GENETIC DIVERSITY, HETEROSIS AND COMBINING ABILITY STUDIES FOR FRUIT YIELD AND ITS COMPONENT TRAITS IN BOTTLE GOURD [*LAGENARIA SICERARIA* (MOLINA) STANDL.]

Thesis Submitted for the Award of the Degree of

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in

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DECLARATION

I, hereby declared that the presented work in the thesis entitled "**Genetic diversity, heterosis and combining ability studies for fruit yield and its component traits in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]**" in fulfilment of degree of **Doctor of Philosophy (Genetics and Plant Breeding)** is outcome of research work carried out by me under the supervision of Dr. Harshal Ashok Avinashe, working as Associate Professor, in the Department of Genetics and Plant breeding, School of Agriculture, of Lovely Professional University, Punjab, India. In keeping with general practice of reporting scientific observations, due acknowledgements have been made whenever work described here has been based on findings of other investigators. This work has not been submitted in part or full to any other University or Institute for the award of any degree.

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CERTIFICATE

This is to certify that the work reported in the Ph. D. thesis entitled "**Genetic diversity, heterosis and combining ability studies for fruit yield and its component traits in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]**" submitted in fulfillment of the requirement for the award of degree of **Doctor of Philosophy (Ph.D.)** in the Department of Genetics and Plant Breeding, School of Agriculture, is a research work carried out by Bunga Anand Paul, 12020429, is Bonafide record of his/her 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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"Genetic Diversity, Heterosis and Combining Ability Studies for Fruit Yield and its Component Traits in Bottle Gourd [*Lagenaria siceraria* (Molina) Standl.]"

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ABSTRACT

Bottle gourd (*Lagenaria siceraria* [Molina] Standl.) is an economically and nutritionally important cucurbit grown across tropical and subtropical regions, valued for its culinary versatility, medicinal properties, and resilience under stress conditions. Despite its potential, commercial bottle gourd improvement in India remains limited, largely due to underutilization of its rich genetic diversity, restricted hybrid options, and insufficient understanding of genotype performance under varying environments. The present research was designed to address these gaps through an integrated study combining genetic diversity estimation, heterosis analysis, combining ability evaluation, and genotype × environment (G×E) interaction assessment for yield and its component traits.

The study was conducted in three sequential phases. In Season I (Summer 2023), 38 diverse genotypes sourced from IIVR, NBPGR, and other institutions were evaluated under an alpha lattice design for 21 qualitative, agro-morphological and yield-related traits. Mahalanobis' D^2 analysis revealed substantial variability, grouping the genotypes into seven clusters. Cluster V had the largest number of genotypes (8), followed by clusters II and III with four each. Inter-cluster distances ranged from 14.05 to 30.21, with the maximum divergence observed between clusters IV and VI, suggesting considerable scope for exploiting heterosis through crosses between these groups. Several genotypes combined early flowering, desirable fruit morphology, and high yield potential, making them promising candidates for hybridization.

Based on diversity results, Season II (Kharif 2023) involved selecting 10 lines and 4 testers representing different clusters and performance groups for hybrid development using the line × tester mating design. Forty F_1 hybrids were generated without emasculation, utilizing controlled pollinations to maintain genetic purity.

Season III (Late Summer to Mid-Kharif 2024) focused on evaluating the 40 F_1 hybrids, their 14 parents, and one commercial check (Malerkotla Special) under three sowing dates: 15 May, 10 June, and 7 July, to simulate environmental variation. An alpha lattice design with two replications per environment was used. Observations were recorded on 14 traits: days to male flowering (DMF), days to female flowering (DFF), sex ratio (SR), number of secondary

branches (NSB), vine length (VL), fruit length (FL), fruit girth (FG), days to first harvest (D1H), days to third harvest (D3H), average fruit weight (AFW), fruit flesh thickness (FFT), rind thickness (RT), fruit yield per plant (FYPP), and total soluble solids (TSS).

Heterosis Analysis revealed substantial hybrid vigor for several traits. For FYPP, **L5×T1** recorded the highest mid-parent heterosis (54.82%), **L4×T1** showed maximum heterobeltiosis (42.17%), and **L1×T1** achieved the highest economic heterosis (38.95%). Positive heterosis was also observed for AFW (**L6×T4**), FL (**L5×T2**), and FFT (**L7×T4**), indicating their potential for direct yield improvement. Negative heterosis for DMF and DFF was noted in **L10×T4**, a desirable feature for earliness breeding.

Line × Tester Analysis provided insights into the genetic control of traits. Among lines, **L1 (IC 284895)** was a superior general combiner for early flowering (-2.81 days), FL (3.84 cm), and FYPP (+2.61 kg). **L8 (IC 371745)** and **L9 (Avinash IV)** exhibited strong GCA effects for VL and AFW. Among testers, **T3 (Narendra Pooja)** and **T4 (Punjab Round)** were identified as reliable contributors to yield-related traits. High SCA effects were found in **L5×T2** (FL: 5.73 cm), **L6×T4** (AFW: 116.42 g), **L7×T4** (FFT: 2.14 mm), and **L10×T4** (earliness and reduced vine length).

Gene Action estimates indicated the involvement of both additive and non-additive effects, with the predominance of additive gene action (GCA/SCA ratio < 1) for most traits, highlighting the suitability of heterosis breeding strategies for yield improvement. Traits such as earliness, fruit size, and weight benefited from dominance variance, while certain traits like fruit length showed notable additive contributions.

AMMI Stability Analysis showed significant G×E effects for yield, with PC1 explaining 61.24% and PC2 explaining 23.47% of the interaction variation. The AMMI biplots and GGE analysis identified **L1×T1**, **L5×T1**, and **L4×T1** as high-yielding and stable across environments, demonstrating their adaptability for diverse planting dates. Other hybrids such as **L6×T4** and **L5×T2** showed potential for specific adaptation to particular sowing windows.

From diversity analysis, heterosis estimation, combining ability studies, and stability testing confirms that careful parental selection based on genetic divergence, coupled with the exploitation of both additive and non-additive effects, can yield hybrids with superior performance and stability. The combination of broad-adapted hybrids (**L1×T1**, **L5×T1**, **L4×T1**) and specifically adapted hybrids offers breeders a strategic toolkit for both wide and targeted recommendations.

In conclusion, the research establishes a robust, multi-faceted breeding framework for bottle gourd improvement. By harnessing genetic diversity, exploiting heterosis, understanding gene action, and evaluating stability across environments, this study delivers elite hybrids and superior parental lines for future programs. The identified hybrids, particularly **L5×T1**, **L4×T1**, and **L1×T1**, have strong potential for commercial cultivation, promising to enhance productivity, adaptability, and profitability of bottle gourd farming in diverse agro-climatic regions.

Keywords: AMMI analysis, Bottle Gourd, Genetic Diversity, Heterosis, Combining Ability, Genotype × Environment Interaction

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Place: Phagwara, Punjab

Date: ……

Bunga Anand Paul

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Abbreviations	
°Brix	Degree Brix
°C	Degree Celsius
cm	Centi metre
mm	Milli metre
gms	Grams
kgs	Kilo grams
max	Maximum
min	Minimum
ml	Milli litre
i.e.	In essence
viz	Namely
vs	Versus
Symbols	
=	Equals
%	Per cent
x	Cross

CHAPTER 1

INTRODUCTION

Bottle gourd (*Lagenaria siceraria* (Molina) Standl.) holds significant importance in sub-Saharan Africa (SSA) and Indian sub-continent for its versatile utility as a crop. It is referred to as Lauki (Hindi), Ghiya (Hindi), Dudhi (Marathi/Gujarati), Sorekayi (Kannada/Telugu), Annapkaya (Telugu), Ladu (Bengali), Calabash etc. Its leaves, fruits, and seeds are prized for their nutritional value, contributing vital elements to diets in the region (Mkhize et al., 2021). Bottle gourd belongs to the genus *Lagenaria* and family *Cucurbitacea*. Genus *Lageniaria* has 5 wild relatives all of which are found in Africa which is believed to be the centre of origin to the only cultivated species from the genus (Mashilo et al., 2017). While bottle gourd remains underexplored and underutilized in India, where commercial varieties are limited, diverse genetic resources in Africa and Asia offer potential for developing improved varieties through selective breeding (Mkhize et al., 2021). Notably, traits like flowering time, plant morphology, and fruit characteristics exhibit considerable variation, presenting opportunities for breeding programs to enhance cultivar performance. In India, bottle gourd holds culinary significance and is recognized for its medicinal properties, including anti-diabetic, anti-cancer, and anti-inflammatory effects (Dhakad et al., 2022; Sithole *et al*., 2023). Fresh bottle gourd juice is commonly employed to alleviate flatulence, manage diabetes mellitus and hypertension, support liver health, and act as a diuretic (Mashilo et al., 2017). Bottle gourd have high content of bio-active compounds like cucurbitacins. The leaves have high amounts of cucurbitacins type E and I while cucurbitacin I was found in mature fruits. Sweet domesticated bottle gourd has low concentration of cucurbitacins. Very high concentration of cucurbitacins causes bitterness and poisionong (Attar and Ghane, 2018, 2019; Chanda et al., 2019; Mkhize et al., 2021). Its nutritional richness and genetic diversity underscore its potential to contribute significantly to horticultural production in India. Both in SSA and Asia, along with the immature tender fruit, its leaves are consumed as a vegetable (Morimoto and Mvere, 2004). Bottle gourd is source to various amino acids and minerals **(Table 1.1)** (Mkhize et al., 2021).

Table 1.1 Range of Amino acid concentrations in bottle gourd

Amino acid	Concentration (µg/g)
Aspartic acid	19.84 - 143.59
Threonine	143.72 - 1593.36
Serine	3.67 - 149.62
Glutamic acid	25.14 - 431.55
Alanine	11.39 - 222.74
Valine	7.93 - 126.06
Leucine	9.00 - 148.30
Phenylalanine	14.19 - 177.84
Lysine	6.18 - 160.97
Arginine	16.15 - 212.42

Cultivation of bottle gourd can be done in wide range of soils but is best suited for heavily manured loamy soils. It performs well in warm and humid conditions. Seedlings can be raised in nursery and be transplanted at 2-3 leaves stage. This method is usually followed if the target is to raise an early crop. Direct sowing of 4-5 seeds in pits is usually done to reduce the cultivation costs. Two crops per year can be taken according to Indian conditions where dry season crop can be sown from October to March and the wet season crop can be sown from March to July (Dhakad et al., 2022).

