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(GPB 596)

"IDENTIFICATION OF GOOD COMBINER IN INDIGENOUS VARIETY OF WHEAT (*Triticum aestivum* L.) FOR YIELD AND ITS COMPONENT TRATIS"

Lovely Professional University, Punjab
In partial fulfillment of the requirements for the
Degree of

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In

Genetics & Plant Breeding

By

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CERTIFICATE

This is to certify that the Dissertation entitled **"Identification of good combiner in indigenous variety of wheat (*Triticum aestivum* L.) for yield and its component triaits"** is a bonafide record of independent research work done by **Gaurav Thakur,** (Reg. No.: 11715378) under our supervision and submitted to Lovely Professional University in partial fulfillment for the award of the Degree of Master of Agriculture. (Genetics & Plant Breeding)

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DECLARATION

I hereby declare that the project work entitle **"Identification of good combiner in indigenous variety of wheat (*Triticum aestivum* L.) for yield and its component triaits"** Is an authentic record of my work carried out at lovely professional university as requirements of project work for the award of degree of Master of Science in Genetics and Plant Breeding, under the guidance of Dr. Madakemohekar Anant Hanumant, Assistant professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab.

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INTRODUCTION

Wheat (*Triticum aestivum*) is the first important and strategic cereal crop for the majority of world's populations. It is the most important staple food of about two billion people (36% of the world population). Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). It exceeds in acreage and production every other grain crop (including rice, maize, etc.). Triticeae is one of the tribes containing more than 15 genera and 300 species including wheat and barley. Wheat belongs to the tribe Triticeae (= Hordeae) in the grass family Poaceae (Gramineae) (Briggle and Reitz, 1963) in which the one to several flowered spikelets are sessile and alternate on opposite sides of the rachis forming a true spike. Wheats (Triticum) and ryes (Secale) together with Aegilops, Agropyron, Eremopyron and Haynalidia form the subtribe Triticineae (Simmonds, 1976). Linnaeus in 1753 first classified wheat. In 1918, Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. This was a turning point in Triticum classification. It separated wheat into three groups. Diploids had 14 (n=7), tetraploids had 28 (n=14) and the hexaploids had 42 (n=21) chromosomes.

Wheat is an edible grain, one of the oldest and most important of the cereal crops. Though grown under a wide range of climates and soils, wheat is best adapted to temperate regions with rainfall between 30 and 90 cm. Winter and spring wheat are the two major types of the crop, with the severity of the winter determining whether a winter or spring type is cultivated. Winter wheat is always sown in the fall; spring wheat is generally sown in the spring but can be sown in the fall where winters are mild. Therefore, today wheat is grown all over the world, with different varieties sown according to the various climates. The greatest portion of the wheat flour produced is used for bread making.

Wheat grown in dry climates is generally hard type, having protein content of 11-15 percent and strong gluten (elastic protein). The sticky gluten of bread wheat entraps the carbon dioxide (CO_2) formed during yeast fermentation and enables leavened dough to rise. The hard type of wheat produces flour best suited for bread making. The wheat of humid areas is softer, with protein content of about 8-10 percent and weak gluten. The softer type produces flour suitable for cakes, crackers, cookies, pastries and household flours. Durum wheat (*Triticum turgidum* L.). Although most wheat is grown for human food and about 10 percent is retained for seed and industry (for production of starch, paste, malt, dextrose, gluten).

Wheat is a crop of global significance. It is grown in diversified environments. It is a staple food of millions of people. Approximately one-sixth of the total arable land in the world is cultivated with wheat. Whereas paddy is mainly cultivated in Asia, wheat is grown in all the continents of the world. It supplies about 20 per cent of the food calories for the world's growing population. Global wheat production touched 622.2 million tonnes and India is the second largest producer of wheat after China. Wheat has a distinct place among the food grain crops.

World trade in wheat is greater than for all other crops combined.Globally, wheat is the leading source of vegetable protein in human food. It has a higher protein content than other major cereals such as maize(corn) or rice .In terms of total production, it is second to rice as the main human food crop and ahead of maize (maize is used more for animal feeds).

