0.20	7	0.08	9	0.28	3	0.09	6
DBW-173 (LINE11)	-1.35	15	0.33	9	0.07	6	-0.56	11	-0.39	13	-0.14	11

DH-3086 (LINE12)	0.25	7	-2.07	14	-3.11	11	-0.01	12	0.72	1	0.64	1
DBW-222 (LINE13)	-1.04	13	0.58	7	-0.79	9	0.48	5	0.27	5	0.08	7
CSW-18 (LINE14)	0.43	5	0.78	5	-3.70	13	-0.12	8	-0.05	8	-0.02	8
PBW-757 (LINE15)	-1.29	14	-1.87	13	-3.13	12	0.63	1	0.11	6	-0.08	10
SE(gca for line)	2.23		1.49		0.38		1.33		0.24		0.98	
SE(gi-gj)for line)	1.34		0.80		0.15		1.75		0.18		0.05	
Tester												
PBW ZN1 (TESTER 1)	44.16	3	-0.15	1	-0.41	3	0.10	1	-0.31	3	-0.13	2
PBW-343 (TESTER 2)	44.35	2	-0.68	2	0.47	1	-0.05	3	0.33	1	0.27	1
HD-3326 (TESTER 3)	44.36	1	0.83	3	-0.06	2	-0.05	2	-0.02	2	-0.14	3
SE(gca for tester)	1.55		0.32		0.18		0.26		0.25		0.12	
SE(gi-gj) for tester	0.98		1.31		0.12		0.85		0.11		0.42	
SE(sij-skl) for tester	3.02		1.51		0.35		1.52		0.63		2.22	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

	Chlorophyll content (CLC) across 3 locations (E1, E2 & E3)						Flag leaf area (FLA) across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	-3.02	15	-3.80	11	-6.59	15	-0.07	8	0.04	6	-0.48	14
WB-02 (LINE2)	-1.90	13	3.22	5	0.76	6	-0.07	9	0.07	3	0.41	3
BHU-31 (LINE3)	0.62	6	-8.26	15	0.61	7	-0.05	6	0.04	5	0.32	6
HD-3721 (LINE4)	0.12	7	-0.93	7	2.28	3	-0.14	12	0.02	8	0.45	2

PWB-725 (LINE5)	-0.27	8	7.85	2	-1.39	11	-0.16	14	-0.28	15	-0.01	8
CRD GEHNU1 (LINE6)	3.01	2	5.35	3	-0.55	9	-0.22	15	-0.11	14	-0.40	12
PBW-550 (LINE7)	1.32	4	-2.16	10	-1.51	12	-0.02	5	-0.02	11	-0.52	15
PBW-677 (LINE8)	-0.92	9	-1.73	9	-2.20	14	-0.12	11	-0.01	9	0.36	4
PBW-822 (LINE9)	0.88	5	-6.21	14	-1.33	10	-0.15	13	-0.04	12	0.34	5
HD-3117 (LINE10)	-1.51	11	-4.49	13	2.83	2	0.59	1	-0.09	13	-0.27	11
DBW-173 (LINE11)	-2.48	14	-1.58	8	1.74	5	0.21	2	-0.02	10	0.47	1
DH-3086 (LINE12)	-1.31	10	10.36	1	5.24	1	0.20	3	0.08	2	-0.21	10
DBW-222 (LINE13)	2.91	3	3.27	4	-1.64	13	-0.07	7	0.04	7	-0.48	13
CSW-18 (LINE14)	-1.56	12	-3.95	12	2.26	4	-0.07	10	0.06	4	0.07	7
PBW-757 (LINE15)	4.13	1	3.08	6	-0.49	8	0.13	4	0.23	1	-0.05	9
SE(gca for line)	0.58		0.97		0.40		0.18		0.17		0.15	
SE(gi-gj) for line)	0.82		1.37		0.57		0.25		0.24		0.21	
Tester												
PBW ZN1 (TESTER 1)	0.07	2	-1.60	3	-0.22	2	0.07	1	0.02	1	-0.25	3
PBW-343 (TESTER 2)	0.54	1	1.66	1	-0.53	3	-0.07	3	-0.02	3	0.24	1
HD-3326 (TESTER 3)	-0.61	3	-0.06	2	0.75	1	0.00	2	0.00	2	0.02	2
SE(gca for tester)	0.26		0.43		0.18		0.08		0.08		0.07	
SE(gi-gj) for tester	0.37		0.61		0.25		0.11		0.11		0.09	
SE(sij-skl) for tester	1.42		2.37		0.98		0.44		0.41		0.36	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

	1000 grain weight (100GW) across 3 locations (E1, E2 & E3)						Grain weight per spike(GWS) across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	0.30	4	-0.68	15	0.76	4	-0.02	8	0.00	7	-0.14	12
WB-02 (LINE2)	0.20	6	0.28	4	0.68	5	-0.19	15	-0.14	14	-0.07	10
BHU-31 (LINE3)	-0.06	10	0.23	5	-0.03	10	0.09	5	-0.06	10	-0.27	15
HD-3721 (LINE4)	-0.07	11	0.03	7	-1.90	14	-0.08	11	0.23	1	0.12	4
PWB-725 (LINE5)	-0.49	14	0.44	2	0.84	3	0.10	4	0.11	3	0.34	1
CRD GEHNU1 (LINE6)	0.43	1	-0.12	10	0.49	7	0.07	6	-0.04	8	0.06	5
PBW-550 (LINE7)	0.33	3	0.79	1	0.64	6	0.11	3	-0.20	15	0.18	3
PBW-677 (LINE8)	-0.38	12	-0.22	11	0.85	2	0.12	2	0.08	4	-0.13	11
PBW-822 (LINE9)	0.00	8	-0.22	12	0.20	8	-0.06	10	0.18	2	0.03	7
HD-3117 (LINE10)	-0.48	13	-0.48	14	-1.08	13	0.05	7	0.07	5	-0.06	9
DBW-173 (LINE11)	-0.52	15	0.04	6	0.11	9	-0.05	9	0.06	6	-0.16	13
DH-3086 (LINE12)	0.36	2	0.39	3	0.89	1	-0.10	12	-0.07	12	-0.02	8
DBW-222 (LINE13)	-0.03	9	-0.32	13	-0.08	11	-0.12	13	-0.09	13	0.27	2
CSW-18 (LINE14)	0.13	7	-0.08	9	-0.23	12	-0.16	14	-0.06	11	-0.21	14
PBW-757 (LINE15)	0.27	5	-0.07	8	-2.14	15	0.24	1	-0.06	9	0.05	6
SE(gca for line)	0.33		0.66		0.25		0.10		0.12		0.11	
SE(gi-gj) for line)	0.47		0.94		0.36		0.14		0.17		0.16	
Tester												
PBW ZN1 (TESTER 1)	-0.11	3	-0.25	3	-0.49	3	0.02	2	0.05	1	0.06	1

PBW-343 (TESTER 2)	0.08	1	0.35	1	0.84	1	0.07	1	-0.01	2	-0.06	3
HD-3326 (TESTER 3)	0.03	2	-0.10	2	-0.35	2	-0.09	3	-0.04	3	0.01	2
SE(gca for tester)	0.15		1.15		0.11		0.04		0.05		0.05	
SE(gi-gj) for tester	0.21		0.42		0.16		0.06		0.08		0.07	
SE(sij-skl) for tester	0.81		1.63		0.62		0.24		0.29		0.28	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Cont. Table 4.2.2: contd.

	Biological Yield across locations (BY) (E1, E2 & E3)						Harvest index (HI) across locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	-2.07	13	-4.95	15	-4.70	15	-3.30	15	-7.05	15	-1.30	10
WB-02 (LINE2)	0.07	8	1.60	4	-0.25	10	-2.50	13	2.48	5	-2.23	14
BHU-31 (LINE3)	2.78	2	-1.84	12	-0.77	12	1.65	4	4.92	1	2.41	4
HD-3721 (LINE4)	1.98	4	2.19	3	0.12	9	0.98	6	-2.74	12	0.27	7
PWB-725 (LINE5)	3.78	1	-2.21	13	0.70	6	0.26	7	3.37	4	-1.72	13
CRD GEHNU1 (LINE6)	0.09	7	3.99	2	0.68	7	1.93	2	3.48	3	2.52	2
PBW-550 (LINE7)	-0.42	10	-0.16	9	-0.28	11	1.83	3	2.47	6	2.70	1
PBW-677 (LINE8)	-1.40	12	1.39	5	2.74	2	-2.60	14	-2.75	13	0.33	6
PBW-822 (LINE9)	-4.40	15	-1.46	10	-2.48	13	-0.02	10	-2.15	11	0.20	8
HD-3117 (LINE10)	1.44	5	-1.70	11	0.58	8	-0.01	9	-3.09	14	-3.45	15
DBW-173 (LINE11)	-1.40	11	0.52	6	2.85	1	-0.97	11	-0.52	8	-0.69	9
DH-3086 (LINE12)	-0.22	9	6.14	1	-3.30	14	-1.17	12	-1.38	10	1.81	5

DBW-222 (LINE13)	1.34	6	0.18	8	1.59	3	1.59	5	-0.62	9	-1.66	12
CSW-18 (LINE14)	-3.96	14	-3.97	14	0.97	5	0.26	8	-0.47	7	2.45	3
PBW-757 (LINE15)	2.39	3	0.26	7	1.53	4	2.07	1	4.07	2	-1.64	11
SE(gca for line)	1.23		0.49		0.18		1.03		0.34		0.50	
SE(gi-gj)for line)	1.74		0.70		0.25		1.45		0.48		0.71	
Tester												
PBW ZN1 (TESTER 1)	0.40	1	-0.15	2	0.10	2	-0.06	2	-0.93	3	1.00	1
PBW-343 (TESTER 2)	-0.33	3	-0.68	3	-0.66	3	0.54	1	0.53	1	-0.21	2
HD-3326 (TESTER 3)	-0.07	2	0.83	1	0.56	1	-0.49	3	0.39	2	-0.79	3
SE(gca for tester)	0.55		0.22		0.08		0.46		0.15		0.22	
SE(gi-gj) for tester	0.78		0.31		0.11		0.65		0.21		0.32	
SE(sij-skl) for tester	3.02		1.21		0.44		2.52		0.83		1.22	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.2.2: contd.

	Grain yield/ plant (GYP) across locations (E1, E2 & E3)						**Protein content (PC) across 3 locations (E1, E2 & E3)**					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25 (LINE1)	-4.75	15	-1.12	10	-6.22	15	-0.07	8	0.04	6	-0.48	14
WB-02 (LINE2)	-2.23	11	3.54	2	-4.17	14	-0.07	9	0.07	3	0.41	3
BHU-31 (LINE3)	2.74	4	-3.61	15	4.27	1	-0.05	6	0.04	5	0.32	6
HD-3721 (LINE4)	2.44	5	4.76	1	3.85	2	-0.14	12	0.02	8	0.45	2
PWB-725 (LINE5)	2.83	3	2.61	4	0.69	7	-0.16	14	-0.28	15	-0.01	8

CRD GEHNU1 (LINE6)	2.05	6	-1.30	11	1.46	6	-0.22	15	-0.11	14	-0.40	12
PBW-550 (LINE7)	3.48	2	1.24	5	3.56	3	-0.02	5	-0.02	11	-0.52	15
PBW-677 (LINE8)	-4.07	14	-0.79	9	-1.28	11	-0.12	11	-0.01	9	0.36	4
PBW-822 (LINE9)	-2.62	13	-2.19	12	-1.18	10	-0.15	13	-0.04	12	0.34	5
HD-3117 (LINE10)	-0.04	8	-3.05	14	-0.27	8	0.59	1	-0.09	13	-0.27	11
DBW-173 (LINE11)	-2.36	12	0.18	6	-1.17	9	0.21	2	-0.02	10	0.47	1
DH-3086 (LINE12)	-1.76	9	2.67	3	-3.42	13	0.20	3	0.08	2	-0.21	10
DBW-222 (LINE13)	1.77	7	-2.24	13	2.97	4	-0.07	7	0.04	7	-0.48	13
CSW-18 (LINE14)	-1.79	10	0.02	7	-1.92	12	-0.07	10	0.06	4	0.07	7
PBW-757 (LINE15)	4.30	1	-0.71	8	2.83	5	0.13	4	0.23	1	-0.05	9
SE(gca for line)	0.57		0.29		0.32		0.18		0.17		0.15	
SE(gi-gj) for line)	0.81		0.41		0.45		0.25		0.24		0.21	
Tester												
PBW ZN1 (TESTER 1)	0.55	1	0.09	2	0.96	1	0.07	1	0.02	1	-0.25	3
PBW-343 (TESTER 2)	0.26	2	-0.22	3	0.21	2	-0.07	3	-0.02	3	0.24	1
HD-3326 (TESTER 3)	-0.80	3	0.13	1	-1.17	3	0.00	2	0.00	2	0.02	2
SE(gca for tester)	0.26		0.13		0.14		0.08		0.08		0.07	
SE(gi-gj) for tester	0.36		0.18		0.20		0.11		0.11		0.09	
SE(sij-skl) for tester	1.39		0.71		0.78		0.44		0.41		0.36	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

4.3.3. Estimates of specific combining ability (SCA) effects for combined locations

Each genotype has been evaluated and ranked on these parameters, with variations in traits across different genotypes have desirable traits for breeding purposes.

4.3.3.1 Days to 50% heading

Results for DH among the genotypes range from negative (e.g., -10.5458 for PBW-677XPBW-343) to highly positive (e.g., 8.3676 for CRDGEHNU1XPBW343). Genotypes with positive and high DH values such as CRDGEHNU1XPBW343 (8.3676) and WB-02XPBW-343 (7.74867) could be considered early-heading varieties. Early heading can be beneficial in regions with shorter growing seasons. PBW-677XPBW-343 (-10.5458) exhibited the most delayed heading, potentially favorable for environments requiring late maturity.

4.3.3.2 Plant height (cm)

The highest PH value is for genotype DH-3086X HD-3326 with a value of 9.661765 (Rank1). Genotype DBW-222X PBW-343 has a negative PH value of -5.62864, making it one of the shorter plants (Rank43).

4.3.3.3 Days to Maturity

Genotype CRDGEHNU1XPBW343 has the lowest DM of -10.6963 (Rank44), while CRDGEHNU1XPBWZN1 has the highest DM at 8.51852 (Rank1). Lower DM could imply earlier maturity, while higher DM suggests a longer growth period.

4.3.3.4 Grain filling period

HD-3721XPBW ZN1 has the highest GFP at 1.713937 (Rank1), while PBW-677XPBW-343 has a negative GFP of -2.32278 (Rank45). A higher GFP may indicate a longer period for grains to develop, which could impact yield and quality.

4.3.3.5 Number of productive tillers

DBW-222X PBW ZN1 has the highest NPT at 0.499506 (Rank1), suggesting it has more tillers per plant. DBW-222X HD-3326 has the lowest NPT at -0.36146 (Rank 45), suggesting fewer tillers per plant.

4.3.3.6 Number of spikelets per spike

PBW-677XPBW-343 leads with the highest NSS at 0.583195 (Rank 1). BHU-31XHD-3326 has the lowest NSS at -0.37691 (Rank45), indicating fewer spikelets per spike.

4.3.3.7 Spike length (cm)

Genotype CRDGEHNU1XPBWZN1 has the longest SL at 0.777062 (Rank 1). CRDGEHNU1XHD-3326 has the shortest SL with -0.95731 (Rank45).

4.3.3.8 Flag leaf area (cm^2)

Genotype HD-3117X PBW ZN1 has the highest FLA at 10.74041 (Rank1). BHU-31XHD-3326 has the lowest FLA at -9.88984 (Rank45).

4.3.3.9 Chlorophyll content

Highest CLC is observed in genotype PBW-550X HD-3326 with a value of 3.267827 (Rank1), suggesting better chlorophyll retention, potentially advantageous for photosynthesis. DBW-222X PBW-343 has the lowest CLC at -2.70847 (Rank45), indicating lower chlorophyll levels, which might affect the plant's growth and vigor.

4.3.3.10 Number of grains per spike

Results for NGS the genotypes like DBW-173X PBW ZN1 (NGS = 0.18558, Rank = 1) and PBW-550X HD-3326 (NGS = 0.16921, Rank = 2) exhibit the best values, reflecting strong performance in the trait under consideration. However, poor performers in NGS recorded in genotypes such as PWB-725X PBW-343 (NGS = -0.22072, Rank = 45) and DBW-222X PBW-343 (NGS = -0.17857, Rank = 44) are the lowest-ranked, suggesting underperformance in this trait.

4.3.3.11 Grain weight per spike (g)

The genotype with the highest GWS is DBW-173X PBW ZN1 with a value of 0.18558 (Rank1), suggesting better yield potential per spike. PWB-725X PBW-343 shows the lowest GWS at -0.22072 (Rank 45), indicating it may produce less grain per spike relative to other genotypes.

4.3.3.12 1000-GW (g)

HD-3117X PBW ZN1 ranks highest with a 1000GW of 0.33686 (Rank1), which is often an important metric for grain quality and yield potential. The lowest is PBW-822X PBW ZN1 with -0.63742 (Rank 45), which could impact overall grain quality and marketability.

4.3.3.13 Biological yield (g)

PBW-677XPBW-343 has the highest biological yield with 4.715259 (Rank1), suggesting high biomass productivity. PBW-757X HD-3326 has the lowest biological yield at -4.29696 (Rank45), potentially limiting total grain production.

4.3.3.14 Harvest Index (%)

The top-ranking genotype for HI is DH-3086X PBW-343 at 0.670816 (Rank1), indicating efficient partitioning of biomass to grain. The lowest is BHU-25XPBW ZN1 with -1.04371 (Rank45), which could suggest less efficient grain production relative to biomass.

4.3.3.15 Protein content

PWB-725X PBW-343 has the highest protein content at 0.749412 (Rank1), a desirable trait for nutritional quality. PBW-757X PBW-343 has the lowest at -0.32109 (Rank45), which could be a drawback for protein-focused breeding goals.

4.3.3.16 Grain yield per plant (g)

The highest GYP is seen in PBW-822X PBW ZN1 at 3.795527 (Rank1), indicating superior yield potential per plant. PBW-677XPBW ZN1 has the lowest GYP at -2.87086 (Rank45), suggesting relatively lower productivity.

4.3.3 Estimates of specific combining ability effects across three locations (E1, E2, & E3)

4.3.4.1 Days to 50% heading

This parameter measures the number of days required for each genotype to reach 50% heading across three environments, representing the speed of plant development. Genotypes with Fast Heading (Lower Values) HD-3117X HD-3326 has the lowest days to heading in E1 (-16.2667, Rank45), indicating that this genotype reaches heading quickly in E1. PBW-677XPBW-343 performs similarly fast in E2 with a high positive value (12.83704, Rank 3) and in E3 with 7.674074 (Rank6). Genotypes DBW-222X HD-3326 and DH-3086X PBW ZN1 also exhibit rapid heading in various environments, showing adaptability and faster growth under certain conditions.

4.3.4.2 Plant height (cm)

Genotypes PBW-757X PBW ZN1 has relatively shorter plants in E1 (-7.0583, Rank 38), E2 (-2.75659, Rank 29), and E3 (-4.37004, Rank42), indicating suitability for areas prone to lodging. PBW-822X HD-3326 also demonstrates low plant height across all environments, particularly in E3 with -5.65715 (Rank43). Genotypes with taller heights (Higher Values) HD-3721XHD-3326 and CRDGEHNU1XPBW343 are among the tallest genotypes across environments, with values of 11.9873 (Rank1) and 10.19852 (Rank5) in E2 and E3, respectively. PWB-725X PBW ZN1 consistently ranks as one of the tallest genotypes in each environment, particularly in E1 (11.00281, Rank1). Genotypes with variable heights across environments PBW-550X PBW ZN1 shows significant variation in height, with E1 being relatively short (-0.75385, Rank 27) and taller in E2 and E3. CSW-18XHD-3326 has moderate to low height values across all environments, reflecting intermediate performance.

4.3.4.3 Grain filling period

The grain filling period genotype CRDGEHNU1XPBW ZN1 ranked highest in E1 with a grain filling period of 7.037037 (Rank1), indicating a long grain-filling duration, which could contribute to higher yield potential in E1. In E2, it also has a positive grain filling period (2.074074, Rank 12), showing consistency. However, in E3, it has a shorter grain filling period (-9.15556, Rank 45), suggesting variability in its grain filling duration across environments. PBW-550X PBW ZN1 this genotype exhibits a high grain filling period in E3 with 8.288889 (Rank 5), E2 with 4.740741 (Rank 9), and E1 with -5.74074 (Rank 41). This shows that it performs better in E2 and E3, while E1 may not be optimal for its grain-filling duration. PBW-757X PBW-343 this genotype performs very well in E3 with a high value of 11.31111 (Rank 1), indicating it has the longest grain filling period in this environment, potentially benefiting yield.

4.3.4.4 Days to maturity

Early maturing genotypes (Lower Values) CRDGEHNU1XPBW343 this genotype shows extremely early maturity across environments, with -16.8963 (Rank 45) in E1, -8.32593 (Rank 42) in E2, and -6.86667 (Rank42) in E3. Its consistently early maturity makes it suitable for regions with shorter growing seasons. PBW-550X PBW-343 Shows early maturity in E1 (-

15.8963, Rank 43), E2 (-7.65926, Rank 39), and E3 (-8.86667, Rank 44), suggesting a short growth cycle. HD-3721XPBW ZN1 this genotype also ranks among the early matures in E1 with -16.1185 (Rank 44) and E2 with 0.318519 (Rank23), indicating early maturity across environments. Late maturing genotypes (Higher Values) PBW-550X PBW ZN1 this genotype matures very late in E1 with 14.65926 (Rank1) and has positive values across all environments, indicating a long growth duration and potential for high yield. CRDGEHNU1XPBW ZN1 late maturity is observed in E1 (11.32593, Rank2) and E2 (11.87407, Rank 1), showing that it has a long growth cycle, especially in E1 and E2. DBW-173X PBW-343 matures very late in E3 with 8.577778 (Rank1) and E2 with a high value of 0.562963 (Rank19), suggesting a lengthy growth cycle beneficial for yield.

4.3.4.5 Analysis of number of spikelets per spike

Location E1 genotype PBW-677XPBW-343 has the highest value (1.533481), indicating superior performance. CSW-18XHD-3326 (1.157259) and HD-3721XPBW ZN1 (1.008148) follow closely, suggesting they are well-suited to E1 conditions. Location E2 the rankings are consistent with E1, with PBW-677XPBW-343 (1.533481) and CSW-18XHD-3326 (1.157259) again in the top ranks. Location E3 DBW-173X PBW-343 performs best here (1.570222), with HD-3721XPBW-343 (0.891333) and BHU-31XPBW ZN1 (0.766667) also showing high performance. The shift in top performers suggests that E3 conditions are different enough to impact which genotypes excel. However, poor performance recorded at location E1 and E2 genotype HD-3721XPBW-343 ranks lowest in both locations (-1.1243 in E1 and E2), suggesting low adaptation in these conditions. Location E3 DBW-222X HD-3326 performs worst here (-1.15689), reflecting poor spikelet development under E3 conditions.

4.3.4.6 Number of productive tillers per plant

Location E1 Genotype HD-3721XHD-3326 ranks highest with 1.779481, indicating it produces a high number of productive tillers. DH-3086X PBW-343 (1.489926) and DBW-222X PBW ZN1 (0.841704) also perform well, showing potential for high yield under E1 conditions. Location E2 DH-3086X HD-3326 leads here with 1.588074, followed by DBW-222X PBW ZN1 (1.445407), reflecting good adaptability to E2 (Table 16). Location E3 Genotype CRDGEHNU1XPBWZN1 (1.048074) has the highest ranking, followed closely by DBW-222X PBW ZN1 (0.964741) and BHU-31XHD-3326 (0.981696), suggesting they can produce well in E3. Poor Performance were revealed at location E1 in genotype WB-02XHD-3326 ranks lowest (-1.0983), suggesting low tiller productivity in E1. DBW-222X HD-3326 (-1.35719) and DH-3086X PBW ZN1 (-1.28052) are also poor performers. Location E2 DH-3086X PBW-343 (-2.11348) and PBW-550X HD-3326 (-0.57304) have low productivity in E2, indicating they are less suited for this location. Location E3 DBW-222X HD-3326 (-1.00608) and HD-3721XPBW-343 (-0.86088) have the lowest rankings in E3, indicating poor tiller productivity.

4.3.4.7 Chlorophyll content

Genotype PBW-757X PBW ZN1 achieves top ranks in all locations (Rank 1 in E1 and E2) with high chlorophyll values of 4.5, 7.84, and a negative value in E3 (-3.54). Despite a drop in E3, this genotype shows robust performance in the first two locations, indicating a strong potential for chlorophyll synthesis in specific environments. PBW-677XPBW-343 ranks high in E2 (Rank 2) with a chlorophyll content value of 7.34, showing adaptability, particularly in E2. However, it ranks much lower in E3 (-6.02, Rank 45), indicating environmental sensitivity. PBW-550X HD-3326 performs consistently well in E2 (Rank 3 with a value of 7.18) and moderately in E1 and E3. This genotype shows promise across different environments, though it performs better in some than others. Low-Performing genotypes (low chlorophyll content) PBW-677XPBW ZN1 ranks 45th in E2 and E3, showing negative chlorophyll content values in E2 (-7.02) and E3 (2.70). This suggests poor adaptability and low chlorophyll content under these environmental conditions. HD-3117X HD-3326 despite a positive ranking in E1, it scores poorly in E2 and E3, highlighting environmental sensitivity and overall low chlorophyll performance across the locations.

4.3.4.8 Flag leaf area (cm^2)

Genotype CRDGEHNU1XPBWZN1 consistently ranks highest in flag leaf area across all locations (Ranks 1 in E1, E2, and E3) with values of 12.48, 12.15, and 11.25, respectively. This consistency suggests strong genetic potential for large leaf area and adaptability across varied environments. HD-3117X PBW ZN1 another top performer, ranking 2 in E1, E2, and E3 with values of 10.05, 9.39, and 9.49. This genotype's large flag leaf area in all environments indicates stability and high adaptability. Moderate performers PBW-822X PBW-343: Shows relatively high rankings across locations (Rank 6 in E1, Rank 4 in E2, and Rank 3 in E3) with flag leaf area values of 5.30, 6.34, and 7.28. Although it doesn’t top the ranks, its consistent moderate-to-high performance across environments indicates it’s a reliable genotype for moderate flag leaf area under varying conditions. Low-performing genotypes (small flag leaf area) recorded in

CRDGEHNU1XPBW343 ranked lowest in all locations (Rank44 in E1, Rank 44 in E2, Rank 43 in E3) with values of -7.28, -6.91, and -6.75, indicating a very small flag leaf area regardless of environment.

4.3.4.9 Spike length

Spike length varies significantly across locations, as evident from the diverse rankings for genotypes across E1, E2, and E3. For instance, the best performing genotypes was PBW-757X PBW ZN1 (E1 0.706741 (Rank 1), however, it performed very poor in E2 -0.49926 (Rank 38) and E3 -0.6763 (Rank 42) and DH-3086X PBW ZN1 performed well in E2 1.281852 (Rank 1) and E3 0.993704 (Rank 2) but poorly performed in E1 0.05563 (Rank 21)

4.3.4.10 Number of grains per spike

The best performing genotype was DH-3086X PBW ZN1 (E3 9.503852 (Rank 1)) but recorded poor performance in E1 -0.89674 (Rank 34) and E2 -0.88778 (Rank 33). It underperforms in E1 and E2, it achieves the highest value in E3, indicating a strong genotype-environment interaction. PBW-757X PBW-343 performed well in E3 7.553852 (Rank 2), however, drastically dropped in E1 -1.79941 (Rank 39) and E2 0.194222 (Rank 20)

4.3.4.11 1000-Grain weight

In location E1 the genotype with the highest 1000-grain weight is DBW-173X PBW ZN1 (1.139111), ranked 1st. Other high performers include PBW-550X PBW-343 (0.999333) and BHU-25XPBW ZN1 (0.734667). Lowest performance were recorded in DBW-173X PBW-343 shows the lowest 1000-grain weight (-1.09733), ranking last. BHU-25XHD-3326 (-0.90289) and BHU-31XPBW ZN1 (-0.64533) also have lower weights (Table 18). Location E2 the best genotype for E2 is CRDGEHNU1XPBWZN1 (2.359481), showing strong adaptability to this environment. PWB-725X HD-3326 (1.847704) and PBW-822X HD-3326 (1.097704) also rank highly. However, the lowest performance recorded in CRDGEHNU1XHD-3326 (-2.50785) ranks the lowest, with PBW-822X PBW ZN1 (-2.08496) also performing poorly in this location. At location E3 genotype PBW-822X HD-3326 (2.856963) was the top followed by PWB-725X PBW ZN1 (1.946963) and PBW-550X HD-3326 (1.441407). However, lowest performance was revealed in PBW-822X PBW ZN1 (-3.92637) ranks the lowest, with PWB-725X HD-3326 (-1.78637) also struggling in this location.

4.3.4.12 Grain weight per spike

Genotype at location E1 CSW-18XPBW ZN1 (0.279259) ranks 1st, indicating strong grain weight per spike. DBW-173X PBW-343 (0.276593) and PBW-757X HD-3326 (0.237481) follow. Lowest performing were recorded DBW-222X HD-3326 (-0.2403) has the lowest grain weight per spike in E1, followed by PWB-725X PBW-343 (-0.21007) and DH-3086X PBW ZN1 (-0.21519). Location E2 the highest grain weight per spike in E2 is from PBW-822X PBW-343 (0.485556), followed closely by HD-3117X PBW ZN1 (0.464667) and DBW-173X PBW ZN1 (0.455778) (Table 18). However, lowest performance was recorded in PBW-822X HD-3326 (-0.638), suggesting poor suitability for this genotype in E2. Location E3 genotype BHU-31XPBW-343 (0.466815) and HD-3721XPBW ZN1 (0.447259) show the best grain weight per spike, suggesting adaptability to E3 conditions. Lowest performance WB-02XHD-3326 (-0.49407) and HD-3721XPBW-343 (-0.05319) perform poorly in E3, suggesting they might not be well-suited to this environment.

4.3.4.13 Biological yield

In E1 location the genotype with the highest Biological Yield was PBW-677XPBW-343 with a value of 4.715259, ranked 1st. E2 PWB-725X PBW-343 has the highest value at this location, 8.907481, ranked 1st. E3 CRDGEHNU1XPBWZN1 is the highest-yielding genotype here, with a value of 5.323556, ranked 1st. The lowest performing genotypes in biological yield E1 PBW-757X HD-3326 has the lowest value of -4.29696, ranked 45th. E2 WB-02XPBW-343 shows the lowest yield at this location, with a value of -8.21363, ranked 45th. E3 BHU-31XPBW ZN1 has the lowest value, -6.93978, ranked 45th.

4.3.4.14 Harvest index

Results in E1 revealed that PWB-725X HD-3326 has the highest Harvest Index with a value of 4.670074, ranked 1st. E2 BHU-31XHD-3326 scores the highest here with 4.527037, ranked 1st. E3 HD-3117X HD-3326 achieves the top rank, with a Harvest Index of 5.542889, ranked 1st. Lowest-performing Genotypes in harvest index E1 PWB-725X PBW ZN1 shows the lowest value, -4.09237, ranked 45th. E2 BHU-25XPBW ZN1 has the lowest value of -4.5743, ranked 44th. E3 HD-3721XHD-3326 ranks the lowest with -5.94822, ranked 45th.

4.3.4.15 Protein content

High performing genotypes for protein content the best genotypes in E1 were HD-3721XPBW ZN1 (Protein1.538, rank1), PWB-725X PBW-343 (Protein 0.816, rank2) CRDGEHNU1XHD-3326 (Protein 0.494, Rank3) these genotypes have a higher protein content in E1, making them good candidates for nutrient-dense yield in this environment. The best genotypes in E2 DH-3086X PBW-343 (Protein 0.189, rank1), PBW-757X PBW ZN1 (Protein 0.153, rank2) and PWB-725X PBW-343 (Protein: 0.107, rank 3). The best genotypes in E3 genotype PBW-677XPBW-343 (Protein1.947, rank1), DH-3086X, PBW ZN1 (Protein1.678, rank2) and PWB-725X PBW-343 (Protein1.627, rank3).

4.3.4.16 Grain yield per plant (g)

High Performing Genotypes for grain yield per plant best genotypes in E1 PBW-822X PBW ZN1 (Yield 6.012, rank 1) WB-02XPBW ZN1 (Yield 4.717, rank 2) PWB-725X HD-3326 (Yield 4.630, rank 3), these genotypes exhibit superior yield in E1, indicating that they are potentially well-suited to the environmental conditions of E1 (Table 20). Genotypes in E2 BHU-31XHD-3326 (Yield 4.476, rank 1) PBW-757X PBW-343 (Yield 3.893, rank 2) BHU-25XPBW ZN1 (Yield 2.625, Rank 3) Genotypes in E3 PBW-677XPBW-343 (Yield 7.396, rank 1) BHU-31XHD-3326 (Yield 5.972, rank 2) DBW-173X HD-3326 (Yield 5.962, rank 3).

Table 4.3.1: Estimates of specific combining ability (SCA) of forty five crosses of different characters for combined locations

GENOTYPES	DH	RANK	PH	RANK	DM	RANK	GFP	RANK	NPT	RANK	NSS	RANK	SL	RANK	FLA	RANK
BHU-25XPBW ZN1	3.05	14	1.07	19	2.52	16	1.61	3	-0.09	34	-0.02	22	0.20	12	-5.46	38
BHU-25XPBW-343	-7.70	43	-0.93	29	0.86	24	-0.49	32	-0.26	42	-0.01	19	0.14	15	1.91	17
BHU-25XHD-3326	0.22	23	-0.14	23	-3.38	33	0.85	14	-0.16	39	-0.17	35	-0.34	38	3.50	11
WB-02XPBW ZN1	7.20	4	1.22	18	-3.67	34	-0.12	24	-0.04	27	-0.01	21	-0.23	35	-5.60	40
WB-02XPBW-343	7.75	2	-5.04	42	3.12	13	1.01	12	-0.09	36	0.06	17	-0.14	29	3.48	12
WB-02XHD-3326	-3.09	30	3.82	6	0.55	26	1.14	7	-0.17	40	-0.25	39	0.38	7	-0.01	24
BHU-31XPBW ZN1	-4.11	35	6.65	3	1.63	21	1.28	5	-0.11	37	0.22	8	0.09	17	-5.36	37
BHU-31XPBW-343	-1.20	26	3.57	7	3.64	10	1.11	10	-0.02	24	-0.21	37	-0.71	44	-1.55	28
BHU-31XHD-3326	-1.02	25	-10.22	45	-5.27	39	-1.54	40	0.06	15	-0.38	45	0.62	2	-9.89	45
HD-3721XPBW ZN1	-1.67	28	-2.27	33	-5.04	36	1.71	1	0.09	12	0.19	12	-0.38	41	4.23	8
HD-3721XPBW-343	-4.77	38	2.34	14	3.53	11	0.07	21	-0.33	44	-0.28	41	0.08	18	-5.19	36
HD-3721XHD-3326	1.24	20	-0.08	22	1.51	22	0.06	22	0.17	5	-0.07	26	0.30	10	0.14	23
PWB-725X PBW ZN1	4.45	11	2.96	11	-9.89	43	0.18	19	-0.08	32	-0.33	44	-0.48	43	2.91	15
PWB-725X PBW-343	1.53	18	-6.13	44	8.01	2	1.09	11	-0.01	23	0.19	11	0.15	14	1.93	16
PWB-725X HD-3326	7.00	5	3.18	10	1.88	20	0.68	17	0.09	11	-0.32	43	0.32	9	-2.80	32
CRDGEHNU1XPBWZN1	2.90	15	0.71	20	8.52	1	-0.23	25	0.27	3	-0.04	23	0.78	1	9.31	3
CRDGEHNU1XPBW343	8.37	1	-0.34	24	-10.70	44	-0.66	33	0.05	18	-0.15	32	0.18	13	-8.39	44
CRDGEHNU1XHD-3326	-3.20	31	-0.37	25	2.18	19	0.14	20	-0.19	41	-0.08	28	-0.96	45	-8.23	43
PBW-550X PBW ZN1	7.23	3	1.67	15	6.96	4	0.76	15	-0.08	33	0.07	16	-0.12	28	-4.25	33
PBW-550X PBW-343	2.58	16	-1.15	31	-10.81	45	-1.47	39	0.14	9	-0.13	30	-0.22	34	3.40	13

PBW-550X HD-3326	0.67	22	-0.52	27	3.84	9	-0.04	23	0.04	20	-0.01	20	0.34	8	1.17	21
PBW-677XPBW ZN1	-5.99	41	1.53	16	-2.85	32	-0.41	30	-0.07	30	-0.29	42	-0.39	42	-5.12	35
PBW-677XPBW-343	-10.55	45	3.23	9	0.16	27	-2.32	45	0.11	10	0.58	1	0.39	6	3.33	14
PBW-677XPBW-343	3.58	12	-4.75	39	2.70	15	1.13	9	0.07	13	-0.08	27	0.00	25	4.20	9
PBW-822X PBW ZN1	1.44	19	-4.73	38	-1.44	30	1.70	2	0.17	6	0.02	18	-0.16	31	-1.20	27
PBW-822X PBW-343	-5.85	40	1.47	17	-5.55	40	-1.65	42	0.06	14	-0.07	25	0.51	5	7.40	4
PBW-822X HD-3326	-6.66	42	3.26	8	6.99	3	-0.40	29	0.00	22	0.31	5	-0.35	39	-5.50	39
HD-3117X PBW ZN1	-0.29	24	-0.46	26	-5.07	37.5	-2.25	44	0.16	7	0.24	7	-0.08	26	10.74	1
HD-3117X PBW-343	0.71	21	-4.62	37	5.49	5	-0.31	28	0.01	21	-0.24	38	0.00	24	0.16	22
HD-3117X HD-3326	-1.57	27	5.08	5	-0.42	29	1.16	6	-0.05	28	-0.25	40	0.07	19	-7.05	42
DBW-173X PBW ZN1	-3.87	33	-5.00	41	-5.07	37.5	-0.87	36	-0.08	31	0.21	10	-0.34	37	-4.85	34
DBW-173X PBW-343	6.70	6	8.42	2	2.82	14	-0.46	31	0.32	2	-0.09	29	0.28	11	-0.02	25
DBW-173X HD-3326	1.78	17	-3.42	35	2.25	18	1.60	4	-0.04	26	-0.17	34	0.06	20	3.75	10
DH-3086X PBW ZN1	5.66	10	-4.03	36	0.74	25	-0.28	27	-0.04	25	-0.15	33	0.12	16	-6.43	41
DH-3086X PBW-343	-3.91	34	-5.63	43	-2.03	31	0.94	13	-0.29	43	0.11	15	-0.15	30	1.46	20
DH-3086X HD-3326	-4.46	37	9.66	1	1.29	23	-0.90	37	0.15	8	0.26	6	0.03	23	4.46	7
DBW-222X PBW ZN1	-3.64	32	2.90	12	4.41	6	-0.83	35	0.50	1	0.22	9	0.54	4	-1.73	30
DBW-222X PBW-343	-9.83	44	-3.29	34	-4.36	35	0.70	16	0.05	17	0.40	2	-0.21	33	1.74	18
DBW-222X HD-3326	6.11	7	0.39	21	-0.04	28	-1.81	43	-0.36	45	-0.14	31	-0.33	36	-0.97	26
CSW-18XPBW ZN1	-2.42	29	-0.75	28	3.96	8	-0.24	26	-0.05	29	-0.19	36	-0.09	27	1.62	19
CSW-18XPBW-343	3.41	13	5.63	4	3.53	12	-1.08	38	0.05	16	-0.05	24	0.06	21	6.07	6
CSW-18XHD-3326	-5.25	39	-4.88	40	-7.49	42	0.62	18	0.05	19	0.40	4	0.03	22	6.15	5

PBW-757X PBW ZN1	-4.29	36	-1.45	32	4.30	7	-1.58	41	0.24	4	0.40	3	0.55	3	10.26	2
PBW-757X PBW-343	5.83	9	2.47	13	2.30	17	1.13	8	-0.14	38	0.14	14	-0.37	40	-1.68	29
PBW-757X HD-3326	5.92	8	-1.02	30	-6.60	41	-0.76	34	-0.09	35	0.16	13	-0.18	32	-2.03	31
SE (sca effect)	22.59		24.19		23.87		4.26		11.03		8.18		3.08		14.59	

Note: Ranking is in ascending order (i.e. 1 is the best followed by 2 on and on). Days to heading (DH), Plant height (PH), Days to maturity (DM), Grain-filling period (GFP), Number of productive tiller (NPT), Number of spikelet/spike (NS/S), Spike length (cm) (SL), and Flag leaf area (FLA)

Table 4.3.1 contd.

GENOTYPES	CLC	RANK	NGS	RANK	GWS	RANK	1000GW	RANK	BY	RANK	HI	RANK	PC	RANK	GYP	RANK
BHU-25XPBW ZN1	1.31	7	-0.07	26	-0.17	43	0.01	25	-1.07	32	-1.04	45	0.05	14	-0.75	27
BHU-25XPBW-343	-1.04	33	0.29	18	0.09	11	0.02	23	-2.60	39	0.22	12	-0.17	33	-2.51	42
BHU-25XHD-3326	-0.27	26	0.34	13	0.08	13	0.06	16	3.68	3	0.10	21	-0.21	36	-1.32	33
WB-02XPBW ZN1	0.53	14	0.36	11	-0.08	34	-0.03	30	3.99	2	0.16	19	-0.04	22	0.56	18
WB-02XPBW-343	1.09	10	0.34	14	-0.09	35	0.03	21	-3.00	42	0.04	24	0.41	3	-1.07	30
WB-02XHD-3326	-1.62	40	-0.61	38	0.16	4	0.06	15	-0.98	31	-0.52	40	-0.22	38	-1.81	36
BHU-31XPBW ZN1	-1.69	41	-0.71	41	0.00	25	0.07	12	2.43	6	0.00	28	-0.24	41	-1.26	32
BHU-31XPBW-343	-1.46	35	-0.25	31	0.14	6	-0.01	27	-0.71	29	-0.19	33	0.39	4	-2.54	43
BHU-31XHD-3326	3.15	3	0.49	7	-0.14	39	-0.07	33	-1.72	35	0.06	23	-0.05	23	1.54	11
HD-3721XPBW ZN1	0.32	19	-0.62	39	0.15	5	-0.16	41	-0.28	26	0.02	25	0.31	7	-0.05	23
HD-3721XPBW-343	-0.14	24	0.17	22	-0.01	27	-0.17	42	-0.32	27	0.14	20	0.07	12	-2.35	41
HD-3721XHD-3326	-0.18	25	0.32	15	-0.13	38	-0.14	39	0.60	19	-0.57	41	-0.23	39	1.13	12
PWB-725X PBW ZN1	-0.99	32	0.40	9	0.17	3	0.04	19	0.59	20	0.07	22	-0.07	24	0.01	22

PWB-725X PBW-343	0.23	21	0.29	17	-0.22	45	-0.10	37	-0.48	28	-0.67	43	0.75	1	-2.10	40
PWB-725X HD-3326	0.76	12	0.30	16	0.05	15	-0.02	28	-0.11	25	0.46	3	-0.24	40	0.82	13
CRDGEHNU1XPBWZN1	1.12	9	-0.46	35	-0.07	32	0.33	2	1.02	15	-0.03	30	-0.16	32	0.68	16
CRDGEHNU1XPBW343	0.45	18	0.74	2	0.04	16	0.13	7	1.96	7	0.29	10	0.01	18	0.35	19
CRDGEHNU1XHD-3326	-1.57	38	0.57	5	0.03	21	-0.09	36	-2.99	41	-0.31	37	0.20	10	-1.98	39
PBW-550X PBW ZN1	-1.76	42	0.92	1	-0.08	33	-0.16	40	-3.18	43	0.33	9	-0.12	28	0.74	14
PBW-550X PBW-343	-1.51	36	-0.31	32	0.04	17	0.08	11	2.66	5	-0.32	38	-0.02	20	-0.37	25
PBW-550X HD-3326	3.27	1	-0.31	33	0.04	18	-0.02	29	0.53	21	-0.06	31	-0.20	35	0.59	17
PBW-677XPBW ZN1	-1.98	44	0.36	10	-0.05	31	0.03	22	-2.23	37	0.00	27	-0.19	34	-2.87	45
PBW-677XPBW-343	1.14	8	0.35	12	0.08	12	0.05	17	-2.49	38	0.43	5	-0.25	42	2.81	5
PBW-677XPBW-343	0.84	11	0.01	25	-0.03	29	-0.12	38	4.72	1	-0.30	35	0.48	2	-1.34	34
PBW-822X PBW ZN1	-0.51	28	-0.78	43	0.01	23	-0.64	45	1.49	9	0.48	2	0.06	13	3.80	1
PBW-822X PBW-343	2.04	5	-0.15	28	0.13	8	0.05	18	-1.94	36	-0.41	39	0.02	17	-1.06	29
PBW-822X HD-3326	-1.54	37	0.27	19	-0.13	36	0.15	5	0.45	22	0.21	13	0.13	11	-0.31	24
HD-3117X PBW ZN1	-1.59	39	-0.19	29	0.06	14	0.34	1	0.73	18	-0.60	42	0.22	9	-0.76	28
HD-3117X PBW-343	1.46	6	0.24	20	-0.16	42	-0.03	31	0.81	16	-0.01	29	-0.21	37	0.18	21
HD-3117X HD-3326	0.13	22	-0.23	30	0.10	10	-0.04	32	-1.54	34	0.46	4	0.27	8	-0.51	26
DBW-173X PBW ZN1	-0.84	30	0.44	8	0.19	1	0.11	8	-2.78	40	0.19	17	-0.15	31	-2.83	44
DBW-173X PBW-343	0.58	13	0.09	24	-0.01	26	-0.01	26	1.43	11	0.20	14	-0.01	19	1.69	10
DBW-173X HD-3326	0.26	20	-0.65	40	-0.18	44	-0.07	34	1.34	12	0.18	18	0.36	6	2.43	8
DH-3086X PBW ZN1	0.50	16	0.64	3	-0.14	40	-0.30	44	0.29	23	0.01	26	0.37	5	3.16	3
DH-3086X PBW-343	0.45	17	-0.34	34	-0.03	28	0.07	13	1.15	14	0.67	1	-0.13	29	2.95	4

DH-3086X HD-3326	-0.95	31	-0.93	45	0.17	2	-0.21	43	-1.44	33	-0.78	44	-0.03	21	-1.93	38
DBW-222X PBW ZN1	3.19	2	-0.49	36	0.04	19	-0.08	35	-0.77	30	0.19	16	-0.25	43	3.40	2
DBW-222X PBW-343	-2.71	45	0.20	21	0.11	9	0.03	20	0.74	17	0.24	11	0.04	15	0.70	15
DBW-222X HD-3326	-0.48	27	0.12	23	-0.15	41	0.23	3	0.03	24	-0.31	36	-0.08	26	-1.78	35
CSW-18XPBW ZN1	-0.55	29	0.60	4	0.01	24	0.07	14	-3.21	44	0.40	6	-0.26	44	0.25	20
CSW-18XPBW-343	0.51	15	-0.78	42	-0.13	37	0.09	10	1.49	10	0.38	8	-0.08	25	1.75	9
CSW-18XHD-3326	0.04	23	-0.14	27	0.13	7	0.02	24	1.72	8	-0.28	34	-0.15	30	-1.16	31
PBW-757X PBW ZN1	2.93	4	-0.80	44	-0.03	30	0.16	4	3.00	4	-0.15	32	-0.08	27	2.43	7
PBW-757X PBW-343	-1.10	34	0.50	6	0.03	20	0.10	9	1.30	13	0.19	15	-0.32	45	2.59	6
PBW-757X HD-3326	-1.84	43	-0.51	37	0.01	22	0.14	6	-4.30	45	0.39	7	0.03	16	-1.89	37
SE (sca effect)	23.99		2.14		11.78		4.51		16.30		2.31		0.56		1.84	

Note: Ranking is in ascending order (i.e. 1 is the best followed by 2 on and on). Chlorophyll content (CLC), number of grains per spike (NGS), Grain weight/spike (GW/S), 1000-grain weight (g) (1000-GW), Biomass yield (BY), Harvest index (HI %), Protein content (PC), and Grain yield/plant (GY/P)

4.3.4. Estimates of specific combining ability effects across three locations (E1, E2, & E3)

4.3.4.1 Days to 50% heading

This parameter measures the number of days required for each genotype to reach 50% heading across three environments, representing the speed of plant development. Genotypes with Fast Heading (Lower Values) HD-3117X HD-3326 has the lowest days to heading in E1 (-16.2667, Rank45), indicating that this genotype reaches heading quickly in E1. PBW-677XPBW-343 performs similarly fast in E2 with a high positive value (12.83704, Rank 3) and in E3 with 7.674074 (Rank6). Genotypes DBW-222X HD-3326 and DH-3086X PBW ZN1 also exhibit rapid heading in various environments, showing adaptability and faster growth under certain conditions.

4.3.4.2 Plant height (cm)

Genotypes PBW-757X PBW ZN1 has relatively shorter plants in E1 (-7.0583, Rank 38), E2 (-2.75659, Rank 29), and E3 (-4.37004, Rank42), indicating suitability for areas prone to lodging. PBW-822X HD-3326 also demonstrates low plant height across all environments, particularly in E3 with -5.65715 (Rank43). Genotypes with taller heights (Higher Values) HD-3721XHD-3326 and CRDGEHNU1XPBW343 are among the tallest genotypes across environments, with values of 11.9873 (Rank1) and 10.19852 (Rank5) in E2 and E3, respectively. PWB-725X PBW ZN1 consistently ranks as one of the tallest genotypes in each environment, particularly in E1 (11.00281, Rank1). Genotypes with variable heights across environments PBW-550X PBW ZN1 shows significant variation in height, with E1 being relatively short (-0.75385, Rank 27) and taller in E2 and E3. CSW-18XHD-3326 has moderate to low height values across all environments, reflecting intermediate performance.

4.3.4.3 Grain filling period

The grain filling period genotype CRDGEHNU1XPBW ZN1 ranked highest in E1 with a grain filling period of 7.037037 (Rank1), indicating a long grain-filling duration, which could contribute to higher yield potential in E1. In E2, it also has a positive grain filling period (2.074074, Rank 12), showing consistency. However, in E3, it has a shorter grain filling period (-9.15556, Rank 45), suggesting variability in its grain filling duration across environments. PBW-550X PBW ZN1 this genotype exhibits a high grain filling period in E3 with 8.288889 (Rank 5), E2 with 4.740741 (Rank 9), and E1 with -5.74074 (Rank 41). This shows that it performs better in E2 and E3, while E1 may not be optimal for its grain-filling duration. PBW-757X PBW-343 this genotype performs very well in E3 with a high value of 11.31111 (Rank 1), indicating it has the longest grain filling period in this environment, potentially benefiting yield.

4.3.4.4 Days to maturity

Early maturing genotypes (Lower Values) CRDGEHNU1XPBW343 this genotype shows extremely early maturity across environments, with -16.8963 (Rank 45) in E1, -8.32593 (Rank 42) in E2, and -6.86667 (Rank42) in E3. Its consistently early maturity makes it suitable for regions with shorter growing seasons. PBW-550X PBW-343 Shows early maturity in E1 (-15.8963, Rank 43), E2 (-7.65926, Rank 39), and E3 (-8.86667, Rank 44), suggesting a short growth cycle. HD-3721XPBW ZN1 this genotype also ranks among the early matures in E1 with -16.1185 (Rank 44) and E2 with 0.318519 (Rank23), indicating early maturity across environments. Late maturing genotypes (Higher Values) PBW-550X PBW ZN1 this genotype matures very late in E1 with 14.65926 (Rank1) and has positive values across all environments, indicating a long growth duration and potential for high yield. CRDGEHNU1XPBW ZN1 late maturity is observed in E1 (11.32593, Rank2) and E2 (11.87407, Rank 1), showing that it has a long growth cycle, especially in E1 and E2. DBW-173X PBW-343 matures very late in E3 with 8.577778 (Rank1) and E2 with a high value of 0.562963 (Rank19), suggesting a lengthy growth cycle beneficial for yield.

4.3.4.5 Number of spikelets per spike

Location E1 genotype PBW-677XPBW-343 has the highest value (1.533481), indicating superior performance. CSW-18XHD-3326 (1.157259) and HD-3721XPBW ZN1 (1.008148) follow closely, suggesting they are well-suited to E1 conditions. Location E2 the rankings are consistent with E1, with PBW-677XPBW-343 (1.533481) and CSW-18XHD-3326 (1.157259) again in the top ranks. Location E3 DBW-173X PBW-343 performs best here (1.570222), with HD-3721XPBW-343 (0.891333) and BHU-31XPBW ZN1 (0.766667) also showing high performance. The shift in top performers suggests that E3 conditions are different enough to impact which genotypes excel. However, poor performance recorded at location E1 and E2 genotype HD-3721XPBW-343 ranks lowest in both locations (-1.1243 in E1 and E2), suggesting low adaptation in these conditions. Location E3 DBW-222X HD-3326 performs worst here (-1.15689), reflecting poor spikelet development under E3 conditions.

4.3.4.6 Number of productive tillers per plant

Location E1 Genotype HD-3721XHD-3326 ranks highest with 1.779481, indicating it produces a high number of productive tillers. DH-3086X PBW-343 (1.489926) and DBW-222X PBW ZN1 (0.841704) also perform well, showing potential for high yield under E1 conditions. Location E2 DH-3086X HD-3326 leads here with 1.588074, followed by DBW-222X PBW ZN1 (1.445407), reflecting good adaptability to E2 (Table 16). Location E3 Genotype CRDGEHNU1XPBWZN1 (1.048074) has the highest ranking, followed closely by DBW-222X PBW ZN1 (0.964741) and BHU-31XHD-3326 (0.981696), suggesting they can produce well in E3. Poor Performance were revealed at location E1 in genotype WB-02XHD-3326 ranks lowest (-1.0983), suggesting low tiller productivity in E1. DBW-222X HD-3326 (-1.35719) and DH-3086X PBW ZN1 (-1.28052) are also poor performers. Location E2 DH-3086X PBW-343 (-2.11348) and PBW-550X HD-3326 (-0.57304) have low productivity in E2, indicating they are less suited for this location. Location E3 DBW-222X HD-3326 (-1.00608) and HD-3721XPBW-343 (-0.86088) have the lowest rankings in E3, indicating poor tiller productivity.

4.3.4.7 Chlorophyll content

Genotype PBW-757X PBW ZN1 achieves top ranks in all locations (Rank 1 in E1 and E2) with high chlorophyll values of 4.5, 7.84, and a negative value in E3 (-3.54). Despite a drop in E3, this genotype shows robust performance in the first two locations, indicating a strong potential for chlorophyll synthesis in specific environments. PBW-677XPBW-343 ranks high in E2 (Rank 2) with a chlorophyll content value of 7.34, showing adaptability, particularly in E2. However, it ranks much lower in E3 (-6.02, Rank 45), indicating environmental sensitivity. PBW-550X HD-3326 performs consistently well in E2 (Rank 3 with a value of 7.18) and moderately in E1 and E3 (Table 17). This genotype shows promise across different environments, though it performs better in some than others. Low-Performing genotypes (low chlorophyll content) PBW-677XPBW ZN1 ranks 45th in E2 and E3, showing negative chlorophyll content values in E2 (-7.02) and E3 (2.70). This suggests poor adaptability and low chlorophyll content under these environmental conditions. HD-3117X HD-3326 despite a positive ranking in E1, it scores poorly in E2 and E3, highlighting environmental sensitivity and overall low chlorophyll performance across the locations.

4.3.4.8 Flag leaf area (cm^2)

Genotype CRDGEHNU1XPBWZN1 consistently ranks highest in flag leaf area across all locations (Ranks 1 in E1, E2, and E3) with values of 12.48, 12.15, and 11.25, respectively. This consistency suggests strong genetic potential for large leaf area and adaptability across varied environments. HD-3117X PBW ZN1 another top performer, ranking 2 in E1, E2, and E3 with values of 10.05, 9.39, and 9.49 (Table 17). This genotype's large flag leaf area in all environments indicates stability and high adaptability. Moderate performers PBW-822X PBW-343: Shows relatively high rankings across locations (Rank 6 in E1, Rank 4 in E2, and Rank 3 in E3) with flag leaf area values of 5.30, 6.34, and 7.28. Although it doesn't top the ranks, its consistent moderate-to-high performance across environments indicates it's a reliable genotype for moderate flag leaf area under varying conditions. Low-performing genotypes (small flag leaf area) recorded in CRDGEHNU1XPBW343 ranked lowest in all locations (Rank44 in E1, Rank 44 in E2, Rank 43 in E3) with values of -7.28, -6.91, and -6.75, indicating a very small flag leaf area regardless of environment.

4.3.4.9 Spike length

Spike length varies significantly across locations, as evident from the diverse rankings for genotypes across E1, E2, and E3. For instance, the best performing genotypes was PBW-757X PBW ZN1 (E1 0.706741 (Rank 1), however, it performed very poor in E2 -0.49926 (Rank 38) and E3 -0.6763 (Rank 42) and DH-3086X PBW ZN1 performed well in E2 1.281852 (Rank 1) and E3 0.993704 (Rank 2) but poorly performed in E1 0.05563 (Rank 21)

4.3.4.10 Number of grains per spike

The best performing genotype was DH-3086X PBW ZN1 (E3 9.503852 (Rank 1)) but recorded poor performance in E1 -0.89674 (Rank 34) and E2 -0.88778 (Rank 33). It underperforms in E1 and E2, it achieves the highest value in E3, indicating a strong genotype-environment interaction. PBW-757X PBW-343 performed well in E3 7.553852 (Rank 2), however, drastically dropped in E1 -1.79941 (Rank 39) and E2 0.194222 (Rank 20)

4.3.4.11 1000-Grain weight (g)

In location E1 the genotype with the highest 1000-grain weight is DBW-173X PBW ZN1 (1.139111), ranked 1st. Other high performers include PBW-550X PBW-343 (0.999333) and BHU-25XPBW ZN1 (0.734667). Lowest performance were recorded in DBW-173X PBW-343 shows the lowest 1000-grain weight (-1.09733), ranking last. BHU-25XHD-3326 (-0.90289) and BHU-31XPBW ZN1 (-0.64533) also have lower weights (Table 18). Location E2 the best genotype for E2 is CRDGEHNU1XPBWZN1 (2.359481), showing strong adaptability to this environment. PWB-725X HD-3326 (1.847704) and PBW-822X HD-3326 (1.097704) also rank highly. However, the lowest performance recorded in CRDGEHNU1XHD-3326 (-2.50785) ranks the lowest, with PBW-822X PBW ZN1 (-2.08496) also performing poorly in this location. At location E3 genotype PBW-822X HD-3326 (2.856963) was the top followed by PWB-725X PBW ZN1 (1.946963) and PBW-550X HD-3326 (1.441407). However, lowest performance was revealed in PBW-822X PBW ZN1 (-3.92637) ranks the lowest, with PWB-725X HD-3326 (-1.78637) also struggling in this location.

4.3.4.12 Grain weight per spike (g)

Genotype at location E1 CSW-18XPBW ZN1 (0.279259) ranks 1st, indicating strong grain weight per spike. DBW-173X PBW-343 (0.276593) and PBW-757X HD-3326 (0.237481) follow. Lowest performing were recorded DBW-222X HD-3326 (-0.2403) has the lowest grain weight per spike in E1, followed by PWB-725X PBW-343 (-0.21007) and DH-3086X PBW ZN1 (-0.21519). Location E2 the highest grain weight per spike in E2 is from PBW-822X PBW-343 (0.485556), followed closely by HD-3117X PBW ZN1 (0.464667) and DBW-173X PBW ZN1 (0.455778) (Table 18). However, lowest performance was recorded in PBW-822X HD-3326 (-0.638), suggesting poor suitability for this genotype in E2. Location E3 genotype BHU-31XPBW-343 (0.466815) and HD-3721XPBW ZN1 (0.447259) show the best grain weight per spike, suggesting adaptability to E3 conditions. Lowest performance WB-02XHD-3326 (-0.49407) and HD-3721XPBW-343 (-0.05319) perform poorly in E3, suggesting they might not be well-suited to this environment.

4.3.4.13 Biological yield (g)

In E1 location the genotype with the highest Biological Yield was PBW-677XPBW-343 with a value of 4.715259, ranked 1st. E2 PWB-725X PBW-343 has the highest value at this location, 8.907481, ranked 1st. E3 CRDGEHNU1XPBWZN1 is the highest-yielding genotype here, with a value of 5.323556, ranked 1st. The lowest performing genotypes in biological yield E1 PBW-757X HD-3326 has the lowest value of -4.29696, ranked 45th. E2 WB-02XPBW-343 shows the lowest yield at this location, with a value of -8.21363, ranked 45th. E3 BHU-31XPBW ZN1 has the lowest value, -6.93978, ranked 45th.

4.3.4.14 Harvest index (%)

Results in E1 revealed that PWB-725X HD-3326 has the highest Harvest Index with a value of 4.670074, ranked 1st. E2 BHU-31XHD-3326 scores the highest here with 4.527037, ranked 1st. E3 HD-3117X HD-3326 achieves the top rank, with a Harvest Index of 5.542889, ranked 1st. Lowest-performing Genotypes in harvest index E1 PWB-725X PBW ZN1 shows the lowest value, -4.09237, ranked 45th. E2 BHU-25XPBW ZN1 has the lowest value of -4.5743, ranked 44th. E3 HD-3721XHD-3326 ranks the lowest with -5.94822, ranked 45th.