The plant can grow on ground or can be trained on trellis or *pandal* system for the vines to grow. With good management, the vines can grow very long. Its stem is usually covered with hair which aids in preventing insect occurrence. The leaves are arranged alternatively with tendrils on the opposite end of the node from where leaves arise. Bottle gourd has a tap root system but most of the roots remain shallow and spread out from the base of the plant. Bottle gourd is monoecious, i.e., it has both male and female flowers on the same plant which promotes cross pollination. It is usually pollinated by bees and other insects. The number of male flowers is higher than the female flowers.

A huge diversity exists in the fruit shape of bottle gourd. Neck of the fruits can be narrow, crooked or straight and fruit itself varies in shapes and sizes such as club shaped, round, bottle shaped, flat, pear shaped, cylindrical, elongated straight, pyriform, oblate, elongated curved, oval and even irregular (Mashilo et al., 2015; Kalyanrao et al., 2016; Ahmad et al., 2022). Fruit

neck also shows significant variance which can be used to select genotypes that can produce bottle gourd for aesthetic value (Gürcan et al., 2015; Mashilo et al., 2015). This variation can be used as a criterion for selection depending upon the region and preference. A significant degree of phenotypic polymorphism is observed across a broad spectrum of agronomically important traits in bottle gourd (Mladenović et al 2012; Mashilo et al., 2015, 2017a). Studies have shown that a direct selection for agronomic traits such as number of female flowers, number of branches, number of fruits, fruit width, vine length etc can has a direct effect on fruit yield (Behera et al., 2015; Yao et al., 2015).

Compared to other cucurbits, bottle gourd has a better performance against drought and has high salinity tolerance and therefore is a preferred rootstock for watermelon (Yang et al., 2015; Yetişir et al., 2016; Mashilo et al., 2017c). Identifying genotypes with high drought tolerance can be an important resource. Understanding the physiological basis can aid in developing effective strategies for breeding. High levels of secondary metabolites are reported in genotypes with good tolerance to drought and heat which can be used as indicators for screening (Mashilo et al., 2018). Bottle gourd is moderately resistant to a host of diseases like papaya ringspot, Fusarium wilt, powdery mildew, cercospora leaf spot, tobacco mosaic virus etc. This is one more reason to chose bottle gourd as one of the rootstocks for watermelon (Mkhize et al., 2021).

Low agricultural productivity and climate change along with reduction in cultivable area and restraints in field labour availability are major concerns for food and nutritional security for the future. Underutilized crops such as bottle gourd are often neglected but can play a vital role in supplementing food availability in poor underdeveloped regions (Padulosi et al., 2002). Realizing the potential of bottle gourd necessitates collaborative research involving experts across disciplines such as plant breeding, agronomy, genetics, and food science. Such collaboration can facilitate knowledge exchange, germplasm sharing, and innovative product development to meet diverse human needs and support the food and feed industry in India (Mkhize et al., 2021).

In the realm of conventional breeding, two foundational elements emerge as indispensable: the presence of diverse germplasm and the existence of substantial genetic variability. Germplasm collections, serving as repositories of genetic wealth, furnish breeders with the raw genetic materials they need to craft improved bottle gourd cultivars. Studies from various scientists show that there exists a considerable genetic variability in bottle gourd (Morimoto et al., 2005,

2006; Mashilo et al., 2015, 2016, 2017b). However, the true power of these collections lies in the nuanced analysis of genetic diversity contained within them. This analysis becomes the compass guiding breeders through a complex landscape.

The study of combining ability and heterosis is crucial in plant breeding as it provides insights into the genetic potential of different genotypes for hybridization. Heterosis, or hybrid vigor, describes the phenomenon where hybrid offspring exhibit enhanced traits compared to their parents. This can include increased growth rates, higher yields, and improved resistance to diseases. Evaluating heterosis is essential for identifying crosses that can significantly outperform their parents in various agronomic traits. High yielding and unrelated parental genotypes with desirable agronomic and horticultural attributes have shown yielding high-performing hybrids (Xu et al., 2011; Yildiz et al., 2015). Various studies have reported heterosis for important agronomic and horticultural traits in bottle gourd such as flowering time in female flowers, fruit weight, 100 seed weight, days to 1st male flowering, sex ratio and number of seeds per fruit (Janaranjani et al., 2016; Mkhize et al., 2021).

Combining ability describes a genotype's capacity to pass favourable traits to its progeny. It comprises general combining ability (GCA)—the mean performance of a genotype across multiple crosses, indicative of additive gene effects—and specific combining ability (SCA), which measures the performance of a particular hybrid combination, reflecting non-additive gene interactions. Understanding these parameters allows breeders to select parent genotypes that will produce superior hybrids and is associated with both additive and non-additive gene action (Falconer and Mackay, 1996; Mkhize et al., 2021). A GCA/SCA ratio of <1 indicates the predominance of non-additive gene action and therefore a hybridization breeding approach among desirable parents could be the best approach whereas a GCA/SCA ratio of >1 indicates the importance of additive gene action over non-additive and recurrent selections should show positive results over time. The integration of combining ability and heterosis assessments enables breeders to make informed decisions about which genotypes to utilize in breeding programs, ultimately leading to the development of high-performing cultivars (Wu et al., 2013).

G×E interaction refers to the phenomenon of differential expression of genotypes under different environmental conditions (Kim et al., 2014). This concept highlights the importance of assessing how consistently a genotype performs across different environments, which is known as agronomic stability. Biologically, a stable genotype is considered one whose

phenotype remains relatively consistent and close to the expected performance across a range of environmental conditions. G×E interaction is plotted as a slope of genotypic performance against an environmental gradient. Non-intersecting slopes of genotypes shows that rank of that genotype doesn't change across environments while intersecting slopes indicate that genotypes maybe suited only to specific environments and therefore careful consideration is needed for recommendation (Leon et al., 2016). Crossover interactions are also called as qualitative interactions while non-crossover interactions are known as quantitative interactions (Leflon et al., 2005). Genetic composition of a genotypes plays a major role not only in it's internal processes but also affects its reaction to environmental conditions. These interactions necessitated the study of G×E interactions beside the mean performance of genotypes (Chandrika et al., 2015; Ulaganathan et al., 2015). There are multiple ways to analyse this interaction and each has its own benefits and limitations. One of the commonly used approach for examining G×E interaction employ the linear regression method of Eberhart and Rusell model, 1966. In this model, the regression coefficients (β-values) quantify each genotype's responsiveness (adaptability) across environments, while the deviation mean square (S^2d) serves as an index of performance stability. The other widely used method is AMMI (Additive Main Effects and Multiplicative Interaction) model approach. The Additive Main Effects and Multiplicative Interaction (AMMI) model combines analysis of variance to capture additive effects with principal component analysis to model multiplicative G×E interaction patterns (Abate, 2015).

Despite extensive investigation into combining ability, gene action, and heterosis in bottle gourd (Xu et al., 2011; Yildiz et al., 2015; Mkhize et al., 2021), critical gaps persist in understanding the stability of these traits under varying environmental conditions, particularly across different sowing dates in subtropical regions like India. Prior studies have often focused on single season evaluations or limited germplasm sets, overlooking the pronounced genotype x environment (G×E) interactions driven by erratic rainfall, temperature fluctuations and shifting cropping calendars, factors exacerbated by climate change (Kim et al., 2014; Leon et al., 2016). For instance, while the Eberhart–Russell regression and AMMI models have been applied occasionally in cucurbits (Eberhart & Russell, 1966; Abate, 2015), their use in bottle gourd has been inconsistent, with few integrating multivariate diversity analysis alongside heterosis and combining ability metrics in multi-environment trials. This oversight limits the development of resilient cultivars suited to India's diverse agroecological zones, where bottle gourd could bolster nutritional security for smallholder farmers by providing drought-tolerant,

high yielding options amid declining arable land and labour shortages (Padulosi et al., 2002; Mashilo et al., 2018). Moreover, identifying hybrids with broad adaptation or specific suitability for early, medium or late sowing windows would optimize production under local constraints, such as overlapping wet and dry seasons (Dhakkad et al., 2022). By synergistically employing Mahalanobis' D^2 for diversity clustering, GCA/SCA estimates for parental selection, heterosis quantification for hybrid vigour and AMMI-based stability analysis for G×E dissection, the present study addresses these deficiencies. This integrated approach not only pinpoints stable, high yielding genotypes but also provides actionable insights for breeding programs, ultimately enhancing bottle gourd's role in sustainable horticulture and food systems in India and similar regions.