Wheat was a key factor enabling the emergence of city-based societies at the start of civilization. It was one of the first crops that could be easily cultivated on a large scale, and its seeds could be stored for long periods in a dry climate.

Wheat, best known and most widely cultivated of the wheat, is cultivated for the grain, used whole or ground. Fine ground, it is the source of flour for the world's bread making. Main use is for flour and bread-stuffs known by various names throughout the world. Grain also is the source of alcoholic beverages, beer, industrial alcohol made into synthetic rubber and explosives. Bran from flour milling also an important livestock feed; germ is valuable addition to feed concentrate. Grain fed to livestock whole or coarsely ground. Starch is used for pastes and sizing textiles. Straw made into mats, carpets, baskets, and used for packing material, cattle bedding, and paper manufacturing. Some wheat is cut for hay.

The magnitude of additive gene effect is particularly useful in the development of pureline varieties. Drought is predominantly controlled by additive genes as has been reported by Solmon *et al*. (2003). Likewise, the information concerning dominance and epistatic gene effects (non-additive components) is also valuable for development of hybrid varieties (Sharma and Tandom, 1997: and Munir *et al*., 2007). Several barley workers have tried to estimate the various gene effects; genetic variance and combining ability through exploiting different mating design, such as, diallel, half-diallel, line x tester, partial-diallel, triallel and generation mean analysis etc.

With these points in view, the present investigation entitled **"Identification of good combiner in indigenous variety of wheat (*Triticum aestivum* L.) for yield and its component triaits"** will be undertaken with the following objectives.

1. To study the nature and magnitude of gene action controlling the inheritance of yield and its contributing characters.
2. To find out the best general and specific combiners for yield and its contributing characters.
3. To identify the good lines on the basis of per se performance.
4. To identify the trait(s) to form the basis of selection to increase the yield in wheat.

2. Review Literature

Various biometrical procedures are used by plant breeders for estimation of genetic value of parents and evaluation of varieties and hybrids in terms of their genetic makeup in different adverse conditions need to review before the start of any research programme. A vast literatures in respect of combining ability and gene action, heterosis and inbreeding depression for various yield e traits have been reviewed and brief account of which are presented in this chapter as follows,

Akinci (2009) studied 6 durum wheat parents and their 15 half-diallel crosses. Two local populations (Beyaziye and Bagacak) and four cultivars (Kunduru 1149, Cakmak-79, Diyarbakir-81 and Duraking) of durum wheats were used as parents in the study. Heterosis percentages for high-parent and midparent were - 2.16 % and - 0.74 % for heading date; - 1.64 % and 3.78 % for 1000 kernel weight; - 2.24 % and 5.24 % for plant yield, respectively. The highest heterosis percentage for mid-parent was determined at the hybrids of 'Kunduru 1149 x Diyarbakir81' (1.10 %) for heading date; 'Kunduru 1149 x Cakmak 79' (12.86 %) for 1000 kernel weight; 'Beyaziye x Duraking' (37.67 %) combination for plant yield. The general combining ability (GCA) and specific combining ability (SCA) components of variance were significant for three traits studied. The levels of heterosis and general and specific combining abilities of parental lines were sufficient to sustainable production of hybrid breeding and early selection of breeding lines.

Ahmad (2010) evaluated 15 F1 hybrids and the six parental cultivars. The data showed that, the mean squares of the genotypes (six parents and 15 F 1 hybrids), GCA and SCA were highly significant for all studied traits except SCA for plant height which was insignificant. The effects of general combining ability (GCA) were highly significant for all the traits measured with the exception of 1000-grain weight trait, while the specific combining ability (SCA) effects were statistically significant for studies traits. The GCA effects clarified that, the parents P1, P3 and P5 were the good general combiners for most studied traits.