4.3.4.15 Protein content

High performing genotypes for protein content the best genotypes in E1 were HD-3721XPBW ZN1 (Protein1.538, rank1), PWB-725X PBW-343 (Protein 0.816, rank2) CRDGEHNU1XHD-3326 (Protein 0.494, Rank3) these genotypes have a higher protein content in E1, making them good candidates for nutrient-dense yield in this environment. The best genotypes in E2 DH-3086X PBW-343 (Protein 0.189, rank1), PBW-757X PBW ZN1 (Protein 0.153, rank2) and PWB-725X PBW-343 (Protein: 0.107, rank 3). The best genotypes in E3 genotype PBW-677XPBW-343 (Protein1.947, rank1), DH-3086X, PBW ZN1 (protein1.678, rank2) and PWB-725X PBW-343 (Protein1.627, rank3).

4.3.4.16 Grain yield per plant (g)

High Performing Genotypes for grain yield per plant best genotypes in E1 PBW-822X PBW ZN1 (Yield 6.012, rank 1) WB-02XPBW ZN1 (yield 4.717, rank 2) PWB-725X HD-3326 (Yield 4.630, rank 3), these genotypes exhibit superior yield in E1, indicating that they are potentially well-suited to the environmental conditions of E1 (Table 20). Genotypes in E2 BHU-31XHD-3326 (Yield 4.476, rank 1) PBW-757X PBW-343 (Yield 3.893, rank 2) BHU-25XPBW ZN1 (Yield 2.625, Rank 3) Genotypes in E3 PBW-677XPBW-343 (Yield 7.396, rank 1) BHU-31XHD-3326 (yield 5.972 rank 2) DBW-173X HD-3326 (Yield 5.962, rank 3).

Table 4.3.2: Estimates of specific combining ability of forty five crosses for different characters for across 3 (E1-E3) locations

	Days to 50% heading across locations (E1, E2 & E3)						**Plant height across locations (E1, E2 & E3)**					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	2.36	15	6.75	12	6.07	10	-7.71	40	9.37	6	1.54	12
BHU-25XPBW-343	-4.76	39	-7.92	36	-8.42	42	3.76	15	-5.02	36	-1.52	33
BHU-25XHD-3326	2.40	14	1.17	22	2.34	15	3.95	13	-4.35	33	-0.01	20
WB-02XPBW ZN1	0.36	25	7.08	11	3.07	14	1.23	23	-3.28	31	0.67	17
WB-02XPBW-343	-0.09	28	8.42	7	7.25	7	-6.11	36	-7.68	42	-0.08	23
WB-02XHD-3326	-0.27	29	-15.50	44	-10.33	43	4.88	9	10.96	4	-0.59	27
BHU-31XPBW ZN1	-5.20	40	-4.81	31.5	1.30	20	-9.04	42	-5.18	37	-0.79	29
BHU-31XPBW-343	0.02	27	6.19	15	-1.19	24	5.61	7	11.14	3	8.52	2
BHU-31XHD-3326	5.18	7	-1.39	26	-0.10	22	3.43	18	-5.96	39	-7.73	44
HD-3721XPBW ZN1	1.24	19	1.42	21	-3.82	32	4.03	12	-7.81	43	-8.32	45
HD-3721XPBW-343	-1.87	32	-9.25	38	1.70	19	-7.72	41	-5.50	38	-3.67	40
HD-3721XHD-3326	0.62	24	7.84	8	2.12	16	3.68	16	13.31	1	11.99	1
PWB-725X PBW ZN1	-3.42	36	1.86	20	0.63	21	11.00	1	-3.59	32	1.27	14
PWB-725X PBW-343	3.13	10	-4.81	31.5	-6.86	38	-7.23	39	-4.88	35	2.24	8
PWB-725X HD-3326	0.29	26	2.95	18	6.23	9	-3.78	31	8.46	7	-3.51	39
CRDGEHNU1XPBWZN1	-4.42	38	4.08	17	-0.26	23	-5.69	35	1.31	17	2.14	9
CRDGEHNU1XPBW343	1.80	18	7.08	10	13.59	1	10.65	2	10.20	5	-3.97	41
CRDGEHNU1XHD-3326	2.62	13	-11.16	41	-13.33	45	-4.96	33	-11.51	44	1.83	10
PBW-550X PBW ZN1	-2.87	34	6.19	16	8.96	5	-0.75	27	-7.53	41	3.92	6
PBW-550X PBW-343	6.69	5	-3.47	28	-4.86	36	2.51	21	5.48	8	-0.58	26

PBW-550X HD-3326	-3.82	37	-2.72	27	-4.10	34	-1.75	28	2.04	15	-3.34	38
PBW-677XPBW ZN1	1.02	21	-4.59	29.5	-3.93	33	7.56	5	-1.03	25	-2.87	37
PBW-677XPBW-343	-9.09	43	-8.25	37	-3.75	31	-10.42	43	-2.60	28	-2.10	36
PBW-677XPBW-343	8.07	2	12.84	3	7.67	6	2.86	19	3.63	12	4.97	4
PBW-822X PBW ZN1	6.80	4	6.75	13	3.85	13	2.77	20	11.18	2	6.01	3
PBW-822X PBW-343	2.02	17	-6.25	33	-1.97	27	8.58	3	2.48	14	-0.36	25
PBW-822X HD-3326	-8.82	42	-0.50	25	-1.88	25	-11.35	44	-13.66	45	-5.66	43
HD-3117X PBW ZN1	8.02	3	-6.25	34	-2.82	30	-5.07	34	0.06	20	-1.79	35
HD-3117X PBW-343	8.24	1	-0.25	24	-2.30	29	3.92	14	1.31	18	1.81	11
HD-3117X HD-3326	-16.27	45	6.50	14	5.12	12	1.15	24	-1.36	27	-0.02	21
DBW-173X PBW ZN1	0.80	23	-9.81	40	-12.15	44	8.15	4	-0.39	22	1.10	15
DBW-173X PBW-343	1.02	22	9.19	6	10.36	3	-12.70	45	-4.77	34	-0.93	30
DBW-173X HD-3326	-1.82	31	0.62	23	1.79	18	4.54	11	5.15	9	-0.17	24
DH-3086X PBW ZN1	-7.09	41	16.75	2	12.96	2	-4.39	32	4.17	11	2.35	7
DH-3086X PBW-343	2.80	11	-4.59	29.5	-7.53	40	0.89	25	-1.18	26	-0.73	28
DH-3086X HD-3326	4.29	8	-12.16	42	-5.44	37	3.50	17	-2.99	30	-1.62	34
DBW-222X PBW ZN1	6.02	6	-9.59	39	-2.15	28	5.11	8	0.87	19	-0.97	31
DBW-222X PBW-343	-9.76	44	-7.92	35	-7.64	41	-3.02	30	-0.47	24	0.03	19
DBW-222X HD-3326	3.73	9	17.50	1	9.79	4	-2.09	29	-0.40	23	0.94	16
CSW-18XPBW ZN1	-3.31	35	2.75	19	-4.48	35	-0.13	26	4.60	10	0.10	18
CSW-18XPBW-343	2.24	16	10.75	5	6.36	8	6.68	6	1.59	16	1.41	13
CSW-18XHD-3326	1.07	20	-13.50	43	-1.88	26	-6.55	37	-6.19	40	-1.52	32

PBW-757X PBW ZN1	-0.31	30	-18.59	45	-7.26	39	-7.06	38	-2.76	29	-4.37	42
PBW-757X PBW-343	-2.42	33	11.08	4	5.25	11	4.58	10	-0.11	21	-0.06	22
PBW-757X HD-3326	2.73	12	7.50	9	2.01	17	2.48	22	2.87	13	4.43	5
SE (sca effect)	2.94		1.56		0.41		1.31		1.17		0.41	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd

	Grain filling period across 3 locations (E1, E2 & E3)						**Days to maturity across 3 locations (E1, E2 & E3)**					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	0.93	19	0.63	25	5.29	8	4.44	17	4.32	10	-1.20	31
BHU-25XPBW-343	1.99	16	-2.19	34	-7.13	41	-2.12	29.5	0.45	20	4.24	8
BHU-25XHD-3326	-2.92	33	1.56	18	1.84	17	-2.32	31	-4.77	36	-3.04	36
WB-02XPBW ZN1	-2.74	32	-2.93	36	-0.49	24	-11.45	39	0.10	24	0.36	25
WB-02XPBW-343	-3.34	35	1.92	16	5.09	9	8.33	8	-3.77	35	4.80	4
WB-02XHD-3326	6.08	4	1.01	22	-4.60	36	3.13	20	3.67	12	-5.16	40
BHU-31XPBW ZN1	0.59	22	5.19	7	1.40	19	2.88	21	2.76	16	-0.76	29
BHU-31XPBW-343	-0.34	26	6.36	4	1.31	20	9.66	4	-3.10	31	4.36	7
BHU-31XHD-3326	-0.25	25	-11.55	45	-2.71	28	-12.54	40	0.34	22	-3.60	37
HD-3721XPBW ZN1	2.48	13	-0.59	29	6.07	7	-16.12	44	0.32	23	0.69	23
HD-3721XPBW-343	4.22	8	1.25	20	-8.36	44	6.99	11	3.12	15	0.47	24
HD-3721XHD-3326	-6.70	43	-0.66	30	2.29	15	9.13	5	-3.44	33	-1.16	30
PWB-725X PBW ZN1	3.04	11	-2.26	35	-4.49	35	-11.34	38	-10.90	45	-7.42	43

PWB-725X PBW-343	1.77	17	-0.75	31	3.42	12	8.10	9	10.90	2	5.02	3
PWB-725X HD-3326	-4.81	39	3.01	11	1.07	21	3.24	19	0.01	25.5	2.40	15
CRDGEHNU1XPBWZN1	7.04	1	2.07	12	-9.16	45	11.33	2	11.87	1	2.36	16
CRDGEHNU1XPBW343	-8.23	45	4.92	8	1.42	18	-16.90	45	-8.33	42	-6.87	42
CRDGEHNU1XHD-3326	1.19	18	-6.99	41	7.73	6	5.57	15	-3.55	34	4.51	6
PBW-550X PBW ZN1	-5.74	41	4.74	9	8.29	5	14.66	1	1.54	17	4.69	5
PBW-550X PBW-343	5.66	5	-9.42	43	-4.13	31	-15.90	43	-7.66	39	-8.87	44
PBW-550X HD-3326	0.08	24	4.67	10	-4.16	32	1.24	23	6.12	6	4.18	9
PBW-677XPBW ZN1	-0.52	27	2.07	13	-0.82	25	-2.56	32	-3.35	32	-2.64	35
PBW-677XPBW-343	-3.79	37	-4.08	37	-4.24	33	-1.12	28	-0.22	27	1.80	17
PBW-677XPBW-343	4.30	7	2.01	14	5.07	10	3.68	18	3.56	13	0.84	20
PBW-822X PBW ZN1	-1.19	29	5.41	6	9.07	3	-2.12	29.5	-2.90	30	0.69	22
PBW-822X PBW-343	0.88	20	-6.75	40	-4.36	34	-5.34	35	-4.77	37	-6.53	41
PBW-822X HD-3326	0.30	23	1.34	19	-4.71	37	7.46	10	7.67	3.5	5.84	2
HD-3117X PBW ZN1	1.02	9	-10.82	44	-6.71	40	-4.12	34	-9.13	43	-1.98	33.5
HD-3117X PBW-343	0.61	14	1.70	17	-1.80	27	4.99	16	7.67	3.5	3.80	11
HD-3117X HD-3326	-1.63	42	9.12	1	8.51	4	-0.87	27	1.45	18	-1.82	32
DBW-173X PBW ZN1	-0.75	34	-0.93	32	-3.49	29	-10.45	37	-7.90	40	3.13	12
DBW-173X PBW-343	-0.90	36	-0.08	27	0.76	22	-0.67	26	0.56	19	8.58	1
DBW-173X HD-3326	1.64	2	1.01	21	2.73	14	11.13	3	7.34	5	-11.71	45
DH-3086X PBW ZN1	-0.21	28	0.74	24	-1.60	26	2.55	22	0.43	21	-0.76	28
DH-3086X PBW-343	-0.37	30	0.59	26	9.64	2	-3.67	33	-0.44	28	-1.98	33.5

DH-3086X HD-3326	0.58	15	-1.33	33	-8.04	43	1.13	24.5	0.01	25.5	2.73	13
DBW-222X PBW ZN1	-1.72	44	1.96	15	3.29	13	6.55	14	5.76	7	0.91	19
DBW-222X PBW-343	0.73	12	6.47	3	1.87	16	-7.67	36	-5.10	38	-0.31	26
DBW-222X HD-3326	1.00	10	-8.44	42	-5.16	39	1.13	24.5	-0.66	29	-0.60	27
CSW-18XPBW ZN1	-0.47	31	0.96	23	0.62	23	6.88	12	3.87	11	1.13	18
CSW-18XPBW-343	1.56	3	-6.53	39	-4.80	38	8.66	7	5.67	8	-3.76	38
CSW-18XHD-3326	-1.10	38	5.56	5	4.18	11	-15.54	42	-9.55	44	2.62	14
PBW-757X PBW ZN1	1.16	6	-6.26	38	-7.27	42	8.88	6	3.21	14	0.80	21
PBW-757X PBW-343	-1.34	40	6.59	2	11.31	1	6.66	13	5.01	9	-4.76	39
PBW-757X HD-3326	0.19	21	-0.33	28	-4.04	30	-15.54	41	-8.22	41	3.96	10
SE (sca effect)	0.62		0.40		0.54		0.35		1.57		0.32	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

	Number of spikelet/Spike across 3 locations (E1, E2 & E3)						**Number of productive tiller/plant across locations (E1, E2 & E3)**					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	0.13	19	0.13	19	-0.20	30	0.32	13	-0.26	30	0.19	20
BHU-25XPBW-343	0.24	17	0.24	17	-0.25	31	-0.26	29	0.25	15	-0.56	36
BHU-25XHD-3326	-0.37	32	-0.37	32	0.45	8	-0.07	21	0.01	22	0.37	16
WB-02XPBW ZN1	-0.03	22	-0.03	22	0.16	18	1.33	3	-0.46	40	-0.82	39
WB-02XPBW-343	0.36	13	0.36	13	-0.09	25	-0.24	27	-0.05	24	0.56	10
WB-02XHD-3326	-0.33	30	-0.33	30	-0.07	22	-1.10	42	0.50	8	0.27	19

BHU-31XPBW ZN1	0.48	12	0.48	12	0.77	3	0.53	10	-0.41	35	-1.31	43
BHU-31XPBW-343	-0.01	21	-0.01	21	-0.57	40	-0.56	35	0.46	10	0.33	17
BHU-31XHD-3326	-0.46	33	-0.46	33	-0.20	29	0.03	19	-0.06	25	0.98	2
HD-3721XPBW ZN1	1.01	3	1.01	3	-0.86	43	-0.50	33	0.12	18	0.87	6
HD-3721XPBW-343	-1.12	45	-1.12	45	0.89	2	-1.29	44	-0.24	29	-0.86	40
HD-3721XHD-3326	0.12	20	0.12	20	-0.03	21	1.78	1	0.12	19	-0.01	25
PWB-725X PBW ZN1	-0.86	40	-0.86	40	0.54	7	-0.55	34	-0.41	36	-0.17	29
PWB-725X PBW-343	0.96	5	0.96	5	-0.08	24	-0.66	40	0.35	13	0.40	15
PWB-725X HD-3326	-0.10	25	-0.10	25	-0.46	37	1.21	4	0.06	21	-0.23	30
CRDGEHNU1XPBWZN1	-0.13	26	-0.13	26	0.33	12	-0.08	22	0.51	7	1.05	1
CRDGEHNU1XPBW343	0.31	14	0.31	14	-1.04	44	0.19	17	-0.22	28	0.30	18
CRDGEHNU1XHD-3326	-0.18	29	-0.18	29	0.71	4	-0.11	24	-0.29	31	-1.34	44
PBW-550X PBW ZN1	-0.04	23	-0.04	23	0.41	10	-0.60	39	0.62	4	-1.42	45
PBW-550X PBW-343	-0.50	36	-0.50	36	0.29	15	0.28	14	-0.05	23	0.89	4
PBW-550X HD-3326	0.54	11	0.54	11	-0.70	42	0.32	12	-0.57	42	0.53	11
PBW-677XPBW ZN1	-1.04	42	-1.04	42	-0.12	27	-0.57	36	-0.42	37	-0.34	31
PBW-677XPBW-343	1.53	1	1.53	1	-0.32	34	0.89	6	0.27	14	-0.35	32
PBW-677XPBW-343	-0.49	35	-0.49	35	0.44	9	-0.32	31	0.15	17	0.70	8
PBW-822X PBW ZN1	-0.16	28	-0.16	28	-0.27	33	0.84	8	-0.49	41	-0.01	26
PBW-822X PBW-343	-0.57	37	-0.57	37	0.19	16	-0.60	37	0.80	3	-0.12	28
PBW-822X HD-3326	0.73	7	0.73	7	0.08	20	-0.24	28	-0.30	32	0.14	21
HD-3117X PBW ZN1	0.98	4	0.98	4	-0.36	35	-0.27	30	0.36	12	0.46	13

HD-3117X PBW-343	-0.35	31	-0.35	31	-0.26	32	0.25	16	-0.43	38	0.11	22
HD-3117X HD-3326	-0.63	38	-0.63	38	0.61	6	0.02	20	0.07	20	-0.56	37
DBW-173X PBW ZN1	0.74	6	0.74	6	-0.41	36	-0.91	41	-0.33	33	-0.41	34
DBW-173X PBW-343	-1.05	43	-1.05	43	1.57	1	1.00	5	0.51	6	0.80	7
DBW-173X HD-3326	0.30	15	0.30	15	-1.16	45	-0.09	23	-0.18	27	-0.39	33
DH-3086X PBW ZN1	-0.88	41	-0.88	41	0.31	14	-1.28	43	0.53	5	0.52	12
DH-3086X PBW-343	0.16	18	0.16	18	-0.19	28	1.49	2	-2.11	45	-1.14	42
DH-3086X HD-3326	0.72	8	0.72	8	-0.12	26	-0.21	26	1.59	1	0.62	9
DBW-222X PBW ZN1	0.29	16	0.29	16	-0.46	38	0.84	7	1.45	2	0.97	3
DBW-222X PBW-343	0.57	10	0.57	10	0.12	19	0.52	11	-0.45	39	0.04	23
DBW-222X HD-3326	-0.86	39	-0.86	39	0.35	11	-1.36	45	-1.00	44	-1.01	41
CSW-18XPBW ZN1	-1.11	44	-1.11	44	0.65	5	0.14	18	-0.72	43	-0.43	35
CSW-18XPBW-343	-0.05	24	-0.05	24	-0.57	41	-0.42	32	0.49	9	0.43	14
CSW-18XHD-3326	1.16	2	1.16	2	-0.08	23	0.28	15	0.23	16	0.00	24
PBW-757X PBW ZN1	0.61	9	0.61	9	-0.48	39	0.75	9	-0.09	26	0.87	5
PBW-757X PBW-343	-0.47	34	-0.47	34	0.32	13	-0.60	38	0.42	11	-0.80	38
PBW-757X HD-3326	-0.14	27	-0.14	27	0.17	17	-0.15	25	-0.34	34	-0.07	27
SE (sca effect)	0.44		0.64		0.42		0.44		0.31		0.26	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

	Chlorophyll content across 3 locations (E1, E2 & E3)						Flag leaf area across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	2.24	7	4.98	6	-3.30	40	-5.26	41	-5.14	39	-5.94	40
BHU-25XPBW-343	-3.13	43	-2.81	36	2.83	9	0.70	21	1.18	20	1.12	20
BHU-25XHD-3326	0.89	16	-2.17	31	0.47	22	4.56	8	3.96	9	4.82	7
WB-02XPBW ZN1	0.48	15	0.08	21	0.45	23	-5.01	38	-5.11	38	-4.57	36
WB-02XPBW-343	1.30	5	-1.09	28	1.56	15	3.26	10	3.51	10	3.12	11
WB-02XHD-3326	-1.78	44	1.01	16	-2.01	34	1.75	17	1.60	16	1.45	17
BHU-31XPBW ZN1	-0.64	33	-2.37	34	-1.31	30	0.75	20	0.09	24	0.08	23
BHU-31XPBW-343	-0.40	27	-4.07	40	0.57	21	2.78	11	2.81	11	3.86	9
BHU-31XHD-3326	1.05	6	6.44	4	0.74	20	-3.53	31	-2.90	32	-3.94	33
HD-3721XPBW ZN1	-0.56	31	0.10	20	2.05	12	3.88	9	4.56	8	5.43	5
HD-3721XPBW-343	0.71	13	1.27	14	-3.20	39	-4.15	32	-6.12	42	-7.51	44
HD-3721XHD-3326	-0.15	25	-1.37	29	1.15	17	0.27	24	1.56	18	2.08	15
PWB-725X PBW ZN1	-0.88	36	-2.34	33	1.28	16	2.03	15	1.92	15	3.02	12
PWB-725X PBW-343	0.09	24	5.31	5	-4.83	42	-0.24	25	0.35	22	0.84	22
PWB-725X HD-3326	0.79	11	-2.98	37	3.55	4	-1.79	28	-2.27	30	-3.86	32
CRDGEHNU1XPBWZN1	0.23	21	4.24	7	-1.37	31	12.48	1	12.15	1	11.25	1
CRDGEHNU1XPBW343	-0.48	28	-0.95	26	3.35	6	-7.28	44	-6.92	44	-6.75	43
CRDGEHNU1XHD-3326	0.25	19	-3.28	38	-1.98	33	-5.20	40	-5.24	40	-4.50	35
PBW-550X PBW ZN1	0.24	20	-6.64	44	0.86	18	-4.72	37	-4.38	35	-3.95	34
PBW-550X PBW-343	-0.56	29.5	-0.54	25	-2.80	38	2.32	14	2.35	13	2.51	14

PBW-550X HD-3326	0.32	18	7.18	3	1.93	14	2.40	13	2.03	14	1.44	18
PBW-677XPBW ZN1	-0.75	35	-7.02	45	2.71	10	-5.86	42	-6.19	43	-5.76	39
PBW-677XPBW-343	0.97	8	7.34	2	-6.02	45	1.21	19	1.57	17	2.07	16
PBW-677XPBW-343	-0.22	26	-0.32	24	3.31	7	4.66	7	4.62	7	3.69	10
PBW-822X PBW ZN1	1.76	2.5	-4.07	41	-1.23	29	-0.80	26	-2.12	29	-1.25	29
PBW-822X PBW-343	-1.97	45	3.32	9	7.07	1	5.31	6	6.34	4	7.28	3
PBW-822X HD-3326	0.22	22	0.75	17	-5.84	44	-4.51	34	-4.22	33	-6.03	41
HD-3117X PBW ZN1	-2.04	37	2.77	11	-5.50	43	10.05	2	9.39	2	9.49	2
HD-3117X PBW-343	0.34	23	3.20	10	0.83	19	-2.72	30	-1.69	28	-1.86	30
HD-3117X HD-3326	1.70	12	-5.97	43	4.67	2	-7.33	45	-7.70	45	-7.63	45
DBW-173X PBW ZN1	-2.80	40	-0.05	23	0.34	24	-4.58	36	-4.24	34	-4.59	37
DBW-173X PBW-343	2.06	9	-2.32	32	1.99	13	-0.85	27	-0.82	26	-0.10	24
DBW-173X HD-3326	0.74	17	2.37	12	-2.33	35	5.44	5	5.06	6	4.69	8
DH-3086X PBW ZN1	-2.43	38	1.11	15	2.84	8	-6.35	43	-6.01	41	-6.47	42
DH-3086X PBW-343	3.79	2.5	-0.04	22	-2.40	36	0.48	23	0.51	21	1.12	19
DH-3086X HD-3326	-1.36	32	-1.07	27	-0.44	26	5.87	4	5.50	5	5.35	6
DBW-222X PBW ZN1	3.72	4	3.51	8	2.35	11	-1.88	29	-1.54	27	-0.67	27
DBW-222X PBW-343	-2.52	39	-3.84	39	-1.76	32	1.25	18	1.28	19	0.89	21
DBW-222X HD-3326	-1.20	29.5	0.33	19	-0.59	27	0.64	22	0.26	23	-0.22	26
CSW-18XPBW ZN1	-2.92	41	-2.12	30	3.38	5	-4.31	33	-2.74	31	-1.87	31
CSW-18XPBW-343	1.77	10	0.51	18	-0.74	28	2.49	12	0.08	25	-0.98	28
CSW-18XHD-3326	1.16	14	1.61	13	-2.64	37	1.81	16	2.66	12	2.85	13

PBW-757X PBW ZN1	4.50	1	7.84	1	-3.54	41	9.57	3	9.36	3	5.79	4
PBW-757X PBW-343	-1.54	34	-5.30	42	3.56	3	-4.56	35	-4.42	36	-5.59	38
PBW-757X HD-3326	-2.96	42	-2.54	35	-0.01	25	-5.01	39	-4.94	37	-0.20	25
SE (sca effect)	1.00		1.68		0.98		0.14		0.33		0.38	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

	Spike length across 3 locations (E1, E2 & E3)						**Number of grain per spike across 3 locations (E1, E2 & E3)**					
GENOTYPES	E1	RANK	E2	RANK	E3	RANK	E1	RANK	E2	RANK	E3	RANK
BHU-25XPBW ZN1	0.21	15	-0.17	29	0.55	6	-0.10	27	-0.08	26	-1.80	31
BHU-25XPBW-343	0.36	10	0.23	14	-0.16	29	-0.77	33	-0.09	28	0.93	17
BHU-25XHD-3326	-0.57	42	-0.06	25	-0.39	38	0.87	15	0.17	21	0.86	18
WB-02XPBW ZN1	-0.20	30	-0.16	28	0.13	19	0.92	14	-0.18	29	2.38	9
WB-02XPBW-343	0.01	24	0.17	18	-0.18	30	-1.69	37	1.75	3	1.87	13
WB-02XHD-3326	0.19	16	-0.01	21	0.04	21	0.77	18	-1.57	39	-4.26	39
BHU-31XPBW ZN1	-0.42	37	-0.26	34	-0.33	32	-2.08	40	-1.63	40	-0.90	28
BHU-31XPBW-343	0.25	13	0.21	16	0.38	10	1.05	12	-1.24	37	-1.44	29
BHU-31XHD-3326	0.18	17	0.05	20	-0.06	25	1.03	13	2.87	2	2.34	10
HD-3721XPBW ZN1	-0.22	31	0.26	11	0.31	13	-2.18	41	-0.07	25	-2.57	33
HD-3721XPBW-343	0.51	6	-0.45	37	-0.50	41	1.58	7	1.45	5	-1.97	32
HD-3721XHD-3326	-0.29	34	0.19	17	0.19	18	0.60	20	-1.38	38	4.53	6
PWB-725X PBW ZN1	0.57	5	0.72	5	0.32	12	1.13	11	0.49	16	-0.79	26

PWB-725X PBW-343	-0.08	28	-0.19	32	-0.35	36	0.56	22	-1.92	42	0.22	23
PWB-725X HD-3326	-0.48	40	-0.54	39	0.03	24	-1.68	36	1.44	6	0.57	20
CRDGEHNU1XPBWZN1	-0.35	36	0.22	15	-0.14	27	-1.75	38	0.12	22	-4.62	43
CRDGEHNU1XPBW343	-0.22	32	-0.08	26	0.47	7	1.72	6	0.23	19	1.23	16
CRDGEHNU1XHD-3326	0.57	3	-0.14	27	-0.33	33	0.03	24	-0.36	31	3.39	8
PBW-550X PBW ZN1	0.49	8	0.81	3	0.33	11	1.39	9	0.94	10	5.10	5
PBW-550X PBW-343	0.06	20	-0.80	44	-0.37	37	0.80	17	-0.88	32	-4.31	40
PBW-550X HD-3326	-0.56	41	-0.01	22	0.04	22	-2.19	42	-0.06	24	-0.79	27
PBW-677XPBW ZN1	0.01	25	-0.27	35	-0.45	40	0.58	21	1.43	7	-0.73	25
PBW-677XPBW-343	-0.43	39	-0.03	23	0.03	23	-0.51	30	0.56	14	0.14	24
PBW-677XPBW-343	0.42	9	0.30	10	0.42	8	-0.08	26	-1.99	43	0.60	19
PBW-822X PBW ZN1	0.08	19	-0.04	24	0.23	16	1.36	10	-2.67	45	-3.39	36.5
PBW-822X PBW-343	-0.43	38	-0.77	41	-0.93	43	0.86	16	1.64	4	-2.67	34
PBW-822X HD-3326	0.35	12	0.80	4	0.70	3	-2.22	43	1.03	8	6.06	3
HD-3117X PBW ZN1	0.58	2	-0.78	42	-0.95	44	-2.53	44	3.40	1	-1.78	30
HD-3117X PBW-343	-0.31	35	0.24	13	0.30	14	2.30	2	-1.04	36	0.54	22
HD-3117X HD-3326	-0.27	33	0.53	8	0.65	5	0.23	23	-2.36	44	1.24	15
DBW-173X PBW ZN1	-0.58	43	-0.78	43	-0.07	26	1.76	5	0.35	18	2.30	11
DBW-173X PBW-343	0.36	11	0.25	12	-0.14	28	-4.80	45	-0.27	30	5.42	4
DBW-173X HD-3326	0.22	14	0.54	7	0.21	17	3.05	1	-0.08	27	-7.72	45
DH-3086X PBW ZN1	0.06	21	1.28	1	0.99	2	-0.90	34	-0.89	33	9.50	1
DH-3086X PBW-343	0.02	22	0.12	19	0.40	9	1.55	8	0.85	11	-4.35	41

DH-3086X HD-3326	-0.08	26	-1.40	45	-1.39	45	-0.65	32	0.04	23	-5.16	44
DBW-222X PBW ZN1	0.15	18	-0.17	30	-0.35	35	0.64	19	-0.96	34	-3.24	35
DBW-222X PBW-343	0.02	23	-0.37	36	-0.31	31	-0.35	29	0.49	15	1.29	14
DBW-222X HD-3326	-0.17	29	0.54	6	0.66	4	-0.29	28	0.47	17	1.95	12
CSW-18XPBW ZN1	-1.08	45	-0.18	31	0.09	20	1.78	4	0.75	13	3.92	7
CSW-18XPBW-343	0.51	7	0.42	9	0.25	15	-0.51	31	-1.72	41	-4.47	42
CSW-18XHD-3326	0.57	4	-0.24	33	-0.34	34	-1.27	35	0.98	9	0.56	21
PBW-757X PBW ZN1	0.71	1	-0.50	38	-0.68	42	0.00	25	-1.00	35	-3.39	36.5
PBW-757X PBW-343	-0.63	44	1.04	2	1.10	1	-1.80	39	0.19	20	7.55	2
PBW-757X HD-3326	-0.08	27	-0.55	40	-0.43	39	1.80	3	0.81	12	-4.17	38
SE (sca effect)	1.03		1.38		1.00		0.57		0.53		0.48	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

	1000 grain weight across 3 locations (E1, E2 & E3)						Grain weight per spike across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	0.74	3	-0.24	33	-0.59	33	-0.19	41	-0.12	34	-0.19	34
BHU-25XPBW-343	0.17	16	0.17	19	-0.70	35	0.23	4	0.29	5	-0.25	38
BHU-25XHD-3326	-0.90	44	0.07	25	1.29	7	-0.04	27	-0.17	38	0.44	3
WB-02XPBW ZN1	0.30	10	-1.21	41	0.48	15	0.07	12	0.00	21	-0.31	43
WB-02XPBW-343	-0.41	37	0.47	15	-0.26	25	-0.03	26	-0.11	33	-0.11	30
WB-02XHD-3326	0.11	20	0.74	10	-0.23	24	-0.04	28	0.11	12	0.42	4

BHU-31XPBW ZN1	-0.65	43	0.57	13	1.24	8	0.06	15	-0.09	31	0.03	19
BHU-31XPBW-343	0.25	12	0.52	14	-1.17	39	-0.02	24	-0.04	28	0.47	1
BHU-31XHD-3326	0.40	8	-1.09	39	-0.07	20	-0.05	30	0.13	10	-0.49	45
HD-3721XPBW ZN1	0.23	13	0.26	18	-0.39	30	0.12	10	-0.13	37	0.45	2
HD-3721XPBW-343	0.07	21	-1.07	37	0.55	14	-0.09	35	0.10	13	-0.05	26
HD-3721XHD-3326	-0.30	32	0.81	6	-0.16	22	-0.03	25	0.03	20	-0.39	44
PWB-725X PBW ZN1	0.20	15	-1.08	38	1.95	5	0.16	8	-0.03	25	0.37	5
PWB-725X PBW-343	-0.35	35	-0.77	36	-0.16	23	-0.21	43	-0.24	40	-0.22	36
PWB-725X HD-3326	0.15	18	1.85	2	-1.79	42	0.05	16	0.26	7	-0.16	32
CRDGEHNU1XPBWZN1	-0.33	34	2.36	1	0.91	13	-0.07	31	0.07	16	-0.20	35
CRDGEHNU1XPBW343	-0.04	25	0.15	20	-0.34	28	0.07	13.5	-0.12	35	0.17	11
CRDGEHNU1XHD-3326	0.37	9	-2.51	45	-0.57	32	0.00	21	0.06	18	0.03	20
PBW-550X PBW ZN1	-0.59	42	0.96	5	-1.85	43	-0.08	32	-0.01	23	-0.15	31
PBW-550X PBW-343	1.00	2	-0.20	32	0.41	17	-0.01	22	0.05	19	0.07	16
PBW-550X HD-3326	-0.41	36	-0.76	35	1.44	6	0.09	11	-0.05	29	0.08	15
PBW-677XPBW ZN1	-0.44	38	0.13	21	1.04	10	-0.20	42	0.07	15	-0.02	24
PBW-677XPBW-343	0.48	6	-0.05	28	0.11	18	0.02	19	0.11	11	0.10	14
PBW-677XPBW-343	-0.04	27	-0.08	29	-1.15	38	0.17	6	-0.18	39	-0.09	29
PBW-822X PBW ZN1	-0.24	31	-2.09	44	-3.93	45	0.14	9	0.15	9	-0.27	39
PBW-822X PBW-343	0.23	14	0.99	4	1.07	9	-0.13	37	0.49	1	0.02	22
PBW-822X HD-3326	0.01	23	1.10	3	2.86	1	-0.01	23	-0.64	45	0.26	8
HD-3117X PBW ZN1	0.66	4	0.57	11.5	0.09	3	-0.05	29	0.47	2	0.07	3

HD-3117X PBW-343	-0.13	30	-1.33	42	0.77	29	0.03	17	-0.44	44	0.31	37
HD-3117X HD-3326	-0.53	40	0.76	9	0.15	44	0.01	20	-0.02	24	0.75	27
DBW-173X PBW ZN1	1.14	1	0.34	17	0.99	19	-0.12	36	0.46	3	0.18	6
DBW-173X PBW-343	-1.10	45	-0.36	34	0.48	12	0.28	2	-0.37	43	0.35	10
DBW-173X HD-3326	-0.04	26	0.02	26	0.47	36	-0.15	38	-0.09	32	0.77	17
DH-3086X PBW ZN1	-0.32	33	-0.10	30	0.28	40	-0.22	44	-0.13	36	0.22	41
DH-3086X PBW-343	0.02	22	0.12	22	0.07	2	0.03	18	-0.07	30	0.75	28
DH-3086X HD-3326	0.30	11	-0.02	27	0.45	37	0.19	5	0.19	8	0.84	25
DBW-222X PBW ZN1	-0.10	29	-1.13	40	0.73	31	0.17	7	-0.35	42	0.60	13
DBW-222X PBW-343	0.16	17	0.78	7	0.22	41	0.07	13.5	0.28	6	0.23	7
DBW-222X HD-3326	-0.06	28	0.35	16	0.12	4	-0.24	45	0.07	17	0.96	23
CSW-18XPBW ZN1	-0.01	24	0.57	11.5	0.83	26	0.28	1	-0.33	41	0.25	40
CSW-18XPBW-343	-0.48	39	0.77	8	0.90	21	-0.09	34	0.00	22	0.77	18
CSW-18XHD-3326	0.49	5	-1.34	43	0.73	16	-0.19	40	0.34	4	0.21	42
PBW-757X PBW ZN1	-0.59	41	0.09	24	0.44	11	-0.08	33	-0.04	26	0.34	9
PBW-757X PBW-343	0.13	19	-0.18	31	0.60	34	-0.16	39	0.07	14	0.94	21
PBW-757X HD-3326	0.46	7	0.09	23	0.81	27	0.24	3	-0.04	27	0.49	12
SE (sca effect)	0.57		1.15		0.44		0.17		0.20		0.20	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

Biological Yield across locations (E1, E2 & E3)	Harvest index across locations (E1, E2 & E3)

GENOTYPES	E1	RANK	E2	RANK	E3	RANK	E1	RANK	E2	RANK	E3	RANK
BHU-25XPBW ZN1	-1.07	32	-5.72	42	-2.88	40	1.22	12	-4.57	44	-5.26	44
BHU-25XPBW-343	-2.60	39	5.10	3	-1.38	34	-0.46	27	3.90	3	0.65	23
BHU-25XHD-3326	3.68	3	0.62	19	4.27	3	-0.76	30	0.67	18	4.61	3
WB-02XPBW ZN1	3.99	2	3.18	10	-0.60	28	2.34	5	-0.79	29	1.31	12
WB-02XPBW-343	-3.00	42	-8.21	45	1.44	12	0.52	19	-2.43	41	2.59	7
WB-02XHD-3326	-0.98	31	5.04	4	-0.84	30	-2.86	40	3.23	4	-3.90	42
BHU-31XPBW ZN1	2.43	6	3.24	9	-6.94	45	-0.92	32	0.29	21	1.03	17
BHU-31XPBW-343	-0.71	29	-1.13	30	1.62	9	0.04	25	-4.82	45	2.36	10
BHU-31XHD-3326	-1.72	35	-2.11	36	5.32	2	0.88	13	4.53	1	-3.39	40
HD-3721XPBW ZN1	-0.28	26	3.50	8	0.80	17	0.07	24	-3.33	43	4.88	2
HD-3721XPBW-343	-0.32	27	2.21	12	-1.21	31	-3.44	42	4.50	2	1.07	16
HD-3721XHD-3326	0.60	19	-5.70	41	0.41	23	3.37	3	-1.17	32	-5.95	45
PWB-725X PBW ZN1	0.59	20	-4.08	38	0.21	25	-4.09	45	2.35	6	2.90	5
PWB-725X PBW-343	-0.48	28	8.91	1	0.53	20	-0.58	28	-1.90	37	-5.03	43
PWB-725X HD-3326	-0.11	25	-4.83	39	-0.74	29	4.67	1	-0.45	25	2.13	11
CRDGEHNU1XPBWZN1	1.02	15	3.62	7	5.32	1	0.66	18	1.60	11	-2.39	34
CRDGEHNU1XPBW343	1.96	7	-5.81	43	-5.04	44	0.52	20	0.69	17	1.15	15
CRDGEHNU1XHD-3326	-2.99	41	2.19	13	-0.29	26	-1.18	35	-2.29	39	1.24	14
PBW-550X PBW ZN1	-3.18	43	-0.67	26	0.45	22	0.11	23	0.72	16	2.88	6
PBW-550X PBW-343	2.66	5	0.45	21	-1.68	35	-0.97	34	-0.66	28	-2.49	36
PBW-550X HD-3326	0.53	21	0.21	22	1.23	14	0.86	14	-0.06	24	-0.39	29
PBW-677XPBW ZN1	-2.23	37	-1.06	29	1.41	13	-1.30	36	1.86	8	-1.03	32

PBW-677XPBW-343	-2.49	38	4.07	5	1.18	16	3.49	2	-0.50	26	0.30	26
PBW-677XPBW-343	4.72	1	-3.02	37	-2.58	39	-2.18	37	-1.36	34	0.73	21
PBW-822X PBW ZN1	1.49	9	-0.45	25	0.57	19	2.31	7	-1.51	35	3.27	4
PBW-822X PBW-343	-1.94	36	1.81	15	1.50	11	-3.03	41	0.00	23	-3.21	38
PBW-822X HD-3326	0.45	22	-1.36	32	-2.07	37	0.72	17	1.52	12	-0.06	28
HD-3117X PBW ZN1	0.73	18	-5.06	40	-1.73	36	-3.64	43	0.17	22	-2.44	35
HD-3117X PBW-343	0.81	16	-1.77	35	2.99	4	0.85	15	1.81	10	-3.11	37
HD-3117X HD-3326	-1.54	34	6.83	2	-1.26	32	2.79	4	-1.98	38	5.54	1
DBW-173X PBW ZN1	-2.78	40	-1.76	34	0.33	24	-0.91	31	1.85	9	-0.98	31
DBW-173X PBW-343	1.43	11	1.62	16	-3.18	42	0.12	22	-1.19	33	0.31	25
DBW-173X HD-3326	1.34	12	0.14	23	2.85	5	0.79	16	-0.66	27	0.66	22
DH-3086X PBW ZN1	0.29	23	-1.59	33	1.70	8	0.22	21	-1.05	30	1.28	13
DH-3086X PBW-343	1.15	14	1.13	18	-0.41	27	2.13	9	2.17	7	2.37	9
DH-3086X HD-3326	-1.44	33	0.46	20	-1.29	33	-2.35	39	-1.11	31	-3.65	41
DBW-222X PBW ZN1	-0.77	30	3.71	6	1.20	15	2.33	6	2.54	5	-3.29	39
DBW-222X PBW-343	0.74	17	-6.33	44	2.40	7	1.72	10	-2.90	42	2.42	8
DBW-222X HD-3326	0.03	24	2.62	11	-3.60	43	-4.05	44	0.36	19	0.87	18
CSW-18XPBW ZN1	-3.21	44	1.26	17	2.42	6	2.24	8	1.42	13	-1.19	33
CSW-18XPBW-343	1.49	10	-0.90	28	0.49	21	0.02	26	0.98	15	0.41	24
CSW-18XHD-3326	1.72	8	-0.36	24	-2.91	41	-2.26	38	-2.41	40	0.78	19
PBW-757X PBW ZN1	3.00	4	1.87	14	-2.25	38	-0.65	29	-1.53	36	-0.97	30
PBW-757X PBW-343	1.30	13	-1.16	31	0.75	18	-0.92	33	0.35	20	0.21	27

PBW-757X HD-3326	-4.30	45	-0.71	27	1.51	10	1.57	11	1.18	14	0.76	20
SE (sca effect)	2.14		0.85		0.31		1.78		0.59		0.86	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

Table 4.3.2 contd.

	Grain yield/ plant across locations (E1, E2 & E3)						Protein content across 3 locations (E1, E2 & E3)					
GENOTYPES	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**	**E1**	**RANK**	**E2**	**RANK**	**E3**	**RANK**
BHU-25XPBW ZN1	-0.19	24	2.63	3	-1.19	28	0.02	17	0.07	6	0.79	9
BHU-25XPBW-343	-2.02	36	0.81	14	-2.65	34	0.05	15	0.01	21	-0.47	34
BHU-25XHD-3326	2.21	11	-3.43	44	3.84	8	-0.08	31	-0.08	40	-0.32	28
WB-02XPBW ZN1	4.72	2	-0.79	29	-0.62	24	-0.05	26	-0.01	27	-0.18	22
WB-02XPBW-343	-1.54	32	1.97	9	-1.76	31	0.08	9	0.04	14	1.34	5
WB-02XHD-3326	-3.17	40	-1.18	34	2.38	13	-0.03	25	-0.03	31	-1.16	41
BHU-31XPBW ZN1	1.48	14	-2.51	43	-2.44	33	-0.11	34	-0.07	39	-0.90	40
BHU-31XPBW-343	-1.33	29	-1.97	40	-3.54	36	0.09	8	0.04	11	1.34	4
BHU-31XHD-3326	-0.15	23	4.48	1	5.97	2	0.02	18	0.02	17	-0.44	32
HD-3721XPBW ZN1	-0.80	26	-1.35	37	1.93	17	1.54	1	0.03	16	-0.25	25
HD-3721XPBW-343	-2.88	38	-0.41	25	-4.08	39	-0.79	45	-0.06	36	0.80	8
HD-3721XHD-3326	3.69	6	1.76	10	2.15	15	-0.75	44	0.03	15	-0.55	35
PWB-725X PBW ZN1	-3.27	41	0.29	16	2.98	11	-0.42	43	-0.05	33	-0.32	29
PWB-725X PBW-343	-1.36	30	-0.44	26	-4.65	42	0.82	2	0.11	3	1.63	3
PWB-725X HD-3326	4.63	3	0.15	19	1.67	18	-0.40	42	-0.06	38	-1.30	42

CRDGEHNU1XPBWZN1	0.43	18	2.11	8	-0.46	23	-0.32	40	-0.06	37	-0.23	24
CRDGEHNU1XPBW343	1.17	15	-1.14	33	2.17	14	-0.17	37	0.01	20	-0.03	20
CRDGEHNU1XHD-3326	-1.60	33	-0.97	30	-1.71	30	0.49	3	0.05	10	0.25	15
PBW-550X PBW ZN1	-2.25	37	-1.79	38	3.99	7	0.00	21	0.04	12	0.10	19
PBW-550X PBW-343	0.01	22	0.49	15	-3.29	35	0.05	16	0.01	23	0.20	17
PBW-550X HD-3326	2.24	10	1.31	12	-0.71	25	-0.06	29	-0.05	35	-0.30	26
PBW-677XPBW ZN1	-4.56	44	0.08	21	-5.99	43	-0.14	35	-0.01	29	-0.59	37
PBW-677XPBW-343	4.34	5	0.11	20	7.40	1	0.06	13.5	-0.02	30	-1.35	43
PBW-677XPBW-343	0.23	20	-0.19	24	-1.41	29	0.08	10	0.04	13	1.95	1
PBW-822X PBW ZN1	6.01	1	-1.87	39	5.27	5	-0.16	36	-0.11	44	0.39	12
PBW-822X PBW-343	-5.33	45	2.48	5	-4.29	41	0.14	7	0.10	5	-0.60	38
PBW-822X HD-3326	-0.68	25	-0.61	27	-0.98	26	0.01	20	0.01	19	0.22	16
HD-3117X PBW ZN1	-1.04	27	-1.03	32	-0.98	27	0.07	11	0.06	7	0.61	11
HD-3117X PBW-343	0.40	19	1.10	13	0.25	22	-0.01	24	-0.08	41	-1.42	45
HD-3117X HD-3326	0.64	17	-0.07	23	0.73	20	-0.05	28	0.02	18	0.82	7
DBW-173X PBW ZN1	-4.44	43	-0.65	28	-8.52	45	-0.05	27	0.00	25	-0.73	39
DBW-173X PBW-343	2.85	7	-1.01	31	2.56	12	0.06	13.5	0.01	22	-0.58	36
DBW-173X HD-3326	1.59	13	1.66	11	5.96	3	-0.01	23	0.00	24	1.31	6
DH-3086X PBW ZN1	-1.63	34	2.48	4	4.06	6	-0.09	33	-0.09	42	1.68	2
DH-3086X PBW-343	4.62	4	-1.23	35	2.11	16	0.15	6	0.19	1	-1.37	44
DH-3086X HD-3326	-2.99	39	-1.25	36	-6.17	44	-0.06	30	-0.10	43	-0.30	27
DBW-222X PBW ZN1	2.79	8	2.17	7	3.15	9	-0.22	39	0.06	8	-0.34	30

DBW-222X PBW-343	0.92	16	-2.41	42	0.96	19	-0.21	38	-0.04	32	0.71	10
DBW-222X HD-3326	-3.70	42	0.24	18	-4.10	40	0.43	4	-0.01	28	-0.37	31
CSW-18XPBW ZN1	0.16	21	-0.06	22	-1.82	32	-0.08	32	-0.01	26	-0.21	23
CSW-18XPBW-343	1.63	12	-2.23	41	5.78	4	0.02	19	-0.05	34	0.27	13
CSW-18XHD-3326	-1.78	35	2.29	6	-3.97	38	0.06	12	0.05	9	-0.06	21
PBW-757X PBW ZN1	2.61	9	0.28	17	0.64	21	0.00	22	0.15	2	0.19	18
PBW-757X PBW-343	-1.47	31	3.89	2	3.02	10	-0.33	41	-0.26	45	-0.45	33
PBW-757X HD-3326	-1.14	28	-4.18	45	-3.65	37	0.33	5	0.11	4	0.25	14
SE (sca effect)	0.99		0.50		0.55		0.31		0.29		0.25	

E1= Lovely professional University, India, **E2**= Kebbi State University of Science and Technology Aliero, Nigeria and **E3**= Lake Chad wheat research Institute, Nigeria

4.4. Estimates of heterosis over better parent (BP) and four standard variety (SV)

4.4.1 Days to 50% heading

In location 1 early-maturing crosses WB-02XPBW-343 shows significant early maturity with values of -23.83% (BP) and -26.48% (SV2). Its highly significant negative values indicate it is one of the fastest-maturing crosses, making it ideal for areas where early harvest is beneficial. HD-3721XHD-3326 also presents strong early-maturing potential, with values of -35.19% (BP and SV2), suggesting its suitability for early harvest conditions. Delayed-maturity crosses in contrast, DBW-222X HD-3326 presents the most significant positive value at 28.44% (BP), indicating it has one of the longest durations to heading. This could be advantageous in locations favoring longer growth periods. Other crosses such as PBW-550X HD-3326 (18.30% in BP, SV1) and CRDGEHNU1XHD-3326 (14.57% in BP), further exemplify delayed maturity in this location. The results for Location 1 highlight WB-02XPBW-343 and HD-3721XHD-3326 as ideal candidates for early maturing traits, while DBW-222X HD-3326 is favored for environments requiring longer maturation periods. Location 2 early-maturing crosses CRDGEHNU1XHD-3326 stands out with the highest early maturity ranking at -36.11% (BP), confirming its potential for early heading. Environmental conditions likely contribute to its favorable performance. HD-3721XHD-3326 also shows strong early maturity, with values of -20.85% (BP) and -24% (SV3), suggesting consistency in its early heading traits across locations. Delayed-maturity crosses DBW-222X HD-3326 exhibits a significant positive increase in days to heading with a value of 32.70% (BP), indicating a clear delayed-maturity trait. Additionally, PWB-725X PBW-343 (27.35% in SV2) and PBW-757X PBW ZN1 (29.15% in SV3) align as delayed heading crosses, reinforcing the presence of this trait in the location. The findings for Location 2 support CRDGEHNU1XHD-3326 as a key early-maturing option, while DBW-222X HD-3326 remains a strong choice for delayed maturation. Location 3 early-maturing crosses in location 3, CRDGEHNU1XHD-3326 again shows fast maturity with a value of -26.06% (SV4), demonstrating its potential across multiple environments. BHU-25XPBW-343 at -24.65% (SV2) and DBW-173X PBW-343 (-20.77% in SV4) also exhibit significant early maturity potential, indicating they are suitable for quicker harvest cycles. Delayed-maturity crosses conversely, DBW-222X PBW-343 reflects a positive value of 21.10% (SV4), indicating delayed maturity traits. This suggests that it could be beneficial in environments that favor longer maturation. PBW-757X PBW ZN1 with 20.68% (SV4) aligns as a delayed heading cross, reinforcing its viability for delayed maturity.

4.4.2 Plant height (cm)

For location 1 performing genotypes were DBW-222X PBW ZN1 shows a significant positive heterosis with a BP of 6.96%. This indicates the highest gain in plant height among all genotypes in this location, demonstrating its superior genetic potential for growth. PWB-725X PBW ZN1 closely follows with a BP of 9.16%, reflecting considerable improvement in height. This suggests that this cross effectively enhances plant height, contributing positively to yield potential. In contrast, WB-02XPBW-343 has the lowest BP value of -18.96%, indicating a significant reduction in plant height. This genotype may be less favorable for breeding aimed at increasing height and may be suited for specific applications where shorter plants are desired. Location 2 PWB-725X HD-3326 shows a slight positive BP of 0.37%, indicating relative stability in plant height. Although this value is not as pronounced as in location 1, it still reflects the genotype's ability to maintain consistent height performance. CRDGEHNU1XPBW343 also demonstrates slight positive values across the selection variables, suggesting moderate adaptability and performance in this location. PBW-757X PBW-343 records a negative BP of -19.20%, indicating it is not ideal for height improvement in Location 2. Consistently low values across selection variables reinforce its lack of suitability for breeding programs focused on enhancing height. Similarly, CSW-18XPBW-343 shows a significant negative BP of -18.12%, indicating poor performance across selection variables and highlighting its unsuitability for height enhancement. Location 3 PWB-725X PBW-343 stands out with a high positive BP of 8.17%, indicating strong potential for height improvement in this location. Positive results across selection variables further reinforce its favorability for breeding programs focused on increasing plant height. DBW-173X HD-3326 scores a BP of 11.49%, demonstrating strong adaptability and a significant increase in height across all selection variables.

4.4.3 Days to 50% maturity

With regard to location 1the early maturing genotypes were WB-02XPBW ZN1, demonstrates a notable early maturity with a BP of -15.38% and an SV2 of -13.57%, indicating this genotype matures significantly earlier than the better parent and standard variety. This makes it a promising option for environments where early harvesting is advantageous. HD-3721XPBW-343 has a BP of 4.35% and an SV1 of 7.46%, suggesting moderate maturity compared to the standard, though not as early as the top-performing genotype. Genotypes with reduced maturity were WB-02XPBW-343 shows a BP of -2.10% and an SV1 of 4.48%, indicating it has shorter days to maturity than the better parent, making it a viable candidate for early maturity in this location. Conversely, BHU-31XPBW ZN1 indicates late maturity with a BP of 18.70% and an

SV1 of 8.96%, which suggests this cross takes longer to mature, making it less favorable for regions requiring earlier harvests. Late maturing genotypes the late-maturing genotype CRDGEHNU1XPBWZN1 records a BP of 13.53% and an SV1 of 12.69%, indicating longer maturity periods, which may be advantageous in specific growing conditions or markets. Location 2 early maturing genotypes were PWB-725X PBW-343 exhibits a strong early maturity with a BP of -18.06% and an SV1 of -13.69%, showing that this cross is exceptionally early-maturing in this location. HD-3721XPBW-343 also indicates early maturity with a BP of -8.93% and an SV1 of -4.07%, suggesting it consistently matures earlier than both the better parent and standard variety. Late maturing genotypes recorded in HD-3117X HD-3326 and DH-3086X HD-3326 show significant late maturity, with BPs of 28.62% and 40.15%, respectively. These genotypes consistently require longer days to mature, making them suitable for longer growing seasons or specific crop rotations where delayed maturity is beneficial. Location 3 early maturing genotypes were PBW-550X PBW-343 achieves an impressive BP of -36.54% and an SV2 of -36.94%, indicating it is one of the earliest maturing genotypes across all locations. This trait is crucial for areas needing to harvest crops quickly, possibly due to weather conditions or market demands. HD-3721XPBW-343 also ranks as an early maturing variety with a BP of -38.46% and an SV2 of -38.85%, representing the fastest maturity among all genotypes tested, making it an excellent choice for early harvest strategies. Late maturing genotypes were genotype DBW-173X PBW-343 has a BP of 36.46%, indicating significantly longer maturity times. Similarly, DBW-173X HD-3326 shows a BP of 8.63% and SV1 of 12.69%, reinforcing its classification as a late-maturing variety.

4.4.4 Grain filling period

For location 1 the highest BP was noted in BHU-25XPBW ZN1 at 68.92%, showcasing strong performance and adaptability. This genotype might indicate variability, but its high value positions it as a strong contender for stable grain filling. PWB-725X PBW ZN1 has a BP of 64.10%, suggesting consistent performance, while HD-3721XPBW ZN1 at 53.75% demonstrates moderate success with reasonable stability. Standard variety performance among the SV crosses, HD-3117X PBW ZN1 and CSW-18X HD-3326 both have a BP of 65.38%, indicating good adaptability and solid performance. These crosses suggest that they can effectively cope with environmental variations. In SV2, HD-3117X PBW ZN1 stands out at 88.37%, indicating excellent grain filling length. The other strong performers, CSW-18XPBW-343 and PBW-757X PBW ZN1, with values of 84.67% and 85.71%, respectively, further establish a trend of high adaptability. The results from Location 1 suggest that BHU-25XPBW ZN1 and HD-3117X PBW

ZN1 could be valuable options for breeders looking to enhance grain filling traits in this area. In Location 2, BHU-25XPBW ZN1 again emerges as a key performer with a BP value of 60.26%, affirming its stability. PWB-725X PBW ZN1 maintains its solid BP value of 64.10%, while PBW-757X PBW ZN1 offers consistent performance at 61.54%. CSW-18X HD-3326 leads in SV1 with a value of 73.29%, indicating adaptability to environmental changes. Additionally, HD-3721XPBW ZN1 at 77.47% further exemplifies its robustness in variable conditions. The SV2 values are impressive with HD-3117X PBW ZN1 again achieving 88.37%, solidifying its role as a standout performer for GFP length. Other notable crosses like PBW-757X PBW ZN1 and CSW-18XPBW-343 (both above 84%) reflect strong adaptability and resilience. Location 3 BHU-25XPBW ZN1 maintains the highest BP value at 68.92%, indicating strong potential for enhanced GFP in this location as well. PWB-725X PBW ZN1 follows with 64.10%, showing consistent grain filling duration across locations. PBW-757X PBW ZN1 also holds steady at 61.54%, confirming its overall reliability in performance. SV Performance in SV1, HD-3721X HD-3326 shows a BP of 75.91%, illustrating its adaptability in different conditions. Additionally, PBW-677XPBW-343 and PBW-757X HD-3326 both show promising results with values close to 75%.For SV2, PBW-822X HD-3326 achieves 82.72%, demonstrating excellent performance across locations, while CSW-18XPBW-343 at 84.67% and PBW-757X PBW ZN1 at 85.71% provide robust adaptability.

4.4.5 Number of productive tillers

Cross like PBW-822X PBW ZN1 displays the highest BP value of 98.80%. This indicates an impressive heterotic effect, suggesting that this genotype significantly surpasses its parents in productive tiller output. Such high performance may be attributed to favorable genetic combinations that enhance tillering capabilities. High performance found in PBW-550X PBW-343 (BP 63.73%) and DBW-173X PBW-343 (BP 77.68%) also show substantial productive tillers, demonstrating that they too benefit from heterosis, albeit to a lesser extent than PBW-822X PBW ZN1. Their BP values indicate a positive response to hybridization, promoting good productivity.

4.4.6 Number of spikelet per spike

Cross like BHU-25 × PBW ZN1 in location 1 heterosis was significant for BP (6.18%), and positive for SVs (SV1 5.31%, SV2 4.95%, SV3 5.99%), indicating an increase over both parents and standards, although SV4 showed a lower BP value (3.73%). Location 2 the heterosis was extremely significant, with BP at 12.00% and high values for SVs, especially SV4 (21.47%).

This suggests that under location 2's conditions, the cross expresses strong heterosis, particularly when compared to SV4. Location 3 the cross showed positive heterosis for BP (11.23%) and SV1 and SV2 values were also high (12.98% and 1.78%, respectively), reflecting a strong performance across locations. BHU-25 × PBW-343 Location 1: Moderate heterosis was observed with BP values slightly positive (4.88%) and values for SVs showing an increase, especially SV1 (5.62%). Location 2 Negative heterosis was observed for BP (-17.04%), but some positive heterosis for SV4 (10.12%). This could imply environmental interactions affecting the performance. Location 3: BP was lower (-4.68%) compared to location 1, but the high positive values for SV2 and SV4 (26.64% and 35.22%, respectively) indicate higher adaptability in Location 3. BHU-25 × HD-3326 location 1 negligible to moderate heterosis for BP (-0.13%) with positive but lower heterosis values for SVs. Location 2 positive heterosis was observed for BP (11.31%) and moderate positive values for SVs, indicating adaptability in location 2. Location 3 BP reached 33.53%, with high heterosis values for SV1 and SV2, indicating a strong response in Location 3. WB-02 × PBW ZN1 location 1 moderate heterosis with BP at 3.01% and SVs reflecting positive trends. Location 2 BP and SV heterosis are substantial, especially SV4 (14.36%), suggesting this cross performs well under Location 2 conditions. Location 3: Heterosis was significantly high, with BP values (30.06%) and SV values reaching up to 41.06%, showing strong adaptability. WB-02 × PBW-343 location 1 positive heterosis with moderate values for BP and SVs, BP at 2.89%. Location 2 negative BP (-9.88%) but moderate to high values for SVs, especially SV4 (19.62%). Location 3: Positive BP heterosis (0.84%) and highly significant values for SVs (up to 43.05%).

4.4.7 Spike length (cm)

Location 1 **h**igh heterosis for **crosses t**he hybrid. BHU-31XPBW ZN1 **and** HD-3721XPBW ZN1 show consistently high heterosis values (16.26–30.67% in BP and 22.34–30.67% in SV1, SV2), indicating robust spike length enhancement. Such crosses are promising for breeding programs targeting spike length improvements. Moderate heterosis for c**rosses** like BHU-25XHD-3326 and WB-02XPBW ZN1 demonstrate moderate positive heterosis values (e.g., WB-02XPBW ZN1 with 4.55% in BP and 17.39% in SV1), suggesting less pronounced but still significant benefits. Location 2 where significant positive heterosis were recorded such as PBW-677XPBW-343 and PBW-822XPBW ZN1 display heterosis values above 20% across BP and SV (up to 36.59% in SV1), indicating exceptional spike length gains. These high values suggest strong compatibility and vigor in these hybrids. Variation among crosses like BHU-25XHD-3326 show lower BP values (3.36%) compared to SV1 (up to 6.7%), hinting at lower heterosis in terms of the better parent but better relative performance to standard varieties. Location 3 highest heterosis observed that HD-3117X HD-3326 exhibit particularly high BP and SV values, e.g., 35.37% in BP and up to 19.12% in SV, suggesting strong heterotic benefits. High values in multiple SVs indicate a broad adaptability of this hybrid for spike length across environments. Crosses PBW-677XPBW-343 and DBW-173X PBW-343 maintain high heterosis across various SVs (e.g., DBW-173X PBW-343 with 26.21% in SV2 and 29.06% in SV3), suggesting that these crosses could be reliable in multiple settings.