The current study is designed with the following objectives in mind:

1. **To estimate genetic diversity using Mahalanobis' D^2 statistic and the grouping of genotypes into clusters.**
2. **To estimate the nature and magnitude of heterosis in fruit yield and its component traits.**
3. **To assess the general combining ability effects of the parents and the specific combining ability effects of crosses on yield and its components.**
4. **To judge the nature and magnitude of gene action involved in the inheritance of traits.**
5. **To find out Genotype x Environment interaction and identification of stable genotypes using AMMI model.**

CHAPTER 2

REVIEW OF LITERATURE

Table 2.1 Review: Diversity

S No	Author and Year	Research Findings
1	Deepthi et al., 2015	They used 24 bottle gourd genotypes for their diversity analysis. They found significant differences among genotypes which yielded five clusters using Mahalanobis' D^2 analysis.
2	Gurcan et al., 2015	They studied 31 diverse exotic accessions. They found out that none of the genotypes grouped based on their geographical origin. They obtained 8 major clusters based on their observations.
3	Shubha et al., 2015	They studied 127 bottle gourd genotypes and recorded 13 morphological characters to assess the diversity. The genotypes were grouped into three major clusters using hierarchical clustering where cluster I comprised of medium length vines.
4	Chetariya and Vaddoria, 2017	Studied 20 genotypes of bottle gourd and found significant diversity among them. They used Mahalanobis' D^2 statistic which yielded 13 clusters suggesting wide genetic diversity.
5	Jatav et al., 2018	The present investigation was carried out using twenty-four bitter gourd genotypes to assess diversity among others. Using Mahalanobis' D^2 analysis they grouped the genotypes into 5 clusters with cluster IV and V having one genotype each while cluster I had twelve genotypes and cluster II and III had five each.
6	Pradhan et al., 2018	They studied eighteen ash gourd genotypes (11 landraces and 7 released varieties) which is an under-exploited vegetable crop for diversity in 2015 and 2016. Genotypes were grouped into three major clusters which contained six, three and nine genotypes respectively.
7	Kandasamy et al., 2019	They studied 20 bottle gourd genotypes for diversity using yield and yield related traits. Using Mahalanobis' D^2 statistic

		they placed the genotypes into six clusters with cluster IV being biggest cluster with 6 genotypes in it
8	Quamaruzzaman, 2020	He conducted an experiment on 22 bottle gourd genotypes and grouped them into 5 clusters using Mahalanobis' D^2 analysis. Significant diversity was found between the clusters based on the intra clusters distances that was reported.
9	Rehan et al., 2020	A trial was conducted on 24 bottle gourd genotypes to assess genetic divergence through Mahalanobis's D^2 analysis. The results revealed significant variability among the accessions, which were partitioned into five clusters. Cluster I contained the greatest number of genotypes, whereas Clusters II, III, and IV exhibited close genetic affinities.
10	Alhariri et al., 2021	They studied fifty-one bitter gourd accessions for diversity. Based on the data recorded for 10 quantitative characteristics, the accessions were grouped into six main clusters using Mahalabosis' D^2 analysis (UPGMA method with arithmetic mean.
11	Harsh et al., 2022	Carried out an investigation using twenty-six muskmelon genotypes for genetic diversity based on 32 morphological and 4 biochemical traits. Based on Mahalabosis' D^2 values, the genotypes were grouped into 12 clusters. Cluster I was the biggest cluster with nine genotypes followed by cluster III which consisted of 7 genotypes while cluster II, IV, V, VI, VII, VIII, IX, X, XI, XII had 1 genotype each.
12	Mahapatra et al., 2022	Ninety-one genotypes were evaluated for genetic diversity using Mahalanobis D^2 analysis, which revealed significant variation in fruit shape. Additionally, the morphological characteristics grouped the genotypes into nine distinct clusters.
13	Mahapatra et al., 2023	They evaluated 91 accessions from around India and found significant diversity in them. Based on Euclidian cluster analysis using Ward's distance, they could able to group the genotypes into 12 clusters.

14	Chakraborty and Chaurasiya, 2024	They studied 30 genotypes for 33 quantitative traits. They obtained seven clusters using Mahalanobis' D^2 statistics. Maximum number of genotypes in cluster was seven.
15	Rani et al., 2025	They used D^2 values to group thirty-two muskmelon genotypes into five clusters. D^2 values ranged from 0.00 to 45.08 within the clusters. Cluster I had the highest intra-cluster diversity with twenty-five genotypes. Cluster III had four genotypes while cluster II, IV and V had 1 genotype each.

Table 2.2 Review: Heterosis

S No	Author and Year	Research Findings
1	Gayakawad et al., 2016	Thirty-six bottle gourd hybrids, along with their respective parents and a commercial check, were evaluated to estimate the extent of heterosis for various growth and yield traits. The cross IC392392 × PSPL recorded the highest heterosis for vine length at 45 days after sowing (71.43%), while IC392392 × AB showed the maximum heterosis for vine length at 75 days after sowing (44.08%). For number of branches at 45 DAS, IC392392 A × PSPL exhibited the highest heterosis (38.70%), whereas IC284953 × AB recorded the maximum heterosis at 75 DAS (8.12%). Significant heterosis for number of fruits per vine (26.67%) was observed in the crosses IC308564 A × PSPL, IC421962 × PS, and IC284953 × AB. The cross IC342078 × PS showed the highest heterosis for average fruit weight (150.00%) over the commercial check. Notably, the hybrid NBBL-12 × PS exhibited the maximum heterosis for both fruit yield per vine (57.00%) and fruit yield per hectare (174.97%) compared to the commercial check.
2	Ghuge et al., 2016	They studied 28 hybrid combinations developed from 8 parent lines to assess heterosis. Among them, 11 hybrids showed positive heterosis in a desirable direction. The cross Aditi × PSPL showed the highest heterosis for the number of fruits per

		plant, followed by Aditi × VRBG 100 and Samrat × VRBG 444, all outperforming the standard variety, Samrat. Overall, hybrids that demonstrated significant yield improvements also tended to show strong heterosis for either fruit weight or the number of fruits per vine.
3	Janaranjani et al., 2016	They evaluated 36 crosses from nine lines and four testers in a RCBD design. Standard heterosis for yield ranged from -23.17 to 133.61(Pusa Naveen x NDBG-164) against the commercial check NDBG-164.
4	Malviya et al., 2017	Evaluated 28 crosses (8 parents in diallel mating pattern). Standard heterosis for fruit yield per plant ranged from -24.66 to 54.24. maximum standard heterosis recorded by cross Coimbatore3 × JBOGL-01-6 which 54.24 per cent, followed by JBOGL01-6 × JBOGL-01-2 (37.11 %) and Pusa Naveen × JBOGL01-6 (31.32 %).
5	Parmar and Pathak, 2018	A study involving eight parental lines and 28 F_1 hybrids of bottle gourd from a half-diallel cross was carried out to assess heterosis for agronomic and quality traits. Significant positive heterosis for fruit weight and marketable yield was observed in the crosses Punjab Komal × PSPL and Gutka Long × Pusa Naveen. For ascorbic acid content, PSPL × Pusa Naveen, PSPL × Punjab Barkat, and Punjab Barkat × PBOG-8 showed highly significant positive heterosis, indicating the potential of these hybrids for yield and nutritional quality improvement.
6	Khot et al., 2019	Thirty hybrids, developed using a line × tester design with 10 lines and 3 testers, were assessed for heterosis. The hybrid Bot.G-6-2 × Arka Bahar demonstrated the highest heterosis over the better parent, mid-parent, and commercial check for all growth parameters except vine length heterobeltiosis. Importantly, the cross Bot.G-6-2 × Pusa Naveen exhibited the highest and statistically significant heterobeltiosis for vine length.

7	Quamruzzaman et al., 2020	They evaluated 21 (7 parents in half diallel) crosses along with their parents. 17 crosses showed significant positive better parent heterosis. P3 x P4 showed an increase of 49.72% followed by P3 x P5 with an increase of 44.97%.
8	Kumar and Ram, 2021	Carried out an experiment using forty-five F1 hybrids from a 10 × 10 half diallel cross to estimate the extent of heterosis. Heterobeltiosis for fruit yield ranged from -36.91(P1 × P4) to 12.15(P4 × P9), and standard heterosis for fruit yield ranged from -24.24(P1 × P9) to 29.21(P1 × P2) percent. Out of forty-five F1s, P4 × P9 was found to be superior overall for eighteen characters compared to the better parent.
9	Masud et al., 2021	Twenty-one crosses, derived from seven lines and three testers, were evaluated. Out of these, 13 crosses exhibited significant positive heterosis for yield per plant. The cross 59-1-1-1-1-8 × BG0048 showed the highest heterosis at 190.41%, followed by 59-1-1-1-1-1-8 × BARI Lau-1 at 158.26%, and 59-1-1-1-1-1-8 × BG0059 at 140.38%. In conclusion, the most promising cross combinations for exploiting heterosis in terms of fruit number and yield are 59-1-1-1-1-8 × BG0048 and 59-1-1-1-1-8 × BARI Lau-1.
10	Mauriya et al., 2021	Forty hybrids generated from ten lines and four testers were assessed for heterosis. Among these, ten crosses exhibited mid-parent heterosis for fruit yield per plant, although overall fruit yield did not show significant heterosis compared to the mid-parent, better-parent, or commercial check. Additionally, mid-parent heterosis was observed in vine length, fruit set percentage, sex ratio, and total soluble solids (T.S.S.).
11	Odedara et al., 2021	Five hybrid combinations—ABG 1 × DBG 5, NDBG 132 × DBG 6, Pusa Naveen × DBG 5, Pusa Naveen × DBG 6, and DBG 5 × DBG 6—were assessed. Crosses NDBG 132 × DBG 6, Pusa Naveen × DBG 5, and Pusa Naveen × DBG 6 exhibited significant and positive heterobeltiosis for fruit yield per plant.