Saad (2010) estimated the heterotic effects of F1 crosses relative to their respective mid and better parents and combining ability analysis for heading and yield and its components.Highly significant differences among the tested entries were detected for different traits, indicating wide genetic variability among studied genotypes for all traits (days to heading, number of spikes per plant, number of kernels per spike, kernels weight per spike (g), 100-kernel weight (g) and grain yield per plant (g)). Results showed that mean square due to both general and specific combining ability were highlysignificant for all characters studied, indicating the importance of both additive and non-additive genes effects in the inheritance of these characters.

Ashutosh *et al.* (2011) Heterosis and combining ability analysis were studied in a 7 × 7 diallel set of bread wheat. Analysis of variance (ANOVA) revealed the presence of significant variance due to general combining ability (GCA)among the parents for all the traits, and due to specific combining ability (SCA) among the crosses forthe all the traits except for number of tillers per plant, plant height and number of spikelets per spike.Combining ability analysis revealed the involvement of both additive and non-additive gene action inthe inheritance of most of the traits. On the basis of GCA, SCA effects and per se performance, parents K 9107 for 6 traits, K 9162 for 4 traits and GW 373 for 3 traits and crosses K 9107 × K 7903 for 2 traits, K68 × K 7903 for 2 traits were found good general and specific combiners, respectively. Significance theterosis over economic parent and mid parent was observed for almost all the traits studied. The magnitude of heterosis was highest (21.74%) for number of spikelets per spike over economic parentand for number of tillers per plant (13.73%) over mid parent.

Pradeep *et al.* (2015) revealed that non-additive genetic variance play a predominant role in the inheritance of most of the traits. The best combinations mostly involved high x low and low x low general combiner for the characters under study. There was very rare case in which high x high general combiner were involved for best combinations. On the basis of gca and sca effects, two parents (i.e. PBW 373 and RAJ 3765) and 17 cross combinations (i.e. five best crosses namely, K 9423 x NW 1014, Unnat Halna x HUW 560, K 9423 x Unnat Halna, K 9162 x NW 1014, K 7903 x HUW 560), were found good general and specific combiners for higher grain yield and also for other yield contributing traits, respectively. These crosses may be used in heterosis breeding programme for developing new wheat genotype with broad genetic base by multiple crossing programmes. Therefore, crosses involving high x low general combiners in respect of different characters in the present study may be utilized for obtaining transgressive segregants in the next generation resulting from dominance gene interaction.

Patial*et al.* (2016) studied six line of wheat by using line x tester analysis. Variance of specific combining ability (SCA) were higher than the general combining ability (GCA) for all the traits which indicated the predominance of non-additive (dominant, overdominance and epistasis) type of gene action in the inheritance of the traits. Hence, selection of superior plants should be deferred to later generation. The GCA estimates suggested that if the yield traits are to be improved through hybridization and selection, then priority should be given to the male parents RD 2668 and female lines HBL 703 and HBL 704. The 2 crosses; HBL 703/RD 2668 and HBL 704/ RD 2751 were found to be good specific cross combinations for grain yield and its related traits having high significant SCA.

Thomas *et al.* (2017) estimated heterosis for yield and its component traits in 10 parents and their 45 F1's under normal and heat stress condition. Cross combination HD-2733 x HUW-468 (50.24 %) depictedhighest positive significant relative heterosis for grain yield followed by

AAI-11 x HUW-468 (47.08%)and K-911 x HUW-468 (43.19%). Similarly AAI-11 x HUW-468 (36.17%) exhibited highest positivesignificant heterobeltiosis for grain yield followed by hybrids HD-2733 x HUW-468 (35.76%) and HD-2733 x AAI-16 (35.04%) in normal condition. In stressed condition, cross NW-1014 x NW-4035 (30.63%) followed by K-9162 x NW-4035 (24.12 %) and K-911 x AAI-11 (22.93%) exhibited highest positivesignificant relative heterosis. Whereas cross combination NW-1014 x NW-4035 (27.76 %) depictedhighest positive significant heterobeltiosis followed by hybrids K-9162 x NW-4035 (19.43%) and NW-4081 x K-9162 (15.99%) which may be exploited for developing hybrids with better yield and yieldrelated traits in wheat. These crosses could be extensively used in breeding programme to developsuperior segregants or better pure lines could be derived in further breeding programmes.