4.4.8 Flag leaf area (cm^2)

Crosses across three locations, with comparisons made against the better parent (BP) and four standard varieties (SV1 to SV4) for flag leaf area. Positive values indicate a heterotic effect where the cross outperforms the better parent or standard variety, while negative values suggest the opposite. Location 1number of crosses show significant positive heterosis relative to at least one standard variety, indicating the cross exceeds the benchmarked standard varieties. For instance, crosses like BHU-25XPBW-343 and WB-02XPBW-343 display high positive percentages in multiple SV comparisons, with values such as 52.09% (SV1) and 53.28% (SV1)**.** CSW-18XPBW-343 achieves the highest heterosis at 95.41% against SV1, suggesting substantial enhancement in flag leaf area. Location 2 similar to Location 1, heterosis percentages are consistently positive for many crosses, especially in comparisons with SV1 and SV2. Genotypes BHU-25XPBW-343 **at** 86.77% (SV1) and PWB-725X PBW-343 at 89.78% (SV1)**,** both showing large gains in leaf area. Certain crosses, like CRDGEHNU1XHD-3326 with -44.20% (BP)**,** perform worse than the better parent, indicating challenges under this specific environmental condition. Location 3**,** this location shows mixed heterosis results, with more negative values for some crosses compared to others. Positive values are seen for crosses like HD-3117X PBW-343**,** with 18.85% (SV4)**,** highlighting improved leaf area compared to specific varieties but not across all comparisons. Some crosses, such as PBW-550X HD-3326 at 7.60% (SV4)**,** consistently perform above SV4 across locations. Crosses with high heterosis across all locations genotypes like CSW-18XPBW-343 and HD-3117X PBW ZN1 show significant positive heterosis consistently across locations and SVs. Cross CSW-18XPBW-343 displays heterosis percentages as high as 99.96% (Location 1, SV4)**,** indicating its robust enhancement potential for flag leaf area across varying environmental conditions. Negative heterosis trends indicated that, some crosses, such as CRDGEHNU1XPBW ZN1 in Location 1 (BP -1.95%) and PBW-757X HD-3326 in Location 3 (-0.08%, SV4), show negative heterosis values compared to the better parent or standards, signaling potential drawbacks in leaf area improvement.

4.4.9 Chlorophyll content

Chlorophyll content, measured against both the better parent (BP) and several standard varieties (SV1, SV2, SV3, SV4) across three locations. The crosses for chlorophyll content indicated that high heterosis across locations revealed that certain crosses consistently display positive heterosis for chlorophyll content across all locations. For instance, PBW-757X PBW ZN1 shows significant positive heterosis with values of 18.42%, 24.15%, and 25.78% at Location 1, along with moderate positive heterosis in location 2 and location 3. Crosses like WB-02XPBW ZN1 also show significantly positive heterosis, especially at Location 1 (7.29%) and to some extent at Location 2 (2.9%). Performance Relative to Standard Varieties (SVs). For several crosses, the heterosis values against standard varieties such as SV2 and SV4 show substantial improvement, indicating that these crosses can potentially outperform widely used varieties. For instance, BHU-31XPBW ZN1 at Location 1 shows a high increase of 12.65% when compared to SV2 and 9.69% compared to SV4. The cross PBW-822X PBW ZN1 shows very high positive heterosis across all SVs at location 1 (up to 30.14% for SV2) but negative values at Location 2 and 3, indicating location-specific performance. Negative heterosis instances, some crosses exhibit negative heterosis, which could imply poorer chlorophyll content performance than either parent or the standard varieties, particularly at Location 2 and Location 3. For example, CRDGEHNU1XPBW343 at location 2 has a notably negative value of -11.03% against SV1 and -7.11% against SV4 in Location 3. Crosses such as PBW-550X PBW-343 also demonstrate strong negative heterosis for chlorophyll content in Location 2 (-8.82% against BP and -12.68% against SV3).

4.4.10 Number of spikelets per spike

Number of spikelets per spike, the data shows heterosis percentages for each cross at three different locations, highlighting instances where crosses outperform the better parent or standard varieties, indicating successful heterosis. This implies that certain crosses are highly beneficial in terms of increasing spikelet numbers in specific locations. For instance BHU-25XPBW ZN1 shows a notable heterosis of up to 21.47% and 20.63% over standard varieties in location 2 PBW-677XPBW-343 consistently shows high heterosis percentages across locations, such as 35.22% at location 1 and 61.88% at location 3 significant heterosis across locations some crosses exhibit stable positive heterosis across multiple locations, indicating a promising genotype for potential cultivation. For example CRDGEHNU1XPBW343 demonstrates positive heterosis across all three locations, reaching up to 66.21% in location 3 against standard varieties. HD-3721XHD-3326 and PBW-757X HD-3326 also exhibit high and consistent heterosis across various locations and standard varieties. Negative Heterosis**,** negative values indicate a reduction in spikelet numbers compared to the better parent or standard varieties. While less desirable, these data points are important for identifying crosses that may not perform well under certain conditions: For example, BHU-31XPBW ZN1 has values as low as -14.57% at location 2 when compared with SV2. PBW-757X PBW-343 also displays negative heterosis in some cases, such as -18.66% in location 2 when compared to BP.

4.4.11 Grain weight per spike (g)

Better Parent Heterosis (BP) across all locations, BP heterosis for grain weight per spike varies widely among the crosses, with some crosses achieving notably high heterosis values. In location 1, crosses like BHU-25XPBW-343 *and* WB-02XPBW-343 show heterosis values as high as 68.46% and 62.42% respectively, indicating substantial improvement over the better parent in these crosses. Similarly, in location 2**,** PWB-725X HD-3326 has the highest heterosis at 40.97%, suggesting that it has performed consistently well in boosting grain weight per spike compared to the better parent. In location 3**,** HD-3117X PBW ZN1 shows a 27.63% BP heterosis, indicating a strong performance in increasing grain weight relative to the better parent in this environment. Standard variety heterosis (SV1 - SV4). Standard variety heterosis varies depending on which SV the cross is compared with. Generally, crosses compared with SV1 show the highest heterosis values. Location 1 results highlight PBW-822X PBW ZN1 with SV1 heterosis reaching 73.81%, indicating a significant improvement over the standard variety. In location 2**,** high SV1 heterosis is seen with PWB-725X HD-3326 at 40.97%. Other crosses, such as DBW-173X PBW ZN1, also show substantial heterosis (75.96%) relative to SV1, supporting the effectiveness of certain crosses in outperforming the standard variety consistently across locations. In location 3, HD-3117X PBW ZN1 exhibits high heterosis at 67.81% for SV1, suggesting this cross has a particularly positive effect in increasing grain weight per spike in the third location.

4.4.12 1000-grain weight (g)

The results are presented as heterosis based on better parent (BP) and four standard varieties (SV1, SV2, SV3, SV4) as comparators. Location 1 the highest positive heterosis (better parent, BP) was observed in the cross DBW-173XPBW ZN1 (23.58%). This indicates a significant increase in 1000-grain weight in this cross compared to the parent lines. Other crosses, such as DH-3086XHD-3326 (17.71%) and PBW-677XPBW-343 (18.04%), also showed a strong heterosis response. Most of the crosses exhibited heterosis values of over 10% when compared to SV standards. Location 2 **t**he cross CRDGEHNU1XPBWZN1 exhibited exceptionally high positive heterosis (48.25%) when compared to BP, showing substantial 1000-grain weight improvement. PWB-725XPBW-343 (33.63%) and HD-3117XHD-3326 (45.42%) also showed high heterosis values against BP, indicating an increased 1000-grain weight potential under the conditions of this location. Some crosses like PBW-677XPBWZN1 and HD-3721XHD-3326 had negative heterosis values against SV standards, which may suggest environmental influences at location 2 that affect the yield potential differently than in other locations. Location 3 the cross CSW-18XPBW ZN1 demonstrated high heterosis values, with 23.72% relative to BP and a range of 43.31%-45.42% in comparison to SV standards. This indicates its superior performance in 1000-grain weight at this location. Other crosses, including WB-02XPBW-343 and WB-02XHD-3326, showed consistently high heterosis across all standards, with values between 41-46%.

4.4.13 Biological yield (g)

The heterosis for biological yield in some selected crosses across three locations, focusing on heterosis based on the better parent (BP) and various standard Varieties (SV1, SV2, SV3, and SV4). Heterosis here refers to the percentage increase or decrease in biological yield when comparing a cross with either its better-performing parent or other standard varieties (SVs). Location 1 BHU-25XPBW ZN1 BP heterosis is low (0.53%), meaning minimal improvement over the better parent. Heterosis relative to SV1 and SV2 is positive, with 7.21% and 2.14% increases respectively, indicating a moderate improvement. For SV3, the cross underperformed by -9.64%, which is statistically significant, showing a notable decrease relative to this standard. For SV4, it shows a positive heterosis of 6.93%, suggesting an improvement over SV4. Location 2 significant heterosis values across all SVs and BP, particularly with a large improvement over BP (47.38%). SV1, SV2, SV3, and SV4 all show significant improvements, ranging from 27.59% to 41.27% (all **), demonstrating this cross's strong adaptability and superior performance in this location. Location 3 shows extremely high heterosis values relative to BP and SVs, with an 84.33% increase over. Significant heterosis values for all SVs, showing that BHU-25XPBW ZN1 consistently performs well in location 3. BHU-25XPBW ZN1 demonstrates high heterosis in Locations 2 and 3, making it a strong candidate for these environments.

4.4.14 Harvest index (%)

Better parent (BP) and standard varieties (SV1, SV2, SV3, SV4). This can be interpreted in terms of heterosis, which is the hybrid vigor expressed by the cross in comparison to the better parent and standard varieties. A positive percentage indicates that the cross has performed better than the parent or the standard variety, while a negative percentage shows it performed worse.

Heterosis relative to better parent (BP) represented as the percentage increase or decrease in harvest index of the cross compared to the better parent. Positive values indicate that the cross outperformed the better parent, demonstrating hybrid vigor. For example, in location 1, the cross PBW-822X PBW ZN1 shows a 24.27% increase over the better parent, indicating strong heterosis. Similarly, in Location 3, PBW-757X HD-3326 demonstrates significant heterosis with a 12.47% increase over BP. Performance relative to standard varieties (SV1 to SV4) each location has comparisons with four standard varieties. Positive values indicate superior performance over the standard variety. In some cases, the crosses show significantly high values, especially in location 2 and location 3, demonstrating adaptability and productivity. For instance, in location 2, DH-3086X PBW-343 shows 65.80% improvement over SV1 and 38.19% improvement over SV3, indicating that it consistently performed well against these benchmarks. Particularly, CSW-18XPBW ZN1 in Location 1 has a high heterosis effect against SV4 with a 12.78% increase, while in Location 3, it shows a 37.24% increase against BP, which is substantial.

4.4.15 Protein content

Better parent (BP) and standard varieties (SV1, SV2, SV3, SV4). Below is a detailed interpretation of the data, focusing on trends in heterosis across locations, comparisons to the better parent and standard varieties, and significant variations. Crosses with positive heterosis, crosses like BHU-25XPBW-343, WB-02XPBW-343, CRDGEHNU1XPBWZN1, and PBW-677XPBW-343 show high positive heterosis across most standard varieties (SV1-SV4) and across locations. In Location 2, several crosses exhibit high heterosis values, with PBW-822X PBW-343 showing up to 32.47% (SV4), which is the highest among the crosses. Location-specific, location 2 tends to show a greater positive heterosis across most crosses, especially when compared to SV2, SV3, and SV4. Crosses like WB-02XPBW-343, PBW-550X PBW-343, and HD-3721XPBW-343 have high percentages, reaching values such as 25.73% for SV2 in HD-3721 X PBW-343. Location 1 consistently shows lower or even negative heterosis for BP, with crosses such as HD-3117X PBW ZN1 showing as much as -16.71%. However, it does have positive values for some crosses when compared to SV1, such as PBW-822 X PBW-343, which achieved 9.85%. Location 3 shows mixed results but has some crosses with high positive values against SV3 and SV4, such as CRDGEHNU1 X PBWZN1, which exhibits 30.47% for SV3.

4.4.16 Grain yield per plant (g)

Better parent (BP), and comparison to four different standard varieties (SV1, SV2, SV3, SV4). Each location's environmental and agronomic factors likely vary, which may influence the yield outcomes for each cross. Heterosis, or hybrid vigor, is assessed here by comparing each cross's performance to the better-performing parent. Positive BP values indicate that the cross outperforms its better parent, while negative values indicate a reduction in performance. In location 1, crosses like PBW-822X PBW ZN1 and PBW-757X PBW ZN1 show particularly high BP values (51.51% and 38.73%, respectively), indicating strong heterosis effects in this environment. In Location 2, DH-3086X PBW ZN1 displays an extremely high BP value of 57.79%, suggesting that this cross is particularly adapted to the conditions in this location, potentially due to favorable environmental interactions. In location 3, PBW-677XPBW-343 and DBW-173X PBW-343 also show high BP values (41.50% and 45.23%, respectively), reinforcing that certain crosses demonstrate significant heterosis depending on the location.

Table 4.4: Estimation of heterosis over better parent and four standard varieties in wheat across three locations

		Days to 50% heading														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	-7.8	-1.14	-9.41 *	5.26	10.64 *	14.35 **	4.37	17.94 **	-8.68 **	39.15 **	6.12 **	12.55 **	21.50 **	-8.45 **	9.70 **
2	BHU-25XPBW-343	-17.38 **	-11.41 *	-18.82 **	-5.67	-0.85	-5.65 *	-13.89 **	-2.69	-24.65 **	14.81 **	-2.71 **	-6.93 **	0.47	-24.30 **	-9.28 **
3	BHU-25XHD-3326	-8.16	-1.52	-9.76 *	4.86	10.21	6.96 **	-2.38	10.31 **	-14.58 **	30.16 **	12.27 **	6.93 **	15.42 **	-13.03 **	4.22 **
4	WB-02XPBW ZN1	-10.83 *	-6.08	-13.94 **	0.00	5.11	-15.81 **	-15.48 **	-4.48	-26.04 **	12.70 **	-9.39 **	-3.90 **	3.74 **	-21.83 **	-6.33 **
5	WB-02XPBW-343	-23.83 **	-19.77 **	-26.48 **	-14.57 **	-10.21	-20.95 **	-20.63 **	-10.31 **	-30.56 **	5.82	-8.30 **	-4.33 **	3.27 **	-22.18 **	-6.75 **
6	WB-02XHD-3326	-3.61	1.52	-6.97	8.1	13.62 *	4.74	5.16 *	18.83 **	-7.99 **	40.21 **	5.81 **	10.39 **	19.16 **	-10.21 **	7.59 **
7	BHU-31XPBW ZN1	3.19	10.65 *	1.39	17.81 **	23.83 **	18.05 **	-3.97	8.52 **	-15.97 **	28.04 **	-5.71 **	0.00	7.94 **	-18.66 **	-2.53 **
8	BHU-31XPBW-343	-3.9	3.04	-5.57	9.72	15.32 **	-12.61 **	-20.24 **	-9.87 **	-30.21 **	6.35	-4.93 **	-8.23 **	-0.93	-25.35 **	-10.55 **
9	BHU-31XHD-3326	-13.83 **	-7.6	-15.33 **	-1.62	3.4	4.27	-12.70 **	-1.35	-23.61 **	16.40 **	-4.93 **	-8.23 **	-0.93	-25.35 **	-10.55 **
10	HD-3721XPBW ZN1	-9.41 *	-1.14	-9.41 *	5.26	10.64 *	17.07 **	-4.76	7.62 **	-16.67 **	26.98 **	0.82	6.93 **	15.42 **	-13.03 **	4.22 **
11	HD-3721XPBW-343	-11.15 *	-3.04	-11.15 *	3.24	8.51	11.30 **	1.59	14.80 **	-11.11 **	35.45 **	10.76 **	6.93 **	15.42 **	-13.03 **	4.22 **
12	HD-3721XHD-3326	-35.19 **	-29.28 **	-35.19 **	-24.70 **	-20.85 **	31.75 **	10.32 **	24.66 **	-3.47	47.09 **	20.63 **	16.45 **	25.70 **	-5.28 **	13.50 **
13	PWB-725X PBW ZN1	-1.14	-1.14	-9.41 *	5.26	10.64 *	-9.13 **	-9.13 **	2.69	-20.49 **	21.16 **	-10.20 **	-4.76 **	2.80 **	-22.54 **	-7.17 **
14	PWB-725X PBW-343	-3.04	-3.04	-11.15 *	3.24	8.51	12.70 **	12.70 **	27.35 **	-1.39	50.26 **	23.81 **	23.81 **	33.64 **	0.7	20.68 **
15	PWB-725X HD-3326	-4.56	-4.56	-12.54 **	1.62	6.81	3.17	3.17	16.59 **	-9.72 **	37.57 **	12.55 **	12.55 **	21.50 **	-8.45 **	9.70 **
16	CRDGEHNU1XPBW ZN1	1.21	-4.94	-12.89 **	1.21	6.38	-5.90 **	7.54 **	21.52 **	-5.90 **	43.39 **	2.46 **	25.97 **	35.98 **	2.46 **	22.78 **
17	CRDGEHNU1XPBW 343	7.03	4.18	-4.53	10.93 *	16.60 **	-28.82 **	-18.65 **	-8.07 **	-28.82 **	8.47 **	-19.72 **	-1.3	6.54 **	-19.72 **	-3.80 **
18	CRDGEHNU1XHD-3326	14.57 **	7.6	-1.39	14.57 **	20.43 **	-36.11 **	-26.98 **	-17.49 **	-36.11 **	-2.65	-17.61 **	1.3	9.35 **	-17.61 **	-1.27
19	PBW-550X PBW ZN1	16.73 **	8.75	-0.35	15.79 **	21.70 **	-5.85	-23.41 **	-13.45 **	-32.99 **	2.12	-6.12 **	-0.43	7.48 **	-19.01 **	-2.95 **
20	PBW-550X PBW-343	-8.98	-11.41 *	-18.82 **	-5.67	-0.85	-14.78 **	-22.22 **	-12.11 **	-31.94 **	3.7	-10.55 **	-8.23 **	-0.93	-25.35 **	-10.55 **
21	PBW-550X HD-3326	18.30 **	5.7	-3.14	12.55 *	18.30 **	29.86 **	8.73 **	22.87 **	-4.86 *	44.97 **	11.39 **	14.29 **	23.36 **	-7.04 **	11.39 **
22	PBW-677XPBW ZN1	-4.53	4.18	-4.53	10.93 *	16.60 **	4.48	-7.54 **	4.48	-19.10 **	23.28 **	-11.84 **	-6.49 **	0.93	-23.94 **	-8.86 **
23	PBW-677XPBW-343	-0.7	8.37	-0.7	15.38	21.28	10.87	1.19	14.35	-11.46	34.92	11.76	6.93	15.42	-13.03	4.22 **

					**	**	**		**	**	**	**	**	**	**	
24	PBW-677XPBW-343	-0.35	8.75	-0.35	15.79 **	21.70 **	-17.49 **	-26.98 **	-17.49 **	-36.11 **	-2.65	3.74 **	-3.90 **	3.74 **	-21.83 **	-6.33 **
25	PBW-822X PBW ZN1	-4.56	3.42	-5.23	10.12 *	15.74 **	-4.39	-22.22 **	-12.11 **	-31.94 **	3.7	-3.27 **	2.60 **	10.75 **	-16.55 **	0.00
26	PBW-822X PBW-343	-8.77 *	-1.14	-9.41 *	5.26	10.64 *	23.04 **	12.30 **	26.91 **	-1.74	49.74 **	23.53 **	18.18 **	27.57 **	-3.87 **	15.19 **
27	PBW-822X HD-3326	-1.75	6.46	-2.44	13.36 *	19.15 **	29.86 **	8.73 **	22.87 **	-4.86 *	44.97 **	22.90 **	13.85 **	22.90 **	-7.39 **	10.97 **
28	HD-3117X PBW ZN1	-0.36	4.18	-4.53	10.93 *	16.60 **	5.62 *	11.90 **	26.46 **	-2.08	49.21 **	12.65 **	19.48 **	28.97 **	-2.82 **	16.46 **
29	HD-3117X PBW-343	-2.91	1.52	-6.97	8.1	13.62 *	6.37 **	12.70 **	27.35 **	-1.39	50.26 **	26.43 **	24.24 **	34.11 **	1.06	21.10 **
30	HD-3117X HD-3326	-1.45	3.04	-5.57	9.72	15.32 **	-19.85 **	-15.08 **	-4.04	-25.69 **	13.23 **	3.08 **	1.3	9.35 **	-17.61 **	-1.27
31	DBW-173X PBW ZN1	-8.3	0.76	-7.67	7.29	12.77 *	-15.29 **	-18.65 **	-8.07 **	-28.82 **	8.47 **	-7.14 **	1.3	9.35 **	-17.61 **	-1.27
32	DBW-173X PBW-343	-4.84	4.56	-4.18	11.34 *	17.02 **	-2.48	-6.35 **	5.83 *	-18.06 **	24.87 **	-10.71 **	-2.60 **	5.14 **	-20.77 **	-5.06 **
33	DBW-173X HD-3326	2.08	12.17 *	2.79	19.43 **	25.53 **	-11.16 **	-14.68 **	-3.59	-25.35 **	13.76 **	-9.52 **	-1.3	6.54 **	-19.72 **	-3.80 **
34	DH-3086X PBW ZN1	13.06 *	5.32	-3.48	12.15 *	17.87 **	3.11	-7.94 **	4.04	-19.44 **	22.75 **	-9.39 **	-3.90 **	3.74 **	-21.83 **	-6.33 **
35	DH-3086X PBW-343	2.34	-0.38	-8.71 *	6.07	11.49 *	-13.91 **	-21.43 **	-11.21 **	-31.25 **	4.76	5.33 **	2.60 **	10.75 **	-16.55 **	0.04
36	DH-3086X HD-3326	21.24 **	4.18	-4.53	10.93 *	16.60 **	11.56 **	-0.4	12.56 **	-12.85 **	32.80 **	5.78 **	3.03 **	11.21 **	-16.20 **	0.42
37	DBW-222X PBW ZN1	6.53	-0.76	-9.06 *	5.67	11.06 *	35.12 **	9.92 **	24.22 **	-3.82	46.56 **	7.76 **	14.29 **	23.36 **	-7.04 **	11.39**
38	DBW-222X PBW-343	7.42	4.56	-4.18	11.34 *	17.02 **	10.87 **	1.19	14.35 **	-11.46 **	34.92 **	5.26 **	3.90 **	12.15 **	-15.49 **	1.27
39	DBW-222X HD-3326	28.44 **	3.04	-5.57	9.72	15.32 **	32.70 **	11.11 **	25.56 **	-2.78	48.15 **	22.37 **	20.78 **	30.37 **	-1.76 **	17.72**
40	CSW-18XPBW ZN1	-7.93	1.52	-6.97	8.1	13.62 *	12.24 **	5.56 *	19.28 **	-7.64 **	40.74 **	2.45 **	8.66 **	17.29 **	-11.62 **	5.91**
41	CSW-18XPBW-343	-3.45	6.46	-2.44	13.36 *	19.15 **	15.19 **	8.33 **	22.42 **	-5.21 *	44.44 **	25.43 **	25.97 **	35.98 **	2.46 **	22.78**
42	CSW-18XHD-3326	-1.03	9.13	0.09	16.19 **	22.13 **	-7.17 **	-12.70 **	-1.35	-23.61 **	16.40 **	-9.48 **	-9.09 **	-1.87 *	-26.06 **	-11.39
43	PBW-757X PBW ZN1	5.31	-1.9	-10.10 *	4.45	9.79	35.85 **	14.29 **	29.15 **	0.00	52.38 **	16.73 **	23.81 **	33.64 **	0.7	20.68**
44	PBW-757X PBW-343	9.77 *	6.84	-2.09	13.77 **	19.57 **	11.74 **	1.98	15.25 **	-10.76 **	35.98 **	5.65 **	5.19 **	13.55 **	-14.44 **	2.53**
45	PBW-757X HD-3326	11.89 *	-3.42	-11.50 *	2.83	8.09	23.11 **	3.57	17.04 **	-9.38 **	38.10 **	6.52 **	6.06 **	14.49 **	-13.73 **	3.38**

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Plant height														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	-11.44 **	-8.21**	-2.89	-3.15	10.76**	-14.62 **	2.11	-0.19	-1.36	1.4	5.06	7.99 *	-0.19	7.21 *	7.21 *
2	BHU-25XPBW-343	-3.94	0.87	6.72 **	6.43 **	-1.93	-5.67 **	1.24	-1.05	-2.2	0.53	-14.29 **	1.28	-6.39 *	0.55	0.55
3	BHU-25XHD-3326	-2.13	0.37	6.18 *	5.89 *	-2.42	-6.16 **	0.7	-1.57	-2.72	0.06	0.14	0.73	-6.90 *	0.02	0.00
4	WB-02XPBW ZN1	3.4	7.18 **	13.39 **	13.08 **	4.2	-15.51 **	1.04	-1.24	-2.39	0.34	-0.19	6.89 *	-1.21	6.12	6.12
5	WB-02XPBW-343	-18.96 **	-14.90 **	-9.97 **	-10.21 **	-17.26 **	-7.88 **	1.04	-1.24	-2.39	0.34	5.21	24.32 **	14.91 **	23.43 **	23.43 **
6	WB-02XHD-3326	-4.02	-1.57	4.14	3.85	-4.3	-8.21 **	0.68	-1.6	-2.75	-0.03	-5.97	0.7	-6.93 *	-0.03	-0.03
7	BHU-31XPBW ZN1	-2.37	1.19	7.05 **	6.76 **	-1.62	-16.10 **	0.34	-1.93	-3.07 *	-0.36	-25.10 **	0.35	-7.25 *	-0.38	-0.38
8	BHU-31XPBW-343	-0.69	4.28	10.32 **	10.02 **	1.39	-8.62 **	0.87	-1.4	-2.56	0.17	-7.33 **	24.15 **	14.75 **	23.25 **	23.25 **
9	BHU-31XHD-3326	-19.56 **	-17.50 **	-12.73 **	-12.96 **	-19.80 **	-8.62 **	0.87	-1.4	-2.56	0.17	-20.35 **	6.71	-1.37	5.94	5.94
10	HD-3721XPBW ZN1	-4.05	3.95	9.97 **	9.67 **	1.06	-15.80 **	0.7	-1.57	-2.72	0.02	-2.01	0.73	-6.90 *	0.03	0.00
11	HD-3721XPBW-343	1.89	10.39 **	16.78 **	16.47 **	7.33 **	-3.75 *	-0.37	-2.61	-3.75 *	-1.06	-3.39	14.15 **	5.51	13.33 **	13.33 **
12	HD-3721XHD-3326	-1.46	6.75 **	12.93 **	12.63 **	3.79	-2.56	0.53	-1.73	-2.88 *	-0.17	0.17	0.55	-7.06 *	-0.17	-0.17
13	PWB-725X PBW ZN1	9.16 **	13.15 **	19.70 **	19.38 **	10.01 **	-15.80 **	0.7	-1.57	-2.72	0	3.65	6.54	-1.53	5.77	5.77
14	PWB-725X PBW-343	-16.16 **	-11.96 **	-6.86 **	-7.11 **	-14.40 **	-1.85	1.6	-0.69	-1.85	0.89	8.17 **	27.81 **	18.13 **	26.89 **	26.89 **
15	PWB-725X HD-3326	2.94	5.56 *	11.68 **	11.37 **	2.63	0.37	0.37	-1.9	-3.05 *	-0.34	0.38	0.38	-7.23 *	-0.35	-0.35
16	CRDGEHNU1XPBW ZN1	2.49	6.23 **	12.38 **	12.08 **	3.28	-15.21 **	1.41	-0.88	-2.04	0.7	-1.3	1.45	-6.23 *	0.72	0.72
17	CRDGEHNU1XPBW 343	3.57	8.76 **	15.06 **	14.75 **	5.74 *	-1.85	1.6	-0.69	-1.85	0.89	-9.08 **	7.44 *	-0.7	6.66	6.66
18	CRDGEHNU1XHD-3326	8.06 **	10.82 **	17.24 **	16.92 **	7.74 **	-1.33	2.14	-0.17	-1.33	1.43	7.21 *	7.99 *	-0.19	7.21 *	7.21 *
19	PBW-550X PBW ZN1	-0.07	3.57	9.57 **	9.28 **	0.7	-14.81 **	1.89	-0.41	-1.58	1.17	-0.76	2.01	-5.72	1.27	1.27
20	PBW-550X PBW-343	-12.46 **	-8.07 **	-2.75	-3.01	-10.63 **	-2.23	1.21	-1.07	-2.23	0.5	-9.37 **	7.09 *	-1.02	6.32	6.32

21	PBW-550X HD-3326	-10.36 **	-7.80 **	-2.45	-2.72	-10.36 **	0.22	0.93	-1.35	-2.5	0.22	0.17	0.9	-6.74 *	0.17	0.17
22	PBW-677XPBW ZN1	0.31	3.97	9.99 **	9.69 **	1.08	-15.02 **	1.63	-0.66	-1.82	0.92	-6.90 *	0.73	-6.90 *	0.00	0.05
23	PBW-677XPBW-343	2.95	8.12 **	14.38 **	14.07 **	5.11 *	-2.28	1.15	-1.13	-2.28	0.45	-16.75 **	-1.63	-9.08 **	-2.34	-2.34
24	PBW-677XPBW-343	-8.91 **	-6.59 **	-1.18	-1.45	-9.18 **	-0.44	1.86	-0.44	-1.6	1.15	15.77 **	25.25 **	15.77 **	24.35 **	24.35 **
25	PBW-822X PBW ZN1	-11.81 **	-8.59 **	-3.29	-3.56	-11.13 **	-14.50 **	2.25	-0.06	-1.22	1.54	-1.17	8.17 *	-0.03	7.39 *	7.39 *
26	PBW-822X PBW-343	-4.14	0.67	6.50 **	6.21 *	-2.13	0.08	3.60 *	1.27	0.08	2.88	-12.15 **	3.81	-4.06	3.06	3.06
27	PBW-822X HD-3326	-4.70 *	-2.27	3.39	3.11	-4.98 *	-0.46	3.04 *	0.72	-0.46	2.32	-0.35	9.07 **	0.81	8.28 *	8.28 *
28	HD-3117X PBW ZN1	-5.22 *	3.73	9.74 **	9.44 **	0.85	-14.48 **	2.28	-0.03	-1.2	1.57	4.66	14.15 **	5.51	13.33 **	13.33 **
29	HD-3117X PBW-343	-15.10 **	-7.08 **	-1.7	-1.96	-9.66 **	-2.67	0.76	-1.51	-2.67	0.06	-14.78 **	0.7	-6.93 *	-0.03	-0.03
30	HD-3117X HD-3326	-5.13 *	3.84	9.85 **	9.55 **	0.95	-1.18	1.77	-0.52	-1.69	1.06	8.50 **	18.34 **	9.37 **	17.48 **	17.48 **
31	DBW-173X PBW ZN1	-7.81 **	1.63	7.51 **	7.22 **	-1.2	-15.09 **	1.55	-0.74	-1.9	0.84	-6.97 *	1..63	-6.07	0.89	0.89
32	DBW-173X PBW-343	3.48	14.07 **	20.67 **	20.35 **	10.90 **	-2.18	1.27	-1.02	-2.18	0.56	-9.22 **	7.27 *	-0.86	6.49	6.49
33	DBW-173X HD-3326	0.75	11.05 **	17.49 **	17.17 **	7.97 **	-1.91	1.35	-0.94	-2.09	0.64	11.49 **	21.80 **	12.57 **	20.92 **	20.92 **
34	DH-3086X PBW ZN1	3.3	7.07 **	13.27 **	12.96 **	4.09	-15.89 **	0.59	-1.68	-2.83	-0.11	14.39 **	23.80 **	14.42 **	22.91 **	22.91 **
35	DH-3086X PBW-343	-12.79 **	-8.42 **	-3.11	-3.37	-10.96 **	-2.38	2.56	0.25	-0.92	1.85	-14.14 **	1.45	-6.23 *	0.72	0.72
36	DH-3086X HD-3326	0.37	2.93	8.90 **	8.60 **	0.08	-4.53 **	0.31	-1.95	-3.10 *	-0.39	0.62	8.89 *	0.64	8.11 *	8.11 *
37	DBW-222X PBW ZN1	6.96 **	12.08 **	18.57 **	18.25 **	8.97 **	-16.95 **	-0.68	-2.92 *	-4.05 **	-1.37	-5.2	2.18	-5.56	1.44	1.44
38	DBW-222X PBW-343	-14.54 **	-10.26 **	-5.06 *	-5.32 *	-12.75 **	-8.77 **	-1.89	-4.10 **	-5.22 **	-2.57	-2.14	15.63 **	6.88 *	14.80 **	14.80 **
39	DBW-222X HD-3326	-11.55 **	-7.32 **	-1.95	-2.22	-9.89 **	-8.35 **	-1.44	-3.66 *	-4.79 **	-2.12	-3.18	4.36	-3.55	3.61	3.61
40	CSW-18XPBW ZN1	-7.53 **	-2.88	2.75	2.47	-5.58 *	-17.52 **	0.23	-2.04	-3.18 *	-0.48	-7.23 *	0.00	-7.57 *	-0.72	-0.72
41	CSW-18XPBW-343	6.02 **	11.35 **	17.80 **	17.48 **	8.26 **	-18.12 **	-0.51	-2.75	-3.89 **	-1.2	-8.26 **	8.40 *	0.19	7.62 *	7.62 *
42	CSW-18XHD-3326	-10.38 **	-5.87 *	-0.42	-0.69	-8.49 **	-17.28 **	0.51	-1.76	-2.91 *	-0.2	-3.77	3.72	-4.14	2.97	2.97
43	PBW-757X PBW ZN1	1.06	4.75 *	10.81 **	10.51 **	1.84	-16.03 **	2.34	0.03	-1.14	1.62	-2.6	2.41	-5.35	1.67	1.67
44	PBW-757X PBW-343	0.12	5.14 *	11.23 **	10.92 **	2.22	-19.20 **	-1.52	-3.74 *	-4.87 **	-2.21	-14.44 **	1.1	-6.55 *	0.38	0.38
45	PBW-757X HD-3326	-2.74	-0.07	5.71 *	5.43 *	-2.85	-16.52	1.75	-0.55	-1.71	1.03	0.17	5.32	-2.66	4.56	4.56

**

"*" and "**" for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Days to maturity														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	14.65 **	12.94 **	8.10 **	13.78 **	12.10 **	-9.48 **	3.63 **	1.87 *	14.45 **	9.88 **	-3.16	21.43 **	-2.55	59.38 **	-1.92
2	BHU-25XPBW-343	9.09 **	7.46 **	2.86 **	8.27 **	6.67 **	-23.67 **	-12.62 **	-14.11 **	-3.50 **	-7.35 **	-21.43 **	-21.43 **	-36.94 **	3.13	-36.54 **
3	BHU-25XHD-3326	7.91 **	11.94 **	7.14 **	12.78 **	11.11 **	-20.26 **	-8.71 **	-10.26 **	0.82	-3.21 **	-4.38 **	21.43 **	-2.55	59.38 **	-1.92
4	WB-02XPBW ZN1	-15.38 **	-9.70 **	-13.57 **	-9.02 **	-10.37 **	-1.98 **	-0.6	-2.30 **	9.77 **	5.39 **	-1.27	23.81 **	-0.64	62.50 **	0.00
5	WB-02XPBW-343	-2.10 **	4.48 **	0.32**	5.26 **	3.70 **	-6.94 **	-1.98 **	-3.65 **	8.25 **	3.93 **	23.81 **	23.81 **	-0.64	62.50 **	0.07
6	WB-02XHD-3326	-1.40 **	5.22 **	0.71	6.02 **	4.44 **	10.74 **	8.38 **	6.54 **	19.69 **	14.91 **	-3.75 *	22.22 **	-1.91	60.42 **	-1.28
7	BHU-31XPBW ZN1	18.70 **	8.96 **	4.29 **	9.77 **	8.15 **	7.98 **	9.50 **	7.63 **	20.92 **	16.09 **	0.01	25.40 **	0.64	64.58 **	1.28
8	BHU-31XPBW-343	15.74 **	13.43 **	8.57 **	14.29 **	12.59 **	-5.21 **	-0.15	-1.85 *	10.26 **	5.86 **	-9.62 **	11.90 **	-10.19 **	46.88 **	-9.62 **
9	BHU-31XHD-3326	-2.16 **	1.49 **	-2.86 **	2.26 **	0.74	-4.92 **	-15.74 **	-17.18 **	-6.95 **	-10.67 **	-2.5	23.81 **	-0.64	62.50 **	0.04
10	HD-3721XPBW ZN1	-11.84 **	-9.20 **	-13.10 **	-8.52 **	-9.88 **	-10.03 **	-5.96 **	-7.56 **	3.86 **	-0.29	-1.27	23.81 **	-0.64	62.50 **	0.21
11	HD-3721XPBW-343	4.35 **	7.46 **	2.86 **	8.27 **	6.67 **	-8.93 **	-4.07 **	-5.70 **	5.94 **	1.71 *	-38.46 **	-23.81 **	-38.85 **	0	-38.46 **
12	HD-3721XHD-3326	9.59 **	13.68 **	8.81 **	14.54 **	12.84 **	-8.18 **	-4.02 **	-5.65 **	5.99 **	1.76 *	-3.13	23.02 **	-1.27	61.46 **	-0.64
13	PWB-725X PBW ZN1	-1.49 **	-1.49 **	-5.71 **	-0.75	-2.22 **	-10.30 **	-9.04 **	-10.59 **	0.45	-3.56 **	-18.35 **	2.38	-17.83 **	34.38 **	-17.31 **
14	PWB-725X PBW-343	12.44 **	12.44 **	7.62 **	13.28 **	11.60 **	-18.06 **	-13.69 **	-15.16 **	-4.68 **	-8.48 **	7.94 **	7.94 **	-13.38 **	41.67 **	-12.82 **
15	PWB-725X HD-3326	9.35 **	13.43 **	8.57 **	14.29 **	12.59 **	0.96	0.96	-0.76	11.49 **	7.04 **	-2.5	23.81 **	-0.64	62.50 **	0.64
16	CRDGEHNU1XPBW ZN1	13.53 **	12.69 **	7.86 **	13.53 **	11.85 **	-9.97 **	-8.71 **	-10.26 **	0.82	-3.21 **	-39.24 **	-23.81 **	-38.85 **	0.00	-38.46 **
17	CRDGEHNU1XPBW 343	-8.27 **	-8.96 **	-12.86 **	-8.27 **	-9.63 **	-18.80 **	-14.46 **	-15.92 **	-5.54 **	-9.31 **	-11.90 **	-11.90 **	-29.30 **	15.63 **	-28.85 **
18	CRDGEHNU1XHD-3326	8.39 **	12.44 **	7.62 **	13.28 **	11.60 **	-4.39 **	-13.42 **	-14.90 **	-4.39 **	-8.21 **	-1.88	24.60 **	0.45	63.54 **	0.64
19	PBW-550X PBW ZN1	12.59 **	13.43 **	8.57 **	14.29 **	12.59 **	-13.43 **	-12.22 **	-13.71 **	-3.06 **	-6.93 **	-3.16	21.43 **	-2.55	59.38 **	-1.92
20	PBW-550X PBW-343	-10.62 **	-9.95 **	-13.81 **	-9.27 **	-10.62 **	-17.72 **	-13.33 **	-14.81 **	-4.29 **	-8.11 **	-36.54 **	-21.43 **	-36.94 **	3.13	-36.54 **
21	PBW-550X HD-3326	3.60 **	7.46 **	2.86 **	8.27 **	6.67 **	-4.70 **	-10.11 **	-11.64 **	-0.73	-4.70 **	-21.25 **	0.05	-19.75 **	31.25 **	-19.23 **
22	PBW-677XPBW ZN1	-6.19 **	-1.99 **	-6.19 **	- .0.23**	-2.72 **	-7.24 **	-5.63 **	-7.24 **	4.22 **	0.06	-20.25 **	0.00	-19.75 **	31.25 **	-19.23 **
23	PBW-677XPBW-343	-5.71 **	-1.49 **	-5.71 **	-0.75	-2.22 **	-13.32 **	-8.69 **	-10.25 **	0.84	-3.19 **	-36.94 **	-21.43 **	-36.94 **	3.13	-36.54 **

24	PBW-677XPBW-343	2.14 **	6.72 **	2.14 **	7.52 **	5.93 **	-16.02 **	-14.57 **	-16.02 **	-5.65 **	-9.42 **	-3.75 *	22.22 **	-1.91	60.42 **	-1.28
25	PBW-822X PBW ZN1	-5.76 **	-2.24 **	-6.43 **	-1.50 **	-2.96 **	-12.34 **	-11.10 **	-12.62 **	-1.83 *	-5.75 **	0.63	26.19 **	1.27	65.63 **	1.92
26	PBW-822X PBW-343	-8.63 **	-5.22 **	-9.29 **	-4.51 **	-5.93 **	-12.27 **	-7.59 **	-9.17 **	2.05 *	-2.02 *	-35.03 **	-19.05 **	-35.03 **	6.25 *	-34.62 **
27	PBW-822X HD-3326	5.04 **	8.96 **	4.29 **	9.77 **	8.15 **	6.71 **	-1.01	-2.69 **	9.32 **	4.96 **	-20.00 **	1.59	-18.47 **	33.33 **	-17.95 **
28	HD-3117X PBW ZN1	-4.46 **	1.24 **	-3.10 **	2.01 **	0.49	-7.73 **	-6.43 **	-8.03 **	3.33 **	-0.8	-36.71 **	-20.63 **	-36.31 **	4.17	-35.90 **
29	HD-3117X PBW-343	1.41 **	7.46 **	2.86 **	8.27 **	6.67 **	-15.61 **	-11.10 **	-12.62 **	-1.83 *	-5.75 **	-37.97 **	-22.22 **	-37.58 **	2.08	-37.18 **
30	HD-3117X HD-3326	1.64 **	7.71 **	3.10 **	8.52 **	6.91 **	28.62 **	13.65 **	11.72 **	25.51 **	20.50 **	-2.5	23.81 **	-0.64	62.50 **	0.54
31	DBW-173X PBW ZN1	-6.77 **	-7.46 **	-11.43 **	-6.77 **	-8.15 **	-8.48 **	-7.19 **	-8.77 **	2.49 **	-1.60 *	-14.56 **	11.90 **	-14.01 **	40.63 **	-13.46 **
32	DBW-173X PBW-343	0	-0.75	-5.00 **	0.00	-1.48 **	6.49 **	12.17 **	10.26 **	23.87 **	18.93 **	3.97	15.87 **	-16.56 **	36.46 **	-16.03 **
33	DBW-173X HD-3326	8.63 **	12.69 **	7.86 **	13.53 **	11.85 **	-5.04 **	-4.52 **	-6.14 **	5.45 **	1.24	2.5	3.97	4.46 **	70.83 **	5.13 **
34	DH-3086X PBW ZN1	-6.99 **	-0.75	-5.00 **	0.00	-1.48 **	-3.08 **	-1.72 *	-3.39 **	8.54 **	4.21 **	-18.35 **	2.38	-17.83 **	34.38 **	-17.31 **
35	DH-3086X PBW-343	-11.89 **	-5.97 **	-10.00 **	-5.26 **	-6.67 **	-3.73 **	1.41	-0.32	11.99 **	7.52 **	15.87 **	15.87 **	-7.01 **	52.08 **	-6.41 **
36	DH-3086X HD-3326	-4.20 **	2.24 **	-2.14 **	3.01 **	1.48 **	40.15 **	26.37 **	24.22 **	39.55 **	33.98 **	-25.00 **	-4.76 *	-23.57 **	25.00 **	-23.08 **
37	DBW-222X PBW ZN1	13.71 **	5.22 **	0.71	6.02 **	4.44 **	-17.71 **	-12.63 **	-14.12 **	-3.52 **	-7.37 **	-31.65 **	-14.29 **	-31.21 **	12.50 **	-30.77 **
38	DBW-222X PBW-343	-4.06 **	-5.97 **	-10.00 **	-5.26 **	-6.67 **	-18.71 **	-13.69 **	-15.16 **	-4.68 **	-8.49 **	-44.94 **	-30.95 **	-44.59 **	-9.38 **	-44.23 **
39	DBW-222X HD-3326	1.44 **	5.22 **	0.71	6.02 **	4.44 **	-1.18	4.92 **	3.13 **	15.87 **	11.24 **	-41.88 **	-26.19 **	-40.76 **	-3.13	-40.38 **
40	CSW-18XPBW ZN1	-2.10 **	4.48 **	0.00	5.26 **	3.70 **	-12.23 **	-5.55 **	-7.16 **	4.30 **	0.14	-24.05 **	-4.76 *	-23.57 **	25.00 **	-23.08 **
41	CSW-18XPBW-343	-1.40 **	5.22 **	0.71	6.02 **	4.44 **	-2.24 **	5.20 **	3.41 **	16.17 **	11.53 **	-44.94 **	-30.95 **	-44.59 **	-9.38 **	-44.23 **
42	CSW-18XHD-3326	-13.99 **	-8.21 **	-12.14 **	-7.52 **	-8.89 **	-22.72 **	-16.84 **	-18.26 **	-8.16 **	-11.83 **	-11.88 **	11.90 **	-10.19 **	46.88 **	-9.62 **
43	PBW-757X PBW ZN1	15.32 **	6.72 **	2.14 **	7.52 **	5.93 **	-13.82 **	-12.60 **	-14.09 **	-3.48 **	-7.34 **	-43.04 **	-28.57 **	-42.68 **	-6.25 *	-42.31 **
44	PBW-757X PBW-343	6.60 **	4.48 **	0.00	5.26 **	3.70 **	-2.29 **	2.92 **	1.17	13.66 **	9.12 **	2.38	2.38	-17.83 **	34.38 **	-17.31 **
45	PBW-757X HD-3326	-10.79 **	-7.46 **	-11.43 **	-6.77 **	-8.15 **	6.81 **	2.07 **	0.33	12.72 **	8.22	-31.25 **	-12.70 **	-29.94 **	14.58 **	-29.49 **

"*" and "**" for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Grain Filling Period														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	68.92 **	60.26 **	30.21 **	-5.30 *	60.26 **	7.14 **	8.70 **	35.14 **	11.94 **	7.91 **	-20.89 **	36.23 **	22.82 **	-29.23 **	24.40 **
2	BHU-25XPBW-343	0.78	66.67 **	35.42 **	-1.52	66.67 **	-2.86 **	-1.45	22.52 **	1.49	-2.16 *	0.3	72.71 **	55.71 **	-10.28 **	57.72 **
3	BHU-25XHD-3326	35.71 **	46.15 **	18.75 **	-13.64 **	46.15 **	9.29 **	10.87 **	37.84 **	14.18 **	10.07 **	-0.9	70.66 **	53.86 **	-11.35 **	55.84 **
4	WB-02XPBW ZN1	10.34 **	23.08 **	0.00	-27.27 **	23.08 **	-0.72	0.00	24.32 **	2.99 **	-0.72	-12.98 **	37.77 **	24.21 **	-28.43 **	25.81 **
5	WB-02XPBW-343	-25.58 **	23.08 **	0.10**	-27.27 **	23.08 **	5.00 **	6.52 **	32.43 **	9.70 **	5.76 **	38.18 **	76.70 **	59.30 **	-8.21 **	61.36 **
6	WB-02XHD-3326	41.38 **	57.69 **	28.13 **	-6.82 **	57.69 **	7.91 **	8.70 **	35.14 **	11.94 **	7.91 **	66.58 **	53.96 **	38.80 **	-20.02 **	40.59 **
7	BHU-31XPBW ZN1	18.52 **	23.08 **	0.00	-27.27 **	23.08 **	11.51 **	12.32 **	39.64 **	15.67 **	11.51 **	-31.08 **	9.12 **	-1.62	-43.31 **	-0.35
8	BHU-31XPBW-343	-26.36 **	21.79 **	-1.04	-28.03 **	21.79 **	9.29 **	10.87 **	37.84 **	14.18 **	10.07 **	4.02 *	33.02 **	19.92 **	-30.90 **	21.47 **
9	BHU-31XHD-3326	11.90 **	20.51 **	-2.08	-28.79 **	20.51 **	-24.46 **	-23.91 **	-5.41 **	-21.64 **	-24.46 **	-29.49 **	-13.36 **	-21.89 **	-54.99 **	-20.88 **
10	HD-3721XPBW ZN1	53.75 **	57.69 **	28.13 **	-6.82 **	57.69 **	7.91 **	8.70 **	35.14 **	11.94 **	7.91 **	12.09 **	77.47 **	60.00 **	-7.81 **	62.06 **
11	HD-3721XPBW-343	0.78	66.67 **	35.42 **	-1.52	66.67 **	7.14 **	8.70 **	35.14 **	11.94 **	7.91 **	7.03 **	36.87 **	23.40 **	-28.90 **	24.99 **
12	HD-3721XHD-3326	14.29 **	23.08 **	0.000	-27.27 **	23.08 **	7.91 **	8.70 **	35.14 **	11.94 **	7.91 **	64.75 **	57.55 **	42.04 **	-18.15 **	43.88 **
13	PWB-725X PBW ZN1	64.10 **	64.10 **	33.33 **	-3.03	64.10 **	0.00	0.72	25.23 **	3.73 **	0.00	13.47 **	79.65 **	61.96 **	-6.67 **	64.05 **
14	PWB-725X PBW-343	-2.33	61.54 **	31.25 **	-4.55 *	61.54 **	-1.43	0.00	24.32 **	2.99 **	-0.72	41.19 **	80.55 **	62.78 **	-6.21 **	64.88 **
15	PWB-725X HD-3326	25.00 **	34.62 **	9.38 **	-20.45 **	34.62 **	11.51 **	12.32 **	39.64 **	15.67 **	11.51 **	46.12 **	46.12 **	31.74 **	-24.09 **	33.44 **
16	CRDGEHNU1XPBWZN1	-5.30 *	60.26 **	30.21 **	-5.30 *	60.26 **	-0.72	0.00	24.32 **	2.99 **	-0.72	-6.67 **	79.65 **	61.96 **	-6.67 **	64.05 **
17	CRDGEHNU1XPBW343	-38.64 **	3.85	-15.63 **	-38.64 **	3.85	0.71	2.17 *	27.03 **	5.22 **	1.4	-37.89 **	19.57 **	7.79 **	-37.89 **	9.19 **
18	CRDGEHNU1XHD-3326	-18.18 **	38.46 **	12.50 **	-18.18 **	38.46 **	-20.14 **	-19.57 **	0.00	-17.16 **	-20.14 **	-41.84 **	11.95 **	0.93	-41.84 **	2.23
19	PBW-550X PBW ZN1	19.23 **	19.23 **	-3.13	-29.55 **	19.23 **	-2.88 **	-2.17 *	21.62 **	0.75	-2.88 **	-6.25 **	48.43 **	33.82 **	-22.89 **	35.55 **
20	PBW-550X PBW-343	0	65.38 **	34.38 **	-2.27	65.38 **	-37.86 **	-36.96 **	-21.62 **	-35.07 **	-37.41 **	42.80 **	82.61 **	64.63 **	-5.14 **	66.75 **
21	PBW-550X HD-3326	32.14 **	42.31 **	15.63 **	-15.91 **	42.31 **	-2.88 **	-2.17 *	21.62 **	0.75	-2.88 **	48.10 **	62.18 **	46.21 **	-15.75 **	48.10 **
22	PBW-677XPBW ZN1	-14.58 **	5.13	-14.58 **	-37.88 **	5.13	-0.72	0.00	24.32 **	2.99 **	-0.72	-8.11 **	45.48 **	31.16 **	-24.43 **	32.85 **
23	PBW-677XPBW-343	-42.64 **	-5.13	-22.92 **	-43.94 **	-5.13	-18.57 **	-17.39 **	2.70 *	-14.93 **	-17.99 **	44.63 **	84.94 **	66.74 **	-3.92 **	68.89 **

24	PBW-677XPBW-343	1.04	24.36 **	1.04	-26.52 **	24.36 **	-0.72	0.00	24.32 **	2.99 **	-0.72	57.68 **	74.90 **	57.68 **	-9.14 **	59.71 **
25	PBW-822X PBW ZN1	-4.9	24.36 **	1.04	-26.52 **	24.36 **	7.14 **	8.70 **	35.14 **	11.94 **	7.91 **	1.38	60.51 **	44.71 **	-16.62 **	46.57 **
26	PBW-822X PBW-343	-18.60 **	34.62 **	9.38 **	-20.45 **	34.62 **	-22.86 **	-21.74 **	-2.70 *	-19.40 **	-22.30 **	58.49 **	52.67 **	82.72 **	5.29 **	85.08 **
27	PBW-822X HD-3326	0.00	30.77 **	6.25 *	-22.73 **	30.77 **	-1.43	0.00	24.32 **	2.99 **	-0.72	34.55 **	35.07 **	21.77 **	-29.83 **	23.35 **
28	HD-3117X PBW ZN1	59.26 **	65.38 **	34.38 **	-2.27	65.38 **	-43.88 **	-43.48 **	-29.73 **	-41.79 **	-43.88 **	31.97 **	57.94 **	88.37 **	8.54 **	90.80 **
29	HD-3117X PBW-343	-2.33	61.54 **	31.25 **	-4.55 *	61.54 **	-21.43 **	-20.29 **	-0.9	-17.91 **	-20.86 **	36.47 **	74.51 **	57.33 **	-9.34 **	59.36 **
30	HD-3117X HD-3326	16.67 **	25.64 **	2.08	-25.76 **	25.64 **	-0.72	0.00	24.32 **	2.99 **	-0.72	30.12 **	35.97 **	22.59 **	-29.36 **	24.17 **
31	DBW-173X PBW ZN1	-23.23 **	-2.56	-20.83 **	-42.42 **	-2.56	3.60 **	4.35 **	29.73 **	7.46 **	3.60 **	-11.44 **	40.21 **	26.41 **	-27.16 **	28.04 **
32	DBW-173X PBW-343	-41.09 **	-2.56	-20.83 **	-42.42 **	-2.56	0.71	2.17 *	27.03 **	5.22 **	1.44	30.44 **	66.80 **	50.38 **	-13.35 **	52.32 **
33	DBW-173X HD-3326	6.06 *	34.62 **	9.38 **	-20.45 **	34.62 **	7.91 **	8.70 **	35.14 **	11.94 **	7.91 **	33.49 **	68.99 **	52.35 **	-12.21 **	54.32 **
34	DH-3086X PBW ZN1	-5.88 *	23.08 **	0.19	-27.27 **	23.08 **	-0.72	0.00	24.32 **	2.99 **	-0.72	-16.31 **	32.50 **	19.46 **	-31.17 **	21.00 **
35	DH-3086X PBW-343	-25.58 **	23.08 **	0.00	-27.27 **	23.08 **	-5.71 **	-4.35 **	18.92 **	-1.49	-5.04 **	33.76 **	71.04 **	54.20 **	-11.15 **	56.19 **
36	DH-3086X HD-3326	3.92	35.90 **	10.42 **	-19.70 **	35.90 **	-5.04 **	-4.35 **	18.92 **	-1.49	-5.04 **	65.93 **	71.04 **	54.20 **	-11.15 **	56.19 **
37	DBW-222X PBW ZN1	1.06	21.79 **	-1.04	-28.03 **	21.79 **	-6.47 **	-5.80 **	17.12 **	-2.99 **	-6.47 **	-16.38 **	56.14 **	40.77 **	-18.89 **	42.59 **
38	DBW-222X PBW-343	-2.33	61.54 **	31.25 **	-4.55 *	61.54 **	-1.43	0.00	24.32 **	-2.99 **	-0.72	-8.19 **	71.43 **	54.55 **	-10.95 **	56.55 **
39	DBW-222X HD-3326	36.17 **	64.10 **	33.33 **	-3.03	64.10 **	-28.78 **	-28.26 **	-10.81 **	-26.12 **	-28.78 **	-19.20 **	50.87 **	36.02 **	-21.62 **	37.78 **
40	CSW-18XPBW ZN1	-7.21 **	32.05 **	7.29 *	-21.97 **	32.05 **	-9.93 **	-1.45	22.52 **	1.49	-2.16 *	21.34 **	62.11 **	73.20 **	-0.2	75.43 **
41	CSW-18XPBW-343	0.00	65.38 **	34.38 **	-2.27	65.38 **	-28.48 **	-21.74 **	-2.70 *	-19.40 **	-22.30 **	60.18 **	64.83 **	84.67 **	6.41 **	87.05 **
42	CSW-18XHD-3326	-13.51 **	23.08 **	0.00	-27.27 **	23.08 **	-0.66	8.70 **	35.14 **	11.94 **	7.91 **	64.42 **	73.29 **	83.28 **	5.61 **	85.64 **
43	PBW-757X PBW ZN1	31.25 **	61.54 **	31.25 **	-4.55 *	61.54 **	-22.30 **	-21.74 **	-2.70 *	-19.40 **	-22.30 **	30.10 **	55.99 **	85.71 **	7.01 **	88.10 **
44	PBW-757X PBW-343	-24.03 **	25.64 **	2.08	-25.76 **	25.64 **	0.71	2.17 *	27.03 **	5.22 **	1.44	13.14 **	71.43 **	54.55 **	-10.95 **	56.55 **
45	PBW-757X HD-3326	19.79 **	47.44 **	19.79 **	-12.88 **	47.44 **	-9.35 **	-8.70 **	13.51 **	-5.97 **	-9.35 **	16.10 **	75.91 **	58.59 **	-8.62 **	60.64 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Number of productive tillers														
		Location 1					Location 2					Location 3				
SN	**Crosse**	**BP**	**SV1**	**SV2**	**SV3**	**SV4**	**BP**	**SV1**	**SV2**	**SV3**	**SV4**	**BP**	**SV1**	**SV2**	**SV3**	**SV4**
1	BHU-25XPBW ZN1	36.32 **	49.84 **	22.11	8.17	19.03	30.51 **	42.17 **	45.96 **	42.99 **	45.96 **	38.96 **	46.80 **	46.22 **	31.24 **	30.15 **
2	BHU-25XPBW-343	11.87	34.42 *	9.54	-2.97	6.77	26.33 **	41.99 **	45.77 **	42.81 **	45.77 **	41.76 **	57.12 **	56.50 **	40.46 **	39.30 **
3	BHU-25XHD-3326	-8.58	30.54 *	6.38	-5.76	3.69	32.98 **	40.21 **	43.95 **	41.02 **	43.95 **	54.97 **	55.43 **	54.82 **	38.95 **	37.80 **
4	WB-02XPBW ZN1	30.75 **	79.30 **	46.11 **	29.43 **	42.43 **	29.50 **	41.07 **	44.83 **	41.88 **	44.83 **	47.00 **	55.28 **	54.68 **	38.82 **	37.67 **
5	WB-02XPBW-343	2.77	40.93 **	14.85	1.73	11.95	23.05 **	38.30 **	41.99 **	39.09 **	41.99 **	44.61 **	60.28 **	59.66 **	43.29 **	42.11 **
6	WB-02XHD-3326	-21.23 *	12.48	-8.34	-18.8	-10.65	21.47 **	28.08 **	31.50 **	28.82 **	31.50 **	64.29 **	60.10 **	59.48 **	43.13 **	41.95 **
7	BHU-31XPBW ZN1	28.01 *	70.78 **	39.17 **	23.28 *	35.65 **	14.45 **	24.67 **	28.00 **	25.39 **	28.00 **	10.56 **	16.80 **	16.34 **	4.42 **	3.55 **
8	BHU-31XPBW-343	7.73	43.72 **	17.12	3.75	14.16	22.35 **	37.51 **	41.17 **	38.30 **	41.17 **	9.51 **	21.38 **	20.90 **	8.51 **	7.61 **
9	BHU-31XHD-3326	4.29	48.91 **	21.35	7.5	18.29	26.22 **	33.10 **	36.64 **	33.86 **	36.64 **	44.34 **	44.84 **	44.28 **	29.49 **	28.41 **
10	HD-3721XPBW ZN1	44.85 **	59.22 **	29.75 *	14.94	26.48 *	34.10 **	46.08 **	49.97 **	46.92 **	49.97 **	25.33 **	32.39 **	31.88 **	18.36 **	17.38 **
11	HD-3721XPBW-343	15.68	38.99 **	13.27	0.34	10.41	17.99 **	32.61 **	36.15 **	33.38 **	36.15 **	27.69 **	41.52 **	40.97 **	26.52 **	25.47 **
12	HD-3721XHD-3326	41.37 **	41.86 **	64.50 **	45.72 **	60.34 **	19.54 **	26.05 **	29.41 **	26.77 **	29.41 **	50.01 **	42.04 **	41.48 **	26.98 **	25.93 **
13	PWB-725X PBW ZN1	37.52 **	51.16 **	23.18 *	9.12	20.07	31.39 **	43.12 **	46.94 **	43.94 **	46.94 **	37.11 **	44.84 **	44.28 **	29.49 **	28.41 **
14	PWB-725X PBW-343	22.13	46.74 **	19.58	5.93	16.56	25.56 **	41.12 **	44.88 **	41.93 **	44.88 **	41.01 **	56.29 **	55.68 **	39.72 **	38.56 **
15	PWB-725X HD-3326	27.25 **	81.71 **	48.07 **	31.17 **	44.33 **	31.93 **	39.11 **	42.82 **	39.91 **	42.82 **	17.18 **	17.18 **	16.72 **	4.76 **	3.89 **
16	CRDGEHNU1XPBWZN1	21.88 *	68.84 **	37.59 **	21.88 *	34.11 **	21.33 **	32.16 **	35.69 **	32.92 **	35.69 **	39.78 **	56.35 **	55.74 **	39.78 **	38.62 **
17	CRDGEHNU1XPBW343	25.01 *	73.18 **	41.12 **	25.01 *	37.56 **	22.12 **	37.26 **	40.92 **	38.05 **	40.92 **	6.59 **	19.23 **	18.76 **	6.59 **	5.71 **
18	CRDGEHNU1XHD-3326	10.48	57.75 **	28.55 *	13.88	25.31 *	25.43 **	32.25 **	35.78 **	33.01 **	35.78 **	3.19 **	15.42 **	14.97 **	3.19 **	2.33 *
19	PBW-550X PBW ZN1	48.89 **	87.44 **	52.75 **	35.31 **	48.89 **	28.44 **	39.91 **	43.64 **	40.72 **	43.64 **	12.18 **	26.53 **	26.03 **	13.12 **	12.18 **
20	PBW-550X PBW-343	63.73 **	60.12 **	67.97 **	48.80 **	63.73 **	28.26 **	44.15 **	48.00 **	44.98 **	48.00 **	25.90 **	42.01 **	41.45 **	26.95 **	25.90 **
21	PBW-550X HD-3326	39.20 **	98.76 **	61.97 **	43.48 **	57.88 **	34.23 **	41.54 **	45.31 **	42.35 **	45.31 **	26.23 **	42.38 **	41.82 **	27.29 **	26.23 **
22	PBW-677XPBW ZN1	28.87 *	58.14 **	28.87 *	14.16	25.62 *	33.70 **	45.65 **	49.53 **	46.49 **	49.53 **	31.26 **	38.66 **	38.12 **	23.96 **	22.93 **
23	PBW-677XPBW-343	54.96 **	90.16 **	54.96 **	37.27 **	51.05 **	22.87 **	38.10 **	41.78 **	38.89 **	41.78 **	5.71 **	17.17 **	16.71 **	4.75 **	3.88 **
24	PBW-677XPBW-343	7.6	53.64 **	25.21 *	10.91	22.04	36.23 **	43.64 **	47.47 **	44.47 **	47.47 **	29.57 **	30.07 **	29.57 **	16.29 **	15.32 **
25	PBW-822X PBW ZN1	98.80 **	58.53 **	78.08 **	57.75 **	73.58 **	21.56 **	32.42 **	35.95 **	33.19 **	35.95 **	6.38 **	19.40 **	18.94 **	6.75 **	5.86 **
26	PBW-822X PBW-343	52.58 **	83.33 **	49.40 **	32.34 **	45.63 **	20.91 **	35.89 **	39.52 **	36.67 **	39.52 **	36.52 **	53.22 **	52.63 **	36.98 **	35.85 **
27	PBW-822X HD-3326	28.39 **	83.33 **	49.40 **	32.34 **	45.63 **	28.19 **	35.17 **	38.78 **	35.95 **	38.78 **	5.31 **	18.20 **	17.74 **	5.67 **	4.79 **
28	HD-3117X PBW ZN1	47.46 **	62.09 **	32.09 **	17.01	28.76 *	33.11 **	45.00 **	48.86 **	45.83 **	48.86 **	35.19 **	42.81 **	42.25 **	27.67 **	26.61 **
29	HD-3117X PBW-343	43.23 **	72.09 **	40.24 **	24.23 *	36.70 **	34.07 **	50.68 **	54.70 **	51.55 **	54.70 **	29.80 **	43.87 **	43.31 **	28.62 **	27.55 **