12	Rambabu et al., 2021	An experiment with six parents and fifteen hybrids obtained from a half diallel mating design showed that four crosses had the highest heterosis. Pusa Sandesh x Arka Bahar, RJBGC-140 x Pusa Samridhi, BOGVAR-2 x Arka Bahar and Arka Bahar x RJBGC-140 were the top performers.
13	Singh et al., 2022	A diallel study of 28 F_1 bottle gourd hybrids (excluding reciprocals) evaluated heterosis for yield and related traits. Significant variation was observed among hybrids. Heterosis for fruit yield per vine ranged from -1.27% to 17.33% over the mid-parent and 0.61% to -22.74% over the better parent. For number of fruits per plant and average fruit weight, heterosis reached up to 46.67% and 41.94%, respectively. Fruit length and earliness also showed notable heterotic effects. Among all, only two hybrids—Arka Bahar × Kashi Ganga and Arka Bahar × Pusa Naveen—showed significant positive heterosis for yield over the better parent. Several crosses, including Arka Bahar × Narendra Dharidar and Pusa Santushti × PSPL, showed significant negative heterosis for earliness.
14	Mkhize et al., 2023	They carried out their experiment on eight parents and twenty-eight hybrids obtained from diallel mating design and evaluated them in non-stressed and drought tressed conditions. They considered fruit yield per plant and seed yield per plant as two of the important characters and on those basis, they identified that under drought stress (DS) conditions, the crosses BG-80 × BG-58, BG-27 × BG-79, BG-79 × BG-52, BG-27 × BG-52, and BG-52 × BG-80 exhibited significant positive mid-parent and better-parent heterosis for FYPP and SYPP. Meanwhile, under normal stress (NS) conditions, the crosses BG-27 × GC, BG-79 × GC, BG-27 × BG-58, and BG-27 × BG-79 also demonstrated high and positive mid-parent and better-parent heterosis for FYPP and SYPP.
15	Vidya et al., 2024	A line × tester study in bitter gourd using nine lines and three testers generated 27 F_1 hybrids to evaluate heterosis was carried

		out. The hybrids HUB-1 × Co-1, HUB-1 × White Long, and Katahi Vaibhav × White Long showed the highest positive heterosis and specific combining ability for earliness, yield, and quality traits. Notably, the gynoecious hybrid HUB-1 × Co-1 exhibited the highest standard heterosis of 104.40% over the commercial check for yield (18.38 t/ha) and also showed resistance to viruses and fruit fly. Additionally, HUB-1 × Co-1 and Jonpuri × White Long demonstrated superior heterosis for quality traits like beta-carotene, ascorbic acid, and iron content, marking them as promising hybrids for yield, quality, and resistance.

Table 2.3 Review: Combining Ability

S No	Author and Year	Research Findings
1	Gayakwad et al., 2016	Thirty-six hybrids, derived from 12 lines and three testers, were evaluated for yield and earliness traits. Lines IC421962, IC342078, and NBBL-12 exhibited strong general combining ability for both fruit yield per vine and yield per hectare. Among specific cross combinations, NBBL-12 × PS, IC421962 × PSPL, and IC308564A × PSPL demonstrated superior specific combining ability for earliness, fruit yield per vine, and yield per hectare.
2	Jha et al., 2016	Conducted a study on 66 crosses from 12 parents for combining ability, gene action and heterosis. P-8 was best general combiner for carbohydrate, ascorbic acid and total soluble solids while, P-11 was best general combiner for yield per plant. Therefore, the above inbred utilized in future bottle gourd breeding programs. The crosses P-3 × P-12 and P-4 × P-7 were best specific combiner for protein, P-1 × P-4 was best specific combiner for carbohydrate, P-11 × P-12, P-3 × P-8 and P-5 × P-6 were found good specific combiner for ascorbic acid, P-5 × P-10 and P-10 × P-11 were found good specific combiner for

		ascorbic acid and total soluble solids, respectively. P-2 × P-7 and P-2 × P-11 were found good specific combiner for yield per plant.
3	Hadiya et al., 2020	A total of 40 hybrids, generated by crossing 10 lines with 4 testers, were evaluated for combining ability of fruit yield per vine and associated traits. Among the parental lines, ABGS 11-23, JBGL 42, JBGL 43, NDBG 104, NDBG 132, NDBG 604, ABG 1, and Pusa Naveen exhibited significant general combining ability (GCA) effects in the favorable direction for yield and its component traits. Specific combining ability (SCA) analysis identified the hybrids JBOGL 01-59 × LCL 1, ABGS 11-17 × PSPL, ABGS 11-17 × ABG 1, DVBG 94 × LCL 1, and JBGL 43 × Pusa Naveen as superior crosses, each showing significant positive SCA effects for fruit yield per vine.
4	Quamruzzaman et al., 2020	A set of 21 F_1 hybrids, generated via a 7 × 7 half-diallel mating design, were assessed for ten traits in a randomized complete block design with three replications. Both general combining ability (GCA) and specific combining ability (SCA) effects were highly significant for all traits except vine length and average fruit weight. Parent P4 showed a significant negative GCA effect for days to first harvest, whereas P6 possessed the largest positive and significant GCA effect for yield per plant, followed by P2 and P7. Moreover, twelve F_1 hybrids exhibited significantly positive SCA effects, with the P3 × P4 cross displaying the greatest SCA effect.
5	Masud et al., 2021	Used twenty-one cross combinations generated using seven inbred lines and three testers for this experiment to study combining ability and heterosis. Both positive and negative significant heteroses were observed for all studied characters. Of the seven lines, two lines showed highly significant negative GCA effects on flowering, and one line (KBG-16) showed highly significant positive GCA effects on yield per plant.

		Cross 59-1-1(S)-7 × BG0048 was found to have significant SCA effects for the no. days to female flowers and cross 59-1-1-1-1-8 × BG0059 had the highest SCA effects on yield per plant.
6	Ahmad et al., 2022	Estimated combining abilities in eighteen inbred lines and forty-five hybrids of bottle gourds generated using Line x Tester. The results indicated positive and significant general combining effects. IC-321410, IC-541393, and IC-310118 were the best general combiners in terms of average fruit weight, fruit per plant, and yield. Specific combining ability effects for days to the first fruit set in IC-394736 × Narendra Rashmi, and average fruit weight were highest for Vallabh Saral × Narendra Madhuri. These parents and crosses can be used in testing and breeding programs.
7	Bhatt et al., 2023	A set of 28 hybrids derived from eight parental lines was assessed for combining ability and heterosis in key quality parameters, including dry matter content, ascorbic acid, reducing sugar, non-reducing sugar, total sugar, and total soluble solids. General combining ability analysis highlighted parent P3 as a superior general combiner for multiple traits. Specific combining ability results further pinpointed the crosses P2 × P6, P5 × P6, and P1 × P4 as particularly promising, exhibiting enhanced performance across several quality metrics.
8	Patel et al., 2023	A study assessed the combining ability of seven lines, three testers, and their hybrids for yield and associated traits. General combining ability (GCA) analysis for fruit yield per vine indicated that line BRBG22-1 was the most promising general combiner, while specific combining ability (SCA) analysis identified the hybrids BRBG-23 × Narendra Rashmi and BRBG-65 × Rajendra Chamatkar as the best specific combiners for fruit yield per vine.

9	Tulluru et al., 2023	They studied 45 hybrids from 10 parents for their combining ability. Out of the ten parents studied Local Round, Pusa Samridhi, Pant Lauki-3 and Kashi Ganga were found to be good general combiners for quality, yield and quality characters. Based on SCA effects, eight cross combinations viz., Pusa Naveen x Arka Bahar, Pusa Naveen x Kashi Ganga, Pusa Naveen x Punjab Bahar, Pusa Samridhi x Pant Lauki-3, Pusa Samridhi x Local Round, Pusa Santhusti x Kashi Ganga, Pant Lauki-3 x Local Round, Pant Lauki-3 x Local Long were identified as promising for fruit yield per vine, fruit length and average fruit weight.
10	Keshari and Singh, 2024	The combining ability of 28 hybrids was assessed, revealing that no single parental line possessed uniformly high general combining ability (GCA) across all traits. Nevertheless, the cross NDBG-104 × Pusa Sandesh, followed by Pant Lauki-4 × Kashi Kirti, emerged as the most promising combinations for the majority of evaluated traits.

Table 2.4 Gene Action

S No	Author and Year	Research Findings
1	Bawkar et al., 2016	Studied 14 characters for various objectives. Their results showed high heritability accompanied by a high genetic advance which indicated the predominance of additive gene action.
2	Anupam et al., 2017	An experiment was conducted to evaluate heterosis and gene action for ten traits in 36 hybrids derived from nine parental lines. The findings revealed that both additive and non-additive genetic effects were involved, with an over mean degree of dominance indicating that non-additive gene action predominantly influences the inheritance of most traits.
3	Jha et al., 2017	Analysis of 66 hybrids derived from 12 parental lines for ten traits revealed that dominance variance components (H_1 and

		H_2) exceeded the additive variance component (D) in every case, indicating that dominance gene action predominates in trait expression. The average degree of dominance exceeded unity for all traits in both seasons, demonstrating overdominance. Moreover, the estimated dominant-to-recessive allele ratio was greater than one for every character, reflecting a higher frequency of dominant alleles.
4	Amangoua et al., 2018	This study found that seed yield, 100-seed weight, and seed number in bottle gourd are primarily governed by genetic factors, with high heritability and controlled by a small number of genes—often close to one—regardless of environmental variation; using calabash-type plants as the maternal parent increased hypothetical heterosis and trait means, indicating maternal effects, and selection for improved seed yield can be achieved efficiently in a few selfing generations (F3–F4) in West African bottle gourd breeding programs
5	Kumar et al., 2018	A half diallel cross of seven inbred bottle gourd lines was analyzed for gene action in thirteen yield and morphological traits. The study found significant additive genetic variance for most characters, notably average fruit weight and fruits per vine, alongside highly significant dominance components, with evidence of over-dominance (except for fruit length). Most traits showed predominance of dominant alleles in the parents. The results support using heterosis breeding for yield improvement in bottle gourd, as both additive and non-additive gene effects play major roles
6	Quamruzzaman et al., 2019	A half diallel cross involving five bottle gourd parents was investigated. The analysis of genetic variance components indicated that additive effects are more influential in determining fruit yield, as evidenced by the higher magnitude of general combining ability relative to specific combining ability.