3. MATERIAL AND METHODS

The materials used and methods applied during the present course of investigation on "Identification of good combiner in indigenous variety of wheat (*Triticum aestivum* L.) for yield and its component traits" are being presented, followed by statistical procedures used. Twenty five elite and diverse pure lines of wheat were received from the B.H.U., Varanasi. The experiments will be conducted at Agricultural Research Farm of School of Agriculture, Lovely Professional University as per following detailed plan of work.

3.1.1 Experimental site

The experiments will conducted during the *rabi* (winter) season of 2017-18 and 2018-19at Agricultural Research Farm of School of Agriculture, Lovely Professional University. The experimental area is quite uniform in respect of topography and fertility. The soil of experimental site is sandy loam.

3.2 Experimental material

25 varieties of wheat will be collect and these genotypes were sown at three dates with a week gap, in two rows of 2 m length having a spacing of 30 cm x 10 cm following single seed per hill to keep the plant population at optimum level.

Testerswill be crossed with lines to produced F_1s' (excluding reciprocals) in line x tester fashion, using testers as female.Standard agronomic practices will be follow to raise a good crop. Cross seeds will be harvested separately for each crosses, dried well and packed to grow next generation.

Selection,hybridization and evaluation of selected genotypes

1st year (*Rabi* season, 2017-18)

- Out of 25 genotypes will be grown and maintained on Agriculture Research Farm, School of agriculture, Lovely Professional University, will be selected on the basis of genotypic diversity for making the crosses.
- These genotypes will be sown at three dates with a week gap, in two rows of 5 m length having a spacing of 25 cm x 10 cm following single seed per hill to keep the plant population at optimum level.

- Three testers will be crossed with six lines to produced 18 F_1s' (excluding reciprocals) in line x tester fashion, using testers as female.
- Standard agronomic practices were followed to raise a good crop.
- Cross seeds will be harvested separately for each crosses to grow next generation.

IInd year (*Rabi* Season, 2013-14)

- The experimental materials (18 F'$_1$s along with their parents including standard check) will be grown in a single row plot of 5 m length in the Compact Family Randomized Block Design with three replications.
- *Per se* performance of parents and crosses will be assessed for various traits.
- Observations on various morphological, physiologic and drought tolerant traits will be recorded on randomly selected plants as detailed in para 3.3.

Table 3.1: Details of selected barley genotypes.

S.No.	Name of Lines/Testers	Source
	Lines	
1.	HUW666	BHU, Varanasi
2.	DL153-2	BHU, Varanasi
3.	HD-2932	BHU, Varanasi
4.	HUW343	BHU, Varanasi
5.	K-68	BHU, Varanasi
6.	HP1744	BHU, Varanasi
	Testers	
1.	HUW- 516	BHU, Varanasi
2.	N1-DW-15	BHU, Varanasi
3.	HS-284	BHU, Varanasi

3.3 Observations recorded

3.3.1 Days to 50 % flowering

The number of days will be taken from sowing to heading in main spike of 50 % plants of a plot will be recorded.

3.3.2 Days to maturity

The number of days will be recorded from sowing to physiological maturity of main spike in hundred per cent plants.

3.3.3 Plant height (cm)

At the physiological maturity, the height of individual tagged/sampled plant will be measured in centimeters from the ground level to the tip of terminal spikelet (excluding the awn) of the main shoot.

3.3.4 Number of effective tillers

At the physiological maturity, the total number of spike bearing tillers in each plant will be recorded.

3.3.5 Spike length (cm)

Length of main spike (cm) will bemeasured from the base to the tip of the terminal spikelet, excluding the awn.

3.3.6 Awn length (cm)

Length of the awn will be measured in centimeter.