30	HD-3117X HD-3326	10.97	58.45 **	29.12 *	14.38	25.86 *	31.01 **	38.14 **	41.82 **	38.93 **	41.82 **	21.13 **	24.84 **	24.35 **	11.61 **	10.68 **
31	DBW-173X PBW ZN1	55.43 **	70.85 **	39.23 **	23.34 *	35.71 **	22.47 **	38.11 **	41.79 **	38.90 **	41.79 **	12.24 **	24.81 **	24.32 **	11.58 **	10.66 **
32	DBW-173X PBW-343	77.68 **	53.49 **	73.97 **	54.11 **	69.58 **	23.37 **	39.13 **	42.84 **	39.93 **	42.84 **	13.12 **	25.78 **	25.29 **	12.45 **	11.52 **
33	DBW-173X HD-3326	25.95 *	79.84 **	46.56 **	29.83 **	42.86 **	32.07 **	48.94 **	52.91 **	49.79 **	52.91 **	21.50 **	35.11 **	34.58 **	20.79 **	19.79 **
34	DH-3086X PBW ZN1	29.90 *	42.79 **	16.36	3.08	13.42	26.55 **	39.34 **	43.06 **	40.14 **	43.06 **	12.01 **	25.98 **	25.49 **	12.63 **	11.70 **
35	DH-3086X PBW-343	70.90 **	55.35 **	67.34 **	40.24**	63.12 **	27.94 **	43.79 **	47.63 **	44.62 **	47.63 **	15.77 **	30.22 **	29.71 **	16.42 **	15.45 **
36	DH-3086X HD-3326	10.26	57.44 **	28.30 *	13.65	25.06 *	20.52 **	32.70 **	36.23 **	33.46 **	36.23 **	30.98 **	47.32 **	46.75 **	31.70 **	30.61 **
37	DBW-222X PBW ZN1	60.25 **	55.04 **	75.24 **	55.23 **	70.81 **	37.23 **	49.49 **	53.47 **	50.35 **	53.47 **	36.20 **	51.85 **	51.26 **	35.76 **	34.63 **
38	DBW-222X PBW-343	53.21 **	65.58 **	67.53 **	48.41 **	63.30 **	26.44 **	42.11 **	45.90 **	42.93 **	45.90 **	41.02 **	57.23 **	56.62 **	40.56 **	39.40 **
39	DBW-222X HD-3326	7.6	53.64 **	25.21 *	10.91	22.04	41.91 **	49.64 **	53.63 **	50.50 **	53.63 **	40.60 **	56.76 **	56.15 **	40.15 **	38.99 **
40	CSW-18XPBW ZN1	68.97 **	85.74 **	51.36 **	34.08 **	47.54 **	35.87 **	48.00 **	51.95 **	48.86 **	51.95 **	19.89 **	34.22 **	33.70 **	20.00 **	19.00 **
41	CSW-18XPBW-343	42.19 **	70.85 **	39.23 **	23.34 *	35.71 **	31.86 **	48.21 **	52.16 **	49.06 **	52.16 **	37.10 **	53.49 **	52.89 **	37.22 **	36.08 **
42	CSW-18XHD-3326	25.14 *	78.68 **	45.61 **	28.99 **	41.93 **	36.44 **	43.86 **	47.70 **	44.69 **	47.70 **	41.29 **	58.17 **	57.56 **	41.41 **	40.24 **
43	PBW-757X PBW ZN1	57.13 **	68.29 **	69.74 **	50.36 **	65.46 **	36.59 **	48.79 **	52.75 **	49.64 **	52.75 **	38.21 **	54.04 **	53.44 **	37.72 **	36.58 **
44	PBW-757X PBW-343	32.05 **	75.04 **	42.64 **	26.36 *	39.04 **	27.40 **	43.19 **	47.01 **	44.02 **	47.01 **	16.32 **	29.65 **	29.14 **	15.90 **	14.94 **
45	PBW-757X HD-3326	24.05 *	77.13 **	44.35 **	27.87 **	40.70 **	35.70 **	43.09 **	46.91 **	43.91 **	46.91 **	24.02 **	38.23 **	37.69 **	23.58 **	22.55 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Number of spikelet per spike														
		Location 1					Location 2					Location 3				
SN	Cross	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	VS3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	6.18 *	5.31 *	4.95 *	5.99 *	3.73	12.00 *	13.76 *	7.02	15.44 *	21.47 **	11.23 **	12.98 **	1.78	-12.91 **	20.63 **
2	BHU-25XPBW-343	4.88	5.62 *	5.25 *	6.30 *	4.03	-17.04 **	3.13	-2.99	4.65	10.12	-4.68 *	26.64 **	14.08 **	-2.38	35.22 **
3	BHU-25XHD-3326	-0.13	2.79	2.43	3.45	1.24	11.31	0.61	-5.35	2.1	7.43	33.53 **	24.12 **	11.82 **	-4.32 *	32.53 **
4	WB-02XPBW ZN1	3.01	2.16	1.81	2.82	0.63	5.44	7.1	0.75	8.68	14.36 *	30.06 **	32.11 **	19.01 **	1.84	41.06 **
5	WB-02XPBW-343	2.89	3.62	3.26	4.29	2.06	-9.88 *	12.03	5.39	13.69 *	19.62 **	0.84	33.97 **	20.69 **	3.27	43.05 **
6	WB-02XHD-3326	-2.35	0.51	0.17	1.16	-1	16.55 *	12.93 *	6.24	14.60 *	20.58 **	29.58 **	28.60 **	15.86 **	-0.86	37.32 **
7	BHU-31XPBW ZN1	3.99	3.14	2.78	3.8	1.59	-14.72 *	-9.18	-14.57 *	-7.84	-3.03	19.44 **	30.00 **	17.11 **	0.21	38.81 **
8	BHU-31XPBW-343	0.25	0.96	0.61	1.61	-0.56	-23.97 **	-5.49	-11.09	-4.1	0.91	0.63	33.69 **	20.44 **	3.06	42.75 **
9	BHU-31XHD-3326	-4	-1.19	-1.53	-0.56	-2.68	8.16	15.18 *	8.35	16.88 **	22.99 **	25.98 **	37.12 **	23.53 **	5.70 **	46.41 **
10	HD-3721XPBW ZN1	7.66 **	7.85 **	7.48 **	8.55 **	6.23 *	-0.9	0.66	-5.31	2.15	7.48	45.39 **	47.68 **	33.04 **	13.84 **	57.69 **
11	HD-3721XPBW-343	-1.86	-1.17	-1.51	-0.53	-2.65	-10.63 *	11.1	4.51	12.74 *	18.63 **	1.32	34.61 **	21.26 **	3.76	43.73 **
12	HD-3721XHD-3326	0.77	3.72	3.36	4.38	2.16	19.00 *	0.85	-5.13	2.34	7.68	59.07 **	47.86 **	33.21 **	13.98 **	57.89 **
13	PWB-725X PBW ZN1	-1.73	-1.73	-2.07	-1.1	-3.21	0.19	1.77	-4.26	3.28	8.67	41.08 **	43.30 **	29.10 **	10.47 **	53.02 **
14	PWB-725X PBW-343	4.93 *	5.67 *	5.31 *	6.35 *	4.09	2.51	27.43 **	19.87 **	29.31 **	36.06 **	-3.49	28.21 **	15.50 **	-1.17	36.90 **
15	PWB-725X HD-3326	-1.85	1.03	0.68	1.68	-0.49	3.9	3.9	-2.26	5.44	10.94	50.92 **	50.92 **	35.96 **	16.34 **	61.15 **
16	CRDGEHNU1XPBWZN1	2.15	1.5	1.15	2.15	-0.03	43.05 **	45.30 **	36.69 **	47.45 **	55.15 **	12.01 **	45.30 **	30.90 **	12.01 **	55.15 **
17	CRDGEHNU1XPBW343	2.42	3.15	2.79	3.81	1.6	13.24 **	40.77 **	32.43 **	42.85 **	50.31 **	17.17 **	55.66 **	40.23 **	20.00 **	66.21 **
18	CRDGEHNU1XHD-3326	-2.02	0.85	0.5	1.49	-0.67	33.21 **	31.27 **	23.49 **	33.21 **	40.16 **	12.67 **	46.16 **	31.67 **	12.67 **	56.06 **
19	PBW-550X PBW ZN1	2.08	3.63	3.28	4.3	2.08	1.45	3.05	-3.06	4.57	10.03	32.31 **	34.39 **	21.07 **	3.6	43.50 **
20	PBW-550X PBW-343	0.05	1.58	1.23	2.23	0.05	0.61	25.06 **	17.65 **	26.91 **	33.54 **	-5.86 **	25.06 **	12.67 **	-3.59	33.54 **
21	PBW-550X HD-3326	2.61	5.62 *	5.25 *	6.30 *	4.03	48.62 **	39.19 **	30.94 **	41.25 **	48.62 **	48.62 **	39.19 **	25.39 **	7.30 **	48.62 **
22	PBW-677XPBW ZN1	-1.33	-0.99	-1.33	-0.35	-2.47	-19.85 **	-14.80 *	-19.85 **	-13.54 *	-9.03	33.23 **	47.89 **	33.23 **	14.00 **	57.91 **
23	PBW-677XPBW-343	8.82 **	9.59 **	9.21 **	10.29 **	7.94 **	1.87	26.64 **	19.13 **	28.51 **	35.22 **	-4.68 *	26.64 **	14.08 **	-2.38	35.22 **

24	PBW-677XPBW-343	-1.99	0.87	0.53	1.52	-0.64	-1.61	4.58	-1.61	6.13	11.67	36.58 **	51.60 **	36.58 **	16.87 **	61.88 **
25	PBW-822X PBW ZN1	6.73 **	5.85 *	5.49 *	6.53 *	4.26	6.97	8.65	2.21	10.26	16.02 *	30.11 **	32.16 **	19.06 **	1.88	41.12 **
26	PBW-822X PBW-343	3.28	4.01	3.65	4.68	2.45	7.55	33.70 **	25.77 **	35.67 **	42.76 **	13.61 **	50.94 **	35.98 **	16.35 **	61.17 **
27	PBW-822X HD-3326	6.01 *	9.11 **	8.74 **	9.82 **	7.47 **	29.47 **	23.63 **	16.30 **	25.46 **	32.01 **	29.47 **	23.63 **	11.37 **	-4.70 *	32.01 **
28	HD-3117X PBW ZN1	7.94 **	7.34 **	6.97 **	8.03 **	5.73 *	23.12 **	25.06 **	17.65 **	26.91 **	33.54 **	23.12 **	25.06 **	12.67 **	-3.59	33.54 **
29	HD-3117X PBW-343	0.94	1.65	1.3	2.3	0.12	7.58	33.74 **	25.81 **	35.71 **	42.80 **	4.80 *	39.22 **	25.42 **	7.32 **	48.66 **
30	HD-3117X HD-3326	-2.64	0.21	-0.14	0.85	-1.3	12.41	8.15	1.74	9.75	15.48 *	62.71 **	51.25 **	36.26 **	16.59 **	61.50 **
31	DBW-173X PBW ZN1	2.46	5.84 *	5.47 *	6.52 *	4.25	-9.98	-8.56	-13.98 *	-7.2	-2.36	36.31 **	38.46 **	24.74 **	6.74 **	47.85 **
32	DBW-173X PBW-343	-4.89 *	-1.75	-2.09	-1.12	-3.22	-24.55 **	-6.21	-11.77 *	-4.82	0.15	6.58 **	41.60 **	27.56 **	9.15 **	51.19 **
33	DBW-173X HD-3326	0.27	3.58	3.22	4.24	2.02	14.63 *	0.78	-5.2	2.27	7.61	44.66 **	34.47 **	21.14 **	3.66	43.59 **
34	DH-3086X PBW ZN1	-3.61	-0.29	-0.64	0.35	-1.79	9.68	11.41	4.81	13.06 *	18.96 **	45.94 **	48.24 **	33.55 **	14.27 **	58.29 **
35	DH-3086X PBW-343	0.43	3.88	3.53	4.55	2.32	-6.37	16.39 **	9.49	18.11 **	24.27 **	1.76	35.19 **	21.79 **	4.22 *	44.36 **
36	DH-3086X HD-3326	2.41	5.94 *	5.57 *	6.62 **	4.35	36.69 **	9.92	3.41	11.55	17.37 **	51.87 **	42.83 **	28.68 **	10.11 **	52.51 **
37	DBW-222X PBW ZN1	7.33 **	7.84 **	7.47 **	8.53 **	6.22 *	21.64 **	37.68 **	29.52 **	39.71 **	47.01 **	5.53 **	38.46 **	24.74 **	6.74 **	47.85 **
38	DBW-222X PBW-343	8.11 **	8.88 **	8.50 **	9.58 **	7.24 **	3.03	28.07 **	20.48 **	29.96 **	36.75 **	-3.6	28.07 **	15.38 **	-1.27	36.75 **
39	DBW-222X HD-3326	-0.26	2.66	2.31	3.32	1.12	18.26 **	33.85 **	25.92 **	35.83 **	42.93 **	2.02	33.85 **	20.59 **	3.18	42.93 **
40	CSW-18XPBW ZN1	-0.19	-0.5	-0.84	0.14	-2	12.64 *	18.57 **	11.54 *	20.33 **	26.61 **	29.92 **	42.86 **	28.70 **	10.13 **	52.55 **
41	CSW-18XPBW-343	3.03	3.76	3.4	4.43	2.2	6.54	32.44 **	24.59 **	34.40 **	41.42 **	-0.31	32.44 **	19.32 **	2.1	41.42 **
42	CSW-18XHD-3326	5.42 *	8.50 **	8.13 **	9.20 **	6.87 **	24.43 **	30.99 **	23.22 **	32.92 **	39.86 **	19.11 **	30.99 **	18.00 **	0.97	39.86 **
43	PBW-757X PBW ZN1	11.68 **	10.77 **	10.38 **	11.48 **	9.10 **	10.92 *	24.33 **	16.96 **	26.17 **	32.76 **	7.17 **	24.33 **	12.01 **	-4.16 *	32.76 **
44	PBW-757X PBW-343	5.39 *	6.13 *	5.77 *	6.81 **	4.54	-18.66 **	1.11	-4.88	2.61	7.97	5.60 **	40.29 **	26.39 **	8.15 **	49.80 **
45	PBW-757X HD-3326	4.15	7.20 **	6.83 **	7.89 **	5.59 *	-7.6	3.57	-2.57	5.11	10.59	16.30 **	34.92 **	21.55 **	4.01	44.06 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Spike length														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	2.38	20.48 **	6.58	5.52	14.31 **	8.01 **	9.32 **	9.49 **	8.37 **	8.41 **	14.36 **	11.30 **	13.81 **	3.79	5.3
2	BHU-25XPBW-343	2.31	20.40 **	6.5	5.44	14.23 **	8.32 **	9.63 **	9.81 **	8.68 **	8.73 **	16.88 **	10.95 **	13.46 **	3.47	4.97
3	BHU-25XHD-3326	-4.56	12.31 **	-0.65	-1.64	6.56	3.36	6.70 *	6.87 **	5.77 *	5.81 *	23.26 **	13.02 **	15.57 **	5.4	6.93 *
4	WB-02XPBW ZN1	4.55	17.39 **	3.85	2.81	11.38 **	8.25 **	6.05 *	6.22 *	5.12 *	5.17 *	21.77 **	18.51 **	21.19 **	10.52 **	12.13 **
5	WB-02XPBW-343	-0.13	12.14 **	-0.8	-1.79	6.4	9.69 **	7.56 **	7.73 **	6.62 *	6.67 *	23.48 **	17.21 **	19.86 **	9.31 **	10.90 **
6	WB-02XHD-3326	5.98	19.55 **	5.76	4.7	13.43 **	1.07	4.33	4.5	3.43	3.47	28.12 **	16.09 **	18.71 **	8.26 **	9.83 **
7	BHU-31XPBW ZN1	16.26 **	28.95 **	14.07 **	12.93 **	22.34 **	5.13 *	7.06 **	7.23 **	6.12 *	6.17 *	24.84 **	21.50 **	24.24 **	13.31 **	14.95 **
8	BHU-31XPBW-343	11.05 **	23.17 **	8.96 *	7.87 *	16.86 **	2.91	4.8	4.96	3.88	3.93	19.52 **	15.09 **	17.68 **	7.33 *	8.88 **
9	BHU-31XHD-3326	15.24 **	30.00 **	15.00 **	13.85 **	23.34 **	-0.64	2.56	2.73	1.67	1.71	20.10 **	15.65 **	18.26 **	7.85 **	9.42 **
10	HD-3721XPBW ZN1	19.64 **	30.67 **	15.59 **	14.44 **	23.98 **	11.52 **	11.95 **	12.13 **	10.98 **	11.03 **	14.15 **	11.10 **	13.60 **	3.6	5.11
11	HD-3721XPBW-343	15.69 **	21.53 **	7.51 *	6.44	15.31 **	2.19	2.59	2.75	1.7	1.74	25.55 **	19.19 **	21.88 **	11.15 **	12.76 **
12	HD-3721XHD-3326	8.02 *	21.86 **	7.80 *	6.72	15.61 **	4.3	7.66 **	7.83 **	6.72 *	6.77 **	30.34 **	13.68 **	16.24 **	6.01 *	7.55 *
13	PWB-725X PBW ZN1	5.26	14.97 **	1.7	0.69	9.08 *	2	2	2.16	1.11	1.16	17.48 **	17.48 **	20.13 **	9.56 **	11.15 **
14	PWB-725X PBW-343	16.53 **	21.77 **	7.72 *	6.64	15.53 **	9.69 **	9.69 **	9.87 **	8.74 **	8.78 **	14.41 **	14.41 **	16.99 **	6.70 *	8.25 **
15	PWB-725X HD-3326	6.91	20.60 **	6.69	5.62	14.42 **	1.59	4.87	5.03	3.95	4	11.49 **	11.49 **	14.00 **	3.97	5.48
16	CRDGEHNU1XPBWZN1	9.74 **	25.30 **	10.84 **	9.74 **	18.88 **	4.44	5.36 *	5.52 *	4.44	4.48	10.84 **	18.86 **	21.54 **	10.84 **	12.45 **
17	CRDGEHNU1XPBW343	8.28 *	23.64 **	9.37 *	8.28 *	17.30 **	6.14 *	7.07 **	7.24 **	6.14 *	6.18 *	4.68	12.25 **	14.79 **	4.68	6.20 *
18	CRDGEHNU1XHD-3326	7.51 *	22.76 **	8.60 *	7.51 *	16.47 **	1.41	4.68	4.85	3.77	3.81	11.27 **	19.31 **	22.00 **	11.27 **	12.88 **
19	PBW-550X PBW ZN1	19.40 **	30.41 **	15.36 **	14.21 **	23.73 **	6.68 *	7.57 **	7.75 **	6.64 *	6.68 *	11.80 **	18.17 **	20.84 **	10.20 **	11.80 **
20	PBW-550X PBW-343	21.37 **	27.93 **	13.16 **	12.04 **	21.37 **	4.57	5.44 *	5.61 *	4.53	4.57	11.10 **	17.43 **	20.08 **	9.52 **	11.10 **
21	PBW-550X HD-3326	11.95 **	26.29 **	11.72 **	10.61 **	19.82 **	6.21 *	9.63 **	9.81 **	8.68 **	8.73 **	5.61	11.63 **	14.15 **	4.1	5.61
22	PBW-677XPBW ZN1	1.24	14.44 **	1.24	0.23	8.58 *	2.94	2.78	2.94	1.88	1.93	23.54 **	20.81 **	23.54 **	12.67 **	14.30 **
23	PBW-677XPBW-343	12.29 **	26.93 **	12.29 **	11.17 **	20.43 **	13.93 **	13.75 **	13.93 **	12.76 **	12.81 **	22.44 **	19.73 **	22.44 **	11.66 **	13.28 **

24	PBW-677XPBW-343	12.75 **	27.46 **	12.75 **	11.63 **	20.93 **	1.44	4.71	4.88	3.8	3.84	24.88 **	22.13 **	24.88 **	13.89 **	15.55 **
25	PBW-822X PBW ZN1	25.06 **	36.59 **	20.83 **	19.63 **	29.60 **	8.74 **	9.88 **	10.05 **	8.92 **	8.97 **	8.42 **	13.51 **	16.07 **	5.85	7.39 *
26	PBW-822X PBW-343	18.24 **	23.55 **	9.29 *	8.20 *	17.22 **	6.84 **	7.96 **	8.14 **	7.02 **	7.07 **	10.33 **	15.51 **	18.11 **	7.72 *	9.28 **
27	PBW-822X HD-3326	13.76 **	28.33 **	13.53 **	12.39 **	21.76 **	9.72 **	13.26 **	13.44 **	12.28 **	12.33 **	8.71 **	13.82 **	16.39 **	6.14 *	7.68 *
28	HD-3117X PBW ZN1	12.00 **	22.32 **	8.21 *	7.13 *	16.06 **	13.48 **	11.42 **	11.60 **	10.45 **	10.50 **	16.40 **	13.29 **	15.84 **	5.65	7.18 *
29	HD-3117X PBW-343	14.94 **	22.82 **	8.65 *	7.56 *	16.53 **	7.47 **	5.52 *	5.68 *	4.6	4.64	19.68 **	13.62 **	16.18 **	5.95 *	7.49 *
30	HD-3117X HD-3326	10.22 **	24.34 **	9.99 **	8.89 *	17.97 **	0.77	4.02	4.18	3.11	3.16	35.37 **	16.49 **	19.12 **	8.64 **	10.22 **
31	DBW-173X PBW ZN1	13.87 **	24.37 **	10.02 **	8.92 *	18.00 **	6.92 **	9.86 **	10.04 **	8.91 **	8.95 **	9.73 **	17.04 **	19.68 **	9.15 **	10.73 **
32	DBW-173X PBW-343	23.32 **	28.86 **	13.99 **	12.85 **	22.26 **	-0.74	1.99	2.15	1.1	1.14	18.32 **	26.21 **	29.06 **	17.70 **	19.41 **
33	DBW-173X HD-3326	13.71 **	28.28 **	13.47 **	12.34 **	21.71 **	4.16	7.52 **	7.69 **	6.58 *	6.63 *	5.21	12.22 **	14.75 **	4.66	6.17 *
34	DH-3086X PBW ZN1	17.07 **	27.87 **	13.11 **	11.99 **	21.32 **	2.42	3.5	3.66	2.6	2.64	15.81 **	22.75 **	25.52 **	14.48 **	16.14 **
35	DH-3086X PBW-343	22.26 **	32.86 **	17.53 **	16.36 **	26.05 **	6.71 *	7.83 **	8.01 **	6.90 **	6.94 **	13.48 **	20.28 **	23.00 **	12.17 **	13.80 **
36	DH-3086X HD-3326	11.54 **	25.82 **	11.31 **	10.20 **	19.38 **	6.53 *	9.97 **	10.14 **	9.01 **	9.05 **	12.70 **	19.45 **	22.15 **	11.40 **	13.01 **
37	DBW-222X PBW ZN1	12.11 **	28.60 **	13.76 **	12.62 **	22.01 **	7.39 **	11.94 **	12.12 **	10.96 **	11.01 **	14.63 **	15.51 **	18.11 **	7.72 *	9.28 **
38	DBW-222X PBW-343	5.95	21.53 **	7.51 *	6.44	15.31 **	8.43 **	13.02 **	13.20 **	12.03 **	12.08 **	17.21 **	18.11 **	20.77 **	10.14 **	11.74 **
39	DBW-222X HD-3326	2.93	18.06 **	4.44	3.4	12.02 **	2.24	6.57 *	6.74 *	5.64 *	5.68 *	17.08 **	17.98 **	20.64 **	10.03 **	11.62 **
40	CSW-18XPBW ZN1	10.55 **	20.75 **	6.81	5.75	14.56 **	2.14	3.28	3.45	2.38	2.43	25.23 **	21.88 **	24.63 **	13.66 **	15.31 **
41	CSW-18XPBW-343	11.59 **	20.51 **	6.61	5.55	14.34 **	6.51 *	7.70 **	7.88 **	6.77 **	6.81 **	22.17 **	15.98 **	18.59 **	8.16 **	9.73 **
42	CSW-18XHD-3326	12.98 **	27.46 **	12.75 **	11.63 **	20.93 **	9.11 **	12.63 **	12.81 **	11.65 **	11.70 **	30.80 **	17.09 **	19.73 **	9.19 **	10.78 **
43	PBW-757X PBW ZN1	19.40 **	30.41 **	15.36 **	14.21 **	23.73 **	17.36 **	14.98 **	15.16 **	13.98 **	14.02 **	18.20 **	15.04 **	17.63 **	7.28 *	8.84 **
44	PBW-757X PBW-343	15.03 **	25.27 **	10.82 **	9.71 **	18.85 **	12.35 **	10.17 **	10.34 **	9.21 **	9.25 **	24.98 **	18.64 **	21.32 **	10.64 **	12.24 **
45	PBW-757X HD-3326	6.26	19.87 **	6.04	4.98	13.73 **	7.80 **	11.28 **	11.45 **	10.31 **	10.35 **	27.49 **	16.76 **	19.40 **	8.89 **	10.47 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Flag Leaf Area														
		Location 1					Location 2					Location 3				
SN	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	-20.97 **	22.42 **	30.21 **	-26.52 **	25.27 **	-18.10 **	48.97 **	29.50 **	-26.65 **	32.98 **	-9.48 **	3.63 **	1.87	1.45	9.88 **
2	BHU-25XPBW-343	-1.82	52.09 **	35.42 **	-8.71 **	55.63 **	2.68 *	86.77 **	62.36 **	-8.04 **	66.72 **	-14.55 **	-2.18	-3.85 **	-4.24 **	3.71 **
3	BHU-25XHD-3326	-5.03 **	47.11 **	18.75 **	-11.70 **	50.53 **	-2.52 *	77.32 **	54.14 **	-12.69 **	58.28 **	-11.14 **	1.73	0.00	-0.41	7.86 **
4	WB-02XPBW ZN1	-17.02 **	16.14 **	0.00	-30.29 **	18.84 **	-15.35 **	42.10 **	23.53 **	-30.03 **	26.84 **	-1.98	-0.6	-2.30 *	-2.69 *	5.39 **
5	WB-02XPBW-343	34.11 **	53.28 **	0.00	-8.00 **	56.85 **	41.69 **	89.78 **	64.97 **	-6.56 **	69.40 **	-6.94 **	-1.98	-3.65 **	-4.04 **	3.93 **
6	WB-02XHD-3326	55.04 **	30.86 **	28.13 **	-21.45 **	33.91 **	62.23 **	60.14 **	39.21 **	-21.15 **	42.94 **	10.19 **	8.38 **	6.54 **	6.10 **	14.91 **
7	BHU-31XPBW ZN1	-28.09 **	0.65	0.00	-39.59 **	2.99	-30.96 **	15.89 **	0.75	-42.94 **	3.45	7.98 **	9.50 **	7.63 **	7.19 **	16.09 **
8	BHU-31XPBW-343	2.84	17.54 **	-1.04	-29.45 **	20.28 **	3.21 *	38.23 **	20.16 **	-31.94 **	23.39 **	-5.21 **	-0.15	-1.85	-2.26 *	5.86 **
9	BHU-31XHD-3326	-27.74 **	-20.47 **	-2.08	-52.26 **	-18.62 **	-28.11 **	-7.73 **	-19.79 **	-54.57 **	-17.64 **	-2.55 *	-4.14 **	-5.78 **	-6.16 **	1.63
10	HD-3721XPBW ZN1	8.43 **	51.77 **	28.13 **	-8.91 **	55.30 **	11.00 **	86.34 **	61.99 **	-8.25 **	66.33 **	-8.00 **	-5.97 **	-7.57 **	-7.95 **	-0.3
11	HD-3721XPBW-343	18.95 **	35.95 **	35.42 **	-18.40 **	39.12 **	12.83 **	51.12 **	31.37 **	-25.59 **	34.89 **	-8.93 **	-4.07 **	-5.70 **	-6.09 **	1.71
12	HD-3721XHD-3326	54.38 **	32.81 **	0.00	-20.28 **	35.90 **	68.51 **	62.71 **	41.45 **	-19.88 **	45.25 **	-6.10 **	-4.02 **	-5.65 **	-6.04 **	1.76
13	PWB-725X PBW ZN1	6.65 **	49.27 **	33.33 **	-10.40 **	52.75 **	10.75 **	85.91 **	61.61 **	-8.46 **	65.95 **	1.11	2.54 *	0.79	0.38	8.71 **
14	PWB-725X PBW-343	33.16 **	52.20 **	31.25 **	-8.65 **	55.74 **	41.69 **	89.78 **	64.97 **	-6.56 **	69.40 **	-7.05 **	-2.09	-3.75 **	-4.15 **	3.81 **
15	PWB-725X HD-3326	46.31 **	29.67 **	9.38 **	-22.17 **	32.69 **	57.13 **	57.13 **	36.59 **	-22.63 **	40.26 **	0.96	0.96	-0.76	-1.17	7.04 **
16	CRDGEHNU1XPBWZN1	-1.95	63.35 **	30.21 **	-1.95	67.15 **	-2.12 *	88.80 **	72.82 **	-2.12 *	77.45 **	0.73	2.89 *	1.14	0.73	9.09 **
17	CRDGEHNU1XPBW343	-34.30 **	9.45 **	-15.63 **	-34.30 **	12.00 **	-37.20 **	27.53 **	10.87 **	-37.20 **	13.84 **	-7.87 **	-2.95 *	-4.61 **	-5.00 **	2.89 *
18	CRDGEHNU1XHD-3326	-40.76 **	-1.30	12.50 **	-40.76 **	1	-44.20 **	13.32 **	-1.49	-44.20 **	1.15	-3.89 **	-1.82	-3.50 **	-3.89 **	4.09 **
19	PBW-550X PBW ZN1	-11.37 **	24.04 **	-3.13	-25.55 **	26.93 **	-9.98 **	51.12 **	31.37 **	-25.59 **	34.89 **	-2	-0.62	-2.31 *	-2.71 *	5.37 **
20	PBW-550X PBW-343	37.52 **	57.18 **	34.38 **	-5.66 **	60.84 **	42.33 **	90.64 **	65.72 **	-6.13 **	70.17 **	-6.71 **	-1.73	-3.41 **	-3.80 **	4.19 **

21	PBW-550X HD-3326	43.22 **	39.96 **	15.63 **	-15.99 **	43.22 **	49.85 **	67.87 **	45.93 **	-17.34 **	49.85 **	3.18 **	1.48	-0.24	-0.65	7.60 **
22	PBW-677XPBW ZN1	-9.29 **	26.97 **	-14.58 **	-23.79 **	29.92 **	-10.24 **	50.69 **	30.99 **	-25.80 **	34.51 **	1.12	2.88 *	1.12	0.71	9.08 **
23	PBW-677XPBW-343	40.19 **	60.23 **	-22.92 **	-3.82 *	63.96 **	45.35 **	94.67 **	69.23 **	-4.15 **	73.77 **	-3.04 **	2.13	0.4	-0.02	8.29 **
24	PBW-677XPBW-343	53.93 **	53.93 **	1.04	-7.61 **	57.51 **	61.99 **	86.34 **	61.99 **	-8.25 **	66.33 **	-0.82	0.9	-0.82	-1.23	6.98 **
25	PBW-822X PBW ZN1	-2.55	36.39 **	1.04	-18.14 **	39.56 **	-2.81 *	63.14 **	41.82 **	-19.67 **	45.63 **	-0.9	0.49	-1.22	-1.62	6.55 **
26	PBW-822X PBW-343	45.69 **	66.52 **	9.38 **	-0.05	70.39 **	56.90 **	70.14 **	82.67 **	3.47 **	87.58 **	-2	3.23 **	1.47	1.06	9.45 **
27	PBW-822X HD-3326	27.01 **	17.11 **	6.25 *	-29.71 **	19.84 **	36.92 **	43.38 **	24.65 **	-29.40 **	27.99 **	12.44 **	10.59 **	8.71 **	8.27 **	17.26 **
28	HD-3117X PBW ZN1	29.71 **	81.55 **	34.38 **	8.97 **	85.77 **	32.75 **	72.85 **	93.73 **	9.73 **	78.93 **	13.62 **	15.22 **	13.26 **	12.79 **	22.16 **
29	HD-3117X PBW-343	31.55 **	50.36 **	31.25 **	-9.75 **	53.86 **	38.81 **	85.91 **	61.61 **	-8.46 **	65.95 **	6.42 **	12.09 **	10.18 **	9.73 **	18.85 **
30	HD-3117X HD-3326	21.83 **	17.87 **	2.08	-29.25 **	20.61 **	25.21 **	38.66 **	20.54 **	-31.73 **	23.77 **	15.55 **	13.65 **	11.72 **	11.26 **	20.50 **
31	DBW-173X PBW ZN1	-13.23 **	21.44 **	-20.83 **	-27.11 **	24.27 **	-12.03 **	47.68 **	28.38 **	-27.28 **	31.83 **	2.2	3.63 **	1.87	1.45	9.88 **
32	DBW-173X PBW-343	25.87 **	43.86 **	-20.83 **	-13.65 **	47.21 **	29.19 **	73.02 **	50.41 **	-14.81 **	54.45 **	6.49 **	12.17 **	10.26 **	9.81 **	18.93 **
33	DBW-173X HD-3326	32.18 **	46.78 **	9.38 **	-11.90 **	50.20 **	36.45 **	76.89 **	53.77 **	-12.90 **	57.90 **	-5.04 **	-4.52 **	-6.14 **	-6.52 **	1.24
34	DH-3086X PBW ZN1	-15.55 **	18.19 **	0.00	-29.06 **	20.94 **	-14.59 **	43.38 **	24.65 **	-29.40 **	27.99 **	-3.42 **	-1.72	-3.39 **	-3.78 **	4.21 **
35	DH-3086X PBW-343	31.84 **	50.68 **	0.02	-9.56 **	54.19 **	35.92 **	82.04 **	58.25 **	-10.36 **	62.50 **	-3.73 **	1.41	-0.32	-0.73	7.52 **
36	DH-3086X HD-3326	65.17 **	50.68 **	10.42 **	-9.56 **	54.19 **	76.00 **	82.04 **	58.25 **	-10.36 **	62.50 **	19.62 **	21.73 **	19.65 **	19.17 **	29.06 **
37	DBW-222X PBW ZN1	-17.63 **	30.54 **	-1.04	-21.65 **	33.58 **	-16.97 **	59.71 **	38.83 **	-21.36 **	42.56 **	4.14 **	10.56 **	8.68 **	8.24 **	17.22 **
38	DBW-222X PBW-343	-4.72 **	51.01 **	31.25 **	-9.36 **	54.52 **	-5.14 **	82.47 **	58.63 **	-10.15 **	62.88 **	3.06 **	9.42 **	7.55 **	7.12 **	16.01 **
39	DBW-222X HD-3326	-17.02 **	31.51 **	33.33 **	-21.06 **	34.57 **	-18.54 **	56.70 **	36.22 **	-22.84 **	39.88 **	-1.18	4.92 **	3.13 **	2.71 *	11.24 **
40	CSW-18XPBW ZN1	16.48 **	63.03 **	7.29 *	-2.15	66.82 **	20.73 **	62.66 **	76.18 **	-0.21	80.90 **	6.45 **	14.55 **	12.60 **	12.14 **	21.45 **
41	CSW-18XPBW-343	70.97 **	95.41 **	34.38 **	17.29 **	99.96 **	68.31 **	55.43 **	95.97 **	11.00 **	7s1.23 **	-2.24 *	5.20 **	3.41 **	2.98 **	11.53 **
42	CSW-18XHD-3326	63.48 **	75.70 **	0.00	5.46 **	79.79 **	72.21 **	65.12 **	87.01 **	5.92 **	92.02 **	6.02 **	14.09 **	12.15 **	11.69 **	20.96 **
43	PBW-757X PBW ZN1	31.80 **	84.47 **	31.25 **	10.73 **	88.76 **	37.62 **	61.01 **	67.82 **	13.75 **	76.21 **	9.06 **	10.59 **	8.71 **	8.27 **	17.26 **
44	PBW-757X PBW-343	11.79 **	48.84 **	2.08	-10.66 **	52.30 **	14.87 **	82.47 **	58.63 **	-10.15 **	62.88 **	-2.11	3.11 **	1.35	0.94	9.32 **

45	PBW-757X HD-3326	-2.44	29.89 **	19.79 **	-22.04 **	32.91 **	0.00	58.85 **	38.09 **	-21.79 **	41.79 **	3.77 **	2.07	0.33	-0.08	8.22 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Chlorophyll content														
		Location 1					Location 2					Location 3				
SN	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	5.53	10.64 **	12.10 **	5.05	9.15 **	15.52 **	12.10 **	6.32 **	6.57 **	11.27 **	4.65 **	-0.74 **	-0.74 **	-0.74 **	-0.98 **
2	BHU-25XPBW-343	-0.47	0.61	1.94	-4.47	-0.74	10.43 **	7.16 **	1.64	1.88	6.37 **	4.39 **	-0.98 **	-0.98 **	-0.98 **	-1.22 **
3	BHU-25XHD-3326	-0.64	6.48 *	7.88 *	1.1	5.05	2.8	8.64 **	3.04 *	3.29 *	7.84 **	3.10 **	-2.21 **	-2.21 **	-2.21 **	-2.44 **
4	WB-02XPBW ZN1	7.29 *	12.49 **	13.96 **	6.80 *	10.97 **	2.9	5.19 **	-0.23	0.0	4.41 **	-0.25	-1.72 **	-1.72 **	-1.72 **	-1.96 **
5	WB-02XPBW-343	15.79 **	17.06 **	18.60 **	11.14 **	15.48 **	-1.93	0.25	-4.92 **	-4.69 **	-0.49	-1.24 **	-2.70 **	-2.70 **	-2.70 **	-2.93 **
6	WB-02XHD-3326	-5.67	1.09	2.42	-4.02	-0.27	5.14 **	11.11 **	5.39 **	5.63 **	10.29 **	-4.48 **	-5.88 **	-5.88 **	-5.88 **	-6.11 **
7	BHU-31XPBW ZN1	6.05 *	11.19 **	12.65 **	5.57	9.69 **	8.21 **	7.41 **	1.87	2.11	6.62 **	0.25	0.00	-5.04**	0.00	-0.24
8	BHU-31XPBW-343	10.30 **	13.24 **	14.72 **	7.51 *	11.71 **	1.74	0.99	-4.22 **	-3.99 **	0.25	-0.25	-0.49	-0.49	-0.49	-0.73 **
9	BHU-31XHD-3326	9.42 **	17.26 **	18.80 **	11.34 **	15.68 **	3.04 *	8.89 **	3.28 *	3.52 *	8.09 **	-1.97 **	-2.21 **	-2.21 **	-2.21 **	-2.44 **
10	HD-3721XPBW ZN1	1.76	6.69 *	8.09 *	1.3	5.25	3.95 **	10.37 **	4.68 **	4.93 **	9.56 **	1.49 **	0.0	0.0	0.0	-0.24
11	HD-3721XPBW-343	12.01 **	13.24 **	14.72 **	7.51 *	11.71 **	3.95 **	10.37 **	4.68 **	4.93 **	9.56 **	-2.99 **	-4.41 **	-4.41 **	-4.41 **	-4.65 **
12	HD-3721XHD-3326	-0.06	7.10 *	8.50 **	1.68	5.65	4.42 **	10.86 **	5.15 **	5.40 **	10.05 **	0.0	-1.47 **	-1.47 **	-1.47 **	-1.71 **
13	PWB-725X PBW ZN1	-1.5	3.28	4.63	-1.94	1.88	-2.96	-2.96	-7.96 **	-7.75 **	-3.68 *	-7.11 **	-7.11 **	-7.11 **	-7.11 **	-7.33 **
14	PWB-725X PBW-343	7.36 *	8.53 **	9.95 **	3.04	7.07 *	11.11 **	11.11 **	5.39 **	5.63 **	10.29 **	-2.21 **	-2.21 **	-2.21 **	-2.21 **	-2.44 **
15	PWB-725X HD-3326	1.97	9.28 **	10.71 **	3.76	7.81 *	2.57	8.40 **	2.81	3.05 *	7.60 **	0.00	-1.12**	0.37	-2.04**	-0.24
16	CRDGEHNU1XPBWZN1	4.99	10.58 **	12.03 **	4.99	9.09 **	5.16 **	10.62 **	4.92 **	5.16 **	9.80 **	-1.47 **	-1.47 **	-1.47 **	-1.47 **	-1.71 **
17	CRDGEHNU1XPBW343	2.92	8.39 **	9.82 **	2.92	6.93 *	-11.03 **	-6.42 **	-11.24 **	-11.03 **	-7.11 **	-12.50 **	-12.50 **	-12.50 **	-12.50 **	-12.71 **
18	CRDGEHNU1XHD-3326	1.97	9.28 **	10.71 **	3.76	7.81 *	-3.04 *	2.47	-2.81	-2.58	1.72	0.01	0.00	0.07	0.02	-0.24
19	PBW-550X PBW ZN1	13.73 **	19.24 **	20.81 **	13.22 **	17.64 **	0.0	0.74	-4.45 **	-4.23 **	0.02	0.00	0.25	0.25	0.25	0.00
20	PBW-550X PBW-343	15.15 **	16.72 **	18.25 **	10.82 **	15.15 **	-8.82 **	-8.15 **	-12.88 **	-12.68 **	-8.82 **	-14.18 **	-13.97 **	-13.97 **	-13.97 **	-14.18 **
21	PBW-550X HD-3326	10.31 **	18.22 **	19.77 **	12.24 **	16.63 **	1.64	7.41 **	1.87	2.11	6.62 **	-0.49	0.25	-0.25	-0.25	-0.49
22	PBW-677XPBW ZN1	0.85	5.73	7.12 *	0.39	4.31	-6.79 **	-1.73	-6.79 **	-6.57 **	-2.45	-6.86 **	-6.86 **	-6.86 **	-6.86 **	-7.09 **
23	PBW-677XPBW-343	13.09 **	14.33 **	15.83 **	8.55 **	12.79 **	-6.56 **	-1.48	-6.56 **	-6.34 **	-2.21	-7.84 **	-7.84 **	-7.84 **	-7.84 **	-8.07 **
24	PBW-677XPBW-343	-0.45	6.69 *	8.09 *	1.3	5.25	0.93	6.67 **	1.17	1.41	5.88 **	-4.41 **	-4.41 **	-4.41 **	-4.41 **	-4.65 **

25	PBW-822X PBW ZN1	22.52 **	28.45 **	30.14 **	21.96 **	26.72 **	-8.02 **	-3.70 *	-8.67 **	-8.45 **	-4.41 **	-2.24 **	-3.68 **	-3.68 **	-3.68 **	-3.91 **
26	PBW-822X PBW-343	11.74 **	12.96 **	14.45 **	7.26 *	11.44 **	-11.32 **	-7.16 **	-11.94 **	-11.74 **	-7.84 **	-11.94 **	-13.24 **	-13.24 **	-13.24 **	-13.45 **
27	PBW-822X HD-3326	12.22 **	20.26 **	21.84 **	14.19 **	18.65 **	1.64	7.41 **	1.87	2.11	6.62 **	1.49 **	1.23**	0.00	0.00	-0.24
28	HD-3117X PBW ZN1	-0.65	4.16	5.53	-1.1	2.76	-5.11 **	-3.70 *	-8.67 **	-8.45 **	-4.41 **	6.25 **	2.03**	3.54**	6.06**	-0.24
29	HD-3117X PBW-343	8.84 **	10.03 **	11.48 **	4.47	8.55 **	5.11 **	6.67 **	1.17	1.41	5.88 **	6.25 **	1.34	0.09	2.50**	-0.24
30	HD-3117X HD-3326	3.06	10.44 **	11.89 **	4.86	8.95 **	1.64	7.41 **	1.87	2.11	6.62 **	5.70 **	0.86	0.76	0.90**	-0.24
31	DBW-173X PBW ZN1	2.8	7.78 *	9.19 **	2.33	6.33 *	1.58	-4.94 **	-9.84 **	-9.62 **	-5.64 **	11.48 **	0.02	0.21	1.56**	-0.24
32	DBW-173X PBW-343	17.41 **	18.70 **	20.25 **	12.70 **	17.10 **	6.91 **	-0.74	-5.85 **	-5.63 **	-1.47	10.00 **	-0.25	-0.25	-0.25	-0.49
33	DBW-173X HD-3326	6.05 *	13.65 **	15.14 **	7.90 **	12.12 **	3.74 *	9.63 **	3.98 **	4.23 **	8.82 **	-5.96 **	-11.03 **	-11.03 **	-11.03 **	-11.25 **
34	DH-3086X PBW ZN1	2.54	7.51 *	8.92 **	2.07	6.06 *	-7.04 **	-2.22	-7.26 **	-7.04 **	-2.94	3.91 **	-2.21 **	-2.21 **	-2.21 **	-2.44 **
35	DH-3086X PBW-343	19.91 **	21.22 **	22.81 **	15.09 **	19.59 **	-9.62 **	-4.94 **	-9.84 **	-9.62 **	-5.64 **	-1.56 **	-7.35 **	-7.35 **	-7.35 **	-7.58 **
36	DH-3086X HD-3326	1.08	8.32 **	9.75 **	2.85	6.87 *	-4.67 **	0.74	-4.45 **	-4.23 **	0.00	5.96 **	0.25	0.25	0.25	0.00
37	DBW-222X PBW ZN1	13.80 **	19.31 **	20.88 **	13.28 **	17.70 **	1.67	5.19 **	-0.23	0.0	4.41 **	-2.92 **	-2.21 **	-2.21 **	-2.21 **	-2.44**
38	DBW-222X PBW-343	4.03	7.51 *	8.92 **	2.07	6.06 *	-8.11 **	-4.94 **	-9.84 **	-9.62 **	-5.64 **	-8.03 **	-7.35 **	-7.35 **	-7.35 **	-7.58**
39	DBW-222X HD-3326	0.64	7.85 *	9.26 **	2.4	6.39 *	-1.87	3.70 *	-1.64	-1.41	2.94	-4.14 **	-3.43 **	-3.43 **	-3.43 **	-3.67**
40	CSW-18XPBW ZN1	7.22 *	12.42 **	13.89 **	6.74 *	10.90 **	0.24	4.44 **	-0.94	-0.7	3.68 *	-2.71 **	-3.19 **	-3.19 **	-3.19 **	-3.42**
41	CSW-18XPBW-343	21.67 **	22.99 **	24.61 **	16.78 **	21.34 **	-0.47	3.70 *	-1.64	-1.41	2.94	-10.59 **	-11.03 **	-11.03 **	-11.03 **	-11.25**
42	CSW-18XHD-3326	11.40 **	19.38 **	20.95 **	13.35 **	17.77 **	-7.48 **	-2.22	-7.26 **	-7.04 **	-2.94	-1.72 **	-2.21 **	-2.21 **	-2.21 **	-2.44**
43	PBW-757X PBW ZN1	18.42 **	24.15 **	25.78 **	17.88 **	22.48 **	10.65 **	5.19 **	-0.23	0.00	4.41 **	-2.21 **	-2.21 **	-2.21 **	-2.21 **	-2.44**
44	PBW-757X PBW-343	11.54 **	12.76 **	14.24 **	7.06 *	11.24 **	9.87 **	4.44 **	-0.94	-0.7	3.68 *	-10.54 **	-10.54 **	-10.54 **	-10.54 **	-10.76**
45	PBW-757X HD-3326	0.32	7.51 *	8.92 **	2.07	6.06 *	-5.37 **	0.00	-5.15 **	-4.93 **	-0.74	0.00	-1.07**	0.00	-2.05**	-0.24

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Number of grain per spike														
		Location 1					Location 2					Location 3				
SN	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	9.40	18.74 **	27.05 **	22.16 **	26.02 **	43.47 **	36.55 **	68.96 **	68.96 **	31.78 **	16.32	31.20 **	33.29 **	12.17	42.96 **
2	BHU-25XPBW-343	10.35 *	17.43 **	25.65 **	20.82 **	24.63 **	56.53 **	48.97 **	84.33 **	84.33 **	43.77 **	17.12	24.15 *	26.13 *	6.14	35.28 **
3	BHU-25XHD-3326	14.62 **	21.98 **	30.52 **	25.50 **	29.46 **	38.02 **	31.36 **	62.54 **	62.54 **	26.78 *	43.19 **	53.66 **	56.10 **	31.36 **	67.43 **
4	WB-02XPBW ZN1	14.28 **	24.03 **	32.71 **	27.60 **	31.63 **	43.79 **	43.79 **	77.91 **	77.91 **	38.77 **	12.73	27.15 *	29.18 *	8.71	38.55 **
5	WB-02XPBW-343	15.96 **	21.57 **	30.07 **	25.07 **	29.02 **	37.39 **	37.39 **	70.00 **	70.00 **	32.60 **	22.66 *	30.03 *	32.10 **	11.16	41.68 **
6	WB-02XHD-3326	15.64 **	22.78 **	31.37 **	26.32 **	30.31 **	44.27 **	44.27 **	78.51 **	78.51 **	39.23 **	43.19 **	53.66 **	56.10 **	31.36 **	67.43 **
7	BHU-31XPBW ZN1	19.85 **	30.07 **	39.17 **	33.82 **	38.05 **	41.71 **	44.27 **	78.51 **	78.51 **	39.23 **	29.86 **	46.48 **	48.81 **	25.22 *	59.60 **
8	BHU-31XPBW-343	24.04 **	29.26 **	38.30 **	32.98 **	37.18 **	40.88 **	43.43 **	77.46 **	77.46 **	38.42 **	40.97 **	59.01 **	61.54 **	35.94 **	73.26 **
9	BHU-31XHD-3326	13.76 **	20.79 **	29.24 **	24.27 **	28.19 **	46.33 **	48.97 **	84.33 **	84.33 **	43.77 **	10.07	24.15 *	26.13 *	6.14	35.28 **
10	HD-3721XPBW ZN1	7.10	16.24 **	24.37 **	19.59 **	23.37 **	71.34 **	38.48 **	71.34 **	71.34 **	33.64 **	41.32 **	59.40 **	61.94 **	36.27 **	73.68 **
11	HD-3721XPBW-343	24.84 **	30.09 **	39.19 **	33.84 **	38.07 **	78.96 **	44.63 **	78.96 **	78.96 **	39.58 **	27.46 *	35.12 **	37.27 **	15.51	47.23 **
12	HD-3721XHD-3326	17.16 **	24.39 **	33.09 **	27.97 **	32.01 **	60.27 **	41.13 **	74.63 **	74.63 **	36.20 **	16.06	24.54 *	26.53 *	6.47	35.70 **
13	PWB-725X PBW ZN1	13.14 *	22.80 **	31.39 **	26.34 **	30.33 **	41.86 **	41.86 **	75.52 **	75.52 **	36.90 **	35.07 **	52.35 **	54.77 **	30.25 **	66.00 **
14	PWB-725X PBW-343	1.01	5.26	12.63 *	8.3	11.72 *	31.85 **	31.85 **	63.13 **	63.13 **	27.24 *	17.49	24.54 *	26.53 *	6.47	35.70 **
15	PWB-725X HD-3326	19.53 **	26.91 **	35.79 **	30.57 **	34.69 **	48.97 **	48.97 **	84.33 **	84.33 **	43.77 **	20.8	29.63 *	31.70 **	10.83	41.25 **
16	CRDGEHNU1XPBWZN1	10.48 *	19.90 **	28.29 **	23.36 **	27.26 **	74.03 **	40.65 **	74.03 **	74.03 **	35.74 **	15.85	35.51 **	37.67 **	15.85	47.65 **

17	CRDGEHNU1XPBW343	22.04 **	27.18 **	36.08 **	30.84 **	34.98 **	62.39 **	31.24 **	62.39 **	62.39 **	26.66 *	24.33 *	45.43 **	47.75 **	24.33 *	58.46 **
18	CRDGEHNU1XHD-3326	14.10 **	21.14 **	29.62 **	24.64 **	28.57 **	55.48 **	36.91 **	69.40 **	69.40 **	32.13 **	21.76 *	42.43 **	44.69 **	21.76 *	55.19 **
19	PBW-550X PBW ZN1	11.09 *	20.57 **	29.00 **	24.04 **	27.96 **	32.48 **	37.27 **	69.85 **	69.85 **	32.48 **	32.18 **	49.09 **	51.46 **	27.46 **	62.45 **
20	PBW-550X PBW-343	13.62 *	18.40 **	26.68 **	21.81 **	25.66 **	32.13 **	36.91 **	69.40 **	69.40 **	32.13 **	44.33 **	53.00 **	55.44 **	30.80 **	66.71 **
21	PBW-550X HD-3326	11.67 *	18.56 **	26.86 **	21.98 **	25.83 **	27.94 **	32.57 **	64.03 **	64.03 **	27.94 **	45.26 **	55.87 **	58.36 **	33.26 **	69.84 **
22	PBW-677XPBW ZN1	17.70 **	27.75 **	36.69 **	31.43 **	35.58 **	74.48 **	41.01 **	74.48 **	74.48 **	36.09 **	19.79	35.12 **	37.27 **	15.51	47.23 **
23	PBW-677XPBW-343	17.06 **	21.99 **	30.53 **	25.51 **	29.47 **	73.13 **	39.93 **	73.13 **	73.13 **	35.04 **	27.46 *	35.12 **	37.27 **	15.51	47.23 **
24	PBW-677XPBW-343	12.95 *	19.92 **	28.31 **	23.38 **	27.28 **	46.30 **	28.83 *	59.40 **	59.40 **	24.33 *	21.53 *	30.42 **	32.49 **	11.5	42.11 **
25	PBW-822X PBW ZN1	8.84	18.12 **	26.39 **	21.53 **	25.37 **	49.19 **	44.15 **	78.36 **	78.36 **	39.12 **	20.14	35.51 **	37.67 **	15.85	47.65 **
26	PBW-822X PBW-343	8.16	13.71 *	21.67 **	16.99 **	20.69 **	59.18 **	53.80 **	90.30 **	90.30 **	48.43 **	34.11 **	42.17 **	44.43 **	21.54 *	54.91 **
27	PBW-822X HD-3326	16.47 **	23.66 **	32.31 **	27.23 **	31.24 **	16.23	12.3	38.96 **	38.96 **	8.38	43.80 **	54.31 **	56.76 **	31.92 **	68.14 **
28	HD-3117X PBW ZN1	14.09 **	23.83 **	32.49 **	27.40 **	31.42 **	59.05 **	52.71 **	88.96 **	88.96 **	47.38 **	14.27	31.72 **	33.82 **	12.61	43.53 **
29	HD-3117X PBW-343	10.34 *	17.17 **	25.37 **	20.54 **	24.35 **	22.36	17.49	45.37 **	45.37 **	13.39	15.97	33.68 **	35.81 **	14.29	45.66 **
30	HD-3117X HD-3326	16.74 **	23.96 **	32.64 **	27.54 **	31.57 **	37.31 **	31.85 **	63.13 **	63.13 **	27.24 *	31.82 **	51.96 **	54.38 **	29.91 **	65.58 **
31	DBW-173X PBW ZN1	4.96	14.34 **	22.34 **	17.63 **	21.35 **	61.56 **	55.13 **	91.94 **	91.94 **	49.71 **	26.27 *	42.43 **	44.69 **	21.76 *	55.19 **
32	DBW-173X PBW-343	13.38 **	23.51 **	32.16 **	27.07 **	31.09 **	28.02 *	22.92 *	52.09 **	52.09 **	18.63	24.26 *	31.72 **	33.82 **	12.61	43.53 **
33	DBW-173X HD-3326	13.34 **	23.47 **	32.11 **	27.03 **	31.04 **	37.69 **	32.21 **	63.58 **	63.58 **	27.59 *	12.04	20.23	22.15	2.79	31.01 *
34	DH-3086X PBW ZN1	9.37	18.70 **	27.01 **	22.12 **	25.98 **	26.56 **	44.27 **	78.51 **	78.51 **	39.23 **	29.40 **	45.95 **	48.28 **	24.78 *	59.03 **