7	Maurya et al., 2020	A half diallel mating design was employed to generate twenty-one hybrids, which were subsequently evaluated to elucidate the gene action mechanisms and the proportional impact of genetic factors on trait manifestation. Significant dominance effects (H_1 and H_2) were observed for all traits except fruit weight, while certain traits also exhibited noteworthy additive variance (D), implying the involvement of both additive and non-additive gene actions. Nonetheless, the relatively smaller dominance effects indicate that additive genetic variance has a more substantial influence on the inheritance of fruit yield and its related traits.
8	Quamruzzaman et al., 2020c	The study analyzed genetic factors affecting yield traits in bottle gourd using 21 F1 hybrids and seven parent lines in Bangladesh. Results showed that non-additive gene action, especially over-dominance, was common for most traits, while fruit length, diameter, and endocarp thickness showed partial dominance. Dominant alleles were more frequent than recessive ones in most traits. Broad-sense heritability was high for all traits, and narrow-sense heritability was especially high for those related to fruit size and thickness. The results suggest that hybrid breeding exploiting heterosis could effectively improve bottle gourd yield
9	Patel and Mehta, 2021	A diallel mating design (excluding reciprocals) was implemented using nine parental lines to produce thirty-six F1 hybrids, aimed at estimating the combining ability for fruit yield and related traits in bottle gourds. The analysis revealed significant general and specific combining ability variances for all traits, indicating that both additive and non-additive genetic effects contribute to their expression. Moreover, a GCA/SCA ratio below one underscores the predominance of non-additive gene action in determining these characteristics.
10	Balat et al., 2022	The study on 21 F1 bottle-gourd hybrids and their seven parent lines in Bangladesh found that yield-related traits are

		predominantly governed by non-additive gene action—mainly over-dominance—while fruit length, diameter, and endocarp thickness exhibit partial dominance; dominant alleles outnumber recessive ones for most characteristics, broad-sense heritability is uniformly high, and narrow-sense heritability is especially strong for fruit size and thickness traits, indicating that heterosis-focused hybrid breeding is a promising route for boosting bottle-gourd yield.
11	Yadav et al., 2025	A line × tester analysis in bottle gourd under salt-affected soil identified NDBG-13, NDBG-Sel-1, and Narendra Rashmi as strong general combiners for yield and key traits, while crosses Narendra Pooja × Pusa Naveen, NDBG-13 × Narendra Rashmi, NDBG-Sel-1 × Narendra Rashmi, and Narendra Kamna × Narendra Rashmi showed the best specific combining ability for yield; most yield and quality traits were governed by non-additive gene action (overdominance), suggesting that heterosis breeding is an effective strategy for crop improvement in this environment

Table 2.5 G×E Interaction

S No	Author and Year	Research Findings
1	Varalakshmi et al., 2018	A three-season evaluation (Rabi–Summer 2011–12, 2012–13, and 2013–14) of 18 bottle gourd varieties was undertaken to characterize genotype × environment (G×E) interactions for fruit yield and its component traits. Highly significant G×E effects for all traits indicated that performance differed markedly across environmental conditions. Among the entries, Narendra Rashmi and IIHR-19-1 exhibited the greatest stability, consistently achieving the highest mean fruit yield per hectare. For fruit number, the genotypes Narendra Dharidhar, KBGR-12, Pusa Samrudhi, and Kalyanpur Long maintained stable performance across environments. Regarding average

		fruit weight, Kashi Ganga, Punjab Komal, and Pant Lauki-3 were both stable and recorded the highest mean values.
2	Khan and Sarolia, 2019	The study analyzed genotype × environment (G×E) interactions in 54 bitter gourd genotypes (36 hybrids, 15 parents, 3 checks) across three environments in Rajasthan using the Eberhart and Russell (1966) model. Significant G×E effects were found for most of the 17 traits, involving both predictable (bi) and unpredictable (S^2di) components. Several hybrids combined high mean performance with non-significant S^2di and either bi<1 (stable in unfavorable environments) or bi>1 (stable in favorable environments) for key traits like yield, fruit weight, and earliness. Notably, L1×T2, L1×T3, L2×T3, L3×T2, L6×T3, L7×T3, L11×T2, and L12×T2 were stable for yield in unfavorable conditions, while L3×T3, L4×T1, L5×T1, L5×T2, L7×T2, L9×T1, and L11×T1 were stable in favorable ones—facilitating targeted breeding for adaptability.
3	Tiwari, 2019	The study assessed genotype × environment (G×E) interactions in 12 advanced spine gourd genotypes over three years using AMMI and GGE biplot analyses for yield stability and adaptability. AMMI showed that G2 and G3 had broad adaptability, while G7 and G6 had specific adaptation; G2 and G5 were most stable, and E2 was the most stable environment. GGE biplot identified G7 as best in E1 and E2, and G4 in E3, defining three mega-environments. Both models highlighted G7 as a high-yielding, stable genotype suitable for widespread cultivation in the Northern Hill Zone of Chhattisgarh.
4	Tiwary and Restogi, 2020	The study examined genotype × environment (G×E) interactions for seed germination in 15 spine gourd genotypes across three conditions—normal field, agroforestry, and greenhouse—using AMMI analysis. Environment had the largest influence on germination, with E2 (agroforestry) performing best. The first two AMMI components explained all G×E variation. Genotypes G10, G2, G4, G8, and G12

		showed stable, high germination across environments, with G10 performing best. Soil factors such as pH, nutrients, and organic matter also affected germination, guiding selection of adaptable genotypes for stable performance.
5	Singh et al., 2023a	They evaluated 48 genotypes of bottle gourd for G×E interaction. Their data showed that P3 x P6 for days to first harvest, P2 x P9 , P3 x P6 , P3 x P9 , P4 x P7 , P3 x P7 , P1 x P3 for fruit length, P4 x P10, P2 x P5 , P1 x P6 for rind thickness, P1 x P6 , P6 x P8 , P9 x P10 for flesh thickness, P6 x P8 , P3 x P9 , P1 x P6 , P8 x P9 , P8 x P10, P4 x P6 for stem girth, P8 x P9 , P6 x P8 , P4 x P8 , P8 x P10 for vine length at final harvest, P4 x P5 and P5 x P6 for yield per vine, P1 x P5 and P1 x P3 for total sugar and P5 x P10, P5 x P9 , P9 x P10, P1 x P2 , P1 x P3 , P1 x P6 and P4 x P7 for non-reducing sugar were exhibited non-significant deviation from regression and regression coefficient. This indicated that the G×E interaction was less on these crosses which will have an impact on stable performance.
6	Singh et al., 2023b	The study evaluated 58 bottle gourd genotypes (10 parents, 45 hybrids, 3 checks) across three environments in Rajasthan using the Eberhart and Russell (1966) model to assess genotype × environment interactions for yield, quality, and growth traits. Stability was judged by mean performance, regression coefficient (bi), and deviation from regression (S^2di), identifying genotypes suited to favorable (bi>1), unfavorable (bi<1), or average (bi≈1) conditions. Several hybrids, such as P4×P5, P5×P6, and P8×P10, showed stable performance for yield or specific traits, enabling targeted selection of varieties adapted to specific environments.
7	Jat et al., 2024	The study assessed genotype × environment (G×E) interactions for three bitter gourd lines (Pusa Rasdar, S32, S57) grown over three years in four environments—hi-tech greenhouse, naturally ventilated polyhouse, insect-proof net house, and

		open field—using a Genotype × Yield × Trait (GYT) biplot approach. Significant G×E effects were found for yield, earliness, antioxidants, and mineral traits, with insect-proof net houses and polyhouses outperforming open fields. Net house × Pusa Rasdar, S32, and S57 combinations showed the highest stability and performance across traits, highlighting that matching genotypes with optimal protected environments maximizes yield and quality.

CHAPTER 3

MATERIALS AND METHODS

This chapter contains the outlines of the materials used in the experiments and the procedures/methods followed for data collection, analysis, and interpretation. The present investigation on "Genetic diversity, heterosis and combining ability studies for fruit yield and its component traits in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]" was carried out during Summer 2023, *Kharif* 2023, Late-summer 2024, *Khariff* 2024, and mid-*Khariff* 2024. The details of the experiment are discussed under the following heads:

3.1 Site of Experiment

3.2 Climatic Conditions

3.3 Experimental Materials

3.4 Methods

3.5 Crossing Program

3.6 Data Recording

3.7 Statistical Analyses

3.1 Site of Experiment

Phagwara is located between the fertile plains between Beas and Sutlej rivers. Lovely Professional University is geographically located at 31° 15' 29" N and 75° 42' 27" E at an altitude of 236 m above MSL (Mean Sea Level) in Chaheru village, under Phagwara sub-district (Kaputhala district), Punjab. The soil type of the experimental location was inceptisols with a slightly basic pH in the range of 7.2 to 7.7.

3.2 Climatic condition

The climate of Phagwara is subtropical with extreme humid conditions during the months of July to September. There is a large variation between summers and winters temperatures with heat index reaching as high as 51° C in summers and -2° C in winters. Fog/Smog is common occurrence during December and January while summer is accompanied by extremely hot dry winds. The normal period of monsoon onset in this region is the 1st week of July, and it lasts

until the end of September, while a brief spell of rain occurs during February-March due to western disturbances. The region receives and average yearly rainfall of about 703.0 mm.

3.3 Experimental materials

The experiment took place in 3 different time frames and the materials used in each season differed according to the objectives of the specific experiment. Season 1 (Summer 2023) consisted of 39 genotypes **(Table 3.2)** which were sourced from Indian Institute of Vegetable Research, Varanasi (IIVR) and National Bureau of Plant Genetic Resources (NBPGR), Pusa, New Delhi. Season 2 (*Kharif* 2023) consisted of 14 genotypes (10 Lines and 4 Testers) (**Table 3.3)** selected from the previous season based on different clusters from the diversity analysis and yield. Season 3 (Late-Summer 2024, *Khariff* 2024, mid-*Khariff* 2024) consisted of 14 parents, 40 F_1 hybrids and 1 commercial check **(Table 3.3 and Table 3.4)**.