3.3.7 Number of grains per spike

The number of grains per spike will be counted from main spike after the harvesting of plant.

3.3.8 1000 grain weight (g)

One thousand threshed grains will be taken randomly after sun drying at 12% moisture level and weighted in gram with the help of electric balance.

3.3.9 Harvest index

Harvest index will be calculated as,

$$\text{Harvest Index} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.3.10 Grain yield per plant (g)

The weight of filled grains of each plant in gramwill berecorded.

3.4 Statistical analysis/ Biometric analysis

3.4.1 Analysis of Variance

The analysis of variance will be completed according to Kempthorne (1957) as described below. The mean data recorded for rainfed (2013-14 and 2014-2015) and irrigated 2014-2015 were formed the basis for analysis of variance for each character.

Table 3.6: ANOVA for line x tester analysis

Source	d.f.	S.S.	M.S.S.	F. ratio
Replication	r- 1	rSS	Mr	Mr/Me
Treatment	n- 1	nSS	Mn	Mn/Me
Parents	p- 1	pSS	Mp	Mp/Me
Parents vs Crosses	1	pcSS	Mpc	Mpc/Me
Crosses	lt- 1	cSS	Mc	Mc/Me
Lines (Male)	l- 1	lSS	M1	σ2e + rσ2lt + rtσ2l
Testers (Female)	t- 1	tSS	M2	σ2e + rσ2lt + rlσ2t
Lines x Testers	(l-1) (t-1)	ltSS	M3	σ2e + rσ2lt
Error	(r-1) (n-1)	eSS	Me	σ2e

Where,

r = number of replications,n = number of treatments,
p = number of parents(l + t),
l = number of male lines,
t = number of female lines,
c = number of crosses(l × t),
MSS = mean sum of squares,
df = degree of freedom

The test of significance was carried out with various MS against eMS using ‘F test’ at the respective degrees of freedom for all the sources of variations except lines and testers where MS

due to lines x tester was used. With the help of expectation, covariance of full sibs and half sibs were estimated by using the formula given below:

$$\text{Covariance of half sibs} = \frac{(M_1 - M_2) + (M_2 - M_3)}{r(l + t)}$$

$$\text{Covariance of full sibs} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r} + \frac{6r\,\text{Cov (H.S.)} - r(l + t)\,\text{Cov (H.S.)}}{3r}$$

3.4.2.1 Estimation of general and specific combining abilities effects

The additive model will be used to estimate the general and specific combining ability effects of ijk^{th} observation is given here:

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

Where,

μ = population mean
g_i = gca effect of i^{th} female parent
g_j = gca effect of j^{th} male parent
s_{ij} = sca effect of ij^{th} combination
e_{ijk} = error associated with the observation X_{ijk}
i = number of female parents
j = number of male parents
k = number of replication

The GCA effects for both male and female parents and SCA effects for each cross combination were calculated with the help of following formula:

$$\mu = \frac{X}{ltr}$$

Where,

X… = Total of all hybrid combination over replication

(i) Lines: GCA effect of i^{th} lines $(g_i) = \frac{Xi..}{tr} - \frac{Xi..}{ltr}$

(ii) Testers: GCA effect of j^{th} testers $(g_i) = \frac{X.j.}{lr} - \frac{X...}{ltr}$

(iii) Crosses: SCA effect of ij^{th} lines $(s_{ij}) = \frac{X..j}{r} - \frac{Xi..}{tr} - \frac{X.j.}{lr} - \frac{X...}{ltr}$

Where,

$X_{i}..$ = Total of i^{th}line over *t* testers and *r*replications
$X_{.j}.$ = Total of j^{th}tester over *l* lines and *r*replications
X_{ij} = ij^{th} combination over all replication

3.4.2.2 Standard Error for the Combining ability effect

The standard errors will be estimated as follows:

$$S.E.gca(line) = \sqrt{Me/_{rt}}$$

$$S.E.gca(tester) = \sqrt{Me/_{rl}}$$

$$S.E.\hat{S}ij(sca) = \sqrt{Me/_{r}}$$

The test of significance for estimates of the GCA and SCA effects were tested as follows:

$$'t'gca\ (line) = \frac{\hat{g}i - 0}{S.E.\hat{g}i}$$

$$'t'gca\ (tester) = \frac{\hat{g}i - 0}{S.E.\hat{g}i}$$

$$'t'sca\ = \frac{\hat{s}ij - 0}{S.E.\hat{s}ij}$$

The calculated't' thus obtained was compared with table value at error degree of freedom at p = 0.05 and p = 0.01.