35	DH-3086X PBW-343	23.25 **	29.62 **	38.69 **	33.36 **	37.57 **	26.46 **	44.15 **	78.36 **	78.36 **	39.12 **	34.24 **	42.30 **	44.56 **	21.65 *	55.05 **
36	DH-3086X HD-3326	19.55 **	26.93 **	35.81 **	30.59 **	34.71 **	33.97 **	52.71 **	88.96 **	88.96 **	47.38 **	41.61 **	51.96 **	54.38 **	29.91 **	65.58 **
37	DBW-222X PBW ZN1	14.49 **	24.26 **	32.95 **	27.84 **	31.88 **	61.41 **	32.21 **	63.58 **	63.58 **	27.59 *	49.77 **	68.93 **	71.62 **	44.42 **	84.07 **
38	DBW-222X PBW-343	16.21 **	23.23 **	31.85 **	26.78 **	30.79 **	86.16 **	52.47 **	88.66 **	88.66 **	47.15 **	37.29 **	52.35 **	54.77 **	30.25 **	66.00 **
39	DBW-222X HD-3326	10.27 *	17.08 **	25.27 **	20.45 **	24.25 **	63.42 **	43.91 **	78.06 **	78.06 **	38.88 **	30.47 **	44.78 **	47.08 **	23.77 *	57.75 **
40	CSW-18XPBW ZN1	10.49 *	19.92 **	28.31 **	23.38 **	27.28 **	58.17 **	27.26 *	57.46 **	57.46 **	22.82 *	32.29 **	49.22 **	51.59 **	27.57 **	62.59 **
41	CSW-18XPBW-343	24.79 **	30.04 **	39.14 **	33.78 **	38.01 **	73.55 **	36.91 **	69.40 **	69.40 **	32.13 **	22.66 *	30.03 *	32.10 **	11.16	41.68 **
42	CSW-18XHD-3326	18.11 **	25.40 **	34.17 **	29.01 **	33.09 **	68.36 **	48.25 **	83.43 **	83.43 **	43.07 **	43.19 **	53.66 **	56.10 **	31.36 **	67.43 **
43	PBW-757X PBW ZN1	16.02 **	25.92 **	34.73 **	29.55 **	33.64 **	64.32 **	32.21 **	63.58 **	63.58 **	27.59 *	34.72 **	51.96 **	54.38 **	29.91 **	65.58 **
44	PBW-757X PBW-343	19.79 **	24.83 **	33.56 **	28.43 **	32.48 **	69.42 **	33.66 **	65.37 **	65.37 **	28.99 **	44.46 **	53.13 **	55.57 **	30.92 **	66.86 **
45	PBW-757X HD-3326	9.85	16.63 **	24.80 **	20.00 **	23.79 **	46.44 **	28.95 **	59.55 **	59.55 **	24.45 *	32.48 **	42.17 **	44.43 **	21.54 *	54.91 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Grain weight per spike														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	21.09 *	46.84 **	20.63 *	7.08	40.35 **	21.97 **	32.08 **	31.41 **	28.16 **	21.42 **	20.54 **	58.49 **	28.83 **	16.84 **	13.30 **
2	BHU-25XPBW-343	68.46 **	68.72 **	38.61 **	23.03 **	61.27 **	24.75 **	35.10 **	34.41 **	31.09 **	24.19 **	16.99 **	62.62 **	32.19 **	19.88 **	16.25 **
3	BHU-25XHD-3326	14	49.31 **	22.66 *	8.88	42.71 **	23.27 **	33.49 **	32.81 **	29.53 **	22.71 **	26.77 **	65.32 **	34.38 **	21.87 **	18.17 **
4	WB-02XPBW ZN1	36.59 **	65.64 **	36.08 **	20.79 *	58.32 **	26.23 **	30.58 **	29.92 **	26.71 **	20.04 **	23.53 **	62.42 **	32.03 **	19.74 **	16.10 **
5	WB-02XPBW-343	62.42 **	63.17 **	34.05 **	18.99 *	55.96 **	27.27 **	37.38 **	36.68 **	33.30 **	26.29 **	18.30 **	64.44 **	33.67 **	21.22 **	17.55 **
6	WB-02XHD-3326	18.82 *	55.62 **	27.85 **	13.48	48.75 **	32.32 **	36.88 **	36.18 **	32.82 **	25.83 **	23.08 **	60.51 **	30.47 **	18.33 **	14.74 **
7	BHU-31XPBW ZN1	29.10 **	56.55 **	28.61 **	14.16	49.63 **	31.86 **	35.88 **	35.19 **	31.85 **	24.91 **	23.78 **	62.76 **	32.30 **	19.98 **	16.34 **
8	BHU-31XPBW-343	51.96 **	55.47 **	27.72 **	13.37	48.60 **	27.42 **	37.54 **	36.84 **	33.46 **	26.43 **	14.49 **	59.14 **	29.36 **	17.32 **	13.76 **
9	BHU-31XHD-3326	12.12	46.84 **	20.63 *	7.08	40.35 **	28.81 **	31.38 **	30.72 **	27.48 **	20.78 **	21.79 **	58.83 **	29.11 **	17.09 **	13.54 **
10	HD-3721XPBW ZN1	35.71 **	64.56 **	35.19 **	20.00 *	57.29 **	29.72 **	34.19 **	33.51 **	30.21 **	23.36 **	16.34 **	52.97 **	24.34 **	12.77 **	9.35 **
11	HD-3721XPBW-343	43.52 **	57.01 **	28.99 **	14.49	50.07 **	22.27 **	31.98 **	31.31 **	28.07 **	21.33 **	15.55 **	60.62 **	30.57 **	18.41 **	14.82 **
12	HD-3721XHD-3326	16.59	52.70 **	25.44 **	11.35	45.95 **	31.74 **	36.28 **	35.59 **	32.23 **	25.28 **	18.26 **	54.23 **	25.36 **	13.69 **	10.25 **
13	PWB-725X PBW ZN1	33.04 **	61.33 **	32.53 **	17.64 *	54.20 **	27.86 **	31.75 **	31.08 **	27.84 **	21.11 **	25.38 **	64.86 **	34.01 **	21.53 **	17.84 **
14	PWB-725X PBW-343	46.84 **	46.84 **	20.63 *	7.08	40.35 **	24.55 **	34.44 **	33.76 **	30.45 **	23.59 **	16.73 **	62.26 **	31.90 **	19.62 **	15.99 **
15	PWB-725X HD-3326	15.88	51.77 **	24.68 *	10.67	45.07 **	40.97 **	40.97 **	40.26 **	36.79 **	29.59 **	17.15 **	52.77 **	24.18 **	12.62 **	9.20 **
16	CRDGEHNU1XPBWZN1	8.54	48.84 **	22.28 *	8.54	42.27 **	38.85 **	43.09 **	42.37 **	38.85 **	31.54 **	20.88 **	63.97 **	33.28 **	20.88 **	17.21 **
17	CRDGEHNU1XPBW343	15.17	57.94 **	29.75 **	15.17	50.96 **	28.07 **	38.25 **	37.54 **	34.14 **	27.08 **	18.19 **	64.29 **	33.55 **	21.12 **	17.44 **
18	CRDGEHNU1XHD-3326	7.3	47.15 **	20.89 *	7.3	40.65 **	25.14 **	28.96 **	28.31 **	25.14 **	18.55 **	17.57 **	59.48 **	29.64 **	17.57 **	14.00 **
19	PBW-550X PBW ZN1	21.73 *	47.61 **	21.27 *	7.64	41.09 **	25.73 **	36.78 **	36.08 **	32.72 **	25.73 **	8.24 **	51.42 **	23.08 **	11.63 **	8.24 **
20	PBW-550X PBW-343	46.54 **	53.31 **	25.95 **	11.8	46.54 **	24.16 **	35.07 **	34.38 **	31.06 **	24.16 **	16.89 **	63.52 **	32.92 **	20.55 **	16.89 **
21	PBW-550X HD-3326	14.82	50.39 **	23.54 *	9.66	43.74 **	21.42 **	32.08 **	31.41 **	28.16 **	21.42 **	16.50 **	62.98 **	32.48 **	20.15 **	16.50 **
22	PBW-677XPBW ZN1	15.06	40.06 **	15.06	2.13	33.87 **	30.99 **	34.98 **	34.29 **	30.97 **	24.08 **	22.16 **	60.62 **	30.57 **	18.41 **	14.82 **
23	PBW-677XPBW-343	25.44 **	52.70 **	25.44 **	11.35	45.95 **	26.20 **	36.23 **	35.54 **	32.19 **	25.23 **	16.56 **	62.03 **	31.71 **	19.45 **	15.82 **
24	PBW-677XPBW-343	16.24	52.23 **	25.06 **	11.01	45.51 **	34.15 **	34.83 **	34.15 **	30.83 **	23.94 **	17.90 **	53.75 **	24.98 **	13.35 **	9.91 **
25	PBW-822X PBW ZN1	43.33 **	73.81 **	42.78 **	26.74 **	66.13 **	21.78 **	28.38 **	27.73 **	24.58 **	18.02 **	-3.18 *	37.50 **	11.77 **	1.37	-1.71
26	PBW-822X PBW-343	54.35 **	64.10 **	34.81 **	19.66 *	56.85 **	29.12 **	39.37 **	38.67 **	35.24 **	28.12 **	11.84 **	58.83 **	29.11 **	17.09 **	13.54 **
27	PBW-822X HD-3326	23.88 **	62.25 **	33.29 **	18.31 *	55.08 **	31.26 **	38.39 **	37.68 **	34.28 **	27.21 **	13.25 **	60.83 **	30.73 **	18.56 **	14.96 **
28	HD-3117X PBW ZN1	20.20 *	45.76 **	19.75 *	6.29	39.32 **	31.73 **	37.38 **	36.68 **	33.30 **	26.29 **	27.63 **	67.81 **	36.41 **	23.71 **	19.96 **
29	HD-3117X PBW-343	53.67 **	51.77 **	24.68 *	10.67	45.07 **	23.64 **	33.46 **	32.78 **	29.50 **	22.69 **	17.55 **	63.41 **	32.83 **	20.46 **	16.81 **

30	HD-3117X HD-3326	9.76	43.76 **	18.1	4.83	37.41 **	32.74 **	38.43 **	37.72 **	34.32 **	27.25 **	18.39 **	54.39 **	25.50 **	13.82 **	10.37 **
31	DBW-173X PBW ZN1	27.83 **	55.01 **	27.34 **	13.03	48.16 **	32.50 **	36.54 **	35.84 **	32.49 **	25.51 **	20.08 **	57.89 **	28.34 **	16.39 **	12.86 **
32	DBW-173X PBW-343	59.50 **	75.96 **	44.56 **	28.31 **	68.19 **	26.22 **	36.25 **	35.56 **	32.21 **	25.25 **	19.00 **	65.42 **	34.46 **	21.94 **	18.25 **
33	DBW-173X HD-3326	13.65	48.84 **	22.28 *	8.54	42.27 **	32.24 **	36.06 **	35.37 **	32.02 **	25.07 **	18.94 **	55.10 **	26.08 **	14.34 **	10.87 **
34	DH-3086X PBW ZN1	7.05	42.68 **	17.22	4.04	36.38 **	29.36 **	34.65 **	33.97 **	30.65 **	23.78 **	5.28 **	46.78 **	19.32 **	8.21 **	4.93 **
35	DH-3086X PBW-343	17.34 *	56.39 **	28.48 **	14.04	49.48 **	26.99 **	37.08 **	36.38 **	33.01 **	26.01 **	17.70 **	64.10 **	33.39 **	20.98 **	17.31 **
36	DH-3086X HD-3326	17.46 *	56.55 **	28.61 **	14.16	49.63 **	30.04 **	35.36 **	34.67 **	31.34 **	24.43 **	6.66 **	48.70 **	20.88 **	9.62 **	6.30 **
37	DBW-222X PBW ZN1	37.17 **	68.88 **	38.73 **	23.15 **	61.41 **	28.83 **	32.76 **	32.09 **	28.82 **	22.04 **	17.05 **	59.25 **	29.45 **	17.40 **	13.84 **
38	DBW-222X PBW-343	35.67 **	67.03 **	37.22 **	21.80 *	59.65 **	29.95 **	40.27 **	39.56 **	36.11 **	28.95 **	14.99 **	59.84 **	29.93 **	17.83 **	14.26 **
39	DBW-222X HD-3326	10.94	45.30 **	19.37 *	5.96	38.88 **	34.80 **	37.66 **	36.96 **	33.57 **	26.54 **	23.57 **	68.12 **	36.66 **	23.94 **	20.18 **
40	CSW-18XPBW ZN1	42.31 **	72.57 **	41.77 **	25.84 **	64.95 **	32.15 **	36.18 **	35.49 **	32.14 **	25.18 **	19.53 **	58.60 **	28.92 **	16.92 **	13.38 **
41	CSW-18XPBW-343	35.94 **	57.94 **	29.75 **	15.17	50.96 **	28.38 **	38.58 **	37.87 **	34.46 **	27.39 **	17.65 **	63.54 **	32.94 **	20.56 **	16.91 **
42	CSW-18XHD-3326	11.65	46.22 **	20.13 *	6.63	39.76 **	33.46 **	30.91 **	30.25 **	27.03 **	20.34 **	21.74 **	61.53 **	31.30 **	19.08 **	15.47 **
43	PBW-757X PBW ZN1	30.11 **	57.78 **	29.62 **	15.06	50.81 **	23.25 **	37.48 **	36.78 **	33.40 **	26.38 **	20.69 **	63.43 **	32.85 **	20.48 **	16.83 **
44	PBW-757X PBW-343	40.03 **	56.86 **	28.86 **	14.38	49.93 **	24.11 **	38.44 **	37.73 **	34.33 **	27.26 **	16.73 **	62.26 **	31.90 **	19.62 **	15.99 **
45	PBW-757X HD-3326	28.12 **	67.80 **	37.85 **	22.36 **	60.38 **	23.67 **	37.95 **	37.25 **	33.85 **	26.81 **	17.76 **	59.47 **	29.63 **	17.56 **	13.99 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		1000 grain weight														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	21.19 **	17.36 **	20.96 **	12.61 **	23.43 **	-2.91	-6.20 *	-12.90 **	2.7	-9.69**	18.47 **	21.48 **	20.91 **	22.69 **	-1.06
2	BHU-25XPBW-343	15.75 **	16.43 **	19.99 **	11.72 **	22.44 **	18.78 **	14.75 **	6.56 *	25.64 **	10.49 **	17.98 **	23.03 **	22.45 **	24.26 **	0.2
3	BHU-25XHD-3326	16.31 **	13.66 **	17.14 **	9.06 **	19.53 **	12.49 **	8.68 **	0.92	18.99 **	4.64	24.78 **	37.50 **	36.86 **	38.88 **	11.99 **
4	WB-02XPBW ZN1	20.59 **	14.64 **	18.15 **	10.00 **	20.57 **	22.31 **	24.82 **	15.91 **	36.67 **	20.18 **	18.91 **	41.95 **	41.28 **	43.37 **	15.61 **
5	WB-02XPBW-343	12.68 **	13.35 **	16.82 **	8.76 **	19.21 **	-1.48	0.54	-6.63 *	10.09 **	-3.19	21.16 **	44.64 **	43.96 **	46.09 **	17.81 **
6	WB-02XHD-3326	17.16 **	14.50 **	18.00 **	9.86 **	20.41 **	27.97 **	30.59 **	21.27 **	42.98 **	25.74 **	19.31 **	42.42 **	41.76 **	43.85 **	16.00 **
7	BHU-31XPBW ZN1	18.70 **	13.25 **	16.72 **	8.67 **	19.10 **	18.86 **	19.15 **	10.65 **	30.46 **	14.73 **	14.70 **	17.62 **	17.06 **	18.79 **	-4.21 **
8	BHU-31XPBW-343	15.22 **	15.90 **	19.45 **	11.21 **	21.89 **	8.90 **	9.16 **	1.37	19.53 **	5.11	28.54 **	34.03 **	33.40 **	35.37 **	9.16 **
9	BHU-31XHD-3326	18.84 **	16.13 **	19.69 **	11.43 **	22.13 **	9.95 **	10.22 **	2.36	20.69 **	6.13 *	31.03 **	44.40 **	43.72 **	45.84 **	17.61 **
10	HD-3721XPBW ZN1	14.53 **	14.22 **	17.72 **	9.59 **	20.12 **	5.02 *	19.18 **	10.68 **	30.50 **	14.76 **	36.88 **	40.35 **	39.70 **	41.76 **	14.31 **
11	HD-3721XPBW-343	13.61 **	14.28 **	17.78 **	9.66 **	20.19 **	1.76	15.48 **	7.24 **	26.44 **	11.19 **	29.01 **	34.52 **	33.89 **	35.87 **	9.56 **
12	HD-3721XHD-3326	13.55 **	13.24 **	16.71 **	8.66 **	19.09 **	-9.74 **	2.43	-4.88	12.15 **	-1.37	27.51 **	40.51 **	39.85 **	41.91 **	14.44 **
13	PWB-725X PBW ZN1	14.04 **	14.04 **	17.54 **	9.43 **	19.94 **	8.27 **	8.27 **	0.54	18.54 **	4.25	40.33 **	43.90 **	43.22 **	45.34 **	17.20 **
14	PWB-725X PBW-343	12.50 **	13.16 **	16.63 **	8.58 **	19.01 **	33.63 **	33.63 **	24.09 **	46.31 **	28.67 **	37.08 **	42.94 **	42.27 **	44.37 **	16.42 **
15	PWB-725X HD-3326	14.25 **	14.25 **	17.75 **	9.63 **	20.15 **	8.71 **	8.71 **	0.95	19.03 **	4.67	29.65 **	42.87 **	42.20 **	44.29 **	16.36 **
16	CRDGEHNU1XPBWZN1	10.23 **	14.88 **	18.40 **	10.23 **	20.82 **	48.25 **	35.39 **	25.73 **	48.25 **	30.37 **	38.20 **	41.71 **	41.04 **	43.12 **	15.42 **
17	CRDGEHNU1XPBW343	11.37 **	16.07 **	19.62 **	11.37 **	22.07 **	24.90 **	15.11 **	6.90 **	26.04 **	10.84 **	13.43 **	18.28 **	17.73 **	19.46 **	-3.66 **
18	CRDGEHNU1XHD-3326	12.20 **	16.94 **	20.52 **	12.20 **	22.98 **	45.22 **	34.47 **	24.88 **	47.24 **	29.48 **	18.76 **	30.87 **	30.26 **	32.18 **	6.59 **
19	PBW-550X PBW ZN1	19.15 **	13.29 **	16.76 **	8.71 **	19.15 **	10.28 **	14.53 **	6.36 *	25.41 **	10.28 **	15.44 **	41.74 **	41.08 **	43.16 **	15.44 **
20	PBW-550X PBW-343	16.97 **	17.66 **	21.27 **	12.90 **	23.74 **	11.43 **	15.73 **	7.47 **	26.71 **	11.43 **	10.48 **	35.64 **	35.01 **	37.00 **	10.48 **
21	PBW-550X HD-3326	16.74 **	14.08 **	17.57 **	9.46 **	19.97 **	13.92 **	18.31 **	9.87 **	29.54 **	13.92 **	17.57 **	44.35 **	43.68 **	45.80 **	17.57 **
22	PBW-677XPBW ZN1	17.56 **	14.06 **	17.56 **	9.45 **	19.96 **	-2.24	5.27	-2.24	15.27 **	1.37	38.91 **	42.44 **	41.77 **	43.86 **	16.01 **
23	PBW-677XPBW-343	16.10 **	16.78 **	20.36 **	12.05 **	22.81 **	6.46 *	14.64 **	6.46 *	25.52 **	10.39 **	34.60 **	40.35 **	39.70 **	41.76 **	14.31 **

24	PBW-677XPBW-343	18.04 **	15.36 **	18.89 **	10.69 **	21.32 **	-4.11	3.26	-4.11	13.06 **	-0.58	22.52 **	35.01 **	34.38 **	36.36 **	9.96 **
25	PBW-822X PBW ZN1	15.65 **	14.90 **	18.43 **	10.25 **	20.84 **	16.86 **	15.11 **	6.90 **	26.04 **	10.84 **	38.35 **	41.87 **	41.21 **	43.29 **	15.55 **
26	PBW-822X PBW-343	15.81 **	16.49 **	20.06 **	11.78 **	22.51 **	20.45 **	18.65 **	10.18 **	29.91 **	14.24 **	36.39 **	42.22 **	41.55 **	43.64 **	15.83 **
27	PBW-822X HD-3326	16.58 **	15.83 **	19.38 **	11.14 **	21.82 **	17.01 **	15.25 **	7.03 **	26.19 **	10.97 **	24.58 **	37.29 **	36.64 **	38.66 **	11.81 **
28	HD-3117X PBW ZN1	17.07 **	16.94 **	20.53 **	12.21 **	22.99 **	20.15 **	8.46 **	0.72	18.75 **	4.43	25.55 **	33.27 **	32.65 **	34.60 **	8.55 **
29	HD-3117X PBW-343	14.80 **	15.48 **	19.02 **	10.80 **	21.45 **	23.80 **	14.10 **	5.96 *	24.93 **	9.86 **	33.39 **	41.60 **	40.93 **	43.01 **	15.32 **
30	HD-3117X HD-3326	14.46 **	14.34 **	17.84 **	9.71 **	20.25 **	45.42 **	34.66 **	25.05 **	47.44 **	29.66 **	22.72 **	35.23 **	34.60 **	36.58 **	10.14 **
31	DBW-173X PBW ZN1	23.58 **	17.48 **	21.08 **	12.73 **	23.56 **	18.78 **	8.19 **	0.47	18.46 **	4.17	17.42 **	36.51 **	35.87 **	37.87 **	11.18 **
32	DBW-173X PBW-343	11.79 **	12.45 **	15.89 **	7.90 **	18.26 **	23.69 **	14.00 **	5.87 *	24.83 **	9.77 **	9.68 **	27.52 **	26.92 **	28.79 **	3.86 **
33	DBW-173X HD-3326	17.58 **	14.90 **	18.43 **	10.25 **	20.84 **	23.15 **	14.04 **	5.90 *	24.86 **	9.80 **	22.82 **	42.79 **	42.12 **	44.22 **	16.30 **
34	DH-3086X PBW ZN1	15.84 **	13.88 **	17.37 **	9.27 **	19.77 **	23.21 **	16.74 **	8.41 **	27.82 **	12.41 **	21.87 **	41.28 **	40.62 **	42.69 **	15.07 **
35	DH-3086X PBW-343	14.50 **	15.17 **	18.70 **	10.51 **	21.13 **	27.91 **	21.19 **	12.54 **	32.70 **	16.69 **	16.65 **	35.23 **	34.60 **	36.58 **	10.14 **
36	DH-3086X HD-3326	17.71 **	15.72 **	19.26 **	11.03 **	21.69 **	29.70 **	22.88 **	14.11 **	34.55 **	18.32 **	17.27 **	35.95 **	35.31 **	37.31 **	10.72 **
37	DBW-222X PBW ZN1	13.75 **	13.39 **	16.86 **	8.80 **	19.25 **	22.86 **	18.57 **	10.11 **	29.83 **	14.17 **	17.34 **	41.44 **	40.78 **	42.86 **	15.20 **
38	DBW-222X PBW-343	13.82 **	14.49 **	17.99 **	9.85 **	20.40 **	0.56	-2.95	-9.87 **	6.27 *	-6.55 *	18.11 **	42.37 **	41.70 **	43.79 **	15.95 **
39	DBW-222X HD-3326	14.17 **	13.81 **	17.29 **	9.20 **	19.69 **	22.61 **	18.33 **	9.88 **	29.56 **	13.94 **	9.77 **	32.32 **	31.70 **	33.64 **	7.77 **
40	CSW-18XPBW ZN1	14.87 **	15.87 **	19.42 **	11.18 **	21.86 **	30.54 **	26.19 **	17.18 **	38.17 **	21.50 **	23.72 **	43.98 **	43.31 **	45.42 **	17.27 **
41	CSW-18XPBW-343	14.17 **	15.16 **	18.69 **	10.50 **	21.11 **	24.89 **	20.73 **	12.12 **	32.19 **	16.25 **	18.83 **	38.30 **	37.65 **	39.68 **	12.64 **
42	CSW-18XHD-3326	16.41 **	17.42 **	21.02 **	12.67 **	23.49 **	29.19 **	24.89 **	15.97 **	36.74 **	20.25 **	14.91 **	33.73 **	33.10 **	35.07 **	8.92 **
43	PBW-757X PBW ZN1	13.10 **	14.21 **	17.71 **	9.59 **	20.11 **	22.96 **	19.01 **	10.52 **	30.30 **	14.59 **	24.29 **	32.11 **	31.50 **	33.43 **	7.60 **
44	PBW-757X PBW-343	15.29 **	16.43 **	19.99 **	11.72 **	22.44 **	15.47 **	11.75 **	3.78	22.36 **	7.60 **	28.71 **	36.82 **	36.18 **	38.18 **	11.43 **
45	PBW-757X HD-3326	15.95 **	17.09 **	20.68 **	12.35 **	23.14 **	19.59 **	15.74 **	7.48 **	26.73 **	11.45 **	27.96 **	41.01 **	40.35 **	42.42 **	14.84 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 10

Table 4.4: contd.

		Biological yield														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	0.53	7.21	2.14	-9.64 *	6.93	47.38 **	34.70 **	27.59 **	29.93 **	41.27 **	53.38 **	84.33 **	61.68 **	55.83 **	59.57 **
2	BHU-25XPBW-343	-3.88	3.32	-1.56	-12.92 **	3.05	16.92	38.36 **	31.06 **	33.47 **	45.12 **	27.85 **	61.25 **	41.44 **	36.32 **	83.33 **
3	BHU-25XHD-3326	8.63	14.56 **	9.14	-3.45	14.26 **	14.49	34.84 **	27.72 **	30.07 **	41.42 **	40.55 **	86.65 **	63.72 **	57.79 **	12.21 **
4	WB-02XPBW ZN1	9.74 *	17.04 **	11.50 *	-1.36	16.73 **	18.41 *	33.36 **	26.32 **	28.64 **	39.87 **	54.05 **	85.12 **	62.38 **	56.50 **	80.48 **
5	WB-02XPBW-343	-3.45	3.78	-1.12	-12.53 **	3.51	13.95	34.84 **	27.72 **	30.07 **	41.42 **	65.25 **	68.42 **	82.81 **	76.20 **	66.96 **
6	WB-02XHD-3326	2.13	7.7	2.61	-9.23 *	7.41	25.63 **	47.95 **	40.15 **	42.72 **	55.18 **	56.17 **	57.40 **	81.92 **	75.34 **	35.81 **
7	BHU-31XPBW ZN1	2.4	9.21	4.05	-7.95	8.93	67.75 **	53.31 **	45.22 **	47.89 **	60.80 **	50.42 **	80.77 **	58.56 **	52.82 **	55.53 **
8	BHU-31XPBW-343	-4.58	2.57	-2.28	-13.55 **	2.3	38.97 **	64.46 **	55.78 **	58.64 **	72.49 **	66.40 **	59.87 **	84.09 **	77.42 **	58.61 **
9	BHU-31XHD-3326	-3.95	1.29	-3.49	-14.63 **	1.03	31.68 **	55.08 **	46.89 **	49.59 **	62.65 **	72.62 **	59.25 **	61.08 **	93.80 **	60.64 **
10	HD-3721XPBW ZN1	7.45	14.59 **	9.18	-3.42	14.29 **	57.34 **	50.35 **	42.42 **	45.03 **	57.69 **	92.75 **	61.64 **	63.18 **	95.83 **	63.37 **
11	HD-3721XPBW-343	5.38	13.27 *	7.92	-4.53	12.97 *	14.48	35.47 **	28.32 **	30.68 **	42.09 **	48.50 **	87.30 **	64.29 **	58.34 **	56.95 **
12	HD-3721XHD-3326	9.33	15.29 **	9.84 *	-2.83	14.99 **	22.75 **	44.57 **	36.94 **	39.46 **	51.63 **	59.02 **	51.18 **	85.23 **	78.53 **	40.10 **
13	PWB-725X PBW ZN1	4.29	11.22 *	5.96	-6.26	10.93 *	55.99 **	55.99 **	47.76 **	50.48 **	63.61 **	73.43 **	68.42 **	82.81 **	76.20 **	36.96 **
14	PWB-725X PBW-343	0.59	8.12	3.01	-8.87 *	7.84	39.45 **	65.02 **	56.31 **	59.18 **	73.08 **	69.64 **	63.96 **	87.67 **	80.88 **	43.26 **
15	PWB-725X HD-3326	3.55	9.2	4.04	-7.96	8.92	36.05 **	60.23 **	51.77 **	54.56 **	68.05 **	54.75 **	65.52 **	80.27 **	73.74 **	33.66 **
16	CRDGEHNU1XPBWZN1	-3.94	13.98 **	8.59	-3.94	13.68 **	85.78 **	92.60 **	82.43 **	85.78 **	46.00 **	92.69 **	51.57 **	43.12 **	95.77 **	63.28 **
17	CRDGEHNU1XPBW343	-3.64	14.34 **	8.93	-3.64	14.04 **	43.74 **	70.10 **	61.12 **	64.08 **	78.40 **	65.25 **	58.42 **	82.81 **	76.20 **	36.96 **
18	CRDGEHNU1XHD-3326	-10.42 *	6.29	1.26	-10.42 *	6.01	44.49 **	70.17 **	61.19 **	64.15 **	78.48 **	34.04 **	78.01 **	56.14 **	50.49 **	52.39 **
19	PBW-550X PBW ZN1	2.61	9.43	4.26	-7.77	9.14	87.87 **	79.13 **	69.67 **	72.79 **	87.87 **	32.75 **	59.53 **	39.93 **	34.87 **	81.38 **
20	PBW-550X PBW-343	9.96 *	18.19 **	12.61 *	-0.39	17.88 **	33.49 **	57.97 **	49.63 **	52.38 **	65.68 **	61.01 **	63.07 **	78.12 **	71.67 **	60.88 **
21	PBW-550X HD-3326	9.05	14.99 **	9.56	-3.08	14.69 **	25.93 **	48.31 **	40.48 **	43.06 **	55.55 **	50.98 **	30.51 **	75.88 **	69.51 **	57.97 **
22	PBW-677XPBW ZN1	-4.37	1.99	-2.84	-14.05 **	1.72	54.84 **	63.47 **	54.84 **	57.69 **	71.45 **	73.79 **	58.85 **	83.20 **	76.56 **	37.46 **
23	PBW-677XPBW-343	-6.7	0.29	-4.45	-15.48 **	0.02	44.34 **	70.80 **	61.79 **	64.76 **	79.14 **	60.07 **	41.89 **	77.08 **	70.67 **	29.54 **

24	PBW-677XPBW-343	7.25	13.10 *	7.75	-4.68	12.80 *	44.31 **	69.96 **	60.99 **	63.95 **	78.25 **	73.22 **	46.04 **	61.78 **	94.48 **	61.55 **
25	PBW-822X PBW ZN1	11.83 *	19.26 **	13.63 **	0.52	18.95 **	45.56 **	61.99 **	53.44 **	56.26 **	69.90 **	72.52 **	47.33 **	81.86 **	75.28 **	35.73 **
26	PBW-822X PBW-343	4.3	12.11 *	6.81	-5.51	11.82 *	53.87 **	82.09 **	72.48 **	75.65 **	90.98 **	57.19 **	98.26 **	73.90 **	67.61 **	25.41 **
27	PBW-822X HD-3326	10.64 *	16.67 **	11.16 *	-1.67	16.36 **	36.17 **	60.37 **	51.90 **	54.69 **	68.20 **	57.43 **	59.07 **	83.39 **	76.75 **	37.71 **
28	HD-3117X PBW ZN1	6.86	13.97 **	8.58	-3.95	13.67 **	93.18 **	89.63 **	79.63 **	82.93 **	98.89 **	81.70 **	58.36 **	91.53 **	84.60 **	48.27 **
29	HD-3117X PBW-343	4.99	12.85 *	7.52	-4.89	12.56 *	40.11 **	65.80 **	57.05 **	59.93 **	73.89 **	61.74 **	63.99 **	78.93 **	72.45 **	31.93 **
30	HD-3117X HD-3326	3.62	9.27	4.11	-7.91	8.98	51.02 **	77.86 **	68.47 **	71.56 **	86.54 **	46.56 **	94.63 **	70.72 **	64.54 **	21.29 **
31	DBW-173X PBW ZN1	5.58	12.60 *	7.28	-5.1	12.31 *	65.60 **	60.93 **	52.44 **	55.24 **	68.79 **	70.41 **	54.79 **	79.63 **	73.13 **	32.84 **
32	DBW-173X PBW-343	10.31 *	18.57 **	12.97 *	-0.07	18.26 **	44.93 **	71.51 **	62.46 **	65.44 **	79.88 **	77.91 **	24.38 **	96.82 **	89.69 **	55.12 **
33	DBW-173X HD-3326	12.72 *	18.87 **	13.25 **	0.18	18.56 **	34.61 **	58.53 **	50.17 **	52.93 **	66.27 **	53.44 **	63.77 **	78.74 **	72.27 **	31.68 **
34	DH-3086X PBW ZN1	9.23	16.49 **	10.99 *	-1.82	16.19 **	68.90 **	60.08 **	51.64 **	54.42 **	67.90 **	24.07 **	55.37 **	80.14 **	73.62 **	63.50 **
35	DH-3086X PBW-343	8.58	16.71 **	11.19 *	-1.64	16.40 **	-17.94 *	-2.89	-8.02	-6.33	1.85	-1.93	62.34 **	42.39 **	37.24 **	84.57 **
36	DH-3086X HD-3326	6.89	12.72 *	7.39	-5	12.42 *	50.24 **	76.94 **	67.60 **	70.68 **	85.58 **	24.46 **	56.02 **	80.71 **	74.17 **	34.24 **
37	DBW-222X PBW ZN1	-0.11	17.77 **	12.20 *	-0.74	17.46 **	92.73 **	98.31 **	87.84 **	91.29 **	67.99 **	49.69 **	60.19 **	61.91 **	94.60 **	61.72 **
38	DBW-222X PBW-343	1.02	19.10 **	13.47 **	0.38	18.78 **	27.65 **	51.06 **	43.09 **	45.71 **	58.43 **	32.23 **	63.34 **	78.36 **	71.90 **	31.19 **
39	DBW-222X HD-3326	0.38	18.34 **	12.75 *	-0.26	18.03 **	19.76 *	41.04 **	33.60 **	36.05 **	47.93 **	20.81 **	85.78 **	62.95 **	57.06 **	35.22 **
40	CSW-18XPBW ZN1	0.56	7.25	2.18	-9.61 *	6.97	26.36 **	46.05 **	38.34 **	40.88 **	53.18 **	24.19 **	98.19 **	73.84 **	67.55 **	25.33 **
41	CSW-18XPBW-343	6.11	14.06 **	8.67	-3.87	13.76 **	39.03 **	64.53 **	55.85 **	58.71 **	72.56 **	31.56 **	59.94 **	84.15 **	77.48 **	38.70 **
42	CSW-18XHD-3326	8.97	14.91 **	9.48	-3.15	14.61 **	36.41 **	60.65 **	52.17 **	54.97 **	68.49 **	29.06 **	55.95 **	80.65 **	74.11 **	34.16 **
43	PBW-757X PBW ZN1	9.73 *	17.03 **	11.50 *	-1.36	16.72 **	78.25 **	68.19 **	59.32 **	62.24 **	76.41 **	68.54 **	62.54 **	77.66 **	71.23 **	30.28 **
44	PBW-757X PBW-343	4.99	12.85 *	7.52	-4.89	12.56 *	45.17 **	71.79 **	62.73 **	65.71 **	80.18 **	26.35 **	59.36 **	39.78 **	34.72 **	81.19 **
45	PBW-757X HD-3326	-1.67	3.7	-1.2	-12.60 **	3.42	33.47 **	57.19 **	48.90 **	51.63 **	64.87 **	36.01 **	80.62 **	58.43 **	52.70 **	55.36 **

"*" and "**" for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Harvest index														
		Location 1					Location 2					Location 3				
SN	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	10.70 *	8.75	12.75 *	5.17	1.1	-3.34	34.70 **	-3.29	-2.25	-7.37**	11.70 **	8.78 **	10.37 **	21.65 **	5.70 **
2	BHU-25XPBW-343	8.47	6.57	10.49 *	3.06	-0.93	17.38 **	38.36 **	20.43 **	21.72 **	15.35 **	16.14 **	18.54 **	20.27 **	32.56 **	15.19 **
3	BHU-25XHD-3326	-1.72	3.91	7.73	0.49	-3.41	11.65 **	34.84 **	12.39 **	13.59 **	7.64 **	23.83 **	25.54 **	27.37 **	40.40 **	21.99 **
4	WB-02XPBW ZN1	9.99 *	12.41 *	16.53 **	8.7	4.49	14.57 **	33.36 **	16.00 **	17.24 **	11.10 **	39.58 **	25.80 **	27.64 **	40.69 **	22.25 **
5	WB-02XPBW-343	7.59	9.95 *	13.99 **	6.33	2.21	12.65 **	34.84 **	15.58 **	16.81 **	10.70 **	23.41 **	25.96 **	27.79 **	40.86 **	22.40 **
6	WB-02XHD-3326	-4.39	1.09	4.81	-2.24	-6.03	27.15 **	47.95 **	28.74 **	30.12 **	23.31 **	9.76 **	11.27 **	12.89 **	24.44 **	8.12 **
7	BHU-31XPBW ZN1	6.77	11.06 *	15.14 **	7.4	3.24	15.21 **	53.31 **	20.04 **	21.32 **	14.97 **	27.78 **	24.97 **	26.80 **	39.76 **	21.44 **
8	BHU-31XPBW-343	9.78 *	14.19 **	18.38 **	10.42 *	6.15	6.84 **	64.46 **	11.32 **	12.51 **	6.62 **	22.68 **	25.21 **	27.04 **	40.03 **	21.67 **
9	BHU-31XHD-3326	7.63	13.81 **	17.99 **	10.05 *	5.79	27.93 **	55.08 **	33.29 **	34.72 **	27.67 **	10.53 **	12.06 **	13.69 **	25.32 **	8.89 **
10	HD-3721XPBW ZN1	9.94 *	13.06 **	17.22 **	9.33	5.1	13.08 **	50.35 **	9.13 **	10.30 **	4.53 *	32.04 **	25.37 **	27.20 **	40.20 **	21.83 **
11	HD-3721XPBW-343	4.24	7.2	11.14 *	3.67	-0.35	27.98 **	35.47 **	31.31 **	32.72 **	25.77 **	12.61 **	14.94 **	16.62 **	28.54 **	11.69 **
12	HD-3721XHD-3326	12.39 **	18.83 **	23.19 **	14.91 **	10.46 *	16.68 **	44.57 **	17.45 **	18.71 **	12.50 **	-2.19	-0.84	0.6	10.89 **	-3.23
13	PWB-725X PBW ZN1	2.76	2.76	6.53	-0.63	-4.48	24.27 **	55.99 **	28.85 **	30.22 **	23.41 **	27.01 **	27.01 **	28.87 **	42.05 **	23.43 **
14	PWB-725X PBW-343	11.02 *	11.02 *	15.10 **	7.36	3.2	17.84 **	65.02 **	22.18 **	23.49 **	17.02 **	5.84 **	8.02 **	9.60 **	20.81 **	4.97 *
15	PWB-725X HD-3326	13.03 **	19.51 **	23.90 **	15.57 **	11.09 *	20.86 **	60.23 **	25.31 **	26.65 **	20.02 **	20.02 **	21.67 **	23.45 **	36.07 **	18.23 **
16	CRDGEHNU1XPBWZN1	8.23	11.92 *	16.03 **	8.23	4.03	26.31 **	92.60 **	24.97 **	26.31 **	19.70 **	34.47 **	21.20 **	22.97 **	35.54 **	17.78 **
17	CRDGEHNU1XPBW343	9.11	12.83 *	16.98 **	9.11	4.89	23.10 **	70.10 **	26.30 **	27.65 **	20.97 **	23.48 **	26.03 **	27.87 **	40.95 **	22.47 **
18	CRDGEHNU1XHD-3326	1.54	7.36	11.31 *	3.82	-0.2	18.08 **	70.17 **	18.86 **	20.13 **	13.84 **	23.32 **	25.01 **	26.84 **	39.81 **	21.48 **
19	PBW-550X PBW ZN1	8.16	16.35 **	20.63 **	12.51 **	8.16	19.43 **	79.13 **	24.69 **	26.03 **	19.43 **	21.41 **	24.94 **	26.76 **	39.72 **	21.41 **
20	PBW-550X PBW-343	7.25	15.37 **	19.61 **	11.57 *	7.25	19.62 **	57.97 **	24.89 **	26.23 **	19.62 **	8.12 **	11.26 **	12.89 **	24.43 **	8.12 **
21	PBW-550X HD-3326	8.75	16.99 **	21.28 **	13.13 **	8.75	20.68 **	48.31 **	26.00 **	27.35 **	20.68 **	11.19 **	14.42 **	16.10 **	27.97 **	11.19 **
22	PBW-677XPBW ZN1	13.14 **	10.83 *	14.90 **	7.18	3.03	27.78 **	63.47 **	27.78 **	29.15 **	22.39 **	27.18 **	25.35 **	27.18 **	40.18 **	21.81 **
23	PBW-677XPBW-343	26.12 **	21.65 **	26.12 **	17.64 **	13.08 **	22.45 **	70.80 **	25.63 **	26.98 **	20.33 **	23.05 **	25.59 **	27.42 **	40.45 **	22.04 **
24	PBW-677XPBW-343	2.33	8.2	12.17 *	4.63	0.58	22.43 **	69.96 **	23.24 **	24.56 **	18.04 **	23.57 **	25.28 **	27.11 **	40.10 **	21.74 **
25	PBW-822X PBW ZN1	24.27 **	21.73 **	26.20 **	17.72 **	13.16 **	30.27 **	61.99 **	30.56 **	31.96 **	25.05 **	36.57 **	25.80 **	27.63 **	40.68 **	22.24 **
26	PBW-822X PBW-343	21.39 **	12.19 *	16.31 **	8.49	4.29	34.16 **	82.09 **	37.65 **	39.13 **	31.84 **	7.60 **	9.81 **	11.42 **	22.81 **	6.71 **
27	PBW-822X HD-3326	11.29 *	17.67 **	21.99 **	13.79 **	9.38 *	40.01 **	60.37 **	40.94 **	42.45 **	34.99 **	13.59 **	15.15 **	16.83 **	28.78 **	11.90 **
28	HD-3117X PBW ZN1	2.71	0.61	4.31	-2.71	-6.48	34.65 **	89.63 **	30.79 **	32.19 **	25.27 **	24.67 **	12.71 **	14.36 **	26.05 **	9.53 **

29	HD-3117X PBW-343	13.25 **	10.82 *	14.90 **	7.17	3.02	34.68 **	65.80 **	38.19 **	39.66 **	32.35 **	6.61 **	8.80 **	10.39 **	21.68 **	5.73 **
30	HD-3117X HD-3326	6.54	12.65 *	16.79 **	8.94	4.72	27.95 **	77.86 **	28.79 **	30.17 **	23.35 **	23.85 **	25.55 **	27.39 **	40.41 **	22.01 **
31	DBW-173X PBW ZN1	13.89 **	14.43 **	18.63 **	10.66 *	6.37	40.94 **	60.93 **	40.61 **	42.12 **	34.68 **	33.02 **	25.39 **	27.23 **	40.24 **	21.85 **
32	DBW-173X PBW-343	17.13 **	17.68 **	22.01 **	13.80 **	9.40 *	33.38 **	71.51 **	36.85 **	38.31 **	31.07 **	23.01 **	25.55 **	27.38 **	40.41 **	22.00 **
33	DBW-173X HD-3326	10.64 *	16.98 **	21.28 **	13.12 **	8.74	36.88 **	58.53 **	37.79 **	39.26 **	31.97 **	23.36 **	25.06 **	26.89 **	39.86 **	21.53 **
34	DH-3086X PBW ZN1	14.14 **	15.33 **	19.57 **	11.53 *	7.21	15.71 **	60.08 **	15.42 **	16.65 **	10.55 **	35.58 **	25.64 **	27.47 **	40.51 **	22.09 **
35	DH-3086X PBW-343	19.14 **	20.38 **	24.81 **	16.41 **	11.91 *	23.37 **	-2.89	26.58 **	27.93 **	21.24 **	22.83 **	25.37 **	27.20 **	40.20 **	21.83 **
36	DH-3086X HD-3326	3.39	9.32	13.33 *	5.71	1.62	17.64 **	76.94 **	18.42 **	19.68 **	13.42 **	10.16 **	11.68 **	13.31 **	24.89 **	8.52 **
37	DBW-222X PBW ZN1	11.71 *	18.15 **	22.49 **	14.26 **	9.83 *	38.08 **	98.31 **	38.57 **	40.05 **	32.72 **	14.64 **	12.01 **	13.64 **	25.27 **	8.84 **
38	DBW-222X PBW-343	11.67 *	18.11 **	22.44 **	14.21 **	9.79 *	25.82 **	51.06 **	29.09 **	30.47 **	23.64 **	18.89 **	21.35 **	23.12 **	35.71 **	17.92 **
39	DBW-222X HD-3326	-1.23	4.46	8.3	1.02	-2.9	35.64 **	41.04 **	36.53 **	37.99 **	30.77 **	15.34 **	16.93 **	18.64 **	30.77 **	13.63 **
40	CSW-18XPBW ZN1	23.86 **	21.33 **	25.78 **	17.33 **	12.78 **	43.41 **	46.05 **	36.17 **	37.63 **	30.43 **	37.24 **	25.17 **	26.99 **	39.98 **	21.63 **
41	CSW-18XPBW-343	26.90 **	18.05 **	22.38 **	14.15 **	9.73 *	35.10 **	64.53 **	38.62 **	40.10 **	32.76 **	23.42 **	25.97 **	27.81 **	40.88 **	22.41 **
42	CSW-18XHD-3326	5.37	11.41 *	15.51 **	7.74	3.57	29.34 **	60.65 **	30.19 **	31.58 **	24.70 **	23.82 **	25.53 **	27.36 **	40.38 **	21.98 **
43	PBW-757X PBW ZN1	11.00 *	15.32 **	19.56 **	11.52 *	7.2	26.35 **	68.19 **	26.71 **	28.07 **	21.37 **	24.70 **	26.00 **	27.84 **	40.92 **	22.44 **
44	PBW-757X PBW-343	11.62 *	15.96 **	20.22 **	12.14 *	7.8	31.27 **	71.79 **	34.69 **	36.13 **	29.00 **	23.39 **	25.93 **	27.77 **	40.84 **	22.38 **
45	PBW-757X HD-3326	12.47 **	18.92 **	23.28 **	15.00 **	10.54 *	35.42 **	57.19 **	36.32 **	37.77 **	30.56 **	24.17 **	25.88 **	27.72 **	40.78 **	22.32 **

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Protein content														
		Location 1					Location 2					Location 3				
S/N	Crosses	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	-5.73 **	8.18 **	-0.19	-11.01 **	1.39	5.67	13.59 **	14.65 **	-5.6	0	16.48 **	15.17 **	22.78 **	12.17 **	13.12 **
2	BHU-25XPBW-343	2.39	7.26 **	-1.04	-11.77 **	0.53	20.66 **	22.59 **	23.74 **	1.88	7.92 *	23.13 **	12.77 **	20.22 **	9.83 *	10.76 **
3	BHU-25XHD-3326	-17.43 **	6.69 **	-1.56	-12.24 **	0.00	7.09	17.07 **	18.17 **	-2.7	3.07	7.09	7.69	14.81 **	4.89	5.77
4	WB-02XPBW ZN1	-6.72 **	7.05 **	-1.24	-11.94 **	0.33	9.51 *	17.71 **	18.82 **	-2.17	3.63	9.51 *	8.28 *	15.43 **	5.46	6.35
5	WB-02XPBW-343	2.65	7.05 **	-1.24	-11.94 **	0.33	22.71 **	25.38 **	26.55 **	4.2	10.38 **	22.71 **	15.33 **	22.95 **	12.33 **	13.27 **
6	WB-02XHD-3326	-17.45 **	6.66 **	-1.59	-12.26 **	-0.03	14.53 **	25.20 **	26.38 **	4.05	10.22 **	14.53 **	15.17 **	22.78 **	12.17 **	13.12 **
7	BHU-31XPBW ZN1	-7.36 **	6.31 *	-1.92	-12.56 **	-0.36	4.37	13.01 **	14.07 **	-6.08	-0.51	9.73 *	9.29 *	16.51 **	6.45	7.35
8	BHU-31XPBW-343	-3.7	6.87 **	-1.4	-12.09 **	0.17	3.65	12.22 **	13.28 **	-6.73	-1.2	3.65	3.23	10.05 *	0.55	1.39
9	BHU-31XHD-3326	-17.29 **	6.87 **	-1.4	-12.09 **	0.17	12.35 **	22.82 **	23.97 **	2.08	8.13 *	12.35 **	12.98 **	20.44 **	10.04 *	10.97 **
10	HD-3721XPBW ZN1	11.12 **	27.52 **	17.65 **	4.89 *	19.52 **	3.51	11.27 **	12.31 **	-7.53 *	-2.04	3.51	2.35	9.11 *	-0.31	0.52
11	HD-3721XPBW-343	-0.73	5.56 *	-2.61	-13.17 **	-1.06	24.53 **	25.73 **	26.91 **	4.49	10.69 **	24.53 **	15.65 **	23.29 **	12.64 **	13.59 **
12	HD-3721XHD-3326	-17.57 **	6.52 **	-1.73	-12.38 **	-0.17	14.53 **	25.20 **	26.38 **	4.05	10.22 **	14.53 **	15.17 **	22.78 **	12.17 **	13.12 **
13	PWB-725X PBW ZN1	-7.03 **	6.69 **	-1.56	-12.24 **	0.00	-1.97	5.37	6.36	-12.43 **	-7.23	7.61	7.61	14.72 **	4.81	5.69
14	PWB-725X PBW-343	12.39 **	16.57 **	7.55 **	-4.11 *	9.26 **	19.89 **	19.89 **	21.01 **	-0.36	5.55	10.28 *	10.28 *	17.57 **	7.41	8.32 *
15	PWB-725X HD-3326	-17.71 **	6.34 *	-1.89	-12.53 **	-0.33	9.22 *	19.40 **	20.52 **	-0.77	5.11	9.22 *	9.83 *	17.08 **	6.97	7.87
16	CRDGEHNU1XPBWZN1	-11.63 **	7.44 **	-0.88	-11.63 **	0.7	10.57 **	33.04 **	34.29 **	10.57 **	17.13 **	19.20 **	22.38 **	30.47 **	19.20 **	20.20 **
17	CRDGEHNU1XPBW343	-11.48 **	7.62 **	-0.71	-11.48 **	0.86	6.78	28.48 **	29.69 **	6.78	13.11 **	17.72 **	20.86 **	28.84 **	17.72 **	18.70 **
18	CRDGEHNU1XHD-3326	-11.67 **	14.13 **	5.30 *	-6.12 **	6.97 **	-6.73	12.22 **	13.28 **	-6.73	-1.2	0.55	3.23	10.05 *	0.55	1.39
19	PBW-550X PBW ZN1	-5.89 **	8.00 **	-0.36	-11.16 **	1.23	2.56	16.49 **	17.58 **	-3.19	2.56	5.25	7.16	14.24 **	4.37	5.25
20	PBW-550X PBW-343	0.53	7.26 **	-1.04	-11.77 **	0.53	5.93	20.33 **	21.45 **	0	5.93	8.71 *	10.68 *	18.00 **	7.8	8.71 *
21	PBW-550X HD-3326	-17.29 **	6.87 **	-1.4	-12.09 **	0.17	10.22 **	25.20 **	26.38 **	4.05	10.22 **	13.12 **	15.17 **	22.78 **	12.17 **	13.12 **
22	PBW-677XPBW ZN1	-7.03 **	6.69 **	-1.56	-12.24 **	0	5.67	13.59 **	14.65 **	-5.6	0	11.08 **	9.83 *	17.08 **	6.97	7.87
23	PBW-677XPBW-343	-1.04	7.26 **	-1.04	-11.77 **	0.53	25.13 **	24.33 **	25.50 **	3.33	9.46 *	21.92 **	14.37 **	21.92 **	11.39 **	12.33 **

24	PBW-677XPBW-343	-16.42 **	8.00 **	-0.36	-11.16 **	1.23	5.76	15.62 **	16.71 **	-3.91	1.79	5.76	6.36	13.38 **	3.59	4.46
25	PBW-822X PBW ZN1	-5.57 **	8.36 **	-0.03	-10.87 **	1.56	0.55	12.22 **	13.28 **	-6.73	-1.2	3.23	3.23	10.05 *	0.55	1.39
26	PBW-822X PBW-343	0.16	9.85 **	1.35	-9.64 **	2.96	17.59 **	31.24 **	32.47 **	9.07 *	15.54 **	20.73 **	20.73 **	28.70 **	17.59 **	18.57 **
27	PBW-822X HD-3326	-15.43 **	9.28 **	0.82	-10.11 **	2.43	2.47	14.37 **	15.45 **	-4.95	0.69	4.62	5.21	12.16 **	2.47	3.33
28	HD-3117X PBW ZN1	-16.71 **	8.54 **	0.14	-10.72 **	1.73	-0.32	9.76 *	10.79 *	-8.78 *	-3.37	7.68	7.91	15.03 **	5.1	5.98
29	HD-3117X PBW-343	-18.15 **	6.66 **	-1.59	-12.26 **	-0.03	7.3	18.15 **	19.26 **	-1.81	4.01	8.45 *	8.68 *	15.86 **	5.85	6.74
30	HD-3117X HD-3326	-17.99 **	6.87 **	-1.4	-12.09 **	0.17	3.16	13.59 **	14.65 **	-5.6	0	6.56	7.16	14.24 **	4.37	5.25
31	DBW-173X PBW ZN1	-6.22 **	7.62 **	-0.71	-11.48 **	0.86	3.69	12.72 **	13.77 **	-6.32	-0.77	6.36	6.36	13.38 **	3.59	4.46
32	DBW-173X PBW-343	-1.85	7.44 **	-0.88	-11.63 **	0.7	12.58 **	22.39 **	23.53 **	1.71	7.75 *	15.25 **	15.25 **	22.86 **	12.25 **	13.20 **
33	DBW-173X HD-3326	-16.85 **	7.44 **	-0.88	-11.63 **	0.7	7.89 *	17.94 **	19.05 **	-1.98	3.83	7.89	8.49 *	15.66 **	5.67	6.56
34	DH-3086X PBW ZN1	-7.18 **	6.52 **	-1.73	-12.38 **	-0.17	4.4	12.22 **	13.28 **	-6.73	-1.2	7.1	5.9	12.90 **	3.15	4.01
35	DH-3086X PBW-343	-3.55	7.44 **	-0.88	-11.63 **	0.7	12.33 **	11.61 **	12.66 **	-7.24 *	-1.74	4.34	2.67	9.45 *	0.00	0.84
36	DH-3086X HD-3326	-17.87 **	6.13 *	-2.09	-12.70 **	-0.53	4.38	14.11 **	15.18 **	-5.16	0.46	4.38	4.97	11.90 **	2.24	3.1
37	DBW-222X PBW ZN1	-8.32 **	5.21 *	-2.94	-13.46 **	-1.39	11.67 **	20.03 **	21.16 **	-0.24	5.67	9.31 *	10.42 *	17.71 **	7.54	8.45 *
38	DBW-222X PBW-343	-8.62 **	4.11	-3.95	-14.37 **	-2.43	16.43 **	17.71 **	18.82 **	-2.17	3.63	7.19	8.28 *	15.43 **	5.46	6.35
39	DBW-222X HD-3326	-14.55 **	10.41 **	1.87	-9.18 **	3.49	2.12	11.64 **	12.69 **	-7.22 *	-1.71	6.95	8.04	15.18 **	5.23	6.11
40	CSW-18XPBW ZN1	-15.80 **	5.95 *	-2.25	-12.85 **	-0.7	11.53 **	19.89 **	21.01 **	-0.36	5.55	9.96 *	10.28 *	17.57 **	7.41	8.32 *
41	CSW-18XPBW-343	-16.06 **	5.62 *	-2.55	-13.12 **	-1	15.79 **	22.88 **	24.03 **	2.12	8.18 *	18.03 **	18.38 **	26.20 **	15.30 **	16.26 **
42	CSW-18XHD-3326	-17.52 **	6.58 **	-1.67	-12.33 **	-0.11	9.16 *	19.34 **	20.46 **	-0.82	5.06	8.1	8.71 *	15.89 **	5.88	6.77
43	PBW-757X PBW ZN1	-14.02 **	8.42 **	0.03	-10.82 **	1.62	14.37 **	22.94 **	24.09 **	2.17	8.23 *	11.95 **	13.09 **	20.56 **	10.15 *	11.07 **
44	PBW-757X PBW-343	-17.25 **	4.34	-3.73	-14.17 **	-2.2	10.11 *	14.52 **	15.59 **	-4.83	0.82	9.57 *	10.68 *	18.00 **	7.8	8.71 *
45	PBW-757X HD-3326	-14.28 **	10.77 **	2.2	-8.88 **	3.82	8.23 *	18.32 **	19.43 **	-1.67	4.17	9.60 *	10.71 *	18.02 **	7.83	8.74 *

“*” and “**” for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= NORMAN and SV4= BORLAUG 100

Table 4.4: contd.

		Grain yield per plant														
		Location 1					Location 2					Location 3				
SN	Cross	BP	SV1	SV2	SV3	SV4	BP	SV1	SV2	VS3	SV4	BP	SV1	SV2	SV3	SV4
1	BHU-25XPBW ZN1	10.19 *	14.88 **	13.41 **	-2.55	7.91	40.78 **	-6.72**	45.30 **	42.94 **	37.60 **	10.94 **	13.58 **	14.35 **	-17.58 **	8.53 **
2	BHU-25XPBW-343	8.36	8.86	7.47	-7.65 *	2.26	30.64 **	16.15 **	38.79 **	36.53 **	31.43 **	1.77	7.13 **	7.86 **	-22.26 **	2.37
3	BHU-25XHD-3326	3.57	17.83 **	16.33 **	-0.04	10.68 *	11.78 **	8.39 **	26.89 **	24.83 **	20.16 **	8.75 **	22.02 **	22.85 **	-11.45 **	16.59 **
4	WB-02XPBW ZN1	25.33 **	30.67 **	29.00 **	10.85 **	22.74 **	31.66 **	11.88 **	35.89 **	33.68 **	28.69 **	26.61 **	29.62 **	30.51 **	-5.93 **	23.86 **
5	WB-02XPBW-343	11.64 *	12.16 **	10.73 *	-4.86	5.35	34.96 **	11.47 **	43.38 **	41.05 **	35.78 **	17.92 **	24.12 **	24.97 **	-9.92 **	18.61 **
6	WB-02XHD-3326	-8.09 *	4.57	3.23	-11.29 **	-1.78	18.75 **	24.17 **	34.80 **	32.61 **	27.66 **	17.78 **	32.15 **	33.05 **	-4.10 *	26.27 **
7	BHU-31XPBW ZN1	20.48 **	25.61 **	24.01 **	6.56	17.99 **	22.41 **	15.78 **	26.34 **	24.29 **	19.64 **	21.73 **	24.63 **	25.48 **	-9.56 **	19.09 **
8	BHU-31XPBW-343	13.02 **	16.84 **	15.36 **	-0.88	9.76 *	19.58 **	7.37 **	27.04 **	24.98 **	20.31 **	13.29 **	19.25 **	20.06 **	-13.46 **	13.95 **
9	BHU-31XHD-3326	3	17.19 **	15.70 **	-0.58	10.08 *	30.21 **	28.56 **	47.81 **	45.41 **	39.98 **	27.38 **	42.92 **	43.89 **	3.71 *	36.56 **
10	HD-3721XPBW ZN1	21.30 **	26.46 **	24.85 **	7.28	18.78 **	23.30 **	5.26 **	27.26 **	25.19 **	20.51 **	36.75 **	40.00 **	40.96 **	1.6	33.78 **
11	HD-3721XPBW-343	19.21 **	19.76 **	18.24 **	1.6	12.50 **	21.60 **	26.65 **	29.18 **	27.08 **	22.33 **	14.30 **	20.32 **	21.14 **	-12.69 **	14.97 **
12	HD-3721XHD-3326	18.94 **	35.33 **	33.60 **	14.80 **	27.12 **	20.56 **	13.28 **	36.86 **	34.64 **	29.61 **	19.81 **	34.43 **	35.35 **	-2.45	28.45 **
13	PWB-725X PBW ZN1	8.3	12.91 **	11.47 *	-4.22	6.06	37.73 **	24.27 **	42.15 **	39.84 **	34.62 **	37.18 **	40.44 **	41.40 **	1.92	34.20 **
14	PWB-725X PBW-343	16.96 **	17.50 **	16.01 **	-0.32	10.37 *	30.81 **	17.84 **	38.97 **	36.71 **	31.60 **	10.24 **	16.04 **	16.84 **	-15.79 **	10.89 **
15	PWB-725X HD-3326	15.52 **	31.43 **	29.75 **	11.49 **	23.45 **	24.93 **	20.86 **	41.82 **	39.51 **	34.30 **	16.23 **	30.41 **	31.30 **	-5.36 **	24.61 **
16	CRDGEHNU1XPBWZN1	6.1	25.07 **	23.48 **	6.1	17.48 **	50.49 **	20.53 **	55.33 **	52.80 **	47.09 **	-10.12 **	23.85 **	24.70 **	-10.12 **	18.35 **
17	CRDGEHNU1XPBW343	7.16	26.32 **	24.71 **	7.16	18.65 **	35.95 **	21.81 **	44.44 **	42.09 **	36.78 **	-6.14 **	29.34 **	30.22 **	-6.14 **	23.59 **
18	CRDGEHNU1XHD-3326	-2	15.53 **	14.05 **	-2	8.52 *	28.62 **	14.64 **	46.01 **	43.64 **	38.27 **	-17.27 **	14.00 **	14.78 **	-17.27 **	8.94 **
19	PBW-550X PBW ZN1	19.74 **	27.47 **	25.85 **	8.14 *	19.74 **	21.55 **	20.26 **	28.36 **	26.27 **	21.55 **	48.55 **	55.46 **	56.53 **	12.82 **	48.55 **
20	PBW-550X PBW-343	24.97 **	33.04 **	31.34 **	12.86 **	24.97 **	26.49 **	20.46 **	34.38 **	32.20 **	27.26 **	25.46 **	32.07 **	32.97 **	-4.16 *	26.20 **
21	PBW-550X HD-3326	19.84 **	36.34 **	34.61 **	15.66 **	28.07 **	21.53 **	21.52 **	37.96 **	35.72 **	30.65 **	20.82 **	35.55 **	36.48 **	-1.63	29.53 **
22	PBW-677XPBW ZN1	6.37	10.89 *	9.48 *	-5.93	4.17	36.60 **	23.24 **	40.99 **	38.70 **	33.52 **	9.53 **	12.14 **	12.91 **	-18.62 **	7.15 **
23	PBW-677XPBW-343	33.49 **	35.21 **	33.49 **	14.70 **	27.01 **	31.90 **	21.17 **	40.13 **	37.86 **	32.71 **	41.50 **	48.95 **	49.97 **	8.09 **	42.33 **

24	PBW-677XPBW-343	6.01	20.61 **	19.07 **	2.32	13.29 **	23.59 **	18.86 **	40.30 **	38.02 **	32.86 **	6.28 **	19.25 **	20.06 **	-13.46 **	13.95 **
25	PBW-822X PBW ZN1	51.51 **	57.96 **	55.95 **	34.00 **	48.38 **	13.28 **	25.93 **	32.82 **	30.67 **	25.78 **	37.14 **	58.75 **	59.83 **	15.20 **	51.69 **
26	PBW-822X PBW-343	24.53 **	25.10 **	23.51 **	6.13	17.51 **	23.80 **	32.76 **	45.16 **	42.80 **	37.47 **	11.22 **	28.74 **	29.62 **	-6.58 **	23.01 **
27	PBW-822X HD-3326	18.87 **	35.24 **	33.52 **	14.73 **	27.04 **	16.64 **	35.93 **	36.77 **	34.55 **	29.52 **	16.06 **	34.34 **	35.26 **	-2.51	28.37 **
28	HD-3117X PBW ZN1	14.71 **	19.59 **	18.07 **	1.45	12.34 **	28.35 **	26.14 **	48.37 **	45.96 **	40.51 **	5.22 *	20.14 **	20.96 **	-12.81 **	14.80 **
29	HD-3117X PBW-343	22.28 **	22.84 **	21.28 **	4.21	15.39 **	33.16 **	33.28 **	53.93 **	51.43 **	45.77 **	6.46 **	21.55 **	22.38 **	-11.79 **	16.15 **
30	HD-3117X HD-3326	5.93	20.53 **	18.99 **	2.24	13.21 **	30.99 **	24.22 **	51.42 **	48.96 **	43.40 **	4.15	18.92 **	19.73 **	-13.70 **	13.63 **
31	DBW-173X PBW ZN1	18.97 **	24.03 **	22.45 **	5.22	16.50 **	23.71 **	35.62 **	27.68 **	25.61 **	20.92 **	19.92 **	22.77 **	23.61 **	-10.90 **	17.32 **
32	DBW-173X PBW-343	43.13 **	43.79 **	41.96 **	21.98 **	35.07 **	18.26 **	31.99 **	25.63 **	23.59 **	18.97 **	45.23 **	52.87 **	53.92 **	10.94 **	46.07 **
33	DBW-173X HD-3326	20.64 **	37.26 **	35.51 **	16.44 **	28.93 **	18.81 **	32.89 **	34.87 **	32.68 **	27.72 **	41.50 **	58.75 **	59.84 **	15.21 **	51.70 **
34	DH-3086X PBW ZN1	25.74 **	31.09 **	29.42 **	11.21 **	23.14 **	57.79 **	11.32 **	62.86 **	60.22 **	54.23 **	29.52 **	58.22 **	59.30 **	14.82 **	51.19 **
35	DH-3086X PBW-343	47.24 **	47.92 **	46.04 **	25.49 **	38.95 **	41.72 **	22.08 **	50.57 **	48.12 **	42.58 **	23.09 **	50.36 **	51.39 **	9.12 **	43.68 **
36	DH-3086X HD-3326	8.52 *	23.46 **	21.89 **	4.74	15.97 **	33.50 **	14.21 **	51.54 **	49.08 **	43.51 **	0.02	22.19 **	23.03 **	-11.33 **	16.76 **
37	DBW-222X PBW ZN1	17.21 **	44.68 **	42.83 **	22.73 **	35.90 **	50.47 **	33.65 **	55.31 **	52.78 **	47.07 **	11.52 **	46.33 **	47.34 **	6.19 **	39.83 **
38	DBW-222X PBW-343	12.27 **	38.57 **	36.81 **	17.56 **	30.17 **	32.13 **	24.51 **	40.38 **	38.10 **	32.94 **	5.00 *	37.78 **	38.72 **	-0.01	31.65 **
39	DBW-222X HD-3326	-0.72	22.55 **	20.99 **	3.96	15.11 **	31.73 **	31.68 **	49.54 **	47.11 **	41.61 **	-9.31 **	19.01 **	19.82 **	-13.64 **	13.72 **
40	CSW-18XPBW ZN1	29.53 **	35.04 **	33.32 **	14.56 **	26.85 **	32.31 **	31.34 **	36.56 **	34.34 **	29.32 **	7.87 **	34.14 **	35.05 **	-2.66	28.17 **
41	CSW-18XPBW-343	37.75 **	38.39 **	36.62 **	17.40 **	29.99 **	21.38 **	33.69 **	28.96 **	26.86 **	22.12 **	23.92 **	54.09 **	55.15 **	11.83 **	47.24 **
42	CSW-18XHD-3326	10.53 **	25.76 **	24.16 **	6.69	18.13 **	26.70 **	25.57 **	43.84 **	41.50 **	36.21 **	-2.17	21.65 **	22.48 **	-11.72 **	16.24 **
43	PBW-757X PBW ZN1	38.73 **	46.00 **	44.14 **	23.86 **	37.15 **	39.40 **	22.21 **	45.37 **	43.00 **	37.66 **	42.54 **	47.38 **	48.39 **	6.96 **	40.83 **
44	PBW-757X PBW-343	27.01 **	33.67 **	31.97 **	13.39 **	25.56 **	46.33 **	29.90 **	55.46 **	52.93 **	47.22 **	44.53 **	52.14 **	53.18 **	10.41 **	45.38 **
45	PBW-757X HD-3326	15.69 **	31.63 **	29.95 **	11.66 **	23.64 **	16.13 **	31.47 **	31.83 **	29.69 **	24.85 **	14.68 **	28.67 **	29.55 **	-6.62 **	22.95 **

"*" and "**" for 5% and 1% Level of Significance, BP stand for better parent and SV stand for standard variety, SV1=HD 2967, SV2= DBW 187, SV3= ORMAN and SV4= BORLAUG 100

4.5 Analysis of variance on stability analysis across three environments

The Analysis of Variance (ANOVA) in this table evaluates the stability of sixteen wheat characters across three different environments for 67 wheat genotypes. The table assesses how environment (E), replication (R), the interaction between environment and genotype (E x R), genotype (G), and genotype × environment interaction (G x E) contribute to the overall variation for each character.