Table 3.1: List of genotypes (Season 1)

S No	Genotype	Source	S No	Genotype	Source
1	IC 541196	NGPGR, Hyderabad	21	NARENDRA POOJA	NDUAT, Faizabad
2	G-2	NDUAT, Faizabad	22	IC 310188	NGPGR, Hyderabad
3	IC 284895	NGPGR, Hyderabad	23	PUSA MEGHDOOT	IIVR, Varanasi
4	IC 538142	NGPGR, Hyderabad	24	IC 322274	NGPGR, Hyderabad
5	IC 470759	NGPGR, Hyderabad	25	IC 566641	NGPGR, Hyderabad
6	NARENDRA RASHMI	NDUAT, Faizabad	26	IC 449080	NGPGR, Hyderabad
7	IC 470859	NGPGR, Hyderabad	27	NAM TAO YAI	IIVR, Varanasi
8	IC 394736	NGPGR, Hyderabad	28	IC 92362	NGPGR, Hyderabad
9	ARKA BAHAR	IIHR, Bengaluru	29	PUSA SUMMER PROLIFIC ROUND	IIVR, Varanasi
10	IC 342077	NGPGR, Hyderabad	30	AVINASH-IV	IIVR, Varanasi
11	IC 438394	NGPGR, Hyderabad	31	PUSA SUMMER PROLIFIC LONG	IIVR, Varanasi
12	PUNJAB ROUND	NGPGR, Hyderabad	32	VRBG-3	NGPGR, Hyderabad
13	AZAD NUTAN	NDUAT, Faizabad	33	N/06-200	NGPGR, Hyderabad
14	SEA-127	NGPGR, Hyderabad	34	VRBG-71	NGPGR, Hyderabad
15	IC 393752	NGPGR, Hyderabad	35	VRBG-47-2	NGPGR, Hyderabad
16	KASHI GANGA	IIVR, Varanasi	36	N/06-40	NGPGR, Hyderabad
17	PANT SHANKAR LAUKI-1	IIVR, Varanasi	37	VRBG-15-1	NGPGR, Hyderabad
18	IC 588086	NGPGR, Hyderabad	38	SEA-83	NGPGR, Hyderabad
19	PUSA MAJIRI	IIVR, Varanasi	39	Malerkotla Special (Commercial Check)	Local
20	IC 371745	NGPGR, Hyderabad			

Table 3.2: List of genotypes (Season 2)

S No	Line/Tester	Genotype
1	Line 1	IC 284895
2	Line 2	VRBG-3
3	Line 3	VRBG-71
4	Line 4	IC 394739
5	Line 5	N/06-40
6	Line 6	IC 393752
7	Line 7	SEA-83
8	Line 8	IC 371745
9	Line 9	Avinash IV
10	Line 10	IC 92362
11	Tester 1	Pusa Majiri
12	Tester 2	Pusa Meghdoot
13	Tester 3	Narendra Pooja
14	Tester 4	Punjab Round

Table 3.3: List of genotypes (Season 3)

S No	Parents/Hybrids	S No	Parents/Hybrids	S No	Parents/Hybrids
1	Line 1 x Tester 1	20	Line 10 x Tester 2	39	Line 9 x Tester 4
2	Line 2 x Tester 1	21	Line 1 x Tester 3	40	Line 10 x Tester 4
3	Line 3 x Tester 1	22	Line 2 x Tester 3	41	IC 284895
4	Line 4 x Tester 1	23	Line 3 x Tester 3	42	VRBG-3
5	Line 5 x Tester 1	24	Line 4 x Tester 3	43	VRBG-71
6	Line 6 x Tester 1	25	Line 5 x Tester 3	44	IC 394739
7	Line 7 x Tester 1	26	Line 6 x Tester 3	45	N/06-40
8	Line 8 x Tester 1	27	Line 7 x Tester 3	46	IC 393752
9	Line 9 x Tester 1	28	Line 8 x Tester 3	47	SEA-83
10	Line 10 x Tester 1	29	Line 9 x Tester 3	48	IC 371745
11	Line 1 x Tester 2	30	Line 10 x Tester 3	49	Avinash IV
12	Line 2 x Tester 2	31	Line 1 x Tester 4	50	IC 92362
13	Line 3 x Tester 2	32	Line 2 x Tester 4	51	Pusa Majiri
14	Line 4 x Tester 2	33	Line 3 x Tester 4	52	Pusa Meghdoot
15	Line 5 x Tester 2	34	Line 4 x Tester 4	53	Narendra Pooja
16	Line 6 x Tester 2	35	Line 5 x Tester 4	54	Punjab Round
17	Line 7 x Tester 2	36	Line 6 x Tester 4	55	Malerkotla Special (Commercial Check)
18	Line 8 x Tester 2	37	Line 7 x Tester 4		
19	Line 9 x Tester 2	38	Line 8 x Tester 4		

3.4 Methods

3.4.1 Trial I (Summer 2023)

First trial took place in Summer 2023 with the objective of evaluating the diversity among the studied genotypes of bottle gourd. The genotypes were sown in a polyhouse on 25th March, 2023 and were later transplanted to the main field on 24th April, 2023 (after hardening for 8 days) on flat beds.

1. Design: Alpha Lattice
2. Number of replications: 2
3. Date of sowing: 25th March, 2023
4. Date of transplanting: 24th April, 2023
5. Plot size: 400 m^2
6. Spacing: 200 cm x 60 cm
7. No. of genotypes: 38 + 1 (Check)

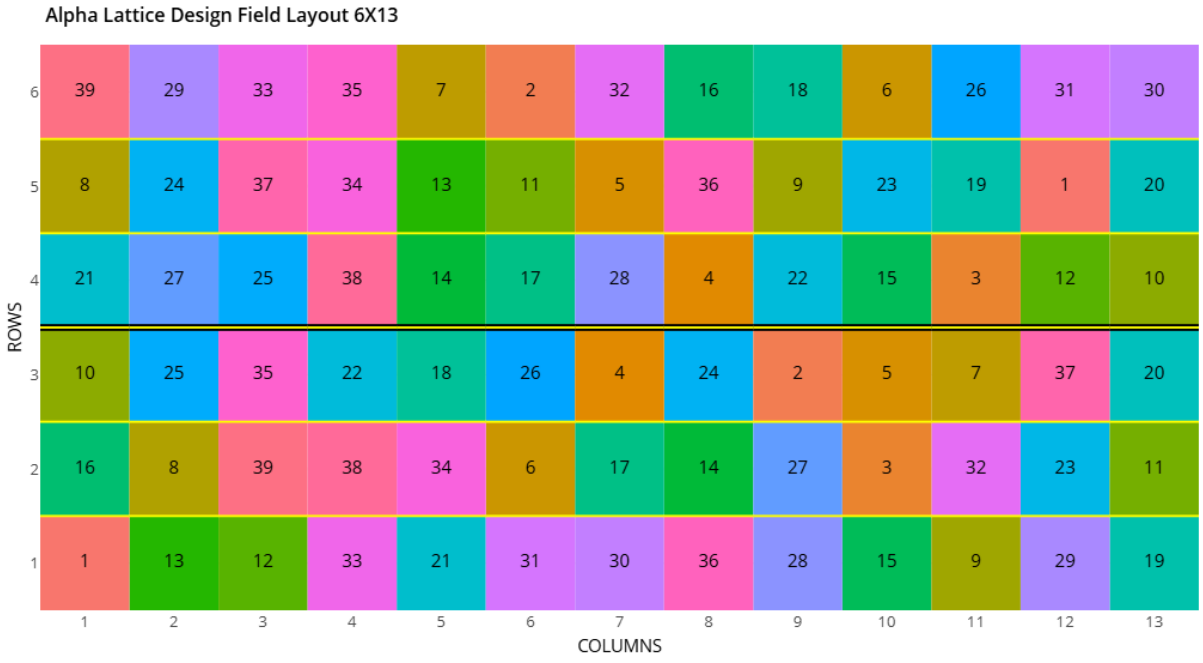


Figure 3.1: Field layout of the first trial (Alpha lattice 6 x 13)

3.4.2 Trial II (*Kharif* 2023)

Second trial was a crossing trial where selected genotypes from the first trial were directly sown on raised beds and were crossed in Line x Tester mating design. A total of 14 parents (10 lines and 4 testers) were selected for crossing.

1. Design: Crossing Block
2. Date of sowing: 14th July (1st stagger)
3. Number of staggers: 3 (15 days interval)
4. Plot size: 250 m^2
5. Spacing: 200 cm x 60 cm
6. No. of genotypes: 14 parents (10 lines and 4 testers)

Tester 1	Tester 2	Tester 3	Tester 4	1st Stagger
Line 9	Line 10	Filler 1	Filler 2	
Line 5	Line 6	Line 7	Line 8	
Line 1	Line 2	Line 3	Line 4	
Tester 1	Tester 2	Tester 3	Tester 4	2nd Stagger
Line 9	Line 10	Filler 1	Filler 2	
Line 5	Line 6	Line 7	Line 8	
Line 1	Line 2	Line 3	Line 4	
Tester 1	Tester 2	Tester 3	Tester 4	3rd Stagger
Line 9	Line 10	Filler 1	Filler 2	
Line 5	Line 6	Line 7	Line 8	
Line 1	Line 2	Line 3	Line 4	

Figure 3.2: Field layout for the crossing block

Crossing Procedure

Bottle gourd [*Lagenaria siceraria* (Mol) Standl.] is a monoecious and predominantly cross-pollinated crop bearing separate male and female flowers on the same plant. Since make and

female flowers are distinct, emasculation is not required for controlled hybridization. Based on the results of genetic diversity analysis and per se performance recorded during Trial I, ten diverse and promising genotypes were selected as lines and four genotypes as testers. These parents were crossed in a Line x Tester mating design.

Healthy and true-to-type plants of each parental genotype were maintained in the crossing block. Female flower buds expected to open the following morning were identified in the late afternoon based on the presence of a well-developed ovary and swollen bud stage. Such buds are carefully covered with butter paper bags and secured using clips to prevent unwanted pollination.

On the following morning, freshly opened male flowers from the designated male parent were collected. Male flowers were selected from vigorous plants to ensure pollen viability. The corolla of the male flower was gently removed to expose the anthers. The previously bagged female flower was uncovered carefully and pollen from one or more freshly collected male flowers was directly dusted onto the receptive stigma by gently rubbing the anthers over it.