3.4.2.3 Critical difference (C.D.) of the estimates

The differences between two estimates were tested by comparing them with C.D. value.

C.D. = S.E. of difference two estimate × t at 5% error degree of freedom.

S.E. of differences of two estimates were calculated as follows

$$S.E.(\hat{g}i - \hat{g}j)line\ = \sqrt{2Me/_{rt}}$$

$$S.E.(\hat{g}i - \hat{g}j)tester\ = \sqrt{2Me/_{rl}}$$

$$S.E.(\hat{s}ij - \hat{s}kl) = \sqrt{2Me/_{r}}$$

3.4.2.4 Proportional contribution of lines, testers and their interactions to total variance

$$\text{Contribution of Lines} = \frac{\text{SS (l)}}{\text{SS (Crosses)}} \times 100$$

$$\text{Contribution of Testers} = \frac{\text{SS (t)}}{\text{SS (Crosses)}} \times 100$$

$$\text{Contribution of Lines} \times \text{Testers} = \frac{SS\ (l \times t)}{SS\ (\text{Crosses})} \times 100$$

3.4.3 Estimation of heterosis

Heterosis in F_1s' will be calculated as the difference of F_1 hybrid performance from the better parents (Heterobeltiosis) and standard checks (Standard heterosis) by using the formulae(Kempthorne, 1957).

$$\text{Heterobeltiosis (\%)} = \frac{(\bar{F}_1 - \bar{BP})}{\bar{BP}} \times 100$$

$$\text{Standard heterosis (\%)} = \frac{(\bar{F}_1 - \bar{C})}{\bar{C}} \times 100$$

Where,

$\bar{F}_1$ = mean performance of F_1

$\bar{F}_2$ = mean performance of F_2

$\bar{BP}$ = mean performance better parent.

$\bar{C}$ = mean performance of check variety.

Test of significance of heterosis

Significance of heterosis will be tested by 't' test. The calculated value of 't' was compared with table value of 't' at error degree of freedom from ANOVA comprising parents and F_1 at p = 0.05 and p = 0.01. t value was estimated s given below:

$$t(H) = \frac{\bar{F}_1 - \overline{BP} or \overline{SC}}{SE(H) over BP or SC}$$

$$SE(H) for BP or SC = \sqrt{\frac{2Mse}{2r}}$$

Where,

Me = error variance obtained by ANOVA comprising parents and F1's

r = Number of replication

3.4.4 Heritability (Narrow sense)

Heritability (h^2) estimate will be worked out by using the formula suggested by Lush (1949) and Burton and De Vance (1953):

$$h^2 \text{ (Narrow sense)} = \frac{\sigma^2_A}{\sigma^2_P} \times 100$$

Where,

h^2 (ns) = Heritability expressed in per cent

$\sigma^2 A$ = Additive genetic variance

$\sigma^2 P$ = Phenotypic variance

The estimates of heritability are categorized as High (>30%), Moderate (>10% and <30%) and Low (<10%).

3.4.5 Expected genetic advance

It will be calculated as per formula suggested by Lush (1949).

(a) Genetic advance (GA) = $(K)\ (h^2)\ (\sigma P)$

(b) Genetic advance as % of mean = $GA/\overline{X} \times 100$

Where,

h^2 = estimates of heritability (absolute value)

σ_P = phenotypic standard deviation

K = selection differential at 5% selection intensity, i.e., 2.06

X = population mean for the concerned character

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