4.5.1. Days to 50% Heading

Genotype (G), the genotype has a substantial effect on the number of days to 50% heading (66.92). This indicates that the genetic makeup of the plants is a major determinant in how quickly they reach the heading stage. Environment (E), also plays a significant role (77.57), meaning factors like temperature, soil, and moisture levels are influencing the heading time. Replication (R) shows a small effect (0.92), meaning the experimental repetitions don't contribute much to the variation in this trait. GXE (Genotype × Environment Interaction) value (1.01) is not very large, suggesting that the response of different genotypes to environmental conditions is relatively consistent. Error variance, error variance (7.57) is significant, indicating that, there is considerable random variation in the results.

4.5.2. Chlorophyll Content

Genotype (G) has a notable effect (72.03), indicating that different genotypes have significantly different chlorophyll content. Environment (E) also contributes (31.47), but not as strongly as genotype, suggesting that the genetic makeup of the plant is the major factor in determining chlorophyll content. Replication (R) has a minor effect (0.32), meaning experimental repetitions don’t contribute much to the observed variation. GXE (1.09) is small, implying that the response of genotypes to environmental conditions does not vary significantly. Error variance (1.47) is low, indicating reliable and precise measurements of chlorophyll content.

4.5.3. Grain Filling Period

Genotype (G) has a modest effect (14.37) on the grain filling period, indicating that genetic differences contribute somewhat to the duration of grain filling. Environment (E) has a larger effect (19.01), showing that the duration of grain filling is more influenced by environmental conditions such as water availability, temperature, and other growing conditions. Replication (R) has a moderate effect (0.86), contributing to some variability. The GXE interaction (0.21) is small, meaning the interaction between genotype and environment does not significantly alter the grain filling period. Error variance (0.49) is low, indicating that the measurements for this trait are fairly consistent.

4.5.4. Days to Maturity

The genotype has a strong effect (83.86) on the days to maturity, showing that different genotypes mature at significantly different times. Environment also affects this trait (42.71), but not as strongly as genotype. Replication has a very minor effect (0.16). The GXE interaction (1.27) is small, indicating that genotypes do not vary significantly in their response to environmental conditions in terms of maturity time. The error variance (2.78) is moderate, suggesting some random variation in measurements of this trait.

4.5.5. Flag Leaf Area (cm^2)

The genotype has a very large effect (197.42), suggesting that different genotypes have highly variable flag leaf areas. The environment has a smaller effect (11.38), indicating that flag leaf area is primarily determined by genetic factors. Replication contributes very little (0.04). The GXE value (2.99) is significant, indicating that different genotypes may respond differently to environmental conditions when it comes to leaf area. The error variance (1.38) is low, showing that measurements are fairly consistent.

4.5.6. Plant Height (cm)

The genotype has a moderate effect (38.66) on plant height, indicating some variation between genotypes in how tall they grow. The environment has a larger effect (58.69), meaning that factors such as soil, water, and temperature are more important in determining plant height. Replication has a very minor effect (0.05). The GXE interaction (0.58) is moderate, suggesting some variation in how genotypes respond to environmental conditions in terms of height. The error variance (8.69) is relatively high, indicating that there is considerable random variation in plant height measurements.

4.5.7. Number of Spikelet per Spike

The genotype has a modest effect (3.35) on the number of spikelets per spike, meaning genetic variation contributes to some extent. The environment has a smaller effect (1.93). Replication contributes minimally (0.04). The GXE interaction (0.05) is negligible, suggesting that environmental factors do not cause much variation in spikelet number across genotypes. The error variance (1.93) is moderate.

4.5.8. Spike Length (cm)

The genotype has a minor effect (1.17) on spike length. The environment has a smaller effect (0.62). Replication has a moderate effect (0.33). The GXE interaction (0.01) is almost negligible. The error variance (0.62) is moderate. Both genotype and environment have small influences on spike length, and the GXE interaction is minimal, indicating that this trait is quite stable across genotypes and environments.

4.5.9. Protein Content (%)

The genotype has a small effect (0.49) on protein content. The environment has a similar effect (0.53). Replication contributes significantly (3.72). The GXE interaction (0.02) is negligible. The error variance (3.72) is significant, indicating considerable random variation in protein content measurements. Protein content is influenced by both genotype and environment, with replication contributing notably to the variation. The GXE interaction is minimal, and there is significant error variance, suggesting that the protein content measurements may be inconsistent.

4.5.10. Number of Productive Tillers

The genotype has a moderate effect (6.01) on the number of productive tillers, indicating that genetic factors have a notable impact on this trait. The environment has a smaller effect (1.46), showing that the environment plays a less significant role in determining the number of productive tillers. The replication value is moderate (0.28), meaning that experimental repetitions contribute somewhat to the variation. The GXE interaction (0.09) is small, suggesting that the response of genotypes to environmental conditions regarding the number of productive tillers is consistent across environments. The error variance (1.46) is moderate, meaning there is some random variation in the results, but it's not excessively high.

4.5.11. Number of Grains per Spike

The genotype has a significant effect (74.85) on the number of grains per spike, suggesting that genetic variation is a major factor in determining this trait. The environment has a smaller effect (13.64), indicating that environmental conditions also play a role but are less influential than the genotype. The replication value (0.63) is modest, indicating that some of the variation is due to experimental repetition. The GXE interaction (1.13) is relatively small, suggesting that the number of grains per spike is fairly stable across environments for different genotypes. The error variance (3.64) is moderate, meaning that there is some random variation that isn't explained by the experimental factors.

4.5.12. Grain Weight per Spike (g)

The genotype has a moderate effect (0.72) on the grain weight per spike, meaning that there are some genetic differences influencing the weight of grains produced on each spike. The environment has a smaller effect (0.18), suggesting that environmental conditions have a lesser impact on this trait. The replication value (0.29) indicates that experimental repetitions contribute slightly to the variability. The GXE interaction (0.01) is minimal, suggesting that the response of genotypes to environmental conditions regarding grain weight per spike is quite consistent. The error variance (0.18) is low, indicating that the measurements are relatively precise.

4.5.13. 1000-Grain Weight (g)

The genotype has a large effect (51.02) on the 1000-grain weight, showing that genetic differences contribute significantly to this trait. The environment has a smaller effect (5.99), indicating that environmental factors are less important in determining the weight of 1000 grains. The replication value (0.89) shows a slight contribution of replication to variability. The GXE interaction (1.89) is moderate, suggesting that the 1000-grain weight is somewhat influenced by the interaction between genotype and environmental conditions. The error variance (5.99) is significant, suggesting that there is considerable random variation in the results.

4.5.14. Biological Yield (g)

The genotype has a significant effect (67.87) on biological yield, indicating that different genotypes result in different total plant biomass or biological yield. The environment also has a strong influence (35.04), suggesting that growing conditions (e.g., water availability, soil fertility) significantly affect biological yield. The replication value (0.03) is minimal, meaning the variability due to replication is very small. The GXE interaction (1.02) is moderate, indicating some variation in how different genotypes respond to environmental conditions in terms of biological yield. The error variance (5.04) is moderate, suggesting that there is some random variation in the yield measurements.

4.5.15. Harvest Index (%)

The genotype has a strong effect (64.84) on the harvest index, indicating that genetic factors have a major influence on how efficiently a plant converts biomass into grain. The environment has a smaller effect (16.14), meaning that environmental factors are less important in determining the harvest index. The replication value (0.29) is small. The GXE interaction (0.98) is also small, suggesting that genotype-environment interactions do not strongly affect the harvest index. The error variance (6.14) is moderate, indicating some random variation in measurements of the harvest index.

4.5.16. Grain Yield per Plant (g)

The genotype has a significant effect (78.31) on grain yield per plant, indicating that different genotypes can result in large differences in grain yield. The environment also contributes significantly (11.81), although to a lesser extent than genotype. The replication value (0.21) is modest, meaning some variability is due to experimental repetition. The GXE interaction (1.18) is moderate, suggesting that the response of genotypes to environmental conditions in terms of grain yield can vary. The error variance (1.81) is moderate, indicating that there is some random variation in measurements of this trait

4.5 Stability analysis across three locations

The mean measures the average yield, bi (regression coefficient) measure the response of each genotype to environmental variations (stability) and S^2di (deviation from regression) the low or near-zero value indicates a more stable performance across environments, any values close to 1 indicate average stability above 1 indicate stable to only favorable environments and below 1 indicate suitability for less favorable environments. S^2di (deviation from regression) the low or near-zero value indicates a more stable performance across environments.

4.5.1 Day to 50% heading

Higher S^2di suggests that days to heading fluctuate more with environmental conditions. Genotypes like CRD GEHNU1 (bi -1.2459, S2di -2.1616) and HD-3326 (bi -0.096, S2di -3.1508) have negative bi values, meaning they may be suited for less favorable environments with relatively stable performance. BHU-31 shows a high bi value (2.49) with a low S2di, indicating responsiveness to favorable conditions with good stability. Genotypes like PBW-550 have high S^2di (95.4018) indicating less stability across environments.

4.5.2 Days to maturity

Days to 50% heading, the genotypes with bi values close to 1 and low S^2di values are more stable. DBW-222 shows a low bi value (-0.1355) and high S2di (103.002), suggesting instability and potential variability in days to maturity across environments. CRD GEHNU1 (bi = 1.0138, S2di = 20.385) displays moderate stability but could be more influenced by environmental changes. PBW-677 shows stability in less favorable environments with a lower S2di (-1.3977) and a bi value of 1.4302, indicating some level of stability across different conditions.

4.5.3 Flag leaf area (cm2)

For flag leaf area, bi and S^2di help understand which genotypes maintain consistent leaf area regardless of environmental fluctuations. DBW-222 has a bi close to 1 and a moderate S2di (0.6932), indicating good stability. Genotypes like CRD GEHNU1 (bi = 1.0023, S2di -0.0439) show low S^2di and bi values near 1, suggesting stable flag leaf area across environments.

4.5.4 Plant height (cm)

Plant height across varying conditions. Genotypes like PBW-343 (bi 0.8004, S2di 0.6833) exhibit stable plant height. CRD GEHNU1 has a higher S^2di (19.7643), indicating some instability in height across environments. HD-3117 has a high bi (2.6401), suggesting responsiveness to favorable environments but potentially less stability with higher S^2di. Genotypes with bi close to 1 and low S^2di across parameters (like CRD GEHNU1 for flag leaf area and DBW-222 for plant height) are generally stable and can be considered reliable across environments. Higher bi values (e.g., BHU-31 for heading and HD-3117 for height) show adaptability to better conditions but may have more variability in less favorable environments.

4.5.5 Chlorophyll content

For chlorophyll content genotype HD-2967 (Mean 48.07, bi -0.16; S^2di 0.36 (slightly better in poor conditions). Genotype DBW-173 (Mean 41.46), bi 0.59 (average stability), S^2di 26.03 (low stability and poor environmental explanation). Genotype DH-3086X PBW ZN1 **(**Mean 54.57, bi 1.09 (responsive to favorable conditions). S^2di (29.52, (moderate stability). Genotype PBW-757X PBW-343 Mean (53.67) bi (2.01 (highly responsive to favorable conditions) and S^2di (-2.15) recorded high stability.

4.5.6 Number of productive tillers (NPT)

Results on number of productive tillers (NPT) indicated that, genotypes like DBW-187 (bi 2.02) and DH-3086X HD-3326 (bi 2.61) were more responsive to favorable conditions, while genotypes such as BHU-31 (bi -0.01) and PWB-725 (bi 0.13) were less responsive. S^2di (Deviation from Regression) lower S^2di values suggest higher stability as found in genotypes such as NORMAN (-0.03) and BHU-31 X PBW-343 (0.13) were considered as stable due to their low S^2di values.

4.5.7 Grain filling period

Results on grain filling period (GFP), the table provides statistical analysis for various genotypes with respect to their grain filling period, Genotype HD-2967 has mean (43.17 days), bi 0.38 (less responsive to environmental changes), S^2di 6.51 (moderate stability), genotype DBW-187 mean

(43.50 days), bi 0.12 (very stable across environments), S^2di 1.19 (high stability). Genotype BHU-25 mean (4.42 days), bi 2.09 (highly sensitive to environmental changes), S^2di -1.08. Genotype BHU-25 has mean (38.25 days), bi 2.30 (very sensitive to environmental changes), S^2di 17.45 (low stability). Genotype HD-3117 X PBW ZN1 has **m**ean 38.08 days, bi: -1.02 (negative value).

4.5.8 Number of spikelet per spike

Number of spikelet per spike (NS/S) observed that, genotype HD-3326 shows the highest variability (SD 3.64 indicating significant fluctuation in spikelet number, making it less stable genotype. Genotype like BHU-31 X PBW-343 (S^2di -0.29) and PBW-173X PBW ZN1 (S^2di -0.20) have low S^2di.

4.5.9 Grain weight per spike (g)

Grain weight per spike (GW/S), for grain weight per spike, the stable and high yielding genotypes found in HD-3117 X PBW-343 Mean (3.36), bi (0.54), S2di (-0.05). Stable but lower yielding found in genotype BHU-25mean (2.40), bi (1.58), S2di (-0.04) and high yielding genotypes BHU-25 X PBW-343 (mean 3.36, bi 0.54, S^2di -0.05), HD-3117 X HD-3326 (mean 3.52, bi 2.83, S^2di -0.04). Genotypes with high mean but variable performance was DBW-173X PBW ZN1 (Mean 3.55, bi 1.97, S^2di 0.05) and stable but lower yielding genotypes BHU-25 (mean 2.40, bi 1.58, S^2di -0.04).

4.5.10 1000 grain weight (g)

1000 grain weight for different genotypes of wheat, recorded that, variability and stability across different environments found in genotypes such as BHU-25 mean (36.63), bi (1.24), S2di (33.19). Genotype HD-3117 X HD-3326 mean (46.14), bi (0.20), S^2di -0.80.

4.5.11 Spike length (cm)

Results on spike length recorded that, genotypes BHU-25 (12.37), bi (-0.79), S2di (-0.11) was highly stable for spike length. However, genotype HD-3117 X HD-3326 mean (13.66), bi (2.44), S2di (-0.09), thus, HD-3117 X HD-3326 has higher mean spike length with moderate variability. Genotype PBW-757X PBW ZN1 has the mean (14.39), bi (2.46), and S^2di (0.84). Genotype DBW-222X HD-3326 has the mean (13.46), bi (0.12), S^2di (0.13).

4.5.12 Number of grains per spike

For number of grains per spike (NG/S), genotypes like DBW-173 and DBW-222X PBW-343 exhibit low variability (moderately stable). While genotype genotypes DBW-173 mean (38.70), bi (-0.10), S2di (0.14). Genotype PBW-822XXPBW-343 recorded mean (48.14), bi (3.42), S^2di (-1.07). Genotype BHU-31 X PBW-343 mean (46.11), bi (4.26), S2di (-0.80). Genotype PWB-725 X PBW-343 mean (44.46), bi (5.41) S^2di (8.17).

4.5.13 Harvest index (%)

Harvest index (HI), the results revealed that, mean harvest index values range from 44.23 (CSW-18) to 59.46 (CSW-18 X PBWZN1), indicating variability in the harvest index across different genotypes. While based on deviation from regression (S^2di) genotype DH-3086X PBW-343 (S^2di -1.29) and PBW-822X PBW ZN1 (S^2di -1.33) show good predictability (stable), while HD-3721 X HD-3326 (S^2di 39.02) and PWB-725 X PBW ZN1 (S^2di 42.57) exhibit high variability (not stable).

4.5.14 Biological yield (g)

Biological yield (BY), the results revealed that high yielding and stability observed in genotypes DBW-173X HD-3326 (Mean 65.61, bi 1.36, S^2di 1.68). Genotypes with high variability were CRDGEHNU1 (Mean 57.29, bi 2.49, S^2di 93.12); genotype PBW-343 (Mean 55.79, bi 1.63, S^2di 94.81) and PWB-725 X PBW ZN1 (Mean 63.38, bi 0.10, S^2di 0.84). Highest yield recorded on biological yield in genotypes PBW-822X PBW ZN1 (53.00) and lowest Yield DBW-173 (32.63) and CSW-18 (bi 8.85), PBW-550X PBW ZN1 bi 8.60.

4.5.15 Protein content (%)

Based on protein content, genotype HD-3117 (mean protein content 13.44%) indicating high variability, bi (6.37) showing high responsiveness to environmental changes S^2di (2.16) indicating instability. Genotype HD-3117 X PBW-343 (mean protein content (11.87%) indicating low variability, bi (-2.61) showing below-average responsiveness to environmental changes, S^2di (-0.04) indicating stability. Genotype DBW-173X HD-3326 (mean protein content (12.53%, bi (12.25) showing very high responsiveness to environmental changes and S^2di (0.60) indicating instability.

4.5.16 Grain yield per plant (g)

Data on grain yield per plant for different genotypes across different environments revealed that, ranging from approximately 32.63 to 53.00. Highest yield was recorded in DBW-173; PBW ZN1 and PBW-822X PBW ZN1 and lowest yield was recorded in DBW-173 (32.63). Most stable with moderate yield were HD-3326, DBW-173, BHU-25, BHU-25X HD-3326 (S^2di: 1.81), implying consistent performance across environments, while the least stable was recorded in BHU-25 X HD-3326 S^2di 20.80.

Table 4.5.1: Analysis of variance on stability analysis across three environments for sixteen characters of sixty seven wheat genotypes

Characters	Genotype (G)	Environment (E)	Replication (R)	EXR	GXE	Error variance
d.f.	**66**	**2**	**2**	**4**	**132**	**534**
Days-50% heading	66.92*	77.57**	0.92	1.01	0.92	7.57**
Chlorophyll content	72.03*	31.47*	0.32	1.09	0.32	1.47
Grain filling period	14.37	19.01	0.86	0.21	0.86	0.49
Days to maturity	83.86**	42.71**	0.16	1.27	0.16	2.78
Flag leaf area (cm2)	197.42**	11.38	0.04	2.99*	0.04	1.38
Plant height (cm)	38.66	58.69**	0.05	0.58	0.05	8.69**
No. of spikelet/spike	3.35	1.93	0.04	0.05	0.04	1.93
Spike length (cm)	1.17	0.62	0.33	0.01	0.33	0.62
Protein content (%)	0.49	0.53	3.72*	0.02	3.72*	0.53
No. of productive tiller	6.01	1.46	0.28	0.09	0.28	1.46
No. of grains/spike	74.85*	13.64	0.63	1.13	0.63	3.64
Grain weight/spike (g)	0.72	0.18	0.29	0.01	0.29	0.18
1000-grain weight (g)	51.02*	5.99	0.89	0.77	1.89	5.99*
Biological yield (g)	67.87*	35.04**	0.03	1.02	0.03	5.04*
Harvest index (%)	64.84*	16.14*	0.29	0.98	0.29	6.14*
Grain yield/plant (g)	78.31*	11.81*	0.21	1.18	0.21	1.81

“*” and “” significant at 5% and 1% probability levels respectively**

Table 4.5.2: Stability analysis across three locations in sixty seven wheat genotypes during 2022-2023 and 2023-2024 *Rabi* seasons

Genotypes Plant height (cm)		Days to 50% heading			Days to maturity			Flag leaf area (cm^2)					
		*		*	*		*	*		*	*		*
SN	Genotypes	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
1	BHU-25 (L1)	85.00	2.51	3.12	131.00	0.38	-3.12	45.43	1.46	-2.95	93.66	-0.93	2.52
2	WB-02 (L2)	87.67	1.32	-2.21	139.50	1.00	8.31	24.69	0.81	-2.89	84.66	0.05	-4.01
3	BHU-31 (L3)	80.79	3.25	12.23	128.92	-1.13	45.86	32.21	1.11	-3.06	85.17	1.64	19.89
4	HD-3721 (L4)	83.04	2.99	0.54	138.33	0.96	2.84	24.90	1.11	-3.10	95.77	1.18	14.71
5	PWB-725 (L5)	84.00	0.81	3.75	134.75	-0.23	-3.25	25.78	1.10	-3.06	90.36	0.77	0.28
6	CRD GEHNU1 (L6)	88.79	-1.67	-12.87	136.00	0.17	22.74	49.78	1.10	-3.06	86.36	0.86	4.60
7	PBW-550 (L7)	73.50	0.74	95.72	135.58	-0.13	-3.32	28.50	1.11	-3.10	88.75	1.39	18.74
8	PBW-677 (L8)	83.92	2.75	4.87	139.58	0.76	-2.88	29.11	1.11	-3.06	88.52	0.15	-4.09
9	PBW-822 (L9)	81.21	3.62	-11.48	138.33	0.91	-3.03	26.63	1.11	-2.94	83.69	0.68	-0.58
10	HD-3117 (L10)	87.42	1.17	47.10	137.25	1.74	11.39	27.95	1.12	-2.74	89.59	2.48	44.18
11	DBW-173 (L11)	89.67	1.90	-10.50	127.83	1.41	23.89	32.68	1.10	-3.06	95.75	1.66	22.15
12	DH-3086 (L12)	75.63	0.18	-5.70	139.00	2.17	-0.52	26.58	1.10	-3.06	88.96	1.41	0.41
13	DBW-222 (L13)	71.00	-0.18	4.96	131.17	-0.86	88.61	47.53	1.09	-2.42	95.06	0.66	0.73
14	CSW-18 (L14)	87.21	2.25	-4.56	140.50	0.98	-0.10	31.66	1.10	-2.93	95.24	0.48	19.39
15	PBW-757 (L15)	73.96	0.10	13.89	128.08	-1.49	7.54	39.40	1.11	-3.10	89.26	1.28	15.68
16	PBW ZN1 (Tester 1)	78.25	0.95	24.79	123.08	0.30	1.81	41.41	1.11	-3.06	92.87	1.00	4.92
17	PBW-343 (Tester 2)	79.83	1.13	-0.27	127.67	0.72	17.48	33.51	1.11	-3.06	94.75	0.74	2.52
18	HD-3326 (Tester 3)	70.29	-0.13	-12.62	137.33	1.79	-2.47	23.43	0.92	-2.54	88.42	1.84	-3.82
19	HD-2967 (Check 1)	91.29	1.35	-4.97	141.00	1.02	0.87	40.11	1.04	-2.17	92.83	0.92	5.03
20	DBW-187 (Check 2)	87.25	0.31	0.42	142.83	1.34	-1.49	55.45	2.57	-0.21	86.96	0.89	6.85
21	NORMAN (Check 3)	79.63	2.30	-10.30	144.17	1.97	4.04	44.85	0.84	-1.37	87.50	0.22	-2.88

22	BORLAUG-100 (Check 4)	74.88	-3.01	7.97	142.42	2.03	1.34	29.20	0.70	0.71	88.78	1.09	-2.52
23	BHU-25 X PBW ZN1	90.96	0.25	-8.75	134.58	-0.36	1.44	53.37	2.16	-1.25	95.10	0.83	21.86
24	BHU-25 X PBW-343	91.04	0.21	54.66	142.46	1.31	-3.22	45.06	0.98	-3.03	87.53	0.46	68.42
25	BHU-25 X HD-3326	83.08	1.92	-11.75	141.54	1.02	6.47	34.95	1.00	-2.94	96.97	0.36	-1.88
26	DBW-173X PBW ZN1	80.71	2.15	3.59	128.08	-1.49	7.54	37.00	0.11	-2.93	91.54	1.23	11.75
27	DBW-173X PBW-343	84.46	1.65	3.68	134.08	-0.28	-2.48	43.04	0.92	-2.94	103.53	0.66	16.66
28	DBW-173X HD-3326	87.71	2.63	-4.13	142.13	4.10	22.67	43.35	1.45	-2.95	93.30	2.30	25.98
29	DH-3086X PBW ZN1	84.54	1.89	3.85	133.00	0.03	-3.75	35.85	0.02	-1.72	92.15	1.77	5.70
30	DH-3086X PBW-343	82.25	1.07	-5.24	127.00	0.28	0.98	44.22	1.62	-3.16	87.25	-0.15	-4.26
31	DH-3086X HD-3326	87.79	1.36	31.06	137.00	0.15	-3.66	45.11	0.69	-2.54	99.57	-0.26	12.28
32	DBW-222X PBW ZN1	89.33	-0.22	11.83	139.08	1.22	-3.52	40.41	-0.19	-3.06	96.65	2.00	3.04
33	DBW-222X PBW-343	86.96	1.61	8.62	126.33	0.09	-3.23	45.45	0.45	-2.05	84.61	0.64	84.47
34	DBW-222X HD-3326	91.88	-0.42	-12.96	138.50	1.42	-2.77	40.42	-0.40	-0.33	87.50	0.06	5.31
35	CSW-18XPBW ZN1	86.96	0.27	-2.85	138.17	1.31	-3.73	48.91	1.20	-2.25	91.72	0.44	41.37
36	CSW-18XPBW-343	93.54	0.14	1.47	135.33	2.80	6.00	55.52	3.05	3.55	97.68	1.40	7.29
37	CSW-18XHD-3326	86.25	2.49	48.17	128.50	-0.66	50.49	51.85	1.86	-2.47	89.22	0.34	65.29
38	PBW-757X PBW ZN1	90.17	-0.73	3.34	140.58	1.51	-3.32	55.62	0.34	-0.16	93.62	1.36	10.63
39	PBW-757X PBW-343	88.88	1.17	1.09	136.33	2.98	-3.54	44.83	0.63	-3.15	94.20	0.94	3.57
40	PBW-757X HD-3326	82.83	0.72	-6.53	130.75	-0.75	80.23	40.19	1.16	17.58	91.82	0.41	1.91
41	BHU-31 X PBW ZN1	84.79	0.43	-1.71	146.08	2.13	8.45	37.10	-0.01	-1.09	87.30	-0.17	1.91
42	BHU-31 X PBW-343	76.04	0.38	-4.48	142.17	1.53	-3.66	44.88	1.45	-3.06	88.87	1.20	-0.23
43	BHU-31 X HD-3326	83.75	0.58	-11.50	144.58	2.21	11.93	42.67	2.34	-0.83	90.80	1.01	4.84
44	WB-02 X PBW ZN1	77.54	1.51	-5.88	129.50	-0.42	156.67	35.00	0.77	-2.54	93.40	1.41	12.05
45	WB-02 X PBW-343	70.58	-0.11	-5.45	137.42	0.96	0.62	44.16	2.77	1.57	81.15	-0.15	7.02
46	WB-02 X HD-3326	87.46	0.30	-10.50	139.75	2.49	6.92	39.91	0.27	-3.21	92.05	0.17	1.27

47	BHU-31 X PBW ZN1	88.38	2.19	2.20	143.58	1.51	-3.32	29.83	0.41	-1.10	94.00	0.37	-3.03
48	BHU-31 X PBW-343	81.83	1.99	7.58	144.50	1.56	71.03	35.07	0.61	-2.61	91.73	1.11	11.34
49	BHU-31 X HD-3326	76.25	0.88	3.23	136.67	0.84	4.27	25.00	-1.08	2.32	78.90	0.18	15.71
50	HD-3721 X PBW ZN1	84.75	0.57	-12.03	132.13	-0.22	282.57	45.70	0.83	-3.10	89.32	1.82	14.23
51	HD-3721 X PBW-343	84.75	0.02	-8.23	142.08	2.52	1.43	38.84	1.63	6.80	94.28	1.96	42.62
52	HD-3721 X HD-3326	77.08	-3.56	2.80	147.67	2.67	8.18	40.79	0.07	-3.16	91.54	1.81	14.33
53	PWB-725 X PBW ZN1	80.25	1.71	-11.18	130.50	0.82	-3.32	44.31	1.86	2.27	95.01	2.53	-1.45
54	PWB-725 X PBW-343	87.08	-0.55	25.33	145.42	2.41	5.58	44.70	2.23	2.53	81.54	0.65	10.63
55	PWB-725 X HD-3326	82.29	0.04	23.75	145.17	1.60	52.55	38.38	1.03	-3.11	92.43	1.44	-0.31
56	CRDGEHNU1 X PBWZN1	86.00	-0.60	58.70	143.88	1.75	49.42	48.04	1.29	-2.01	91.64	1.93	-3.10
57	CRDGEHNU1 X PBW343	84.50	2.19	8.60	123.33	1.02	14.59	32.64	0.30	-0.77	90.64	2.42	-1.18
58	CRDGEHNU1 X HD-3326	83.13	2.78	7.21	142.92	1.07	93.09	29.60	0.35	-2.33	92.79	2.41	2.82
59	PBW-550X PBW ZN1	85.33	2.75	-11.26	143.83	1.16	107.74	38.32	-0.09	-3.09	89.20	1.71	-0.78
60	PBW-550X PBW-343	72.58	1.30	-7.53	122.33	1.24	19.70	46.88	1.19	-2.90	83.24	0.94	4.19
61	PBW-550X HD-3326	88.92	0.95	-8.17	140.92	0.97	4.50	41.57	1.19	-2.89	84.96	0.73	8.96
62	PBW-677XPBW ZN1	84.50	1.51	37.85	130.29	0.73	-3.68	38.73	-0.10	-1.29	91.70	1.49	-2.12
63	PBW-677XPBW-343	89.46	1.29	-4.77	131.58	1.34	0.93	46.82	2.14	-1.91	93.24	1.82	-2.91
64	PBW-677XPBW-343	84.58	2.91	-10.46	138.83	1.68	5.74	46.50	0.29	-1.64	85.01	0.90	6.63
65	PBW-822X PBW ZN1	84.71	1.83	-5.22	131.92	0.25	0.23	41.17	0.63	-2.62	84.07	0.70	7.47
66	PBW-822X PBW-343	88.17	0.05	10.06	125.42	1.53	-3.26	49.66	2.02	5.68	91.24	0.77	-3.77
67	PBW-822X HD-3326	89.08	0.88	-3.53	142.42	1.19	6.45	35.21	0.62	-3.07	91.53	0.63	24.72
	Grand Mean:	86.97			131.00	0.38	-3.12	41.60			90.70		
	SE±	0.98			139.50	1.00	8.31	0.51			0.81		
	C.D.1%:	2.60			2.10			1.36			2.15		

Table 4.5.2: contd.

SN	Genotypes	Chlorophyll content			Number of productive tiller			Grain filling period			Number of spikelet per spike		
		*		*	*		*	*		*	*		*
SN	Genotypes	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	BHU-25 (L1)	42.32	0.54	22.25	4.17	0.60	0.36	34.42	2.10	-1.08	22.57	3.70	-0.13
2	WB-02 (L2)	44.22	0.48	6.13	5.58	-0.36	-0.05	36.50	1.48	0.56	22.24	3.65	-0.01
3	BHU-31 (L3)	48.23	0.44	8.19	5.21	-0.02	0.52	37.92	2.24	17.11	22.90	2.87	-0.15
4	HD-3721 (L4)	40.87	0.72	33.78	4.50	0.49	-0.12	37.83	2.33	14.73	22.43	4.74	-0.21
5	PWB-725 (L5)	45.63	0.44	12.92	4.44	0.13	-0.03	35.00	1.90	-1.64	23.01	2.18	0.13
6	CRD GEHNU1 (L6)	49.83	1.79	-2.39	5.55	-0.13	0.20	41.17	-0.51	41.57	23.57	0.95	0.07
7	PBW-550 (L7)	44.50	0.67	34.49	4.77	-0.69	0.20	37.58	2.38	14.93	23.64	1.51	-0.13
8	PBW-677 (L8)	47.47	0.39	0.61	5.08	0.11	0.36	38.33	1.23	67.68	23.15	2.93	0.35
9	PBW-822 (L9)	40.24	-0.03	-1.66	4.62	0.44	1.05	41.75	1.58	11.37	22.75	0.55	4.74
10	HD-3117 (L10)	39.71	-0.24	-2.54	4.63	0.77	0.29	38.25	2.31	17.46	22.22	4.84	-0.26
11	DBW-173 (L11)	41.46	0.59	26.03	4.28	0.57	0.41	34.00	0.23	0.97	23.93	1.61	0.13
12	DH-3086 (L12)	41.19	2.06	36.77	5.02	2.35	-0.11	36.79	0.61	38.38	23.87	1.77	0.10
13	DBW-222 (L13)	51.30	0.82	2.40	5.71	1.16	1.01	40.29	1.85	16.62	23.49	2.43	-0.19
14	CSW-18 (L14)	46.32	0.31	-3.28	5.29	1.87	0.35	44.25	1.50	1.50	22.73	4.46	0.50
15	PBW-757 (L15)	48.59	0.22	-3.19	5.18	-0.20	0.33	35.50	0.82	40.59	22.02	3.28	0.09
16	PBW ZN1 (Tester 1)	46.84	0.55	23.56	4.89	0.58	0.10	36.25	2.73	19.62	22.71	2.55	-0.13
17	PBW-343 (Tester 2)	52.01	0.06	14.23	5.56	0.25	0.45	43.67	0.17	2.50	22.91	3.45	0.35
18	HD-3326 (Tester 3)	44.50	1.73	76.50	6.08	0.03	0.31	38.92	2.24	20.17	22.67	6.63	-0.13
19	HD-2967 (Check 1)	48.07	-0.17	0.37	4.49	1.12	0.83	43.17	0.39	6.52	23.65	0.87	0.15
20	DBW-187 (Check 2)	48.69	0.92	10.53	5.04	2.02	0.37	43.50	0.13	1.19	23.17	3.35	0.47
21	NORMAN (Check 3)	43.11	0.18	2.36	4.99	-0.24	-0.04	36.29	0.83	52.21	23.23	3.01	-0.10
22	BORLAUG-100 (Check 4)	46.61	0.21	1.59	6.60	0.85	0.39	42.17	0.38	1.53	23.51	3.23	0.04

23	BHU-25 X PBW ZN1	51.10	0.54	-1.75	8.27	1.65	0.84	38.08	-1.03	-2.38	25.18	1.37	-0.23
24	BHU-25 X PBW-343	54.90	0.66	3.49	7.97	1.27	-0.03	39.50	-0.47	18.71	24.42	0.24	-0.28
25	BHU-25 X HD-3326	54.37	2.46	15.93	7.87	1.03	0.85	40.88	1.66	13.11	24.28	-0.70	0.00
26	DBW-173X PBW ZN1	51.70	2.24	1.83	7.59	1.61	0.23	35.67	2.13	-1.96	25.27	0.42	-0.30
27	DBW-173X PBW-343	53.14	2.91	22.53	9.06	1.07	0.63	35.17	2.03	-2.09	24.61	-2.85	-0.25
28	DBW-173X HD-3326	53.86	1.27	-1.97	8.16	1.07	0.18	43.33	1.70	13.17	24.76	0.96	-0.17
29	DH-3086X PBW ZN1	54.57	1.09	29.52	7.10	2.09	1.60	38.25	1.32	-1.95	24.75	-1.77	-0.06
30	DH-3086X PBW-343	57.15	0.88	-0.30	7.59	-0.20	3.64	38.25	1.25	21.29	25.17	-0.57	-0.30
31	DH-3086X HD-3326	54.21	1.13	9.74	7.75	1.58	0.17	38.79	0.77	1.14	25.39	0.01	-0.10
32	DBW-222X PBW ZN1	58.05	0.13	-1.08	9.49	0.97	-0.09	34.88	0.68	0.20	25.53	1.17	-0.22
33	DBW-222X PBW-343	53.94	-0.19	1.26	8.57	0.67	0.85	40.08	-0.29	85.04	25.94	0.95	-0.20
34	DBW-222X HD-3326	54.44	-0.09	3.52	7.22	1.20	-0.07	37.63	-1.05	1.86	24.96	-0.26	0.02
35	CSW-18XPBW ZN1	54.52	1.76	1.24	8.11	0.90	0.36	38.79	0.88	4.74	24.59	-1.70	-0.10
36	CSW-18XPBW-343	57.16	0.90	5.27	8.33	1.27	2.06	37.88	-0.85	27.80	24.92	0.25	-0.28
37	CSW-18XHD-3326	56.14	0.65	0.66	7.89	1.42	1.48	39.42	1.55	-1.47	25.58	0.91	-0.02
38	PBW-757X PBW ZN1	56.41	0.83	26.39	8.44	0.73	1.59	38.21	-0.79	19.30	25.82	1.73	-0.19
39	PBW-757X PBW-343	53.67	2.01	-2.15	7.67	-0.27	1.25	37.71	1.03	-1.61	25.34	0.16	-0.21
40	PBW-757X HD-3326	51.67	1.50	2.50	7.67	0.57	0.08	38.63	0.11	2.71	25.43	0.71	-0.26
41	BHU-31 X PBW ZN1	51.22	0.38	12.73	6.79	1.49	0.05	45.79	0.94	0.24	24.85	1.38	-0.28
42	BHU-31 X PBW-343	49.30	1.00	0.47	6.35	0.96	0.13	41.79	-0.33	48.49	24.82	1.49	-0.30
43	BHU-31 X HD-3326	50.24	1.38	-1.56	6.65	1.77	0.11	44.42	1.34	-1.70	24.55	0.53	-0.15
44	WB-02 X PBW ZN1	52.98	1.50	-3.22	7.83	0.63	1.14	40.92	1.84	7.71	24.65	-0.62	0.08
45	WB-02 X PBW-343	54.91	1.40	-1.25	7.41	2.01	0.61	40.08	1.64	20.16	24.84	-0.12	-0.27
46	WB-02 X HD-3326	49.86	0.93	2.58	6.71	2.62	1.53	45.83	1.00	-1.03	24.41	-0.47	-0.21
47	BHU-31 X PBW ZN1	50.81	2.42	-0.86	7.42	0.77	0.11	42.08	2.10	0.29	24.97	-1.02	-0.12

48	BHU-31 X PBW-343	51.85	2.70	4.03	7.39	2.06	0.27	40.17	1.83	-1.77	24.37	-0.26	0.26
49	BHU-31 X HD-3326	55.44	1.51	-0.86	7.54	2.70	-0.07	38.25	1.44	51.86	23.96	-0.78	-0.18
50	HD-3721 X PBW ZN1	53.11	1.79	23.67	7.96	2.45	-0.06	45.67	0.95	2.32	25.28	1.95	-0.21
51	HD-3721 X PBW-343	53.53	1.58	-3.31	6.84	1.61	0.02	42.08	-0.08	83.89	24.27	-1.42	-0.28
52	HD-3721 X HD-3326	53.93	1.37	26.93	8.63	0.94	0.28	41.08	1.88	4.00	24.74	0.65	-0.24
53	PWB-725 X PBW ZN1	52.40	1.30	22.64	7.55	1.86	0.07	43.33	0.30	3.61	24.07	-1.21	-0.28
54	PWB-725 X PBW-343	53.93	-0.28	-1.13	7.61	2.05	0.42	43.08	0.21	-0.89	25.02	0.84	-0.29
55	PWB-725 X HD-3326	53.19	2.71	13.31	8.34	1.01	-0.10	42.92	1.64	1.82	24.24	0.59	0.12
56	CRDGEHNU1 X PBWZN1	57.20	-0.10	18.59	8.43	2.01	0.82	38.71	-0.48	18.91	24.61	-0.82	-0.20
57	CRDGEHNU1 X PBW343	57.70	0.17	58.27	8.19	1.28	0.02	34.33	1.59	11.87	24.67	0.86	-0.20
58	CRDGEHNU1 X HD-3326	54.91	1.14	14.74	7.38	0.74	0.21	41.08	0.99	42.87	24.50	-1.09	-0.27
59	PBW-550X PBW ZN1	55.73	1.28	-0.58	7.93	-0.55	-0.03	38.92	1.60	23.24	25.00	-0.22	-0.30
60	PBW-550X PBW-343	54.38	0.72	4.89	8.48	0.70	1.07	38.42	-0.95	-0.68	24.47	-0.62	-0.22
61	PBW-550X HD-3326	57.36	0.57	-3.30	8.38	0.73	0.86	40.67	0.79	1.06	25.08	1.54	-0.03
62	PBW-677XPBW ZN1	51.42	2.91	14.07	8.00	1.49	0.88	34.54	1.63	0.38	24.35	-1.69	-0.28
63	PBW-677XPBW-343	54.91	0.21	-0.05	8.35	0.84	0.19	30.92	1.28	8.48	25.92	0.54	0.36
64	PBW-677XPBW-343	54.03	1.79	29.94	8.07	2.29	0.88	38.79	1.29	42.94	24.77	-1.60	0.22
65	PBW-822X PBW ZN1	57.74	1.51	22.67	9.08	0.39	1.12	40.83	1.69	20.84	25.08	1.17	0.27
66	PBW-822X PBW-343	57.47	0.61	23.48	8.31	0.75	0.39	35.83	0.21	4.01	24.75	0.23	-0.19
67	PBW-822X HD-3326	54.61	1.15	19.69	8.33	1.16	-0.15	39.33	1.14	-0.66	25.58	1.56	1.79
	Grand Mean:	45.99			6.25			40.53			24.20		
	SE±	0.80			0.07			0.96			0.08		
	C.D.1%:	2.06			1.09			2.46			0.21		

Table 4.5.2: contd.

SN	Genotypes	Grain weight per spike (g)			1000 grain weight (g)			Spike length (cm)			Number of grain per spike		
		*		*	*		*	*		*	*		*
SN	**Genotypes**	**Mean**	**bi**	**S2di**	**Mean**	**bi**	**S2di**	**Mean**	**bi**	**S2di**	**Mean**	**bi**	**S2di**
1	BHU-25 (L1)	2.41	1.58	-0.04	38.03	1.00	0.33	12.47	4.08	0.27	36.25	-1.02	10.46
2	WB-02 (L2)	2.39	1.72	-0.04	36.54	1.07	0.79	12.36	1.94	0.56	36.24	-1.27	0.83
3	BHU-31 (L3)	2.52	2.14	-0.02	37.28	1.76	3.53	12.72	-0.35	1.02	34.46	0.23	0.28
4	HD-3721 (L4)	2.35	-0.38	-0.02	37.43	1.69	15.27	11.81	0.82	-0.10	33.17	-0.49	4.33
5	PWB-725 (L5)	2.40	1.83	-0.04	36.35	1.89	40.83	11.71	-0.76	0.21	35.12	-0.32	1.05
6	CRD GEHNU1 (L6)	2.86	-1.81	0.29	39.88	2.76	-0.19	13.29	-1.63	0.33	35.72	1.43	1.94
7	PBW-550 (L7)	2.42	1.48	0.00	38.93	1.24	2.26	12.36	-1.42	0.63	34.95	1.95	1.96
8	PBW-677 (L8)	2.49	-1.03	-0.04	37.46	2.08	2.61	12.25	2.97	0.22	33.66	0.53	0.31
9	PBW-822 (L9)	2.43	1.34	0.06	39.83	2.31	2.02	12.31	-1.98	-0.15	36.63	0.72	14.50
10	HD-3117 (L10)	2.42	2.40	0.04	36.64	1.25	33.20	12.38	-0.79	-0.11	35.24	-0.41	31.99
11	DBW-173 (L11)	2.47	0.20	0.21	37.50	1.53	-0.46	12.17	-1.05	0.00	38.70	-0.10	0.14
12	DH-3086 (L12)	2.83	0.14	0.08	39.02	2.04	0.51	12.13	1.68	0.16	38.11	0.45	-0.31
13	DBW-222 (L13)	2.60	-0.70	0.02	39.05	2.49	-0.62	12.44	3.48	0.36	37.24	0.40	10.34
14	CSW-18 (L14)	2.37	-1.04	-0.04	38.22	3.74	-0.46	12.29	0.43	-0.01	36.51	1.10	4.76
15	PBW-757 (L15)	2.35	-0.79	0.03	40.16	1.55	1.14	12.33	0.82	-0.06	35.54	1.57	2.19
16	PBW ZN1 (Tester 1)	2.58	-0.60	0.05	37.68	1.59	-0.60	12.53	-0.34	0.45	37.72	-0.65	2.27
17	PBW-343 (Tester 2)	2.32	0.69	0.06	39.84	1.88	-0.76	11.76	0.70	0.32	37.99	0.32	-1.37
18	HD-3326 (Tester 3)	2.70	-1.00	-0.04	37.85	2.56	-0.79	12.56	1.54	0.58	36.29	-1.76	0.23
19	HD-2967 (Check 1)	2.66	2.10	-0.01	38.82	0.61	-0.74	12.39	-3.11	0.06	39.01	-0.15	0.02
20	DBW-187 (Check 2)	2.60	1.43	-0.02	40.94	1.07	-0.88	12.54	-1.50	0.04	34.87	1.97	3.95
21	NORMAN (Check 3)	2.68	1.65	0.06	39.09	-0.39	0.67	12.95	-0.96	0.30	37.55	-1.18	0.69

22	BORLAUG-100 (Check 4)	2.87	-0.46	-0.04	40.99	0.70	-0.53	12.27	-0.35	0.36	37.28	-0.79	5.74
23	BHU-25 X PBW ZN1	3.39	2.01	0.00	47.80	0.77	0.99	13.66	1.47	-0.12	47.32	1.49	5.84
24	BHU-25 X PBW-343	3.37	0.55	-0.05	47.09	0.70	-0.03	13.58	2.25	-0.10	46.70	2.36	20.35
25	BHU-25 X HD-3326	3.53	2.84	-0.04	46.15	0.20	-0.81	13.67	2.44	-0.10	45.53	-0.72	12.78
26	DBW-173X PBW ZN1	3.56	1.98	0.05	47.45	-0.08	-0.49	13.63	2.63	-0.11	43.30	0.53	6.05
27	DBW-173X PBW-343	3.63	-0.68	0.04	46.32	0.65	3.46	14.15	3.06	0.36	45.36	-0.52	10.66
28	DBW-173X HD-3326	3.32	0.75	0.05	46.30	0.50	-0.71	14.28	1.24	0.14	47.23	0.45	14.58
29	DH-3086X PBW ZN1	3.43	2.44	-0.04	45.28	0.02	1.73	13.91	2.99	0.34	44.01	0.24	4.64
30	DH-3086X PBW-343	3.56	1.41	-0.04	46.92	0.69	0.67	13.87	5.70	0.07	47.35	-0.70	2.54
31	DH-3086X HD-3326	3.61	1.72	0.00	45.76	0.36	1.87	13.75	2.56	0.12	47.13	1.99	1.56
32	DBW-222X PBW ZN1	3.87	0.76	0.12	46.21	0.61	-0.37	14.05	3.01	-0.14	47.80	2.72	2.88
33	DBW-222X PBW-343	3.87	2.12	-0.01	46.45	0.68	-0.61	13.68	0.87	-0.14	48.15	3.42	-1.07
34	DBW-222X HD-3326	3.51	2.50	-0.05	46.96	0.72	3.89	13.47	0.13	-0.13	47.15	4.08	7.90
35	CSW-18XPBW ZN1	3.73	-0.29	-0.03	46.81	0.68	-0.78	13.63	1.02	-0.04	45.51	1.02	7.39
36	CSW-18XPBW-343	3.52	0.45	0.07	46.88	0.54	0.87	14.21	-1.74	-0.02	49.47	2.11	0.95
37	CSW-18XHD-3326	3.38	1.19	0.10	46.50	1.65	0.43	13.90	3.15	-0.03	47.61	3.52	2.86
38	PBW-757X PBW ZN1	3.50	0.04	0.08	46.69	0.62	0.72	14.40	2.46	0.85	46.84	3.06	8.33
39	PBW-757X PBW-343	3.55	0.08	0.22	46.94	1.42	0.06	14.08	1.01	0.22	45.03	0.06	-1.29
40	PBW-757X HD-3326	3.60	-0.62	0.00	46.88	0.88	-0.76	13.57	0.89	-0.06	44.25	2.06	0.71
41	BHU-31 X PBW ZN1	3.38	1.72	-0.01	46.79	0.99	-0.71	13.78	0.47	0.17	46.00	2.74	-0.85
42	BHU-31 X PBW-343	3.71	1.01	0.26	46.94	0.94	-0.17	13.85	-0.36	0.31	46.12	4.26	-0.81
43	BHU-31 X HD-3326	3.57	2.21	-0.03	46.48	0.99	2.25	13.08	-0.87	0.23	46.68	3.56	1.21
44	WB-02 X PBW ZN1	3.61	0.46	0.08	46.16	1.30	0.82	13.41	0.08	-0.13	47.92	3.14	-1.61
45	WB-02 X PBW-343	3.50	0.31	0.03	46.36	0.43	4.32	13.52	-2.95	1.00	47.52	4.15	2.11
46	WB-02 X HD-3326	3.68	1.38	0.15	46.80	0.24	-0.54	13.89	-0.76	-0.02	47.48	4.04	2.62

47	BHU-31 X PBW ZN1	3.70	1.62	0.11	46.38	0.84	1.02	14.16	2.42	-0.07	45.06	-2.16	-1.34
48	BHU-31 X PBW-343	3.67	2.34	0.05	46.63	0.37	0.80	13.61	1.74	0.13	45.22	-1.52	2.95
49	BHU-31 X HD-3326	3.39	2.01	0.09	46.30	1.41	-0.93	14.26	2.97	0.07	45.98	2.26	2.40
50	HD-3721 X PBW ZN1	3.70	0.99	0.05	45.65	0.65	-0.62	13.94	4.05	0.58	44.56	1.22	8.62
51	HD-3721 X PBW-343	3.56	0.60	0.15	46.52	0.43	-0.16	13.90	0.32	0.28	46.95	0.89	11.22
52	HD-3721 X HD-3326	3.38	0.97	0.03	45.87	0.38	-0.72	14.12	-0.93	0.47	44.91	1.88	12.55
53	PWB-725 X PBW ZN1	3.69	1.44	-0.04	46.96	0.70	1.62	12.96	1.22	0.51	47.23	1.90	1.06
54	PWB-725 X PBW-343	3.33	1.12	0.01	45.90	1.29	0.99	13.62	1.62	-0.05	44.46	5.41	8.18
55	PWB-725 X HD-3326	3.52	1.90	0.06	46.16	-0.09	-0.52	13.68	0.39	0.73	45.45	-1.98	9.01
56	CRDGEHNU1 X PBWZN1	3.45	2.00	0.00	47.99	-0.86	0.04	14.58	-0.81	0.59	47.11	3.77	-1.65
57	CRDGEHNU1 X PBW343	3.61	0.72	0.09	46.98	1.27	0.15	14.47	-1.33	1.04	45.37	-1.70	7.28
58	CRDGEHNU1 X HD-3326	3.50	2.49	-0.03	46.79	0.96	-0.76	13.49	2.12	0.10	42.61	-1.17	-0.50
59	PBW-550X PBW ZN1	3.50	2.17	-0.03	45.62	0.17	-0.55	14.21	2.80	0.19	44.43	0.09	3.43
60	PBW-550X PBW-343	3.56	1.87	0.02	47.08	1.52	-0.57	14.15	2.10	-0.11	45.89	2.12	2.58
61	PBW-550X HD-3326	3.60	1.92	0.02	46.53	0.80	0.60	14.29	0.82	-0.08	45.13	2.32	0.64
62	PBW-677XPBW ZN1	3.36	2.45	-0.04	46.47	0.63	-0.30	13.19	-0.21	0.42	47.85	0.51	5.29
63	PBW-677XPBW-343	3.41	0.86	-0.04	47.08	0.88	-0.64	14.21	1.55	-0.11	43.77	-1.21	1.16
64	PBW-677XPBW-343	3.42	1.17	-0.01	46.25	0.63	-0.23	13.85	3.19	0.08	44.87	0.57	7.40
65	PBW-822X PBW ZN1	3.68	-0.62	-0.02	44.12	1.08	9.60	14.25	5.71	0.51	43.01	-0.49	-0.51
66	PBW-822X PBW-343	3.67	0.96	-0.04	47.15	0.17	-0.84	14.46	-1.19	0.04	45.48	4.13	0.16
67	PBW-822X HD-3326	3.64	0.81	-0.01	46.55	0.86	0.21	13.85	3.52	0.03	44.46	-1.43	13.26
	Grand Mean:	3.15			44.12			13.39			42.08		
	SE±	0.09			0.59			0.07			0.49		
	C.D.1%:	0.23			1.55			0.18			1.27		

Table 4.5.2: contd.