Immediately after pollination, the female flower was re-covered with a fresh butter paper bag to avoid contamination from stray pollen. Care was taken to ensure that only the designated male parent contributed pollen to the female flower. Each pollinated flower was tagged immediately after pollination. The tag contained the following details:

- Female parent name
- Male parent name
- Cross combination number
- Date of pollination

Pollinated fruits were allowed to develop to full physiological maturity on the vine. Fruits were harvested when they attained characteristic maturity symptoms such as hard rind and change in external colour. Mature fruits from each cross were harvested separately and labelled carefully. Seeds were extracted manually by cutting open the mature fruits. The extracted seeds were washed thoroughly with clean water to remove adhering pulp and then shade-dried for 5 3-5 days to reduce seed moisture.

3.4.3 Trial III (Late Summer 2024 – mid *Kharif* 2024)

Third trial was an evaluation trial with multiple objectives. The evaluation was for testing the hybrids that were obtained by the crossing of 14 parents in the previous season. 40 F_1 hybrids along with their 14 parents and 1 commercial check were directly sown on raised beds in an alpha lattice design at 3 different dates of sowing (at least 25 days apart).

1. Design: Alpha lattice
2. No of replications: 2
3. Date of 1st Sowing: 15th May, 2024
4. Date of 2nd Sowing: 10th June, 2024
5. Date of 3rd Sowing: 7th July, 2024
6. Plot size: 600 m^2
7. Spacing: 200 cm x 60 cm
8. No. of genotypes: 55 (40 hybrids, 14 parents and 1 commercial check)

In addition to the 40 F_1 hybrids and 14 parental lines, one commercially grown cultivar, Malerkotla Special was included as a standard check to facilitate comparison of hybrid performance and estimation of economic heterosis. The check grown under the same experimental conditions and experimental design as the other entries.

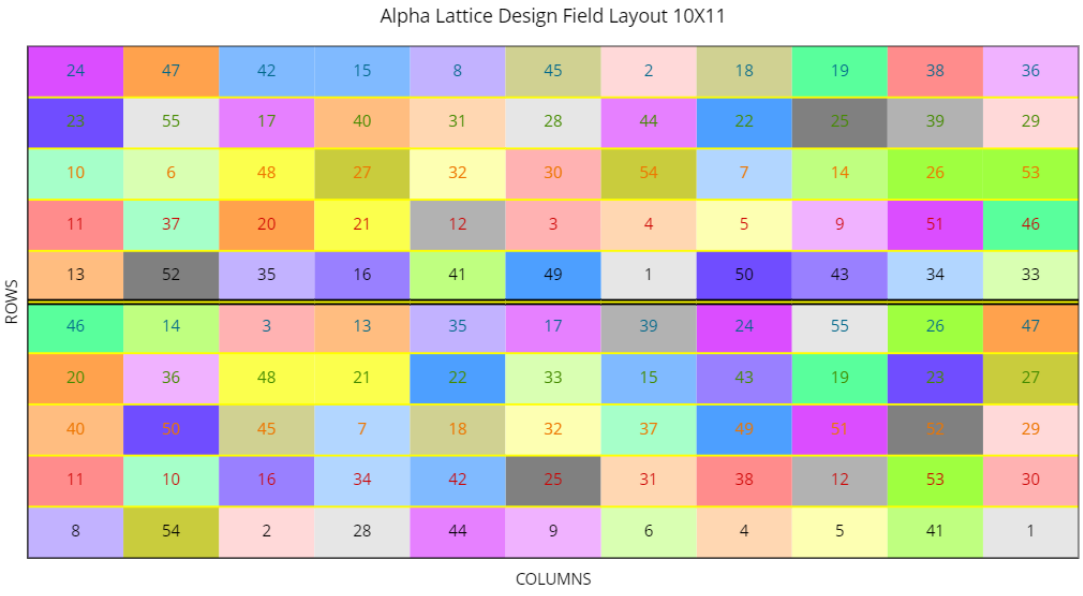


Figure 3.3: Field layout for Environment 1 (Alpha lattice 10 x 11)

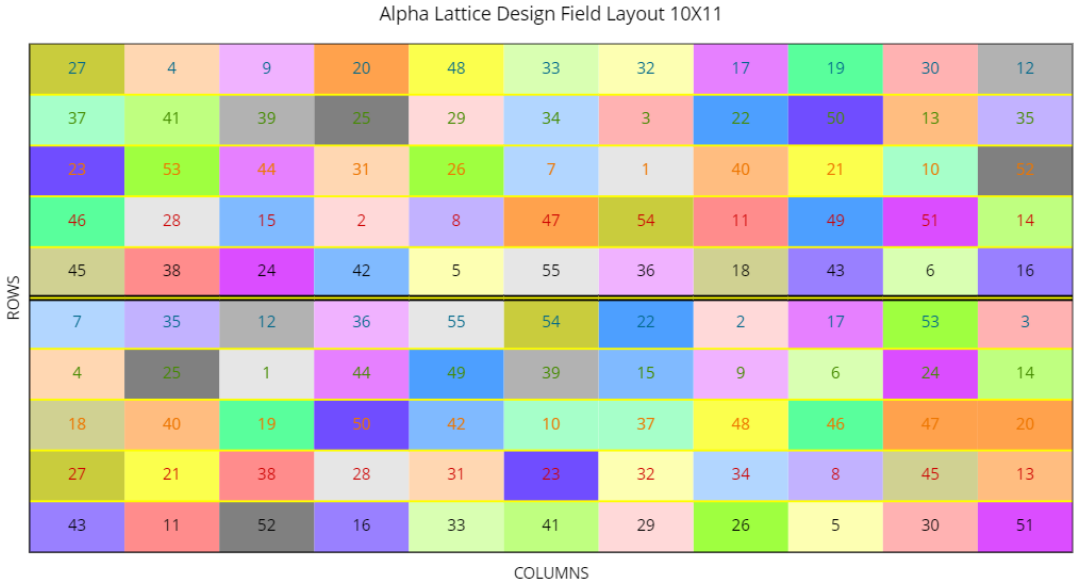


Figure 3.4: Field layout for Environment 2 (Alpha lattice 10 x 11)

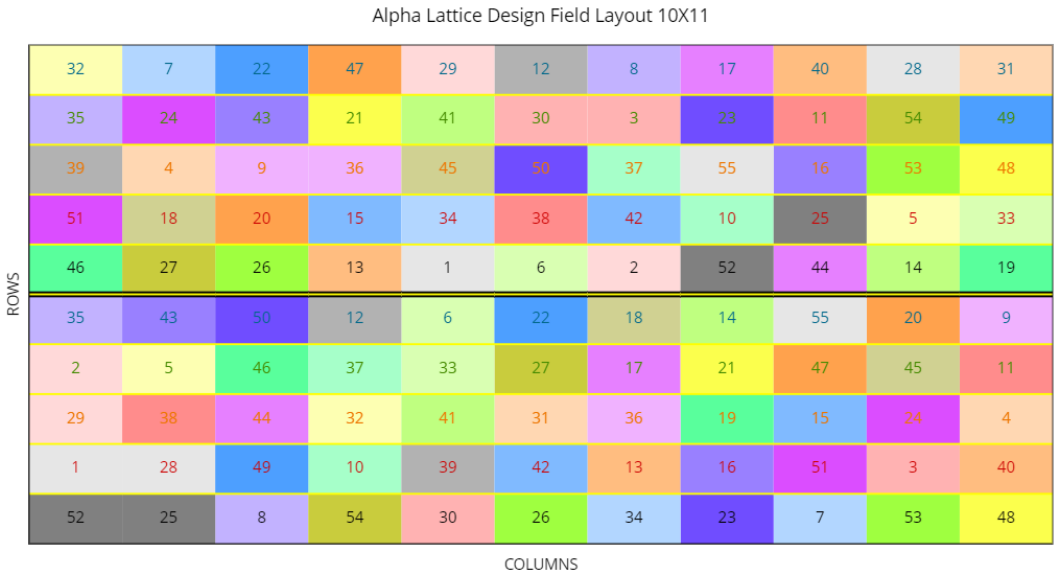


Figure 3.5: Field layout for Environment 3 (Alpha lattice 10 x 11)

3.4.4 Management Practices

1. Land Preparation

The experimental field was ploughed twice with tractor drawn disc plough followed by harrowing to obtain a fine tilth. Raised beds of 1.5m width were prepared for sowing/transplanting in two rows (towards the edge of the raised beds).

2. Fertilizer Application

A recommended dose of fertilizer @ 100:50:50 kg $N:P_2O_5:K_2O$ per hectare was applied. Half of nitrogen and full dose of phosphorus and potassium were applied as basal at the time of transplanting. The remaining nitrogen was applied in two equal splits at 30 and 45 days after transplanting as outlined by PAU package and practices.

3. Irrigation

Irrigation was provided through furrow method at 7-10 day intervals depending on prevailing weather conditions. During flowering and fruit development stages, irrigation frequency was increased to avoid moisture stress.

4. Weed Management

One manual weeding was carried out at 30 days after sowing to maintain weed free conditions.

5. Plant protection Measures

Only a small population of red pumpkin beetle were seen during the trial so no insecticide was sprayed. For powdery mildew management, wettable sulphur (2g/L) was sprayed at 15 day intervals as required.

6. Pollination management

In evaluation trials, natural insect-mediated pollination was allowed. In the crossing block, controlled hand pollination was carried out during early morning hours (7:00 – 09:00 am) and pollinated flowers were tagged and covered to prevent contamination.

Table 3.4: Number of successful crosses for each cross-combination

	Tester 1	Tester 2	Tester 3	Tester 4
Line 1	3	2	2	3
Line 2	4	1	2	3
Line 3	2	4	2	5
Line 4	3	3	1	2
Line 5	2	2	1	3
Line 6	3	3	2	4
Line 7	2	3	3	3
Line 8	2	2	2	2
Line 9	1	2	1	2
Line 10	3	4	2	1

3.5 Data Recording

Observations were recorded on fourteen agronomic and yield related traits of bottle gourd. Data were collected from five randomly selected and tagged plants in each plot and all the data was recorded from these plants. Observations were recorded at appropriate growth stages following standard horticultural procedures. Observations for the following characters were recorded:

3.5.1 Days to first male flowering (DMF)

The trait was quantified as the number of days elapsed from the date of sowing until the anthesis of the first male flower observed within each experimental plot.