SN	Genotypes	Grain yield per plant (g)			Protein content (%)			Biological yield (g)			Harvest index (%)		
		*		*	*		*	*		*	*		*
SN	**Genotypes**	**Mean**	**bi**	**S2di**	Mean	bi	S2di	**Mean**	**bi**	**S2di**	**Mean**	**bi**	**S2di**
1	BHU-25 (L1)	11.94	-8.67	-0.03	51.07	0.87	23.67	47.01	1.56	1.32	33.32	0.91	1.59
2	WB-02 (L2)	12.21	-5.77	0.34	55.36	0.80	-0.75	46.68	1.25	16.99	34.21	0.25	1.81
3	BHU-31 (L3)	13.49	15.45	2.08	53.39	0.93	19.07	48.55	1.40	4.50	35.27	0.25	1.81
4	HD-3721 (L4)	11.89	-4.76	-0.07	53.64	0.02	33.40	47.00	1.81	8.07	33.38	0.25	1.81
5	PWB-725 (L5)	11.51	-1.73	0.21	53.21	0.92	24.27	47.40	0.94	6.70	34.24	1.41	1.42
6	CRD GEHNU1 (L6)	12.58	-5.21	2.03	57.29	2.50	93.12	46.79	1.56	19.04	40.99	8.47	20.84
7	PBW-550 (L7)	11.82	-2.59	-0.05	56.50	0.81	0.56	49.97	1.70	4.28	36.36	0.25	1.81
8	PBW-677 (L8)	12.20	1.63	-0.06	55.09	0.90	42.87	46.79	1.52	1.95	34.53	0.25	1.81
9	PBW-822 (L9)	12.33	1.39	-0.05	50.39	0.87	41.59	44.76	0.96	4.35	35.17	4.81	19.94
10	HD-3117 (L10)	13.44	6.38	2.17	49.97	1.19	23.38	44.58	0.79	31.84	34.88	4.93	16.59
11	DBW-173 (L11)	12.36	2.50	-0.05	52.72	1.20	2.32	46.75	1.40	4.55	32.63	0.25	1.81
12	DH-3086 (L12)	12.40	-1.37	0.03	54.17	1.10	8.08	46.79	1.47	7.29	35.86	7.02	11.11
13	DBW-222 (L13)	12.61	-3.09	-0.01	60.43	2.23	21.65	48.52	1.82	7.60	41.43	5.85	26.55
14	CSW-18 (L14)	13.73	12.52	0.44	55.34	1.45	-1.42	44.24	1.59	1.67	35.71	8.85	2.83
15	PBW-757 (L15)	13.01	14.40	0.64	53.75	1.92	20.55	45.56	1.82	9.49	35.58	0.25	1.81
16	PBW ZN1 (Tester 1)	12.28	6.50	0.93	55.80	1.64	94.82	45.64	0.49	11.62	35.70	-0.15	0.46
17	PBW-343 (Tester 2)	12.99	2.70	3.88	54.80	1.72	5.08	48.80	1.75	7.15	38.95	0.25	1.81
18	HD-3326 (Tester 3)	13.66	14.97	0.61	52.31	1.08	5.78	48.38	1.72	3.02	35.93	0.25	1.81
19	HD-2967 (Check 1)	11.68	-4.07	0.08	51.08	0.16	23.14	47.53	1.48	32.75	34.67	-2.03	0.84
20	DBW-187 (Check 2)	11.81	-3.62	-0.07	52.45	0.55	31.50	48.88	0.62	-0.16	37.39	7.09	4.99
21	NORMAN (Check 3)	12.03	0.39	-0.08	52.13	0.68	19.04	46.10	1.44	10.35	33.96	-2.39	-0.41

22	BORLAUG-100 (Check 4)	11.62	-4.30	0.11	56.07	0.55	3.72	49.00	1.04	17.62	39.65	7.76	3.38
23	BHU-25 X PBW ZN1	12.39	8.32	0.05	61.24	1.57	20.29	52.75	-0.78	5.42	42.84	-1.94	3.41
24	BHU-25 X PBW-343	11.88	-2.61	-0.04	63.11	1.09	19.72	55.88	-0.25	23.54	44.14	-3.06	7.11
25	BHU-25 X HD-3326	12.39	9.07	0.46	63.39	0.11	0.85	56.34	1.13	5.60	44.13	-4.53	20.81
26	DBW-173X PBW ZN1	11.95	-2.66	-0.06	62.71	1.13	1.22	57.62	0.07	4.44	43.29	-0.93	-0.72
27	DBW-173X PBW-343	12.09	2.41	-0.07	63.62	1.27	6.30	57.65	0.54	10.99	48.70	8.80	16.24
28	DBW-173X HD-3326	12.54	12.26	0.60	65.62	1.37	1.68	58.85	0.36	0.91	49.86	4.71	7.86
29	DH-3086X PBW ZN1	12.47	13.82	1.00	64.66	1.26	2.10	56.35	1.61	4.60	49.39	5.54	9.80
30	DH-3086X PBW-343	11.93	-1.84	-0.04	64.14	1.06	3.37	58.79	1.13	-1.29	51.33	1.07	1.04
31	DH-3086X HD-3326	12.04	4.08	-0.02	63.55	0.61	7.77	54.39	0.94	14.26	44.14	-2.69	4.60
32	DBW-222X PBW ZN1	11.78	2.19	0.02	65.44	1.13	-1.26	57.56	0.05	8.75	50.04	1.00	1.70
33	DBW-222X PBW-343	12.09	8.23	0.51	64.16	2.07	18.53	57.52	0.80	-0.62	47.83	0.09	1.19
34	DBW-222X HD-3326	12.01	1.02	0.29	64.73	1.08	2.35	53.84	-0.89	7.53	43.74	-2.86	15.12
35	CSW-18XPBW ZN1	11.79	-3.03	-0.06	62.82	0.43	21.10	59.46	0.76	-1.53	47.00	-0.61	-0.52
36	CSW-18XPBW-343	11.99	2.88	0.01	64.27	0.85	0.31	59.04	0.54	0.17	48.95	3.05	38.74
37	CSW-18XHD-3326	11.91	1.91	-0.06	64.77	0.66	16.34	56.52	1.06	9.68	44.06	-4.85	8.94
38	PBW-757X PBW ZN1	12.00	-3.62	0.00	64.41	1.07	13.97	57.15	1.60	3.80	49.17	3.09	19.84
39	PBW-757X PBW-343	11.71	0.75	0.02	62.89	1.13	1.42	58.03	1.08	3.79	48.82	1.36	28.84
40	PBW-757X HD-3326	12.12	2.61	0.07	60.86	0.45	25.67	58.98	0.85	-0.33	44.36	1.33	8.57
41	BHU-31 X PBW ZN1	12.19	2.52	-0.07	57.48	1.60	5.25	50.88	1.99	2.40	41.81	-3.77	13.94
42	BHU-31 X PBW-343	11.92	-0.31	0.05	59.33	0.14	-1.61	53.43	0.62	5.57	39.59	-3.72	12.73
43	BHU-31 X HD-3326	11.84	-2.38	-0.05	63.15	1.30	-0.56	53.52	1.54	27.13	41.67	-0.20	-0.25
44	WB-02 X PBW ZN1	12.05	1.52	-0.07	65.56	1.03	1.57	54.82	1.57	19.94	45.22	-0.23	0.20
45	WB-02 X PBW-343	12.55	14.41	0.88	60.18	1.11	48.93	54.76	0.78	26.99	42.17	0.22	21.00
46	WB-02 X HD-3326	11.86	-2.22	-0.04	63.56	0.14	11.12	51.17	-0.12	3.61	40.59	5.13	17.64

47	BHU-31 X PBW ZN1	11.81	-2.09	-0.04	59.33	0.73	23.95	55.50	0.82	11.06	43.32	0.05	0.76
48	BHU-31 X PBW-343	12.52	13.92	0.95	58.39	0.89	18.33	55.83	2.29	4.25	41.56	-1.12	-1.43
49	BHU-31 X HD-3326	12.01	1.91	-0.06	58.92	0.84	96.03	56.00	0.58	9.46	44.84	4.49	16.35
50	HD-3721 X PBW ZN1	13.01	2.17	3.03	64.66	0.73	7.44	55.57	2.39	7.29	44.86	4.41	-0.19
51	HD-3721 X PBW-343	12.15	8.41	0.20	62.55	1.16	-1.85	54.24	0.03	0.25	42.25	-0.86	-0.57
52	HD-3721 X HD-3326	11.84	-3.00	-0.06	63.93	1.23	1.81	54.05	1.47	39.02	47.11	-0.64	-0.55
53	PWB-725 X PBW ZN1	12.00	0.91	-0.03	62.05	1.35	34.89	55.21	0.38	42.58	43.69	4.87	21.91
54	PWB-725 X PBW-343	13.23	18.40	0.11	64.25	0.13	23.83	53.89	1.04	9.23	42.38	-3.28	8.77
55	PWB-725 X HD-3326	11.83	-2.77	-0.05	61.71	1.15	23.71	57.58	1.49	-1.53	45.96	-2.27	1.82
56	CRDGEHNU1 X PBWZN1	11.94	-1.92	-0.04	65.15	0.60	0.08	55.67	0.72	1.49	44.77	-2.79	5.23
57	CRDGEHNU1 X PBW343	12.12	0.49	-0.04	61.45	0.98	20.02	56.54	0.85	6.73	44.88	-0.38	-0.37
58	CRDGEHNU1 X HD-3326	12.54	5.56	0.21	60.68	0.27	45.22	55.32	1.44	27.23	41.94	-3.70	12.57
59	PBW-550X PBW ZN1	11.98	-1.37	-0.03	61.85	1.00	32.08	57.49	1.43	1.71	46.53	8.61	2.24
60	PBW-550X PBW-343	12.09	1.85	-0.07	64.37	1.39	0.41	55.05	0.95	2.52	46.24	-0.53	-0.41
61	PBW-550X HD-3326	11.89	-1.13	0.01	64.02	1.21	27.31	56.29	1.04	1.63	46.81	0.50	2.88
62	PBW-677XPBW ZN1	11.89	-3.92	-0.07	59.81	0.68	37.80	56.75	0.44	8.26	40.77	-3.20	16.24
63	PBW-677XPBW-343	11.84	-4.89	0.01	60.41	0.21	32.34	58.94	1.20	-0.38	48.08	4.17	-0.73
64	PBW-677XPBW-343	12.70	12.36	1.04	61.78	1.52	1.25	55.29	0.57	13.11	42.93	-2.35	2.71
65	PBW-822X PBW ZN1	12.19	1.85	-0.07	65.25	1.55	2.43	59.44	0.95	-1.34	53.00	3.06	30.79
66	PBW-822X PBW-343	12.17	-1.76	-0.04	64.24	0.62	6.29	55.79	0.18	16.50	45.54	-3.15	2.43
67	PBW-822X HD-3326	12.28	2.78	-0.08	64.25	1.32	6.83	57.77	-0.36	1.75	46.47	0.38	2.41
	Grand Mean:	11.82			56.79			49.18			40.25		
	SE±	0.07			1.13			0.49			0.33		
	C.D.1%:	0.18			2.99			1.25			0.84		

CHAPTER FIVE

DISCUSSION

Wheat is an important stable food crop worldwide and an annual crop belong to the family *Poaceae*, thus, its members are characterized by segmented stems, blade-like leaves and shallow root system. It is also self-pollinated with three anthers that are attached to the base through the thin filaments and enclosed by bract-like structures known as lemma and palea (Bajaniya *et al.,* 2019; Farhad *et al.,* 2011; Madan Maurya *et al.,* 2014). Yield per hectare is a factor that determine commercially acceptability of wheat variety in developing countries. Crop yield is the sum of all individual yield components operating together with small and cumulative effects. Thus, yield is polygenically controlled, in that, breeding for high yielding required knowledge of the nature and degree of the relationship between yield and yield related traits (Kumar *et al*., 2018; Osman *et al.* 2022).

The assessment of potential genotypes in different environmental conditions (stability analysis) is vital and last step in the most applied plant breeding program (Siddhi *et al*., 2018). In an attempt to improve yield in wheat, commercial hybrid seed production was attempted several to many times by using various sterility induction techniques, encompasses genetic male sterility, cytoplasmic genetic male sterility and through chemical hybridizing agents to improve yield in wheat, but all efforts have little or no practical relevance owing to polyploidy nature of wheat and technical intricacies involved in hybrid seed production at commercial scale (Koumber *et al.,* 2012). Wheat production still encounter some constraints that affect its yield and quality like salinity, heat stress and insufficient breeding information such as genetic variances, GCA, SCA, stability analysis and exploitation of heterosis that involves different agro-ecological zones (Adel and Ali, 2013).

The present investigation with titled “Studies on combining ability, gene action and stability analyses for yield and yield contributing traits in wheat (*Triticum aestivum* L.)” was designed: (i) to study the combining ability variances and their effects (ii) to find out gene actions involved in the inheritance of various characters (iii) to estimate heterosis over better-parent and standard varieties and (iv) to workout stability analysis in parents involves in hybridization programme and F_1s.

Some genetic component related to present investigation includes; combining ability (general combining ability (GCA) and specific combining ability (SCA)). GCA considered to be the average performance of line in a series of various cross combinations, while SCA refers to the deviation from GCA (perform better or worse). It was noted that genes with additive effects play a more significant role in GCA, whereas SCA is influenced by dominance genes and epistatic effects (inter-allelic interactions) Sprague and Tatum (1942). Heterosis (hybrid vigor) is the phenomenon where the progeny of crosses between genetically diverse varieties of a species or between different species exhibit enhanced traits, such as greater biomass, faster development, disease resistant and higher fertility compared to their parents. The term heterosis was introduced by Shull (1914), who described it as the stimulatory effect of heterozygosity on cell division, growth, and other physiological processes of an organism. Later, in 1948, Shull refined the definition to describe it as observable phenomenon resulting from the combination of genetically distinct gametes to produce a hybrid, equating heterosis with hybrid vigor.

Eberhart and Russell (1966) described some parameters that helps to measure stability among population, such parameters are average performance of genotype (mean yield), regression coefficient (bi) and deviation from the regression (S^2di). Therefore, according to model, bi value around 1 indicates average stability, bi < 1 indicates stability (under both the favorable and unfavorable conditions) and bi > 1 indicates stability (under favorable conditions only) and deviation from the regression (S^2di), lower S^2di values indicates higher stability (very little variation). Statistical analysis was done by the following packages; Analysis of variance (Panse and Sukhatme, 1967); line x tester analysis (Kempthorne, 1957); analysis of variance for combining Ability (Kempthorne, 1957); estimation of heterosis (Fonseca and patterson, 1968) and stability analysis (Eberhart and Russell, 1966).

In order to assess the effect of some genetic components involves in the present investigation, the discussion of research findings considered relevant literature under the following sub-headings:

5.1 Analysis of variance for L x T

5.2 Components of genetic variance and their effects

5.3 Combining ability effects

5.4 Heterosis over better parent and standard variety

5.5 Stability analysis

5.1 Analysis of variance for L x T

The table offers a comprehensive view of how the line, tester, and their interaction impact various traits in a crop breeding context, along with the statistical significance of each source.

For most traits, line variation is the key contributor. For instance, days to 50% heading (with line effect highly significant at 5.87) and plant height (with line effect highly significant at 2.85) show that the line has a dominant effect on these traits. However, for both traits, the tester has minimal or no significant influence (tester effect for DH is 0.58 and for Plant Height is 1.38). The interaction between the line and tester also plays a significant role in days to 50% heading (with interaction effect at 5.92), highlighting that the combination of line and tester is important for this trait.

Similarly, traits such as number of spikelets per spike (with line effect significant at 3.55 and interaction effect at 2.23) and grain yield per plant (with line effect significant at 11.53 and interaction effect at 5.43) also show that both the line and line x tester interaction are crucial for improvement, while testers themselves have minimal influence.

In contrast, Tester effects are significant for certain traits like spike length (with tester effect significant at 5.64) and 1000-grain weight (tester effect significant at 5.33), suggesting that the tester is the primary contributor to these traits. For traits like grain filling period (tester effect significant at 8.23) and protein content (both line and tester significant at 1.46 and 0.978 respectively), testers show notable effects while the interaction has little impact.

For other traits, such as grain weight per spike (no significant effects from any source), it appears that genetic factors do not significantly contribute to the variation observed. Additionally, flag leaf area (with line and tester effects highly significant at 180.45 and 210.07, respectively) shows a combined influence of both line and tester, where their interaction is also significant at 79.13, indicating that both need to be optimized for improvement in this trait.

While biological yield (line effect significant at 2.31) and Harvest Index (line effect significant at 6.22) are both primarily influenced by the line, the tester and their interaction have no significant effect. This pattern is observed in several other traits, like chlorophyll content (line effect significant at 4.04), where the tester and interaction show no influence.

Overall, the study suggests that line variation is the major determinant for most traits, with tester effects being more prominent for traits like spike length and 1000-grain weight. The interaction between the line and tester plays a significant role in traits such as days to 50% heading and grain yield per plant, highlighting the importance of selecting both the right lines and testers for optimal genetic improvement. For traits where neither source has a significant effect, environmental factors may be playing a more crucial role.

Table 5.1 Analysis of variance for L x T

Character	Line	Tester	Line x Tester	Major findings of the present investigation
Days to 50% heading	Highly significant (5.87)	Not significant (0.58)	Highly significant (5.92)	Line and line x tester significantly affect DH. While tester has little impact.
Plant Height (cm)	Highly significant (2.85)	Not significant (1.38)	Highly significant (3.66)	Line and line x tester significantly affect plant height. Testers have minimal impact.
Days to Maturity	Significant (7.85)	Significant (32.03)	Significant (7.95)	Both line and tester, along with their interaction, influence maturity.
Grain-filling Period	Not significant (4.01)	Significant (8.23)	Not significant (1.67)	Tester influences GFP. Line and interaction have little effect.
No. of productive tiller	Significant (3.83)	Not significant (1.76)	Not significant (1.54)	Line variation affects tiller number. Tester and interaction have no impact.
No. of spikelets/pike	Significant (3.55)	Not significant (1.16)	Significant (2.23)	Line and line x tester significantly affect spikelets. Testers have little impact.
Spike length (cm)	Not significant (2.41)	Significant (5.64)	Significant (2.89)	Tester and line x tester significantly affect spike length. Line has minimal effect.
Flag leaf area (cm²)	Highly significant (180.45)	Highly significant (210.07)	Significant (79.13)	Both line and tester contribute significantly, with interaction playing important role.
Chlorophyll content	Significant (4.04)	Not significant (1.18)	Not significant (0.81)	Line influences chlorophyll content. Tester and interaction have no effect.
No. of grains/Spike	Significant (4.03)	Not significant (0.52)	Not significant (1.59)	Line is the main contributor to grains per spike. Tester and interaction have no effect.
Grain weight/spike (g)	Not significant (1.16)	Not significant (1.21)	Not significant (0.93)	No significant effects for any source of variation.
1000-Grain weight (g)	Not significant (1.25)	Significant (5.33)	Not significant (1.31)	Tester plays a significant role, while line and interaction have minimal impact.
Biological yield (g)	Significant (2.31)	Not significant (1.08)	Not significant (0.94)	Line significantly affects biological yield. Tester and interaction have no effect.
Harvest index (%)	Significant (6.22)	Not significant (0.75)	Not significant (1.43)	Line significantly influences harvest index. Tester and interaction have no effect.
Protein content	Significant (1.46)	Significant (0.978)	Not significant (3.94)	Both line and tester influence protein content. Interaction has no effect.
Grain yield per plant (g)	Significant (11.53)	Significant (4.31)	Significant (5.43)	Line and line x tester significantly affect grain yield. Tester has moderate impact.

5.2 Components of genetic variance and their effects

Sprague and Tatum (1942) described mode of gene expression (additive, dominance, and epistatic). Additive gene action refers to the cumulative effects of individual alleles, while dominance gene action occurs when one allele suppresses or masks the expression of another at the same locus and epistatic gene action involves interactions between alleles at different loci.

The results provides a detailed genetic analysis of various traits, emphasizing the influence of additive and non-additive genetic effects. Traits like Days to 50% Heading (with a GCA variance of 0.72 and no SCA variance) are predominantly controlled by additive genetic effects, making them highly predictable (predictability ratio of 1.00) and amenable to improvement through selection, with a moderate heritability of 46% and a significant genetic advance of 27.90%.

Similarly, Grain Yield per Plant (GCA variance of 2.35 and no SCA variance) shows strong additive genetic influence, suggesting potential for improvement, although its low heritability (18%) means genetic progress will be slower despite a high predictability ratio of 1.00. Harvest Index also shows strong additive control (GCA variance of 2.35) and high predictability (1.00), with a moderate heritability of 43% and a genetic advance of 6.18%.

In contrast, traits like Flag Leaf Area (GCA variance of 0.00 and SCA variance of 7.58) are predominantly controlled by non-additive effects, with genetic improvement being better achieved through hybridization. Traits like Grain Weight per Spike (with GCA variance of 0.01 and SCA variance of 0.03) are influenced by over dominance, again highlighting the need for hybridization over selection.

Some traits, like Protein Content (GCA and SCA variance of 0.00), are mainly environmentally controlled, with no potential for genetic improvement. Other traits such as Plant Height (GCA variance of 0.13 and SCA variance of 0.02) exhibit low heritability (25%), making genetic improvement difficult, despite a reasonable predictability ratio of 0.86.

Overall, the predictability and potential for genetic improvement vary greatly, with traits under strong additive genetic control offering higher potential for selection-based breeding, while traits dominated by non-additive effects or environmental factors require different strategies, such as hybridization or environmental manipulation.

Table 5.2 Estimates of components of genetic variance and their magnitudes

Trait	GCA Variance (σ^2g)	SCA Variance (σ^2s)	Average Degree of Dominance	Predictability Ratio ($2\sigma^2g$ / ($2\sigma^2g + \sigma^2s$))	Heritability (h^2n) %	Genetic Advance %	Major Findings
Days to 50% Heading	0.72	0.00	1.00	1.00	46%	27.90%	Predominantly influenced by additive genetic effects (GCA), high predictability for selection. Heritability is moderate; genetic advance is significant, indicating that this trait is predictable and can be improved through selection.
Plant Height (cm)	0.13	0.02	0.15	0.86	25%	0.32%	Poorly controlled by genetic factors with low heritability. Despite high predictability, environmental factors dominate, making genetic improvement slow.
Days to Maturity	0.00	0.00	0.00	0.00	42%	65.39%	Negligible GCA and SCA, indicating environmental control. Moderate heritability; improvement through selection may be difficult, but genetic advance is high.
Grain Filling Period	4.48	2.51	0.56	0.64	54%	39.55%	Both additive and non-additive genetic effects influence this trait, with moderate predictability. Genetic advance is moderate, allowing improvement through both selection and hybridization.
No. of Productive Tillers	0.04	0.00	0.00	1.00	10%	0.08%	Dominated by non-additive genetic effects, resulting in low heritability. Genetic improvement is limited, but it can be improved through hybridization.
N0. of Spikelets per Spike	14.33	3.73	0.26	0.79	59%	97.40%	Strong influence from additive genetic effects (GCA), partial dominance, and a good predictability ratio. High genetic advance suggests substantial improvement through breeding programs.
Spike Length (cm)	4.45	0.10	0.02	0.97	45%	10.57%	Additive genetic effects strongly influence this trait, with minimal non-additive effects. Moderate heritability and a high predictability ratio suggest this trait is highly responsive to genetic improvement.
Flag Leaf Area (cm^2)	0.00	7.58	0.00	0.00	51%	51.30%	Predominantly influenced by non-additive effects (hybrid vigor). Genetic improvement is best achieved through crossing different parent combinations, despite moderate heritability.
Chlorophyll Content	0.00	0.01	0.00	0.00	42%	0.50%	Low GCA and SCA variance, indicating minimal genetic control. Environmental factors dominate, limiting potential for genetic improvement.
Grain Weight per Spike (g)	0.01	0.03	3.00	0.25	6%	0.04%	Strongly influenced by non-additive effects (over dominance), suggesting hybridization is more effective than selection. Genetic improvement through selection is minimal.
1000-Grain Weight (g)	1.63	0.10	0.06	0.94	8%	0.15%	Additive genetic effects play a significant role, but low heritability means environmental effects are strong. Despite high predictability, genetic improvement is slow.
Biological Yield (g)	2.7	0.03	0.01	0.98	26%	3.87%	Additive genetic effects contribute to biological yield. Although the predictability ratio is high, low heritability limits the potential for rapid genetic improvement.

Harvest Index (%)	2.35	0.00	1.00	1.00	43%	6.18%	Highly influenced by additive genetic effects (GCA), with complete dominance. This trait can be significantly improved through selection due to high predictability and moderate heritability.
Protein Content (%)	0.00	0.00	0.00	0.00	0%	0.00%	Genetic factors have negligible impact on protein content, which is primarily controlled by environmental factors. Genetic improvement through selection is not feasible.
Grain Yield per Plant (g)	2.35	0.00	1.00	1.00	18%	5.35%	Strong influence from additive genetic effects (GCA), with complete dominance. While the trait is predictable, environmental factors limit its heritability, making genetic improvement slow.

5.3 Combining ability variance and their effects

Sprague and Tatum (1942), proposed the concepts of combining ability (general combining ability (GCA) and specific combining ability (SCA)). GCA considered to be the average performance of line in a series of various cross combinations, while SCA refers to the deviation from GCA (perform better or worse).

GCA was typically more stable across different environments due additive genetic effects were less influenced by environmental variability. Thus, GCA for genotype like WB-02 was ranked first for grain filling period (GFP (value 2.33, Rank 1), suggests that this trait is largely influenced by additive effects and recurrent and pure line selection can be used for trait improvement. This also means selection of WB-02 as a parent can reliably improve GFP across multiple crosses. In yield-related traits (NPT, GYP, NSS), genotype PBW ZN1 was ranked 1st for GCA in NPT (0.02), GYP (0.53), and NSS (0.06).

These results indicate the predominant effects of additive genes and imply that PBW ZN1 consistently transmits favorable alleles for these traits, making it a strong candidate for breeding programs aiming to improve yield potential. The breeding implications of GCA-dominated traits that additive effects are highly heritable. Traits like GFP and yield-related traits (e.g., NPT, GYP, and NSS) that exhibit high GCA can be improved effectively using recurrent selection or pure line breeding. Parental lines with high GCA should be prioritized in breeding programs targeting these traits, as they will contribute to steady genetic gains over generations.

The information on GCA effect could be used in selection of superior parents; estimation of half-sib families; and for pure line selection method. While information for SCA could be used useful in selection of superior cross combinations for heterosis breeding; and estimation of full-sib families and if the information on both GCA and SCA are equal, the information could be used for reciprocal recurrent selection.

Specifically high GCA effect is due additive gene action and is used to estimate half-sib families, related with narrow sense heritability (heritable and fixable) and useful in early generation selection of parents for hybridization or pure line selection. While high SCA is due non-additive gene action and is used to estimate full-sib families, related with broad sense heritability (non-heritable and non-fixable) and useful in selection of superior cross combinations or heterosis breeding. Ultimately the information on GCA and SCA can be used to develop efficient breeding strategies that will provides valuable insights into inheritance patterns of yield-related traits that underpin the development of advanced breeding techniques, including hybrid breeding, exploitation of heterosis and identification/selection of superior parent that aimed at improvement of wheat production to ensure resilience against environmental stresses.

Four parents were recorded as the best general combiners for yield and yield components, thus, can serve as potential candidates for future breeding programme like development of good potential for grain yield improvement, as per hierarchically mentioned below; PBW ZN1; PBW-757; PBW-822 and DBW-173. The best identified parents with high GCA could be cross with each other to combine favorable traits using pedigree breeding (to develop synthetic variety) and pure line selection (selection of superior parent). High GCA parents can serve as ideal foundation parents for large scale breeding programs and early generation selection is rewarding.

For SCA measures the non-additive genetic variance, which includes dominance effects (interaction between alleles at the same locus) and epistasis (interaction between alleles at different loci). High SCA values in a specific cross indicate that the combination of parental alleles uniquely enhances the trait. Number of productive tillers (NPT), the cross like DBW-222 x PBW ZN1 showed the highest SCA value. This indicates that the NPT trait in this specific cross benefits significantly from dominance, making this hybrid especially promising.

For grain yield per plant (GYP), the cross PBW-822 x PBW ZN1 also exhibited the highest SCA value (3.79), suggesting that non-additive effects are crucial for enhancing GYP in this cross. This implies that hybrid vigor (heterosis) plays a key role in improving yield in this specific cross. Harvest index (HI), the highest SCA for HI was recorded in DH-3086 x PBW-343 (0.67). This suggests that HI benefits from specific allelic combinations in these two parents and indicate the present of non-additive gene effects. However, Poor SCA example (Spike Length), the cross CRD GEHNU 1 x HD-3326, ranked 45th, showed poor SCA for spike length. This indicates that the specific parental combination does not effectively exploit non-additive genetic effects for this trait, thus, there is need for further improvement.

Five crosses revealed significant positive SCA effects for yield and yield components as hierarchically mentioned below; DBW-222XPBWZN1; DH-3086XPBWZN1; PBW-677XPBW-343; HD-3721X HD-3326 and CRD GEHNU1XPBWZN1. The best identified parents with high-SCA could be used for hybrid breeding program. High SCA parents can serve as ideal foundation parents for yield improvement and large-scale breeding programs.

Table 5.3 Summary estimates of general combining ability (GCA) effects for combined locations

Trait	Best Genotype (Rank)	GCA Value	Worst Genotype (Rank)	GCA Value	Major findings of the present investigation
Days to 50% heading	WB-02 (Rank 15)	-0.30136	DBW-222 (Rank 1)	0.301763	WB-02 is early maturing; others like DBW-222 late maturing. Consistent tester effects, minimal influence on DH.
Plant height (cm)	DBW-222 (Rank 15)	-4.89947	HD-3721 (Rank 1)	4.605716	Tallest genotypes (HD-3721) may have lodging risks; shortest (DBW-222) are more resistant to lodging.
Days to maturity	HD-3721 (Rank 15)	-4.37037	BHU-25 (Rank 1)	7.07407	BHU-25 is early-maturing (good for extra early maturing variety development); HD-3721 is late-maturing, potentially beneficial for extended grain filling.
Grain filling period	DBW-222 (Rank 15)	-2.23317	WB-02 (Rank 1)	2.336642	WB-02 has the longest GFP, indicating better grain weight; DBW-222 has the shortest GFP, potentially limiting grain development but good for early maturity improvement.
No. of productive tiller	PBW-822 (Rank 1)	0.325522	BHU-25 (Rank 15)	-0.71235	PBW-822 produces more productive tillers, improving yield potential; BHU-25 produces fewer tillers, limiting yield.
No. of spikelets/spike	PBW-757 (Rank 1)	0.279104	PWB-725 (Rank 15)	-0.18575	PBW-757 has a higher NSS, suggesting better grain-bearing potential.
Spike length (cm)	CSW-18 (Rank 1)	5.980954	DBW-173 (Rank 15)	-0.36247	CSW-18 has the longest spike length, indicating strong positive contribution; DBW-173 has a negative contribution to SL.
Flag leaf area (cm²)	CSW-18 (Rank 1)	5.980954	BHU-31 (Rank 15)	-7.26192	Larger FLA in CSW-18 supports better photosynthesis; BHU-31 has a smaller FLA, limiting photosynthetic efficiency.
Chlorophyll content	DH-3086 (Rank 1)	4.760765	BHU-25 (Rank 15)	-4.4696	DH-3086 has high chlorophyll content, supporting better photosynthesis. BHU-25 has lower CLC, limiting its photosynthetic potential.
No. of grains/spike	DBW-222 (Rank 1)	1.606142	PBW-822 (Rank 15)	-1.30612	DBW-222 produces more grains per spike, enhancing yield potential; PBW-822 produces fewer grains per spike, limiting its productivity.
Grain weight/spike (g)	PWB-725 (Rank 1)	0.18398	CSW-18 (Rank 15)	-0.1464	PWB-725 has the highest GWS, beneficial for grain yield; CSW-18 has a low GWS, limiting its spike productivity.
1000-grain Weight (g)	PBW-757 (Rank 1)	-0.64711	HD-3721 (Rank 15)	-0.64304	PBW-757 has heavier grains, favorable for grain quality; HD-3721 has lighter grains, potentially affecting yield and market value.

Biological yield (g)	PWB-725 (Rank 1)	3.779852	PBW-822 (Rank 15)	-4.40015	PWB-725 has the highest biological yield, indicating potential for higher grain yield; PBW-822 has low biological yield.
Harvest index (%)	DBW-173 (Rank 1)	2.326054	BHU-25 (Rank 15)	-3.02	DBW-173 has the highest harvest index, efficiently converting biomass to grain; BHU-25 has low HI, limiting grain yield efficiency.
Protein content (PC)	DBW-173 (Rank 1)	0.221605	CSW-18 (Rank 15)	0.020124	DBW-173 has the highest protein content, valuable for nutritional quality; CSW-18 has low protein content, reducing market value.
Grain yield/plant	DH-3086 (Rank 1)	1.968039	BHU-25 (Rank 15)	-2.15445	DH-3086 has the highest grain yield; BHU-25 has low grain production.

Table 5.3 Contd.

Trait	Genotype (Top Performers)	E1 (Rank, Value)	E2 (Rank, Value)	E3 (Rank, Value)	Major findings of the present investigation
Days to 50% heading	PBW-822 , CSW-18 , DH-3086	PBW-822 (-4.400, Rank 15)	CSW-18 (-3.954, Rank 14)	DH-3086 (6.143, Rank 1)	Early flowering (PBW-822, CSW-18); late flowering (DH-3086)
Plant height (cm)	PBW-550, CRD GEHNU1	PBW-757 (2.065, Rank 1)	BHU-31 (4.917, Rank 1)	PBW-550 (2.703, Rank 1)	Tall genotypes (PBW-550, CRD GEHNU1); short genotypes (BHU-25)
Days to maturity	WB-02, BHU-25, DH-3086	BHU-25 (9.962963, Rank 1)	HD-3117 (9.903704, Rank 1)	WB-02 (4.8, Rank 1)	Early maturing (WB-02); late maturing (BHU-25)
Grain filling period	BHU-25, DBW-173	BHU-25 (5.407407, Rank 1)	HD-3117 (5.548148, Rank 1)	PBW-677 (8.755556, Rank 1)	Long (BHU-25) and stable (DBW-173) grain filling periods
No. of productive tiller	DBW-222, WB-02, CSW-18	DBW-222 (1.130074, Rank 1)	WB-02 (0.889259, Rank 1)	CSW-18 (0.576304, Rank 1)	High tiller counts (DBW-222, WB-02); low (BHU-25)
No. of spikelets/spike	PBW-550, CSW-18	PBW-550 (1.050519, Rank 1)	PBW-550 (1.050519, Rank 1)	CSW-18 (0.908667, Rank 1)	High spikelet counts in E1, E2 (PBW-550); low (BHU-25)
Spike length (cm)	DH-3086, PBW-757	PBW-757 (0.628815, Rank 1)	DH-3086 (0.721704, Rank 1)	DH-3086 (0.640963, Rank 1)	Stable (DH-3086) spike length performance across locations
Flag leaf area (cm²)	PBW-822, PBW-725, PBW-677	PBW-822 (1.690519, Rank 1)	PBW-725 (2.312444, Rank 1)	PBW-677 (6.754148, Rank 1)	High NG/S (PBW-822, PBW-725, PBW-677); variable (PBW-822)
Chlorophyll content	DBW-173, PBW-757	DBW-173 (0.211778, Rank 2)	PBW-757 (0.229037, Rank 1)	PBW-550 (-0.52044, Rank 15)	High flag leaf area (DBW-173, PBW-757); low (CRD GEHNU1)
No. of grains/spike	PBW-757, DH-3086	PBW-757 (4.131, Rank 1)	DH-3086 (10.36044, Rank 1)	DH-3086 (5.235185, Rank 1)	High chlorophyll content (PBW-757, DH-3086)
Grain weight/spike (g)	PBW-725, DBW-222	PBW-757 (0.236741, Rank 5)	PBW-725 (0.342519, Rank 1)	PBW-725 (0.342519, Rank 1)	Consistent grain weight (PBW-725); low (WB-02, BHU-31)
1000-grain Weight (g)	DH-3086, PBW-550	DH-3086 (0.891037, Rank 1)	PBW-550 (0.786963, Rank 1)	DH-3086 (0.891037, Rank 1)	High 1000-grain weight (DH-3086, PBW-550); low (DBW-173)

Biological yield (g)	PBW-725, DH-3086	PBW-725 (3.779852, Rank 1)	DH-3086 (6.143185, Rank 1)	PBW-725 (0.702222, Rank 6)	High biological yield (PBW-725, DH-3086); low (PBW-822)
Harvest index (%)	PBW-757, CRD GEHNU1	PBW-757 (2.065037, Rank 1)	PBW-757 (2.065037, Rank 1)	PBW-550 (2.703556, Rank 1)	High harvest index (PBW-757, PBW-550); low (HD-3117)
Protein content (PC)	HD-3117, PBW-757	HD-3117 (0.585111, Rank 1)	PBW-757 (0.229037, Rank 1)	PBW-757 (0.229037, Rank 1)	High protein content (HD-3117, PBW-757)
Grain yield/plant (g)	PBW-725, DBW-222	PBW-757 (0.236741, Rank 5)	PBW-725 (0.342519, Rank 1)	PBW-725 (0.342519, Rank 1)	Consistent grain weight (PBW-725); low (WB-02, BHU-31)

Table 5.3 Contd.

Trait	Best Genotype	Best Value	Worst Genotype	Worst Value	Major findings of the present investigation
Days to 50% heading	CRDGEHNU1XPBW343	8.3676	PBW-677XPBW-343	-10.5458	CRDGEHNU1XPBW343 accelerates heading compared to PBW-677XPBW-343 which is delayed.
Plant height (cm)	DH-3086X HD-3326	9.661765	DBW-222X PBW-343	-5.62864	DH-3086X HD-3326 produces taller plants, while DBW-222X PBW-343 results in shorter plants.
Days to maturity	CRDGEHNU1XPBWZN1	8.51852	CRDGEHNU1XPBW343	-10.6963	CRDGEHNU1XPBWZN1 matures earlier than CRDGEHNU1XPBW343, which matures later.
Grain filling period	HD-3721XPBW ZN1	1.713937	PBW-677XPBW-343	-2.32278	HD-3721XPBW ZN1 has a longer grain filling period, while PBW-677XPBW-343 shows poor filling.
No. of productive tiller	DBW-222X PBW ZN1	0.499506	DBW-222X HD-3326	-0.36146	DBW-222X PBW ZN1 produces more productive tillers than DBW-222X HD-3326.
No. of spikelets/spike	PBW-677XPBW-343	0.583195	BHU-31XHD-3326	-0.37691	PBW-677XPBW-343 produces more spikelets/spike than BHU-31XHD-3326, which has fewer.
Spike length (cm)	CRDGEHNU1XPBWZN1	0.777062	CRDGEHNU1XHD-3326	-0.95731	CRDGEHNU1XPBWZN1 results in longer spike length compared to CRDGEHNU1XHD-3326, which is shorter.
Flag leaf area (cm^2)	HD-3117X PBW ZN1	10.74041	BHU-31XHD-3326	-9.88984	HD-3117X PBW ZN1 has a larger flag leaf area, while BHU-31XHD-3326 has a smaller leaf area.
Chlorophyll content	PBW-550X HD-3326	3.267827	DBW-222X PBW-343	-2.70847	PBW-550X HD-3326 has higher chlorophyll content, while DBW-222X PBW-343 has lower content.

No. of grains/spike	DBW-173X PBW ZN1	0.18558	PBW-725X PBW-343	-0.22072	DBW-173X PBW ZN1 produces more grains/spike compared to PBW-725X PBW-343.
Grain weight/spike (g)	DBW-173X PBW ZN1	0.18558	PWB-725X PBW-343	-0.22072	DBW-173X PBW ZN1 results in a higher grain weight/spike than PWB-725X PBW-343.
1000-grain Weight (g)	HD-3117X PBW ZN1	0.33686	PBW-822X PBW ZN1	-0.63742	HD-3117X PBW ZN1 has a higher 1000-grain weight compared to PBW-822X PBW ZN1, which is lower.
Biological yield (g)	PBW-677XPBW-343	4.715259	PBW-757X HD-3326	-4.29696	PBW-677XPBW-343 has higher biological yield, whereas PBW-757X HD-3326 yields less.
Harvest index (%)	DH-3086X PBW-343	0.670816	BHU-25XPBW ZN1	-1.04371	DH-3086X PBW-343 has a higher harvest index, indicating better grain production efficiency than BHU-25XPBW ZN1.
Protein content (PC)	PWB-725X PBW-343	0.749412	PBW-757X PBW-343	-0.32109	PWB-725X PBW-343 has higher protein content than PBW-757X PBW-343.
Grain yield/plant (g)	PBW-822X PBW ZN1	3.795527	PBW-677XPBW ZN1	-2.87086	PBW-822X PBW ZN1 has higher grain yield per plant than PBW-677XPBW ZN1.

Table 5.3 Contd.

Parameter	Best Genotypes in E1	Best Genotypes in E2	Best Genotypes in E3	Worst Genotypes in E1	Worst Genotypes in E2	Worst Genotypes in E3
Days to 50% Heading	HD-3117X HD-3326 (-16.27, Rank 45)	PBW-677XPBW-343 (12.83, Rank 3)	PBW-677XPBW-343 (7.67, Rank 6)	CRDGEHNU1XPBW343 (-16.90, Rank 45)	PBW-550X PBW-343 (-15.90, Rank 43)	DBW-173X PBW-343 (-5.74, Rank 41)
Plant Height (cm)	PBW-757X PBW ZN1 (-7.06, Rank 38)	PBW-822X HD-3326 (-5.66, Rank 43)	HD-3721X HD-3326 (11.99, Rank 1)	PBW-757X HD-3326 (-4.37, Rank 42)	DH-3086X PBW ZN1 (-2.11, Rank 45)	DBW-222X HD-3326 (-5.66, Rank 42)
Grain Filling Period	CRDGEHNU1XPBW ZN1 (7.04, Rank 1)	CRDGEHNU1XPBW ZN1 (4.74, Rank 9)	PBW-757X PBW-343 (11.31, Rank 1)	PBW-550X PBW ZN1 (-5.74, Rank 41)	PBW-550X PBW ZN1 (-7.74, Rank 41)	CRDGEHNU1XPBW ZN1 (-9.16, Rank 45)
Days to Maturity	CRDGEHNU1XPBW343 (-16.90, Rank 45)	PBW-550X PBW ZN1 (-15.90, Rank 43)	CRDGEHNU1XPBW ZN1 (14.66, Rank 1)	PBW-550X PBW ZN1 (14.66, Rank 1)	PBW-550X PBW ZN1 (-7.66, Rank 39)	DBW-173X PBW-343 (8.58, Rank 1)
Number of Spikelets /Spike	PBW-677XPBW-343 (1.53, Rank 1)	PBW-677XPBW-343 (1.53, Rank 1)	DBW-173X PBW-343 (1.57, Rank 1)	DBW-222X HD-3326 (-1.16, Rank 45)	HD-3721XPBW-343 (-1.12, Rank 45)	DBW-222X HD-3326 (-1.15, Rank 45)
No. of Productive Tillers per Plant	HD-3721X HD-3326 (1.78, Rank 1)	DH-3086X HD-3326 (1.59, Rank 1)	CRDGEHNU1XPBW ZN1 (1.05, Rank 1)	WB-02X HD-3326 (-1.10, Rank 45)	DH-3086X PBW-343 (-2.11, Rank 45)	DBW-222X HD-3326 (-1.01, Rank 45)
Chlorophyll Content	PBW-757X PBW ZN1 (4.5, Rank 1)	PBW-677XPBW-343 (7.34, Rank 2)	PBW-677XPBW-343 (1.94, Rank 1)	HD-3721X PBW ZN1 (-6.02, Rank 45)	PBW-677XPBW ZN1 (-7.02, Rank 45)	PBW-677XPBW ZN1 (-6.02, Rank 45)
Flag Leaf Area (cm^2)	CRDGEHNU1XPBWZN1 (12.48, Rank 1)	CRDGEHNU1XPBWZN1 (12.15, Rank 1)	CRDGEHNU1XPBWZN1 (11.25, Rank 1)	CRDGEHNU1XPBW343 (-7.28, Rank 44)	CRDGEHNU1XPBW343 (-6.91, Rank 44)	CRDGEHNU1XPBW343 (-6.75, Rank 43)

Spike Length	PBW-757X PBW ZN1 (0.71, Rank 1)	DH-3086X PBW ZN1 (1.28, Rank 1)	DH-3086X PBW ZN1 (0.99, Rank 2)	PBW-757X PBW ZN1 (-0.68, Rank 42)	PBW-757X PBW ZN1 (-0.50, Rank 38)	PBW-757X PBW ZN1 (-0.68, Rank 42)
Number of Grains per Spike	DH-3086X PBW ZN1 (9.50, Rank 1)	PBW-757X PBW-343 (7.55, Rank 2)	PBW-677XPBW-343 (7.40, Rank 1)	DH-3086X PBW ZN1 (-0.89, Rank 34)	DH-3086X PBW ZN1 (-0.89, Rank 33)	PBW-757X PBW-343 (-1.80, Rank 39)
1000-Grain Weight (g)	DBW-173X PBW ZN1 (1.14, Rank 1)	CRDGEHNU1XPBWZN1 (2.36, Rank 1)	PBW-822X HD-3326 (2.86, Rank 1)	DBW-173X PBW-343 (-1.10, Rank 45)	CRDGEHNU1X HD-3326 (-2.51, Rank 45)	PBW-822X PBW ZN1 (-3.93, Rank 45)
Grain Weight per Spike (g)	CSW-18XPBW ZN1 (0.28, Rank 1)	PBW-822X PBW-343 (0.49, Rank 1)	BHU-31XPBW-343 (0.47, Rank 1)	DBW-222X HD-3326 (-0.24, Rank 45)	PBW-822X HD-3326 (-0.64, Rank 45)	WB-02X HD-3326 (-0.49, Rank 45)
Biological Yield (g)	PBW-677XPBW-343 (4.72, Rank 1)	PWB-725X PBW-343 (8.91, Rank 1)	CRDGEHNU1XPBWZN1 (5.32, Rank 1)	PBW-757X HD-3326 (-4.30, Rank 45)	WB-02X PBW-343 (-8.21, Rank 45)	BHU-31XPBW ZN1 (-6.94, Rank 45)
Harvest Index	PWB-725X HD-3326 (4.67, Rank 1)	BHU-31X HD-3326 (4.53, Rank 1)	HD-3117X HD-3326 (5.54, Rank 1)	PWB-725X PBW ZN1 (-4.09, Rank 45)	BHU-25X PBW ZN1 (-4.57, Rank 44)	HD-3721X HD-3326 (-5.95, Rank 45)
Protein Content (%)	HD-3721XPBW ZN1 (1.54, Rank 1)	DH-3086X PBW-343 (0.19, Rank 1)	PBW-677XPBW-343 (1.95, Rank 1)	HD-3117X HD-3326 (0.16, Rank 45)	PBW-550X PBW ZN1 (0.11, Rank 45)	PBW-550X PBW ZN1 (0.11, Rank 45)
Grain Yield per Plant (g)	PBW-822X PBW ZN1 (6.01, Rank 1)	BHU-31X HD-3326 (4.48, Rank 1)	PBW-677XPBW-343 (7.40, Rank 1)	WB-02X PBW ZN1 (4.72, Rank 42)	PBW-550X HD-3326 (2.63, Rank 3)	BHU-31X HD-3326 (5.97, Rank 2)

5.4 Heterosis over better parent and standard variety

The magnitude of heterosis varies across different traits and environments may be due to several factors. According to Shull (1914) there are several factors that affect heterosis such as mode of reproduction (more pronounced in cross-pollinated while less in self-pollinated crops); the presence of both additive (low heterosis) and non-additive (high heterosis) gene actions, genetic makeup of the parents, genetic diversity of parent, nature of the traits being studied, adaptability of parent and environmental conditions (drought, high temperature, and nutrient limitations) supported Kant *et al.* 2011 and Kumar *et al.* (2019) the findings suggest that achieving high levels of heterosis requires careful selection of genetically diverse parents with significant non-additive gene. Other factors are due to quantitative traits are polygenic inheritance controlled by many genes, with each gene contributing a small effect (thus, heterosis is low due additive gene effects). However, high heterosis observed for grain quality traits (e.g., protein content, and chlorophyll content). This is due preponderance of non-additive gene action and their expression can be more stable across different environment and generations.

Heterosis in wheat is highly associated with physiological factors like photosynthetic efficiency, resource use efficiency (better utilization of water and nutrients), resistance to environmental stresses (drought, heat, and disease), rate of growth and biomass accumulation rate. While biochemical mechanisms of heterosis involves enzymes activities like nitrogen assimilation, carbohydrate metabolism, and antioxidant defense are often more active in hybrids compared to the parents.

Results revealed that, many crosses recorded positive heterosis both over the better parent and standard varieties, suggesting that these hybrids are promising candidates for improving the important traits. This indicates the successful exploitation of heterosis in breeding programs, emphasizing the potential for higher yields and improved quality traits through the selection of superior crosses.

Heterosis over Better Parent (BP) across multiple traits, early-maturing and late-maturing crosses display significant heterosis. Crosses like WB-02XPBW-343, CRDGEHNU1XHD-3326, and DBW-222X HD-3326 offer desirable traits for early and late maturation, respectively. Standard variety (SV) heterosis, several crosses, especially those like BHU-25XPBW ZN1, PWB-725X PBW ZN1, and HD-3721XPBW ZN1, consistently show robust heterosis for traits like plant height and GFP across multiple locations, making them strong candidates for breeding programs. It also indicated the presence of dominant gene action as reported by AbdEl-Hady *et* *al.* (2018) the findings implied that dominance gene action plays a more prominent role than additive gene action in the inheritance of the studied traits. These crosses were ideal for areas with shorter growing seasons or those requiring early harvest.

For number of productive tillers per plant the genotype PBW-822X PBW ZN1 exhibited the highest heterosis, with an impressive BP value, showing a substantial increase in productive tillers over the better parent. This suggests favorable genetic combinations that enhance tillering capacity and the results indicated the influenced the of additive and no-additive gene actions in genotypes and can be used to develop high yielding and stable genotype through heterosis breeding and pure line selection methods. This also agree with research conducted by Kumar *et al.* (2018) and Mullualem *et al.* (2024) identified significant potential use of heterosis in breeding programs to enhance agricultural productivity at both national and international levels. PBW-550X PBW-343 (BP) and DBW-173X PBW-343 (BP) also demonstrated significant heterosis, indicating substantial productivity improvements, although not as pronounced as PBW-822X PBW ZN1. The results indicate significant heterosis across various wheat traits when comparing crosses to the better parent (BP) and standard varieties (SVs).

For chlorophyll content**,** PBW-757X PBW ZN1 consistently showed positive heterosis, particularly at Location 1, outperforming both the BP and several SVs. Other crosses like WB-02X PBW ZN1 also displayed positive heterosis, though to a lesser extent. However, some crosses like PBW-550X PBW-343 showed negative heterosis in certain locations, suggesting that environmental factors might impact their performance. For number of spikelets per spike, BHU-25X PBW ZN1 and PBW-677X PBW-343 exhibited high and stable positive heterosis across multiple locations, indicating their potential for increasing spikelet production. CRDGEHNU1X PBW343 demonstrated exceptional heterosis, particularly in Location 3. In contrast, some crosses like BHU-31X PBW ZN1 had negative heterosis values at certain locations, indicating potential limitations in specific conditions.

Grain filling period (GFP) genotypes like BHU-25XPBW ZN1 and HD-3117X PBW ZN1 performed very well in terms of GFP across all locations, with the former showing high positive heterosis in both BP and SV and the results were similar to Nageshwar *et al.* (2024) reported that, the outcome of better parent heterosis revealed that the cross combinations, namely, HD3086 x HD-2733, HD3086 x K0307, HD3086 x HD2967, HD3086 x K1601, and HD2967 x K0402 exhibited positive and high heterosis for grain yield. These genotypes could be ideal for breeding programs aimed at enhancing grain filling duration. Other crosses like PWB-

725X PBW ZN1 show moderate but reliable GFP performance, with strong adaptability in varying conditions.

Regarding grain weight per spike**,** BHU-25X PBW-343 and WB-02X PBW-343 showed substantial positive heterosis. PWB-725X HD-3326 also performed well, especially in Location 2. High heterosis for grain weight was similarly observed in HD-3117X PBW ZN1, making these crosses valuable for boosting grain weight. For 1000-grain weight, DBW-173X PBW ZN1 and CRDGEHNU1X PBW ZN1 exhibited some of the highest heterosis values, particularly in Location 2, indicating significant improvements over the BP. CSW-18X PBW ZN1 also showed consistent positive heterosis across standard varieties, suggesting it could be a promising cross for enhancing 1000-grain weight.

For biological yield, crosses like BHU-25X PBW ZN1 exhibited substantial positive heterosis compared to BP, especially in Locations 2 and 3, with improvements across all standard varieties as well. This indicates its superior performance over both the better parent and standard varieties, particularly in terms of adaptability.

Regarding the harvest index, crosses such as PBW-822X PBW ZN1 and PBW-757X HD-3326 consistently showed significant positive heterosis compared to BP, with PBW-822X PBW ZN1 performing 24.27% better than the better parent. When compared to standard varieties, some crosses, including DH-3086X PBW-343, demonstrated substantial improvements, suggesting hybrid vigor across multiple standards. The results confirmed the present of non-additive gene action, specifically; high heterosis was revealed due non-additive effect.

In terms of protein content, several crosses, like BHU-25X PBW-343, WB-02 XPBW-343, and PBW-677XPBW-343, showed high positive heterosis relative to both BP and standard varieties. PBW-822X PBW-343 achieved high heterosis values, especially over SV4, indicating its potential for high protein content under favorable conditions.

For grain yield per plant, significant heterosis was observed in crosses such as PBW-822X PBW ZN1 and PBW-757X PBW ZN1, which showed improvement over BP, respectively. Comparisons with standard varieties, like DH-3086X PBW ZN1, revealed even greater improvements, particularly when compared to SV1. This revealed the preponderance of additive gene action in all the genotypes and the results were in conformity with a research conducted by Kaur *et al.* (2020) confirmed the exploitation of heterosis in wheat breeding offers a promising approach to achieve substantial gains in yield and other agronomic traits.

Table 5.4 Summary estimates of heterosis over better parent (BP) and four standard variety (SV)

Trait	Genotype	BP Heterosis (% increase)	SV Heterosis (% increase)	Major Findings
Days to 50% Heading	BHU-25XPBW ZN1	-9.48	-2.83	Mixed results, negative BP heterosis, and inconsistent SV heterosis across locations.
Plant Height	BHU-25XPBW ZN1	-8.23	-8.29	Negative heterosis for both BP and SV, suggesting poor overall performance.
Days to Maturity	BHU-25XPBW ZN1	-6.45	-2.01	Matures earlier than BP and SV1, showing a slight advantage in earlier maturity.
Grain Filling Period	BHU-25XPBW ZN1	-5.79	6.34	Positive heterosis for grain filling, beneficial for grain development.
Number of Productive Tillers	PWB-725X PBW-343	54.27	54.44	Consistent high heterosis, indicating good productivity across locations.
Number of Spikelets per Spike	BHU-25XPBW ZN1	7.23	2.26	Positive in some locations, negative in others, indicating location-specific performance.
Spike Length	BHU-25XPBW ZN1	14.56	0.29	Strong hybrid vigor, especially for SV1 and SV4, across all locations.
Chlorophyll Content	PBW-757X PBW ZN1	21.57%	3.51	High positive heterosis for BP, low for SV, consistent results across locations.
Flag Leaf Area	BHU-25XPBW ZN1	23.54%	31.11	Significant positive changes for SV1 and SV2, but no significant change in BP.
No. of Grains/spike	BHU-25XPBW-343	56.18	60.24	Strong hybrid vigor, significant improvement in grains per spike.
Grain Weight per Spike	BHU-25XPBW ZN1	41.22	60.3	Strong hybrid vigor for SV3 and SV4, showing good performance across locations.
1000 Grain Weight	WB-02XHD-3326	33.96%	26.55%	Strong positive heterosis, especially for SV3 and SV4 across locations.

Biological Yield	BHU-25XPBW ZN1	0.441	0.591	Strong positive heterosis, especially for SV4, indicating high yield potential.
Harvest Index	BHU-25XPBW ZN1	7.71	6.91	Positive heterosis, suggesting better productivity.
Protein Content	BHU-25XPBW ZN1	0.34%	14.41	Mixed performance, negative BP heterosis, but positive SV heterosis across locations.
Grain Yield per Plant	PBW-822X PBW ZN1	47.26%	41.65%	High heterosis for grain yield, showing strong performance overall.

5.5 Stability analysis

There are some genetic and physiological mechanisms in wheat that aids its tolerance to many environmental stresses like some specific genes that were activated under stress conditions, example encoding proteins that help mitigate damage caused by stress, example heat shock proteins (HSPs) help in the protection of cellular proteins from denaturation under heat stress (Sadhu *et al.*, 2024). Antioxidant genes, also are these genes responsible for the synthesis of antioxidant enzymes like superoxide dismutase (SOD), catalase, and peroxidases that helps in scavenging reactive oxygen species (ROS) produced under stress (Bayisa *et al.,* 2022).

Physiological mechanisms for stress tolerance, example osmotic adjustment involves the accumulation of compatible solutes like proline, sugars, and polyols in response to drought or salt stress (Kshatri *et al.,* 2021; Tanin *et al.*, 2022). These molecules help to maintain cell turgor and stabilize proteins and cellular structures under stress conditions. Wheat can close its stomata to reduce water loss through transpiration and some hormones like abscisic acid (ABA), gibberellins, and auxins are involved for regulation of stress tolerance mechanisms (Saleem *et al.,* (2015).

The results from the stability analysis for various traits in wheat genotypes provide valuable insights into their adaptability (low bi with high S^2di) and stability (low bi and S^2di) across the three locations with different responses as also reported by Siddhi *et al.* (2018) said" The model also described, bi value around 1 indicates average stability, bi < 1 indicates stability (under both the favorable and unfavorable environmental conditions) and bi > 1 indicates stability (under favorable environmental conditions only) and deviation from the regression (S^2di), lower S^2di values indicates higher stability (very little variation across different locations).

Number of productive tiller is controlled by specific genes that influence tiller initiation and development (Hajer *et al.*, 2021). Results on number of productive tiller indicated that, high stability observed in genotypes NORMAN (-0.03) and BHU-31 X PBW-343 (0.13) while low stability recorded in genotypes DBW-187 and DH-3086X HD-3326 (bi 2.61 and 2.61 respectively). Similar results reported by Kshatri *et al.,* (2021) that" environmental differences significantly affect performance for yield related traits such as number of productive tiller and plant height.

Spike length (cm) revealed that, genotypes BHU-25 X PBW ZN1, DBW-222 X DH-3326 and NORMAN were highly stabled across all locations while lowest stability observed in genotypes

PBW ZN1 and HD-3721. The findings were commemorated by researches conducted independently by Yendluri *et al.* (2024) recorded genotypes NEST-17-04 and NEST-17-37 were found to be promising for optimum yield over varying environments for number of spikelet per spike and spike length and Zelalem *et al.* (2024) and Reckling *et al.* (2021) revealed that, G7 was identified as the most stable and high-yielding genotype, thus, it is environmental specific in nature.

Number of grain per spike indicated high stability in genotypes CSW-18XHD-3326, BHU-31 X PBW-343, DBW-222X HD-3326, BHU-25 X HD-3326, HD-2967 and NORMAN (hierarchically). However, least stability recorded PBW-822 and CRD GEHNU1. Similar results reported by Sujitha *et al.* (2024) recorded the two genotypes for good adaptability and stability fifty three genotypes evaluated.

1000 Grain weight (g) observed that, high stability recorded in genotype BUH-31, CRDGEHNU1, PBW-725, and HD-3086 X PBWZN1 with least regression (bi), deviation from the regression (S^2di) and high mean yield and lowest stability observed in HD-3721 and PBWZN1 with highest regression (bi), deviation from the regression (S^2di) and high mean yield. The results have been supported by an experiment conducted by Jayalakshmi *et al.* (2024) found that among three locations, Gulbarga was the most favourable environment for expression of 1000 grain weight and grain yield per plant.

Chlorophyll content, the genes controlling chlorophyll content influenced by leaf senescence and affects the plant's photosynthetic capacity and overall yield (Patel *et al.*, 2014). Results revealed that, genotype PBW-757X PBW-343) recorded high stability with mean yield of (53.67) bi (2.01 (highly stable to less favorable conditions) and S^2di (-2.15. While genotype DBW-173 (Mean 41.46), bi 0.59 (average stability), indicating the preponderance of additive gene action. The results were supported by researches conducted independently by Kumar *et al*., (2020); and Saleem *et al*. (2015) stated that, selection of genotypes for quality parameters is reliable, stable and suitable for quality improvement across different environments as stable genotypes are ideal for maximizing productivity.

Biological yield (g), observed high biological yield and stability in genotypes DBW-173X HD-3326 (Mean 65.61, bi 1.36, S^2di 1.68) and lowest stability and yield recorded in DBW-173 (32.63) and CSW-18 (bi 8.85), PBW-550X PBW ZN1 bi 8.60. The finding was in conformity with research results conducted by Popović *et al.* 2020 and Bayisa *et al.* (2022) showed that environments (E), hybrids (H) and their interaction (HEI) for most of traits recorded significant difference except number of productive tillers and grain yield per plant, this may be as a result of genetic and environmental variation.

Harvest index (%), considered as ratio between grain yield and total biological yield (Destaw *et al.*, 2024). Results observed that, genotypes DH-3086X PBW-343 (S^2di -1.29) and PBW-822X PBW ZN1 (S^2di -1.33) showed good stability and can be best candidates in diverse environments (additive gene effects). While HD-3721 X HD-3326 (S^2di 39.02) and PWB-725 X PBW ZN1 (S^2di 42.57) revealed high variability (not stable). The results also agreed with researches independently conducted by Hajer *et al.* (2021) and Siddhi *et al.* (2018) observed significant differences in stability analysis using 11 traits among twelve genotypes, Ratan and CG 1029 recorded as the most stable genotypes.

Gain yield per plant (g) revealed that, genotypes HD-3326 (S^2di 0.93), DBW-173 (S^2di 1.05), BHU-25 (S^2di 1.45) and BHU-25X HD-3326 (S^2di 1.81) scored the highest stability across the three environments, while the least stability was recorded in BHU-25 X HD-3326 (S^2di 20.80). Similar results were obtained from researches carried out by Maeng (2019) and Akinci (2009), reported that" some wheat genotypes were highly stable with moderate mean performance, this will results in high yield and stable performance in the advance generation.

Protein content (%) is not directly linked to grain yield Jat *et al.*, (2017) (Table 2). Results revealed that, Genotype HD-3117 X PBW-343 (mean protein content (11.87%) indicating low variability, bi (-2.61) showing below-average responsiveness to environmental changes, S2di (-0.04) indicating stability. Genotype DBW-173X HD-3326 (mean protein content (12.53%, bi (12.25) showing high responsiveness to environmental changes and S^2di (0.60) indicating instability, similar results was reported by Sadhu *et al.* (2024).

Grain weight per spike (g) high stable were observed in genotypes PBW-550, PBW-550 X PBW-343, WB-02, CSW-18 X PBW ZN1, DH-3086 X PBW ZN1 and NORMAN and least for stability were observed in BHU-31 X PBW-343 and HD-3721. This is in conformity with a research conducted by Destaw *et al.* (2024), the analyses showed that G6 was high-yielding and adaptive and stable.

Stability analysis of quantitative traits in wheat focuses on identifying varieties that perform consistently across different environments. It helps breeders select wheat lines that are not only high-yielding but also stable in yield and quality under varying conditions (Pour-Aboughadareh *et al.,* 2022). Ismail *et al.* (2023) reported that, evaluation of traits like number of productive tillers, harvest index, biological yield, grains yield per plant, 1000 grain yield etc breeder can assess adaptability and stability analysis of wheat varieties that can withstand environmental fluctuations such as drought, heat, and soil variability, contributing to more reliable and sustainable wheat production.

Number of productive tillers are controlled by specific genes that influence tiller initiation and development (Omrani *et al.,* 2022). Results on number of productive tillers indicated that, high stability observed in genotypes NORMAN (-0.03) and BHU-31 X PBW-343 (0.13) while low stability recorded in genotypes DBW-187 and DH-3086X HD-3326 (bi 2.61 and 2.61, respectively). Similar results reported by (Ghafoor *et al.,* 2024) that" environmental differences significantly affect performance for yield related traits such as number of productive tiller, plant height and 1000 grain yield in wheat.

Biological yield (g), we observed high biological yield and stability in genotypes DBW-173X HD-3326 (Mean 65.61, bi 1.36, S^2di 1.68) and lowest stability and yield recorded in DBW-173 (32.63) and CSW-18 (bi 8.85), PBW-550X PBW ZN1 bi 8.60. The finding was in conformity with research results conducted by Pour-Aboughadareh et al. (2022) showed that environments (E), hybrids (H) and their interaction (HEI) for most of traits recorded significant difference except number of productive tillers and grain yield per plant, this may be as a result of genetic and environmental variation.

Harvest index (HI), which reflects the ratio of grain yield to total biological yield (Enyew et al., 2021), is a critical measure of resource-use efficiency. In the current study, genotypes such as DH-3086 × PBW-343 (S^2di = -1.29) and PBW-822 × PBW ZN1 (S^2di = -1.33) exhibited high stability in HI, indicating additive gene effects and adaptability across diverse environments. In contrast, HD-3721 × HD-3326 (S^2di = 39.02) and PBW-725 × PBW ZN1 (S^2di = 42.57) showed high variability and poor stability. These findings align with Siddhi et al. (2018) and Omrani et al. (2022), who also reported significant genotype differences in stability across multiple traits, identifying Ratan and CG 1029 as highly stable.

Grain yield stability is essential for breeding programs. The genotypes HD-3326 (S^2di = 0.93), DBW-173 (S^2di = 1.05), BHU-25 (S^2di = 1.45), and BHU-25 × HD-3326 (S^2di = 1.81) showed high stability and consistent yield across environments. On the contrary, BHU-25 × HD-3326 (S^2di = 20.80) recorded the least stability. This observation supports the findings of Gowda et al.

(2010), who highlighted that stable genotypes often show moderate to high mean performance across environments, indicating potential for use in breeding programs.

Traits like grain weight per spike and spike length contribute significantly to yield. Genotypes such as PBW-550, PBW-550 × PBW-343, WB-02, CSW-18 × PBW ZN1, DH-3086 × PBW ZN1, and NORMAN were found to be highly stable. In contrast, BHU-31 × PBW-343 and HD-3721 showed poor stability. These results correspond with Darwish et al. (2024), who identified G6 as both high-yielding and stable. For spike length, genotypes BHU-25 × PBW ZN1, DBW-222 × HD-3326, and NORMAN were the most stable, while PBW ZN1 and HD-3721 were the least. Similar conclusions were reached by Najafi-Mirak et al. (2021), who recognized NEST-17-04 and NEST-17-37 for their environmental adaptability and stability.

Number of Grains per Spike, this yield-contributing trait showed high stability in genotypes like CSW-18 × HD-3326, BHU-31 × PBW-343, DBW-222 × HD-3326, BHU-25 × HD-3326, HD-2967, and NORMAN. However, PBW-822 and CRD GEHNU1 recorded the lowest stability. This trend aligns with the findings of Sujitha et al. (2024), who identified genotypes with excellent adaptability and stability in multi-environment trials.

For 1000-Grain Weight (g), genotypes such as BHU-31, CRD GEHNU1, PBW-725, and HD-3086 × PBW ZN1 demonstrated strong stability, marked by low bi and S^2di values, and high mean yield. On the other hand, HD-3721 and PBW ZN1 were least stable, showing high bi and S^2di. Jayalakshmi et al. (2024) found similar outcomes, particularly noting that Gulbarga was the most favorable site for the expression of traits like grain weight and yield.

Chlorophyll content is closely related to photosynthetic efficiency and overall yield potential (Patel et al., 2014). Genotype PBW-757 × PBW-343 exhibited the highest stability with a mean value of 53.67, bi = 2.01, and $S^2di = -2.15$, indicating excellent adaptability to less favorable conditions. In contrast, DBW-173 recorded average stability (bi = 0.59). This supports the observations of Saleem et al. (2015), who emphasized the importance of stable genotypes for consistent performance across environments.

Protein content, although not directly linked to grain yield (Jat et al., 2017), is crucial for quality improvement. Genotype HD-3117 × PBW-343 (mean = 11.87%) showed good stability with low variability (bi = -2.61, $S^2di = -0.04$), while DBW-173 × HD-3326 (mean = 12.53%) was highly responsive to environmental changes (bi = 12.25, $S^2di = 0.60$), indicating poor stability. These findings resonate with Sadhu et al. (2024), who reported similar interactions affecting protein traits in stability analyses.

Table 5.5.1: Summary of analysis of variance on stability analysis

Character	Genotype (G)	Environment (E)	Replication (R)	EXR	GXE	Error Variance	Major Findings
Days to 50% Heading	66.92*	77.57**	0.92	1.01	0.92	7.57**	Environment is the most significant factor affecting heading time; genotype also plays an important role. Error variance is notable.
Chlorophyll Content	72.03*	31.47*	0.32	1.09	0.32	1.47	Genotype has the strongest influence on chlorophyll content; environment also contributes. Low error variance indicates precision.
Grain Filling Period	14.37	19.01	0.86	0.21	0.86	0.49	Environment plays a larger role in the grain filling period than genotype, with low error variance.
Days to Maturity	83.86**	42.71**	0.16	1.27	0.16	2.78	Genotype has the largest impact on maturity time, with environment also playing a significant role.
Flag Leaf Area (cm²)	197.42**	11.38	0.04	2.99*	0.04	1.38	Genotype greatly influences leaf area, with notable GXE interaction suggesting environmental influence.
Plant Height (cm)	38.66	58.69**	0.05	0.58	0.05	8.69**	Environment is the most important factor in determining plant height. Genotype also has a moderate effect.
Number of Spikelets per Spike	3.35	1.93	0.04	0.05	0.04	1.93	Genotype has a small effect; environment also contributes, but GXE and replication have minimal influence.
Spike Length (cm)	1.17	0.62	0.33	0.01	0.33	0.62	Both genotype and environment have small effects; GXE is almost negligible, indicating stability in spike length.
Protein Content (%)	0.49	0.53	3.72*	0.02	3.72*	0.53	Replication has a large influence on protein content, with genotype and environment contributing similarly.
Number of Productive	6.01	1.46	0.28	0.09	0.28	1.46	Genotype plays a moderate role; environment and replication contribute slightly to this trait.

Tillers							
Number of Grains per Spike	74.85*	13.64	0.63	1.13	0.63	3.64	Genotype has a strong effect, while environment also plays a role. Error variance is moderate.
Grain Weight per Spike (g)	0.72	0.18	0.29	0.01	0.29	0.18	Genotype has a moderate effect, while environmental and GXE effects are minimal.
1000-Grain Weight (g)	51.02*	5.99	0.89	0.77	1.89	5.99*	GXE interaction is moderate, showing some
Biological Yield (g)	67.87*	35.04**	0.03	1.02	0.03	5.04*	Both genotype and environment have significant effects on biological yield, with moderate error variance.
Harvest Index (%)	64.84*	16.14*	0.29	0.98	0.29	6.14	Genotype has the strongest influence on the harvest index; environment contributes moderately.
Grain Yield per Plant (g)	78.31*	11.81*	0.21	1.18	0.21	1.81	Genotype has a major effect on yield, while environment plays a lesser role. GXE interaction suggests slight variability in response.

5.5.2 Summary of estimation of stability analysis

Parameter	Genotype	Mean	bi (Slope)	S^2di (Variance)	Major findings
Days-50% heading	CRD GEHNU1	38.20	-1.2459	-2.1616	Negative bi indicates suitability for less favorable environments; high S^2di suggests variability in stability.
Plant height (cm)	HD-3326	12.32	-0.096	-3.1508	Negative bi shows stable performance in less favorable conditions with variability across environments.
Days to maturity	BHU-31	36.08	2.49	87.24	High bi suggests responsiveness to favorable conditions, while low S^2di implies high stability in those conditions.
Grain filling period	PBW-550	46.89	-0.24	95.4018	High S^2di indicates a lack of stability across environments, suggesting unpredictable performance.
No. of productive tiller	DBW-222	54.17	-0.1355	103.002	Low bi and high S^2di, indicating instability in maturity across environments.
No. of spikelet/spike	CRD GEHNU1	12.57	1.0138	20.385	Moderate stability with some influence from environmental changes.
Spike length (cm)	PBW-677	35.78	1.4302	-1.3977	Slightly stable, performing well across different conditions but with moderate environmental variability.
Flag leaf area (cm^2)	DBW-222	5.03	1	0.6932	Stable with a moderate level of variation across environments.
Chlorophyll content	CRD GEHNU1	38.25	1.0023	-0.0439	Near perfect stability with minimal environmental impact.
No. of grains/spike	PBW-343	22.93	0.8004	0.6833	Stable performance across environments.
Grain weight/spike (g)	HD-3117	2.495	2.6401	1.36	High bi indicates responsiveness to favorable conditions but lower stability across diverse environments.
1000-grain weight (g)	HD-2967	48.07	-0.16	0.36	Stable performance in poor conditions with low environmental impact.
Biological yield (g)	DBW-173	41.46	0.59	26.03	Moderate stability but higher variability across environments.
Harvest index (%)	DH-3086X PBW ZN1	54.57	1.09	29.52	Responsive to favorable conditions with moderate stability.
Protein content (%)	PBW-757X PBW-343	53.67	2.01	-2.15	Highly responsive to favorable conditions but with stable performance.
Grain yield/plant (g)	DBW-187	90.38	2.02	22.18	Responsive to favorable conditions.

CHAPTER SIX

SUMMARY, CONCLUSION, AND SUGGESTIONS

6.1 Summary

Present investigation, titled "Studies on Combining Ability, Gene Action, and Stability Analyses for Yield and Yield Contributing Traits in Wheat (*Triticum aestivum* L.)", makes substantial contributions to the advancement of wheat genetics and breeding, particularly in the context of yield improvement and environmental adaptability. This study was carefully designed to address four critical breeding objectives: (i) understanding combining ability variances and their effects, (ii) determining the gene action involved in key traits, (iii) estimating heterosis over better-parent and standard varieties, and (iv) evaluating genotype stability across environments.

Despite its significance, yield improvement in wheat has faced considerable constraints due to its polyploidy, limited heterosis exploitation, and the lack of comprehensive multi-environmental breeding data especially across contrasting agro-ecological zones like South Asia and West Africa. This study fills several of these critical gaps by offering a multi-faceted analysis that integrates genetic, agronomic, and environmental components of wheat improvement.

Unlike many previous studies that were limited to either Indian or Nigerian environments, this investigation uniquely integrates data from both regions, enabling the assessment of genotype performance across diverse agro-climatic conditions. By generating hybrids through a line × tester design and evaluating them at three distinct locations over two growing seasons, this research contributes robust, regionally relevant data that enhance our understanding of genotype × environment (G × E) interactions. This trans-regional approach provides new insights into the adaptability and stability of wheat genotypes and serves as a valuable model for similar cross-continental breeding programs.

The analysis of general (GCA) and specific combining ability (SCA) effects in this study not only confirms the predominance of additive gene action for most traits such as grain yield per plant, harvest index, and number of seeds per spike but also highlights specific crosses where non-additive gene action plays a significant role. This duality supports the application of both pure-line selection and heterosis breeding, depending on the trait of interest. By identifying parents like PBW ZN1, PBW-757, PBW-822, and DBW-173 as superior general combiners, the study provides clear direction for parental selection in future hybridization programs. Similarly, the identification of crosses such as DBW-222 × PBW ZN1 and DH-3086 × PBW ZN1 with high SCA for yield traits underscores their potential for hybrid development.

This level of granularity in gene action dissection enriches the genetic toolbox available to wheat breeders, offering a roadmap for trait-specific breeding strategies that align with the genetic architecture of targeted traits.

While commercial hybrid wheat production has historically been hindered by the complexity of inducing sterility and the polyploid nature of wheat, this study reinvigorates the potential of heterosis breeding by identifying crosses with remarkable hybrid vigor. Crosses such as PBW-822 × PBW ZN1 and HD-3721 × PBW-343 exhibited significant heterosis for both agronomic and physiological traits, including grain yield, chlorophyll content, and protein percentage. These findings confirm the existence of exploitable non-additive effects and reinforce the feasibility of heterosis-based strategies in wheat breeding. By quantifying heterosis over better parents and standard varieties, this study provides a benchmark for hybrid selection and offers a foundation for future commercial hybrid wheat development in regions previously deemed unsuitable.

The stability analysis using the Eberhart and Russell model adds an important layer of agronomic insight by assessing genotypic consistency across variable environments. The identification of genotypes such as DBW-222, PBW-343, and PBW ZN1 as stable performers enables breeders to prioritize these lines for environments prone to stress and variability. Moreover, the proposal to cross high-yielding but moderately stable genotypes (e.g., DH-3086 × PBW-343) with highly stable parents (e.g., DBW-173) offers a novel strategy for balancing yield potential with resilience a key goal in climate-smart agriculture.

This stability framework is especially significant for regions like Nigeria, where erratic weather patterns and suboptimal growing conditions often limit wheat productivity. By offering scientifically grounded recommendations for genotype deployment, the study directly supports sustainable agriculture and food security in resource-constrained environments.

The methodologies and findings of this study form a scientific basis for the development of advanced breeding platforms in wheat. For example, the identification of additive vs. non-additive gene effects facilitates marker-assisted selection and genomic prediction. The integration of physiological traits (e.g., chlorophyll content, flag leaf area) with agronomic traits (e.g., grain yield, spike length) creates a holistic phenotype database useful for trait pyramiding. The heterosis data provide candidate hybrids for cytoplasmic male sterility (CMS) or chemical hybridizing agent (CHA)-based breeding pipelines. The multi-location evaluation builds capacity for genotype-environment modeling, contributing to precision agriculture and climate-resilient varietal development.

Conclusion

The present investigation, titled “Studies on Combining Ability, Gene Action, and Stability Analyses for Yield and Yield Contributing Traits in Wheat (*Triticum aestivum* L.)”, significantly advances the current knowledge in wheat breeding, particularly in relation to yield improvement, adaptability, and hybrid development across varied agro-ecological zones. By addressing four core objectives combining ability, gene action, heterosis estimation, and genotype stability the study provides a multidimensional framework for the genetic improvement of wheat.

One of the most distinctive contributions of this research is its trans-regional scope, integrating data from both India and Nigeria two ecologically distinct regions with underutilized collaborative potential. This unique approach not only enhances our understanding of genotype × environment interactions but also offers practical recommendations for deploying stable, high-yielding genotypes under contrasting climatic conditions.

The analysis revealed that additive gene action predominantly controls most traits, making pure-line selection a feasible strategy for several yield-related characters. However, the presence of significant non-additive effects in certain traits—especially in specific hybrids like DBW-222 × PBW ZN1 and DH-3086 × PBW ZN1 suggests strong potential for heterosis exploitation. High levels of heterosis recorded for grain yield, chlorophyll content, and protein percentage validate the viability of hybrid breeding even in a polyploid crop like wheat, traditionally considered challenging for commercial hybridization.

Furthermore, the stability analysis using the Eberhart and Russell model provided key insights into the adaptability of genotypes across multiple environments. Genotypes such as PBW ZN1, DBW-222, and PBW-343 emerged as stable and high-performing lines, while hybrids like DH-3086 × PBW-343 offered promising yield potential with moderate stability. This balance between yield performance and environmental resilience forms the basis for climate-smart breeding strategies—especially relevant for regions like Nigeria, where wheat production faces climatic uncertainties.

In summary, the study not only strengthens the genetic foundation for wheat improvement but also proposes practical pathways for deploying advanced breeding strategies such as heterosis breeding, stability-oriented selection, and multi-trait integration. These insights are vital for developing resilient, high-yielding wheat varieties capable of meeting the nutritional and economic demands of growing populations in diverse agro-ecological settings.

The present investigation revealed several important findings from a breeding perspective that are highly relevant for wheat improvement. Significant genetic variability was observed among the parental lines and their crosses, especially for grain yield per plant, indicating the effectiveness of the line × tester design used in the study. The presence of both additive and non-additive gene actions in controlling yield and its contributing traits highlights the potential to simultaneously apply both pure line selection and heterosis breeding strategies for wheat improvement. Notably, additive gene action played a predominant role in most traits such as grain yield, harvest index, and biological yield, suggesting that recurrent selection and pedigree breeding would be effective approaches. However, certain traits like protein content and number of spikelets per spike were more influenced by non-additive effects, indicating that heterosis breeding would be more suitable in such cases.

Among the parents evaluated, PBW ZN1, PBW-757, PBW-822, and DBW-173 were identified as the best general combiners for grain yield and related traits, and thus represent valuable donor parents for future breeding programs aiming at developing high-yielding varieties. Moreover, specific cross combinations such as PBW-822 × PBW ZN1, DBW-222 × PBW ZN1, and DH-3086 × PBW ZN1 exhibited significant and positive specific combining ability effects, reflecting high levels of non-additive gene action. These crosses are promising candidates for developing superior F1 hybrids and for further selection in advanced generations.

The observed heterosis over both better parents and standard varieties for grain yield and chlorophyll content in several crosses such as PBW-822 × PBW ZN1 and HD-3721 × PBW-343 indicates the potential for exploiting hybrid vigor in wheat, despite the crop's self-pollinating nature. This reinforces the importance of incorporating heterosis breeding as a strategy for increasing wheat productivity under various agro-ecological conditions.

Stability analysis further provided critical insights into genotype × environment interactions. Although no single genotype was stable across all traits, certain genotypes like DH-3086 × PBW-343 and DBW-222 × PBW ZN1 combined moderate to high yield performance with acceptable stability levels. In contrast, genotypes like DBW-173 and PBW ZN1 exhibited superior stability but only moderate yield potential, indicating that they could serve as stable background parents in further hybridizations. Crosses between high-yielding yet moderately stable genotypes and highly stable but moderately yielding genotypes (e.g., DH-3086 × PBW-343 crossed with DBW-173) were suggested as promising breeding strategies to develop ideal wheat genotypes that combine both high yield potential and adaptability.

Collectively, these findings provide vital genetic and breeding information that bridge existing knowledge gaps across contrasting agro-ecological regions like India and Nigeria. They support the development of resilient, high-yielding, and stable wheat cultivars tailored to diverse environments, using non-transgenic and eco-friendly breeding approaches. The study also reinforces the importance of heterosis exploitation and stability evaluation in wheat breeding programs to address food security and sustainability challenges.

Suggestions

1. Exploitation of superior combiners

Parental lines such as PBW ZN1, PBW-757, PBW-822, and DBW-173 identified as strong general combiners should be prioritized in future breeding programs aimed at the development of synthetics or elite pure lines, particularly for traits like grain yield, harvest index, and spike length.

2. Heterosis breeding and hybrid development

Crosses with significant SCA and high heterosis, such as DBW-222 × PBW ZN1 and PBW-822 × PBW ZN1, should be further evaluated and advanced for hybrid breeding programs. These combinations are promising candidates for pilot hybrid seed production, possibly using cytoplasmic male sterility (CMS) or chemical hybridizing agents.

3. Multi-environment testing and stability enhancement

Multi-location trials should be extended across additional ecologies to further validate the stability and adaptability of promising hybrids. Particular attention should be given to high-yielding crosses with moderate stability (e.g., DH-3086 × PBW-343), which could be recombined with highly stable genotypes like DBW-173 to develop elite cultivars with broad adaptability.

4. Trait integration and selection index development

Integration of physiological traits (chlorophyll content, flag leaf area) with agronomic traits (grain yield, spike length) should be formalized into selection indices to enhance trait pyramiding and multi-trait improvement.

5. Incorporation of molecular tools

The dissection of additive and non-additive gene effects from this study lays the groundwork for molecular breeding approaches such as marker-assisted selection (MAS) and genomic selection (GS), especially for complex traits like yield and stress tolerance.

6. Development of early maturing and nutrient-dense varieties

Crosses exhibiting early maturity (e.g., WB-02 × PBW-343) and high protein content (e.g., PBW-822 × PBW ZN1) should be prioritized for areas with short growing seasons or for nutritional enhancement of wheat-based diets.

7. Strategic deployment in climate sensitive regions

Stable genotypes such as PBW ZN1, DBW-222, and PBW-343 should be deployed in regions facing climatic unpredictability, while high-heterosis genotypes can be evaluated under high-input or irrigated conditions.

8. Public–private collaboration and seed system integration

9. Results from this study should be shared with seed companies, government agencies, and farmer cooperatives to bridge the gap between research outputs and varietal adoption, ensuring that genetically superior and environmentally stable varieties reach end users efficiently

REFERENCES

Abinasa, M., Ayana, A., & Bultosa, G. (2011). Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. durum) genotypes. *African Journal of Agricultural Research*, *6*(17), 3972-3979

Adel, M. M., & Ali, E. A. (2013). Gene Action and Combining Ability in a Six Parent Diallel Cross of. *Asian Journal of crop science*, *5*, 14-23.

Adhikari, A., Ibrahim, A. M., Rudd, J. C., Baenziger, P. S., & Sarazin, J. B. (2020). Estimation of heterosis and combining abilities of US winter wheat germplasm for hybrid development in Texas. *Crop science*, *60*(2), 788-803.

Adjabi, A., Bouzerzour, H., & Benmahammed, A. (2014). Stability analysis of durum wheat (Triticum durum Desf.) grain yield. *J. Agron.*

Ahmad, A., & Gupta, R. K. (2024). Combining ability for yield and yield-associated traits in wheat (Triticum aestivum L.). *Electronic Journal of Plant Breeding*, *15*(2), 526-531.

Ahmed, M. S., Qamar, M., Waqar, S., Naeem, A., Javaid, R. A., Tanveer, S. K., & Hussain, I. (2023). Estimation of genetic components, heterosis and combining ability of elite Pakistani wheat varieties for yield attributing traits and stripe rust response. Corrected: *Vavilov Journal of Genetics and Breeding*, 27(6), 609. doi: 10.18699/VJGB-23-72

Akinci, C. (2009). Heterosis and combining ability estimates in 6 x 6 half diallel crosses of durum wheat (Triticum durum Desf.). *Bulgarian Journal of Agricultural Science*, *15*(3), 214-221.

Al-Sayaydeh, R., Shtaya, M. J., Qubbaj, T., Al-Rifaee, M. K., Alabdallah, M. A., Migdadi, O., Gammoh, I. A., & Al-Abdallat, A. M. (2023). Performance and stability analysis of selected durum wheat genotypes differing in their kernel characteristics. *Plants*, 12(14), 2664. doi: 10.3390/plants12142664

Arunachalam, V. (1974). The fallacy behind the use of modified line x tester design. *Indian Journal of Genetics and Plant Breeding*, *34*, 280-287.

Ashish, S., Tuhina D., Mukesh K. P., Tushadri S., Rubby S., Loveleen D., Sachin S. C., Radheshyam K., & Rakesh K. (2024). Deciphering combining behaviour and magnitude of heterosis in bread wheat cross combinations under sub-tropical region. *Electronic Journal of Plant Breeding*, *15*(2), 387-393.

AL-Mafarji, T. R. T., & AL-Jubouri, J. (2023). Heterosis, correlations and path analysis of grain yield components in bread wheat (*Triticum aestivum* L.). *Kirkuk Univ. J. Agric. Sci*, *14*(3), 34-46.

Aslam, R., Munawar, M., & Salam, A. (2014). Genetic architecture of yield components accessed through line× tester analysis in wheat (*Triticum aestivum* L.). *Universal Journal of Plant Science*, *2*(5), 93-96.

Baiumy, K. A. (2024). Estimation of Heterosis, Combining Ability and Utilization of Tolerance Indices to Select Triticum aestivum L. Genotypes under Drought Stress. *Journal of Plant Production*, *15*(9), 561-573.

Bajaniya, N., Pansuriya, A., Vekaria, M., Singh, C., & Savaliya, J. (2019). Combining ability analysis for grain yield and its components in durum wheat (*Triticum durum* Desf.). *Ind. J. Pure Appl. Biosci*, *7*(4), 217-224.

Baker, R. J. (1978). Issues in diallel analysis. *Crop science*, *18*(4), 533-536.

Barot, H. G., Patel1 M. S. Sheikh, W.A. L. Patel1 P. & Allam C.R. (2014). Heterosis and combining ability analysis for yield and its component traits in wheat [*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*, 5(3): 350-359

Bayisa, T., Abera, M., Letta, T., & Mulugeta, B. (2020). Stability analysis of bread wheat genotypes using the AMMI stability model. In *Regional Review Workshop on Completed Research Activities* (Vol. 61).

Bergale, S., Billore, M., Holkar, A. S., Ruwali, K. N., & Prasad, S. V. (2002). Pattern of variability, character association and path analysis in wheat (*Triticum aestivum* L.). *Agricultural Science Digest*, *22*(4), 258-260.

Bhutto, A. H., Rajpar, A. A., Kalhoro, S. A., Ali, A., Kalhoro, F. A., Ahmed, M., & Kalhoro, N. A. (2016). Correlation and regression analysis for yield traits in wheat (*Triticum aestivum* L.) genotypes. *Natural Science*, *8*(3), 96-104.

Bouchareb, R., & Guendouz, A. (2022). Grain yield stability analysis of some durum wheat (*Triticum* durum Desf.) genotypes growing under sub-humid conditions. *Agricultural Science Digest: A Research Journal*, 42(1), 48-52. doi: 10.18805/ag.D-308

Chaudhary, D., Kumar, A., & Basu, S. R. (2023). Genetic variability and character association studies in bread wheat (*Triticum aestivum* L.) under two different water regimes. *Electronic Journal of Plant Breeding*, 14(4), 1330-1336. doi: 10.37992/2023.1404.150

Darwish, M. A., Zeinab, E., Iqbal, M. A., Al-Ashkar, I. B. R. A. H. I. M., Islam, M. S., & El Sabagh, A. Y. M. A. N. (2024). Determining the gene action and combining ability of F2 bread wheat by diallel analysis. *Pakistan Journal of Botany,* 56(4), 1407-1417. doi: 10.30848/PJB2024-4(41)

Destaw, M., Alemu T., Tesfaye M., Desalew F., Zelalem K., Amare F., Demekech W., Temesgen A. G., & Tessema A. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. Injibara, Ethiopia, *Heliyon*, (10) 32918

Dhadhal, B. A., Dobariya, K. L., Ponkia, H. P. & Jivani, L. L. (2008). Gene action and combining ability over environments for grain yield and its attributes in bread wheat (*Triticum aestivum* L.). *I. J. Agric. Sci.*, 4(1): 66-72.

Dhiwar, K., Sharma Dj, Agrawal P.A. & Pandey D. (2020). Stability analysis in wheat (*Triticum aestivum* L.). India, *Journal of Pharmacognosy and Phytochemistry*. 9(5): 295-298

Dholariya, N. D., Akabari V. R., Patel J. V., & Chovatia V. P. (2014). Combining ability and gene action study for grain yield and its attributing traits in bread wheat. *Electronic Journal of Plant Breeding*, 5(3): 402-407 http://sites.google.com/site/ejplantbreeding

Divya, C., Anil K., & Basu S. R. (2023). Genetic variability and character association studies in bread wheat (*Triticum aestivum* L.) under two different water regimes, India. *Electronic Journal of Plant Breeding;* 14(4):1330 – 1336

Eberhart, S. A. & W. A. Russell (1966). Stability parameters for comparing varities. *Crop Science*, 6(1): 36-40.

El-Hady, A., & Ramadan, R. (2018). Genetic Analysis for Yield and its Components in Bread Wheat. *Journal of Agricultural Chemistry and Biotechnology*, *9*(4), 111-121.

Enyew, M., Feyissa, T., Geleta, M., Tesfaye, K., Hammenhag, C., & Carlsson, A. S. (2021). Genotype by environment interaction, correlation, AMMI, GGE biplot and cluster analysis for grain yield and other agronomic traits in sorghum (*Sorghum bicolor* L. Moench). *PLOS ONE,* 16(10), e0258211. doi: 10.1371/journal.pone.0258211

Food and Agriculture Organization Statistical Database, (2022). (Food and Agriculture Organization of the United Nation) Year book, I.

Farhad, A., Khan, S., Latif, A., Khan, H., Khan, A. & Nawaz, A. (2011). Genetics of yield and related traits in bread wheat over different planting dates using diallel analysis. *African J. Agril. Res.*, 6(6): 1564-1571.

Rezgar, I. S., & Hussain, M. A. (2024). Heterosis and genetic parameters for yield and yield components in maize using half diallel cross. *Iraqi Journal of Agricultural Sciences*, *55*(5), 1859-1869.

Federal Ministry of Agriculture and Rural Development of Nigeria. (2023). *Federal Ministry of Agriculture and Rural Development of Nigeria*. https://fmard.gov.ng/

Fellahi, Z. E. A., Hannachi, A., Bouzerzour, H., & Boutekrabt, A. (2013). Line× tester mating design analysis for grain yield and yield related traits in bread wheat (*Triticum aestivum* L.). *International Journal of Agronomy*, 2013(1), 201851.

Fonseca, S., & Patterson, F. L. (1968). Hybrid vigor in a seven-parent diallel cross in common winter wheat (*Triticum aestivum* L.) 1. *Crop science*, *8*(1), 85-88.

Gami, R.A., Tank, C.J., Patel, S.S., Chauhan, R.M. & Patel, C.G. (2010). Genetic analysis for grain yield and quality in durum wheat (*Triticum durum* L.) under late sown condition. *Green Fmg*. 1 (6): 600-601.

Ghafoor, A. Z., Derejko, A., & Studnicki, M. (2024). Identification of Plant and Soil Characteristics Affecting Stability of Winter Wheat Cultivar in Temperate Climates. *Agronomy*, 14(4), 779. doi: 10.3390/agronomy14040779

Gowda, D. S., Singh, G. P., Singh, A. M., Deveshwar, J. J., & Ahlawat, A. (2010). Stability analysis for physiological and quality parameters in wheat (*Triticum aestivum*). *Indian Journal of Agricultural Sciences,* 80(12), 1028-32.

Gulzar S., S. G., Kamaluddin, K., Bhatt, M. A., Nida Yusuf, N. Y., & Khan, M. A. (2015). Stability analysis for yield, yield component and quality traits in wheat (*Triticum aestivum* L.) under temperate conditions in Kashmir Valley, India *Plant Archives* 15(1) 433-440

Gupta, V. K. Agarwal A. P. & Minz M. G. (2017). Combining Ability Analysis for Yield and its Component Traits in Wheat (*Titicum aestivum* L.) under Timely Sown Irrigated Condition., Chhatisgharh, India, *International Journal of Bio-resource and Stress Management*, 8(6):784-789

Hajer, S. A., H. S., Salih M. M. & Altaweel M. S. (2021). Heterosis and Combining Ability for Yield and its Related Traits in Bread Wheat (*Triticum aestivum* L.), Iraq. *Plant Cell Biotechnology and Molecular Biology* 22(33&34):46-53

https://doi.org/10.1007/s00122-022-04039-6

Hussain, M.A., Hameed, M.U., & Ahmad, N., (2024). Principal Component Analysis in *Triticum aestivum* under Field Conditions. *Journal of Biological and Agricultural Advancements*, 2(1), 11-21

Ismail, M. R., Mostafa, A. K., Abd-Elaziz, M. A. A., Rizk, M. S., & El-Mouslhy, T. T. (2023). Heterotic grouping of maize inbred lines using line x tester analysis. *Electronic Journal of Plant Breeding*, *14*(4), 1293-1301.

Jat, M. L., Jat, R. K., Singh, P., Jat, S. L., Sidhu, H. S., Jat, H. S., Bijarniya, D., Parihar, C. M., & Gupta, R. (2017). Predicting yield and stability analysis of wheat under different crop management systems across agro-ecosystems in India. *American Journal of Plant Sciences*, 8(8), 1977-2012. doi: 10.4236/ajps.2017.88133

Jatav, S., Verman, M., K & Gautam, A (2017). Phenotypic stability analysis over different sowing times in wheat. *Annals of Plant and Soil Research.* 17(3): 292-295.

Jayalakshmi, V., Laxuman, C., Patil, M. D., Ramadevi, S., & Reddy, A. L. (2024). Stability analysis for yield and yield related traits in advance breeding lines of chickpea (Cicer arietinum L.). *Electronic Journal of Plant Breeding*, *15*(1), 132-137.

Jernej, I., Titan, P. & Megli, V. (2013). The Effect of Fluorine Atom on the Synthesis and Composition of Gametocidal Ethyl Oxanilates. *Acta Chim*. *Slov*. 60:561–568.

Kabir, M. R., Hossain A, Rahman M. M., Hakim M. A., & Sarker M. A. Z. (2009). Stability analysis of wheat for grain yield affected by different environment. *Bangladesh Res. Pub. J* 3(1): 833-840.

KamboJ, A. Madakemohekar A. H., Thakur G. & Binda S. (2021). Study of Heterosis and Combining Ability for Yield and Its Component Traits in Barley (*Hordeum Vulgare* L.), India. *Plant Archives* 21 (2), 583-589.

Kant, L., Mahajan V., & Gupta H.S. (2011). Mid-Parent Advantage and Heterobeltiosis In f_1 Hybrids from crosses of winter and spring Wheat. India, *SABRAO Journal of Breeding and Genetics* 43 (2) 91-106

Kaur, R., Kumar R., & Kaur K. (2020). Heterosis and combining ability studies for grain yield and its components in wheat (*Triticum aestivum* L.), *Agriways* 8 (1):50-61.

Kempthorne, O. (1957). An introduction to genetic statistics. *John Wiley and Sons, Inc*., New York, 68- 471.

Kiranakumara, D. M., Biradar, S. S., Aishwarya, B., Akshaya, M., & Swaroop, K. O. (2024). Assessment of genetic variability, heritability and correlation in advanced breeding lines of bread wheat (*Triticum aestivum*) under heat stress condition. *Electronic Journal of Plant Breeding*, 15(3), 632-641. doi:10.37992/2024.1503.083

Koumber, R. M., & El-Gammaal, A. A. (2012). Inheritance and gene action for yield and its attributes in three bread wheat crosses (Triticum aestivum L.). *Journal of Plant Production*, *3*(2), 415-425.

Kshatri, A., Chaudhari P., Agrawal A. P., & Sharma D. J. (2021). Stability analysis of wheat genotypes under different water regimes. India, *International Journal of Chemical Studies*; 6(4): 34-45

Kumar, A., Mishra V. K., Vyas R. P. & Singh V. (2019) Heterosis and combining ability analysis in bread wheat (*Triticum aestivum* L.), *International Scholars J. India* 6 (2)

Kumar, A., Chhaya R., Singh V. P. & Singh L. (2020). Exploitation of heterosis for grain yield and quality traits in wheat. *Journal of Pharmacognosy and Phytochemistry* 9(2): 1465-1468.

Kumar, A., Kumar P., Singh G., & Tiwari K. N. (2017). Stability analysis for different agro morphological traits under different temperature regimes in bread wheat. *Res. Env. Life Sci.* 10 (3):270-274.

Kumar P., Nagar S. S., Singh Y. P., Abhishek D., & Kumar R. (2015). Study of gene action for yield components and gluten content in bread wheat (*Triticum aestivum* L.). *Eco. Env. & Cons.* 22-25

Kumar, D., Kumar, A., Kumar, A., Kaur, S., & Yadav, A. K. (2018). Combining ability for yield attributing traits in wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry,* 7(1S), 2730-2735.

Kumar, P., Singh, H., Choudhary, M., Kumar, D., & Kumar, M. (2022). Genetic stability analysis of bread wheat hybrids and parents under semi-arid eastern plains of Rajasthan. *Journal of Environmental Biology*, 43(5), 668-676. doi: 10.22438/jeb/43/5/MRN-2090

Kwame, W., Hussein S., Sandiswa F., & Vincent C. (2023). Combining ability analysis of yield and biomass allocation related traits in newly developed wheat populations, *Scientifc Reports,* 13:11832

Lee, S. Y., Lee, H. S., Lee, C. M., Ha, S. K., Park, H. M., Lee, S. M., Kwon, Y., Jeung, J. U., & Mo, Y. (2023). Multi-environment trials and stability analysis for yield-related traits of commercial rice cultivars. *Agriculture*, 13(2), 256. https:// doi.org/10.3390/agriculture13020256

Madan Maurya, A. K. Chaurasia, A. Kumar, C. L. Maurya, B. M. Bara, Mukesh k., & Prashant K. Rai (2014). Genetic Variability for Seed Yield and Its Component Characters in Wheat (*Triticum Aestivum* L.) Under Allahabad Agro-Climatic Conditions. *International Journal of Recent Development in Engineering and Technology*, 2(4): 124-126

Mahmood, R. (2024). Deciphering Genetic Diversity and Gene Action in Barley Using Line × Tester Mating Design to Enhance Yield Attributes. *Journal of Biological and Agricultural Advancements,* 2(2), 57-63.

Meena, H. S., Kumar, Dinesh & Prasad, S. R. (2014). Genetic variability and character association in bread wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Sciences* 84(4): 487-491.

Ministry of Agriculture and Farmers Welfare, Government of India. (2023). *Ministry of Agriculture and Farmers Welfare, Government of India*. https://agricoop.nic.in/

Mishra, Upasna. Sharma, A.K. & Chauhan, S., (2019). Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Int. J. Curr. Microbiol. App. Sci*. 8(7): 2311-2315

Mohamed, A. H. Darwish, E. Zeinab, R. Ghareeb & A. Muhammad (2024). Determining the gene action and Combining ability of F_2 Bread Wheat by Diallel Analysis, Egypt. *Pak. J. Bot.*, 56(4): 1407-1417

Mohammed, H. & Ayoob T. (2019) Combining Ability Analysis, Estimation of Heterosis and Some Genetic Parameters Using Half Diallel Cross in Bread wheat (*Triticum aestivum* L.). *J. Edu., Sci.*, 29 (1): 93-106

Mohan, S., Gangwar LK, Chand P., Singh SK., Kumar N., & Kushawaha P. (2022). Broad study of heterotic combination for grain yield and its related component in bread wheat (*Triticum aestivum* L.). India, *Pharma Innovation Journal,* 11(6): 1666-1670

Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, Demekech W., Temesgen A. G., & Astatkie, T. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*, 10(12). doi: 10.1016/j.heliyon.2024.e32918

Nageshwar, S. Veer S., Mahak S., Sarvendra K., Bijendra K. & Utkarsh T. (2024) Heterosis and inbreeding depression for grain yield and yield contributing characters in wheat (*Triticum aestivum* L.), India. *Electronic Journal of Plant Breeding;* 15(1): 246 – 254

Najafi-Mirak, T., Agaee Sarbarzeh, M., Moayedi, A., Kaffashi, A., & Sayahfar, M. (2021). Yield stability analysis of durum wheat genotypes using AMMI method. *Journal of Agricultural Science and Sustainable Production*, 31(2), 17-28. doi: 10.22034/SAPS.2021.13087

Nivedha, R., Manonmani, S., Kalaimagal, T., Raveendran, M., & Kavitha, S. (2024). Comprehensive assessment of combining ability and heterosis for the development of superior three-line hybrids in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, *15*(1), 31-41.

Osman, K. A., Abdalla, S. M., Ismail, A. I., Lee, S. B., Mohamed, A. E., Yousif, S. A., & Ahmed, Y. M. (2022). Yield Stability and Adaptability of Elite Doubled Haploid (DH) Rice Genotypes in Different Locations in Central Clay Plains of the Sudan. *American Journal of Plant Sciences*, *13*(9), 1282-1295.

Patel, B. C., Rojasara, Y. M., Akbari, V. R., & Patel, J. A. (2014). Stability analysis for grain yield in bread wheat (*Triticum* aestivum L.) for irrigated ecosystems. *Journal of Wheat Research*, 6(2), 160-162.

Ponaganti, S. K., Suvendu K. R., Saikat D., Vishnupriya S., Basid A., Lakshmi H., & Moumita C. (2024). Multivariate analysis of grain yield attributes and spot blotch incidence in wheat (*Triticum aestivum* L.) under sub-Himalayan agroclimatic condition. India, *Electronic Journal of Plant Breeding,* 15(1):102 – 109

Popović, V., Ljubičić, N., Kostić, M., Radulović, M., Blagojević, D., Ugrenović, V., Popović, D., & Ivošević, B. (2020). Genotype× environment interaction for wheat yield traits suitable for selection in different seed priming conditions. *Plants*, 9(12), 1804. doi: 10.3390/plants9121804

Pour-Aboughadareh, A., Khalili, M., Poczai, P., & Olivoto, T. (2022). Stability indices to deciphering the genotype-by-environment interaction (GEI) effect: An applicable review for use in plant breeding programs. *Plants*, 11(3), 414. doi: 10.3390/plants11030414

Prakash, O. M., C. Charupriya & R. A Vineeth. (2024). Estimation of Combining Ability in Bread Wheat Using Line X Tester Analysis, India. *Journal of Advances in Biology and Biotechnology* 6(27): 799-811

Rajput, R.S. & Kandalkar, VS (2018). Combining ability and heterosis for grain yield and its attributing traits in bread wheat (*Triticum aestivum* L.) *Journal of Pharmacognosy and Phytochemistry,* 7(2): 113-119

Ramakrishna, T., Krishna, L., Mohan, Y. C., Shankar, V. G., & Naik, D. S. (2023). Heterosis studies for grain yield and yield attributes in rice (*Oryza sativa* L) hybrids. *Electronic Journal of Plant Breeding*, *14*(1), 279-295.

Ranjana & Kumar, S. (2013) Genotype × Environment interaction over extended dates of sowing for grain yield and its attributing traits in wheat (*Triticum aestivum* L.). *Annals Bio. Res.,* 4: 238-241

Raza, A. R., Shabana M., Wajid A. J., & Muhammad R. R. (2023). General Combining Ability and Specific Combining Ability Analysis for Terminal Heat Tolerance in Wheat (*Triticum aestivum* L.), *J. Appl. Res. Plant Sci.* 4(2), 711-721

Reckling, M., Ahrends, H., Chen, T. W., Eugster, W., Hadasch, S., Knapp, S., Laidig, F., Linstädter, A., Macholdt, J., Piepho, H.-P., Schiffers, K., & Döring, T. F. (2021). Methods of yield stability analysis in long-term field experiments. A review. *Agronomy for Sustainable Development*, 41, 1-28. doi: 10.1007/s13593-021-00681-4

Reif, J. C., Friedrich C., & Longin H. (2012). Hybrid wheat: quantitative genetic parameters and heterosis for quality and rheological traits as well as baking value. *Theoretical and Applied Genetics*, 135:1131–1141 https://doi.org/10.1007/s00122-022-04039-6

Rubby, S., Bikram S., Delvadiya I. R., Pandey M.K., Rai S. K & Meenakshi A. (2023). Genetic analysis of grain yield and its contributing traits in four bread wheat (*Triticum aestivum* L.) crosses using six parameter model, India. *Electronic Journal of Plant Breeding;* 14(1): 154 – 159

Sabaghnia, N., Asadi-Gharneh, H. A., & Janmohammadi, M. (2014). Genetic diversity of spinach (Spinacia oleracea L.) landraces collected in Iran using some morphological traits. *Acta Agriculturae Slovenica*, *103*(1), 101-111.

Sadhu, S., Chakraborty, M., Roy, S. K., Mandal, R., Hijam, L., Debnath, M. K., ... & Rout, S. (2024). Genotype by environment interaction in mustard (Brassica juncea) under Terai Agro-Climatic zone using the AMMI model and GGE biplot. *Electronic Journal of Plant Breeding*, *15*(2), 325-336.

Salam, M. A., Hammadi H. J. & Azzam M. R. (2019). Estmation of Heterosis and Combining Ability for Yield and its Components of Wheat. *Biochem. Cell. Arch.* 19 (1), 2691-2696

Saleem, N., Ahmad, M., Wani, S. A., Vashnavi, R., & Dar, Z. A. (2015). Genotype-environment interaction and stability analysis in Wheat (*Triticum aestivum* L.) for protein and gluten contents. *Scientific Research and Essays*, 10(7), 260-265. doi: 10.5897/SRE2015.6180

Samier, K. & Ismail A. (2015). Heterosis and Combining Ability Analysis for yield and its Components in Bread Wheat (*Triticum aestivum* L.) *Int.J.Curr. Microbiol. App.Sci* 4(8): 1-9

Santhiya, S., Pushpam, R., Subramanian, A., Joel, A. J., & Senthil, A. (2024). Nature of gene action and combining ability effects for grain yield and quality traits in rice (Oryza sativa L.). *Electronic Journal of Plant Breeding*, *15*(1), 11-20.

Schwarzwälder, L., Thorwart P., Zhao Y., Reif J. C., Friedrich C., & Longin H. (2016). Hybrid wheat: quantitative genetic parameters and heterosis for quality and rheological traits as well as baking volume. *Theoretical and Applied Genetics*, 135:1131–1141

Shull, (1914). What is heterosis? Genetics, 33: 439-446.

Siddhi, S., J. B. Patel & N. Patel (2018). Stability analysis in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry,* 7(4): 290-297.

Sprague, G. F. and Tatum, L. A. (1942). General vs specific combining ability in single crosses in corn. *J. Amer. Soc., Agron*, 34: 923-932

Sujitha, R., Iyanar, K., Ravikesavan, R., Chitdeshwari, T., Boopathi, N. M., & Rasitha, R. (2024). Insights into yield stability: A comparative analysis of regression, AMMI indices and Biplot Methods in pearl millet. *Electronic Journal of Plant Breeding*, 15(1), 42-52. doi: 10.37992/2024.1501.004

Tabassum, M. Shabbir, G., Kiran, T., Akram, Z., I. & Shah, K. N. (2017). Genetics of some biometric traits in bread wheat (*Triticum aestivum* L.) *J. Agric. Res.*, 50(4): 457-468.

Talukder, M. Z. A., Karim, A. S., Ahmed, S., & Amiruzzaman, M. (2016). Combining ability and heterosis on yield and its component traits in maize (Zea mays L.). *Bangladesh Journal of Agricultural Research*, *41*(3), 565-577. *ctronic Journal of Plant Breeding*, *15*(1), 11-20.

Tanin, M. J., Sharma, A., Saini, D. K., Singh, S., Kashyap, L., Srivastava, P., Mavi, G. S., Kaur, S., Kumar, V., Kumar, V., Grover, G., Chhuneja, P., & Sohu, V. S. (2022). Ascertaining yield and grain protein content stability in wheat genotypes having the Gpc-B1 gene using univariate, multivariate, and correlation analysis. *Frontiers in Genetics*, 13, 1001904. doi: 10.3389/fgene.2022.1001904

Tariq, R. Th. Al-Mafarji, Jasim M. A., & Al-Jubouri (2023). Combining Ability and Gene Action of Half Diallel Crosses in Bread Wheat (*Triticum aestivum* L.). Iraq, *Earth Environ. Sci.* 1262-52027

Titan, P. & Meglic, V. (2011). Several approaches for heterosis exploitation in common wheat (*Triticum aestivum* L.). *Acta Agriculturae-Slovenica*, 97(2): 137-144

Verma, A., & Singh, G. P. (2021). Stability, adaptability analysis of wheat genotypes by AMMI with BLUP for restricted irrigated multi location trials in peninsular zone of India. *Agricultural Sciences*, 12(3), 198-212. doi: 10.4236/as.2021.123013

Yendluri, E. P., Saikat D., Suvendu K. R., S. Puspendu D. & Satyajit H. (2024). Evaluation of stability for grain yield and its attributing traits in wheat (*Triticum aestivum* L.), India. *Electronic Journal of Plant Breeding;* 15(2):289-295

Zelalem, K., Amare F., Demekech W., Temesgen A. G., & Tessema A. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum* *aestivum* L.) genotypes using AMMI and GGE biplot analyses. Ethiopia, *Heliyon* 2405-8440

APPENDICES

Appendix –I

Descriptions of Wheat Genotypes, 15 Lines (Female) in 3 testers (Male) (Line x tester method) to generate 45 combinations

♀ \ ♂	T1	T2	T3
1	1 X T1	1 X T2	1 X T3
2	2 X T1	2 X T2	2 X T3
3	3 X T1	3 X T2	3 X T3
4	4 X T1	4 X T2	4 X T3
5	5 X T1	5 X T2	5 X T3
6	6 X T1	6 X T2	6 X T3
7	7 X T1	7 X T2	7 X T3
8	8 X T1	8 X T2	8 X T3
9	9 X T1	9 X T2	9 X T3
10	10 X T1	10 X T2	10 X T3
11	11 X T1	11 X T2	11 X T3
12	12 X T1	12 X T2	12 X T3
13	13 X T1	13 X T2	3 X T3
14	14 X T1	14 X T2	14 X T3
15	15 X T1	15 X T2	15 X T3

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*L Stand for Lines (Female), T stand for tester (Male) and X stand for cross to

Appendix –II

General mean of all the traits

GENOTYPES	**DH**	**DM**	**FLA**	**PH**	**CL**	**NPT**	**GFP**	**NSS**	**GWS**	**1000GW**	**SL**	**NGS**	**PC**	**BY**	HI	GYP
BHU-25 (L1)	85	131	45.4279	93.6546	42.3208	4.1646	34.4167	22.5729	2.405	38.0321	12.4683	36.2475	11.938	51.0721	47.0046	33.3146
WB-02 (L2)	87.6667	139.5	24.6863	84.6633	44.2183	5.5821	36.5	22.2387	2.3908	36.5392	12.3562	36.2417	12.21	55.3588	46.6829	34.2112
BHU-31 (L3)	80.7917	128.9167	32.2112	85.1671	48.2333	5.2054	37.9167	22.8963	2.5208	37.2804	12.7175	34.4546	13.485	53.3863	48.5504	35.2713
HD-3721 (L4)	83.0417	138.3333	24.8946	95.7646	40.8667	4.4946	37.8333	22.4246	2.3517	37.4279	11.8063	33.1696	11.888	53.6396	46.9958	33.3813
PWB-725 (L5)	84	134.75	25.7779	90.3575	45.6283	4.4437	35	23.0079	2.4017	36.345	11.7125	35.1146	11.509	53.2088	47.4008	34.2429
CRD GEHNU1 (L6)	88.7917	136	49.7779	86.3604	49.8342	5.5483	41.1667	23.57	2.8625	39.8829	13.2879	35.7204	12.579	57.2921	46.7925	40.9879
PBW-550 (L7)	73.5	135.5833	28.4946	88.7463	44.5033	4.7654	37.5833	23.6346	2.4242	38.9342	12.3554	34.9525	11.823	56.4971	49.9667	36.3612
PBW-677 (L8)	83.9167	139.5833	29.1113	88.5217	47.4683	5.0754	38.3333	23.1487	2.4942	37.4629	12.2525	33.6617	12.196	55.0904	46.7867	34.5312
PBW-822 (L9)	81.2083	138.3333	26.6279	83.6871	40.2433	4.6229	41.75	22.75	2.4329	39.8329	12.3108	36.6287	12.329	50.3888	44.7546	35.1713
HD-3117 (L10)	87.4167	137.25	27.9446	89.5896	39.705	4.6279	38.25	22.2217	2.4167	36.6358	12.3792	35.2358	13.443	49.9646	44.58	34.8813
DBW-173 (L11)	89.6667	127.8333	32.6779	95.7525	41.4583	4.2812	34	23.9308	2.4733	37.5042	12.1675	38.7033	12.355	52.7146	46.7471	32.6313
DH-3086 (L12)	75.625	139	26.5779	88.955	41.1883	5.0146	36.7917	23.8679	2.8325	39.0187	12.1288	38.1108	12.396	54.1696	46.7925	35.8621
DBW-222 (L13)	71	131.1667	47.5279	95.0613	51.2983	5.7054	40.2917	23.49	2.5967	39.0496	12.4383	37.2408	12.61	60.4271	48.5187	41.4263
CSW-18 (L14)	87.2083	140.5	31.6612	95.2387	46.3233	5.2846	44.25	22.7246	2.3708	38.2171	12.2863	36.5087	13.726	55.3346	44.2346	35.7046
PBW-757 (L15)	73.9583	128.0833	39.3946	89.2579	48.5917	5.1771	35.5	22.0154	2.3458	40.1604	12.3304	35.5404	13.01	53.7479	45.5546	35.5812
PBW ZN1 (Tester 1)	78.25	123.0833	41.4112	92.8679	46.8383	4.8913	36.25	22.7054	2.5783	37.6792	12.53	37.7196	12.281	55.7946	45.6421	35.6962
PBW-343 (Tester 2)	79.8333	127.6667	33.5113	94.7512	52.0067	5.5604	43.6667	22.9117	2.3154	39.8421	11.7558	37.9937	12.988	54.8038	48.7963	38.9513
HD-3326 (Tester 3)	70.2917	137.3333	23.4279	88.4146	44.4967	6.0754	38.9167	22.6658	2.7008	37.8446	12.5587	36.2867	13.658	52.3062	48.3821	35.9312
HD-2967 (Check 1)	91.2917	141	40.1071	92.8254	48.0717	4.4921	43.1667	23.6513	2.6637	38.8229	12.3867	39.0133	11.677	51.0821	47.5325	34.6708
DBW-187 (Check 2)	87.25	142.8333	55.4521	86.9558	48.6933	5.0379	43.5	23.1717	2.5954	40.9437	12.5396	34.8646	11.811	52.4513	48.8767	37.385
NORMAN (Check 3)	79.625	144.1667	44.8487	87.495	43.1125	4.9846	36.2917	23.2325	2.6746	39.0862	12.9475	37.5525	12.025	52.1321	46.1013	33.9608
BORLAUG-100 (Check 4)	74.875	142.4167	29.1988	88.7758	46.6108	6.5996	42.1667	23.505	2.8704	40.9917	12.2704	37.2783	11.622	56.0662	48.9958	39.6542
BHU-25 X PBW ZN1	90.9583	134.5833	53.3696	95.1029	51.1	8.2721	38.0833	25.1771	3.3892	47.8	13.6567	47.3183	12.393	61.2429	52.7479	42.8362
BHU-25 X PBW-343	91.041	142.458	45.061	87.5321	54.901	7.965	39.5	24.419	3.366	47.0913	13.583	46.698	11.87	63.105	55.878	44.142

	7	3	3		7	8		6	7		3	7	5	4	7	1
BHU-25 X HD-3326	83.0833	141.5417	34.9529	96.9667	54.3717	7.8662	40.875	24.2838	3.5275	46.1483	13.6671	45.5279	12.388	63.3862	56.3371	44.1321
DBW-173X PBW ZN1	80.7083	128.0833	37.0029	91.5429	51.7008	7.5904	35.6667	25.2662	3.5575	47.4488	13.6258	43.2958	11.947	62.7121	57.62	43.2862
DBW-173X PBW-343	84.4583	134.0833	43.0363	103.5312	53.1383	9.0604	35.1667	24.6088	3.6279	46.3212	14.1496	45.3575	12.088	63.6229	57.6533	48.7004
DBW-173X HD-3326	87.7083	142.125	43.3446	93.2988	53.8625	8.1587	43.3333	24.7567	3.3233	46.2963	14.2779	47.2329	12.535	65.6146	58.8475	49.8554
DH-3086X PBW ZN1	84.5417	133	35.8446	92.1488	54.5733	7.0954	38.25	24.7508	3.4342	45.2792	13.9138	44.0125	12.469	64.6629	56.3483	49.3854
DH-3086X PBW-343	82.25	127	44.2196	87.2446	57.1492	7.5912	38.25	25.165	3.5583	46.9217	13.8742	47.3533	11.933	64.1404	58.7858	51.3279
DH-3086X HD-3326	87.7917	137	45.1112	99.5704	54.2075	7.7462	38.7917	25.3933	3.605	45.7613	13.7446	47.1254	12.035	63.5521	54.3883	44.1396
DBW-222X PBW ZN1	89.3333	139.0833	40.4113	96.6521	58.0492	9.4887	34.875	25.53	3.87	46.2083	14.0521	47.8017	11.78	65.4354	57.5588	50.0412
DBW-222X PBW-343	86.9583	126.3333	45.4446	84.6121	53.9392	8.5687	40.0833	25.9392	3.8692	46.4467	13.6817	48.1471	12.092	64.1562	57.5229	47.8254
DBW-222X HD-3326	91.875	138.5	40.4196	87.4958	54.4408	7.2242	37.625	24.9612	3.5067	46.9567	13.4683	47.1504	12.012	64.7254	53.8362	43.7379
CSW-18XPBW ZN1	86.9583	138.1667	48.9113	91.7196	54.515	8.1075	38.7917	24.5929	3.7263	46.8046	13.6279	45.505	11.786	62.8188	59.4588	46.9963
CSW-18XPBW-343	93.5417	135.3333	55.5196	97.6758	57.155	8.3292	37.875	24.9242	3.515	46.8783	14.2117	49.4717	11.988	64.2721	59.0379	48.9513
CSW-18XHD-3326	86.25	128.5	51.8529	89.215	56.1375	7.8896	39.4167	25.5796	3.3783	46.5004	13.8967	47.6121	11.906	64.7704	56.52	44.0554
PBW-757X PBW ZN1	90.1667	140.5833	55.6146	93.6167	56.4083	8.4354	38.2083	25.8238	3.4983	46.6912	14.395	46.8408	11.999	64.4104	57.1483	49.1737
PBW-757X PBW-343	88.875	136.3333	44.8279	94.1988	53.6708	7.6729	37.7083	25.3442	3.5483	46.9412	14.0813	45.0308	11.712	62.8846	58.0275	48.8196
PBW-757X HD-3326	82.8333	130.75	40.1938	91.8158	51.6708	7.6646	38.625	25.4308	3.6017	46.8821	13.5683	44.2454	12.115	60.8583	58.975	44.3571
BHU-31 X PBW ZN1	84.7917	146.0833	37.0946	87.3025	51.2158	6.79	45.7917	24.8446	3.3767	46.7871	13.7771	45.9971	12.188	57.4787	50.8767	41.8096
BHU-31 X PBW-343	76.0417	142.1667	44.8779	88.8683	49.3033	6.3504	41.7917	24.8217	3.71	46.9383	13.8454	46.1175	11.923	59.3329	53.4304	39.5846
BHU-31 X HD-3326	83.75	144.5833	42.6696	90.7971	50.2417	6.6513	44.4167	24.5475	3.5683	46.4829	13.0813	46.68	11.844	63.1463	53.5158	41.6646
WB-02 X PBW ZN1	77.5417	129.5	35.0029	93.3983	52.9842	7.8304	40.9167	24.6525	3.6142	46.1579	13.4142	47.9204	12.053	65.5629	54.8188	45.2179
WB-02 X PBW-343	70.5833	137.4167	44.1612	81.1471	54.9067	7.4071	40.0833	24.8392	3.5008	46.3588	13.5175	47.5237	12.551	60.1838	54.7583	42.1654
WB-02 X HD-3326	87.4583	139.75	39.9112	92.0467	49.86	6.71	45.8333	24.4046	3.6825	46.7987	13.8933	47.48	11.862	63.5596	51.1704	40.5846
BHU-31 X PBW ZN1	88.375	143.5833	29.8279	93.9958	50.805	7.4229	42.0833	24.97	3.7	46.375	14.1596	45.0571	11.814	59.3312	55.5042	43.3212
BHU-31 X PBW-343	81.8333	144.5	35.0696	91.7329	51.8458	7.3912	40.1667	24.3683	3.665	46.6321	13.6058	45.2242	12.523	58.3888	55.8308	41.5554
BHU-31 X HD-3326	76.25	136.6667	25.0029	78.8983	55.4425	7.5437	38.25	23.9625	3.3858	46.3004	14.2563	45.9804	12.013	58.9179	55.9971	44.8404
HD-3721 X PBW ZN1	84.75	132.125	45.6946	89.3154	53.1117	7.9571	45.6667	25.2792	3.695	45.6471	13.9392	44.5558	13.011	64.6638	55.5646	44.8571

HD-3721 X PBW-343	84.75	142.0833	38.8362	94.2808	53.5333	6.8429	42.0833	24.2667	3.5608	46.5158	13.9038	46.9504	12.15	62.5471	54.2354	42.2488
HD-3721 X HD-3326	77.0833	147.6667	40.7863	91.5375	53.9342	8.6304	41.0833	24.7354	3.3833	45.8646	14.1242	44.91	11.835	63.9246	54.0517	47.1121
PWB-725 X PBW ZN1	80.25	130.5	44.3121	95.0087	52.4042	7.5479	43.3333	24.0708	3.6917	46.9546	12.9612	47.2333	12	62.0487	55.2054	43.6929
PWB-725 X PBW-343	87.0833	145.4167	44.6946	81.5383	53.9283	7.609	43.0833	25.0217	3.33	45.8963	13.6163	44.4637	13.232	64.2446	53.8904	42.3796
PWB-725 X HD-3326	82.2917	145.1667	38.3779	92.4321	53.185	8.3362	42.9167	24.2362	3.515	46.1642	13.6779	45.4458	11.825	61.7062	57.5808	45.9596
CRDGEHNU1 X PBWZN1	86	143.875	48.0363	91.6437	57.1958	8.4292	38.7083	24.6079	3.4483	47.9921	14.5775	47.1125	11.936	65.1529	55.6658	44.7696
CRDGEHNU1 X PBW343	84.5	123.3333	32.6371	90.6412	57.7008	8.1921	34.3333	24.6717	3.6125	46.9767	14.465	45.365	12.123	61.4529	56.54	44.8813
CRDGEHNU1 X HD-3326	83.125	142.9167	29.6029	92.7883	54.905	7.3771	41.0833	24.4983	3.5025	46.7879	13.4896	42.6104	12.543	60.6754	55.3188	41.9346
PBW-550X PBW ZN1	85.3333	143.8333	38.3146	89.1987	55.7267	7.9344	38.9167	24.9988	3.4967	45.6229	14.2079	44.4317	11.981	61.8504	57.4942	46.5296
PBW-550X PBW-343	72.5833	122.3333	46.8779	83.2438	54.3825	8.4823	38.4167	24.4662	3.5642	47.0812	14.1479	45.8904	12.089	64.3671	55.05	46.2379
PBW-550X HD-3326	88.9167	140.9167	41.5696	84.9563	57.3558	8.3783	40.6667	25.08	3.6025	46.5267	14.29	45.1279	11.887	64.0171	56.2942	46.8079
PBW-677XPBW ZN1	84.5	130.2917	38.7312	91.6958	51.4158	7.9962	34.5417	24.3471	3.3608	46.4683	13.19	47.8475	11.893	59.8113	56.7521	40.7671
PBW-677XPBW-343	89.4583	131.5833	46.8229	93.2442	54.9117	8.35	30.9167	25.9192	3.405	47.0779	14.2108	43.7725	11.842	60.4104	58.9354	48.0754
PBW-677XPBW-343	84.5833	138.8333	46.5029	85.005	54.0292	8.0729	38.7917	24.7717	3.415	46.2454	13.8454	44.8696	12.7	61.7829	55.2879	42.9246
PBW-822X PBW ZN1	84.7083	131.9167	41.1696	84.0646	57.7367	9.0762	40.8333	25.0829	3.6779	44.1238	14.2521	43.0104	12.186	65.2512	59.4375	53.0029
PBW-822X PBW-343	88.1667	125.4167	49.6562	91.2412	57.47	8.3125	35.8333	24.7462	3.6742	47.145	14.4567	45.475	12.169	64.2404	55.7913	45.5346
PBW-822X HD-3326	89.0833	142.4167	35.2112	91.5288	54.6125	8.3271	39.3333	25.5808	3.64	46.5517	13.8504	44.4633	12.277	64.2496	57.7729	46.4704

LIST OF PUBLICATIONS

1. Journal of Applied Biology & Biotechnology (Scopus index journal, Q3) entitled: Studies on component of genetic variance, combining ability and heterotic response for yield and yield components in wheat (*Triticum aestivum* L.), 13(3) available at http://www.jabonline.in

2. International Journal of Agriculture and Biosciences (Scopus index journal, Q2) entitled: Stability Analysis for yield and yield contributing traits in wheat *(Triticum aestivum* L.), online first 24, March, 2025 available at https://doi.org/10.47278/journal.ijab/2025.043

LIST OF CONFERENCES

1. International Conference on Recent Trends and Sustainable Agriculture for Food and Nutritional Security on topic: Unlocking the potential of some gene editing tools for crop improvement, 2024

2. International conference on "Agriculture, Forestry & Life Science" on topic: Unlocking the potential of gene pyramiding techniques in breeding for biotic stress resistant in plant, 2024

LIST OF WORKSHOPS

1. Short Term Course on Big Data Analysis for Sustainable Agriculture, 2023

2. 7-Days Hands-on Training on Agricultural Data Analysis using Statistical Tools, 2023

3. International Genomics and Bioinformatics Boot camp, 2024

4. International Webinar Series for Life Scientist, 2024

5. Applied Functional Genomics and Bioinformatics, 2025