3.5.2 Days to first female flowering (DFF)

The trait was quantified as the number of days elapsed from the date of sowing to the occurrence of anthesis in the first female flower observed within each experimental plot.

3.5.3 Sex ratio (SR)

It was recorded as the ratio between number of female flowers to number of male flowers.

3.5.4 Number of secondary branches (NSB)

It was recorded as the number of secondary branches originating from the primary branches at the time of last picking from five selected plants and the averages were calculated.

3.5.5 Vine length (VL)

It was recorded in centimetres as the length of the from base of the shoot till the longest primary branch at the time of last picking from five selected plants and the averages were calculated.

3.5.6 Fruit length (FL)

Length of the edible fruits were measured in centimetres as the length from the point of attachment of the stalk to the blossom end from one fruit from each selected plant and the averages were calculated.

3.5.7 Fruit girth (FG)

Length of the edible fruits were measured in centimetres. The circumference at the thickest part was measured using a thread and a ruler from one fruit from each selected plant and the averages were calculated.

3.5.8 Days to 1st harvest (D1H)

The trait was measured as the number of days elapsed from the date of sowing to the date of the first harvestable fruit (or yield component) collected from each experimental plot.

3.5.9 Days to 3rd harvest (D3H)

The trait was quantified as the number of days elapsed from the date of sowing to the date of the third harvestable fruit (or yield component) collected from each experimental plot.

3.5.10 Average fruit weight (AFW)

All the marketable fruits from the selected plants were weighed in grams and averages were calculated.

3.5.11 Fruit flesh thickness (FFT)

Cross section of one marketable fruit from the selected plants was taken and the thickness of the fleshy part, after removing the rind, was measured using a vernier calliper and averages were calculated.

3.5.12 Rind thickness (RT)

Rind thickness was measured in millimeters using a vernier calliper by measuring the thickness of the outer fruit rind at the middle portion of the fruit.

3.5.13 Fruit yield per plant (FYPP)

All the marketable fruits were harvested and weighed in grams till the complete of the season from the selected plants and the sums of all fruits per plant were averaged of that plot to get the FYPP.

3.5.14 Total soluble solids (TSS)

One marketable fruit from each vine was selected. The flesh was crushed to release the juices and the strained juice was placed on a digital refractometer and reading was noted in degrees Brix (ºBrix). The average from the five fruit was calculated to get TSS.

3.6 Statistical Analysis

Data recorded for the above experiments were recorded according to the above-mentioned methods and were subjected to the following statistical procedures.

1. Analysis of variance (Experimental design)
2. Components of Variance
3. Estimation of Genetic diversity
4. L x T Analysis
5. Combining ability variances
6. Estimation of Heterosis
7. AMMI Model

3.6.1 Analysis of variance (Alpha Lattice Design)

The analysis of variance (ANOVA) for the experimental design was conducted using the approach outlined by Patterson and Williams (1976). The F-test was utilized to determine the statistical significance of differences among treatment means. A fixed effects model under the alpha lattice design was applied to test the hypothesis, as described below:

$$Y_{ijk}=\mu+R_i+B_{ij}+T_k+\epsilon_{ijk}$$

where:

- Y_{ijk} = observed response of the k^{th} treatment in the j^{th} block of the i^{th} replication

- μ = overall mean
- R_i = effect of the i^{th} replication (i=1,2,… r)
- B_{ij} = effect of the j^{th} incomplete block within the i^{th} replication (j=1,2,…,b)
- T_k = effect of the k^{th} treatment (k=1,2,…,t)
- ϵ_{ijk} = residual error associated with each observation, presumed to be independent and identically distributed following a normal distribution with a mean of zero and a constant variance σ^2

The significance of mean squares was tested using the F-test at 5% and 1% levels of significance.

Table 3.5: Analysis of variance for Alpha lattice design

Source of Variation	**Degrees of Freedom(df)**	**Mean Square(MS)**	**Expected Mean Square(EMS)**
Replications(R)	r−1	MS_R	$\sigma^2+b\sigma_R^2$
Blocks within Replications(B(R))	r(b−1)	MS_B	$\sigma^2+\lambda\sigma_B^2$
Treatments(TTT)	t−1	MS_T	$\sigma^2+r\sigma_T^2$
Error(EEE)	(r−1)(t−1)	MS_E	σ^2
Total	rt−1		

where:

- r = number of replications
- b = number of incomplete blocks per replication
- t = number of treatments
- σ_R^2 = variance due to replications
- σ_B^2 = variance due to blocks
- σ_T^2 = variance due to treatments
- σ^2 = residual error variance

- λ = efficiency factor of block adjustment, depends on design structure

3.6.2 Estimation of coefficient of variability

The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), and environmental coefficient of variability (ECV) were estimated according to the formulae proposed by Burton and De Vane (1953).

$$Genotypic\ coefficient\ of\ variation\ (GCV\%) = \frac{\sigma_g}{\bar{x}}$$

$$Penotypic\ coefficient\ of\ variation\ (PCV\%) = \frac{\sigma_p}{\bar{x}}$$

where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\overline{x}$ = grand mean

3.6.3 Heritability

Broad-sense heritability (h^2_{bs}) was estimated using the formulae outlined by Burton and De Vane (1953) and Johnson et al. (1955).

$$Heritability\ (broad\ sense)(h^2_{bs}) = \frac{V_G}{V_P}$$

were,

h^2_{bs}= heritability

V_G= genotypic variance

V_P = Phenotypic variance

3.6.4 Genetic advance

The expected genetic advance (GA) from selection of the top 5 percent of individuals was estimated using the method described by Burton and De Vane (1953) and Johnson et al. (1955).

$GA = K \times \sigma_p \times h^2_{(bs)}$

where,

K = 2.06 (selection differential at 5% selection intensity)

$h^2_{(bs)}$ = heritability (broad sense) (σ^2_g/σ^2_p)

σ_p = phenotypic standard deviation

$$Genetic\ advance\ as\ percentage\ mean\ (GA\%) = \frac{Expected\ GA}{Grand\ mean}\ x\ 100$$

For categorizing the magnitude of different parameters, the following limits were arbitrarily used:

PCV and GCV	> 25%	-	High
	15% - 25%	-	Moderate
	< 15%	-	Low
Heritability (H^2)	> 70%	-	High
	50% - 70%	-	Moderate
	< 50%	-	Low
Genetic advance (GA)	> 50%	-	High
	25% - 50%	-	Moderate
	< 25%	-	Low

3.6.5 Estimation of Genetic diversity (Mahalanobis D^2 Statistics)

Mahalanobis (1936) introduced a measure of multivariate distance for assessing divergence among groups based on multiple traits. Considering x_1, x_2, x_3 ……. x_p as the set of p quantitative variables measured on each individual, and d_1, d_2, d_3 …….. d_p as the differences between the means of two populations for each variable (i.e., $x_1^{-1} – x_1^{-2}$, $x_2^{-1} – x_2^{-2}$ ……x_p-1 – x_p^{-2}), the Mahalanobis D^2 statistic is defined as follows:

$$pD_2 = b_1d_1 + b_2d_2 + \ldots\ldots\ldots\ldots\ldots b_pd_p$$

Here, the b_1 values are to be estimated such that the ratio of variance between the populations to the variance within the populations are maximized. In terms of variances and covariances, the D^2 value is obtained as follows:

$$pD^2 = W_{ij} (x_i^{-1} – x_i^{-2}) (x_j^{-1} – x_j^{-2})$$

where,

W_{ij} is the inverse of estimated variance covariance matrix.

3.6.5.1 Test of significance

A simultaneous test of differences among mean values for multiple correlated variables was conducted using the 'V' statistic, which is based on Wilks' criterion. This analysis was performed at 'pq' degrees of freedom, where **p** represents the number of variables and **q** is the number of genotypes minus one.

Testing of significance of D^2 values

The D^2 value computed for each pair of populations was treated as the calculated value of chi-square (χ^2) and compared to the corresponding tabulated χ^2 value at 'p' degrees of freedom, where 'p' denotes the number of characters evaluated.

3.6.5.2 Grouping of genotypes into various clusters

Based on the D^2 values, the genotypes were grouped into distinct clusters using Tocher's method, as described by Rao (1952).

3.6.5.3 Average intra- and inter-cluster distance

$$\text{Average intra – cluster } D^2 = \Sigma D_i^2/n$$

where,

ΣD_i^2 = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

$$\text{Average inter- cluster distance } D^2 = \Sigma D_{ij}^2/n_i.n_j$$

where,

ΣD_{ij}^2= sum of all distances between all possible combinations ($n_i.n_j$) of the genotypes between the clusters.

n_i= number of genotypes in i^{th} cluster

n_j= number of genotypes in j^{th} cluster

3.6.5.4 Cluster mean

Cluster means of common bean genotypes falling under different clusters in individuals as well as combined over environments were also calculated.

3.6.6 Line x tester analysis

Line × Tester analysis was conducted on a limited scale to estimate the general combining ability (GCA) and specific combining ability (SCA) of multiple lines. This methodology corresponds to the "North Carolina Design II" as formulated by Comstock and Robinson (1952). In this design framework, a random sample of *l* lines is crossed with each of the *t* testers, following the procedure described by Singh and Chaudhary (1977). The associated analysis of variance model is provided below:

Table 3.6: Analysis of variance for Line x Tester

Source of variation	**df**	**SS**	**MSS**
Replications	(r-1)	-	-
Lines (Females)	(l-1)	SS (l)	M(l)
Testers (Males)	(t-1)	SS (t)	M(t)
Lines x Testers	(l-1)(t-1)	SS(lt)	M(lt)
Error	(r-1)(T-1)	SS(e)	M(e)

where

r = number of replications

T = total number of treatments

l = number of lines

t = number of testers

3.6.7 Combining ability effects

Combining ability variances and effects were estimated using the line × tester approach as outlined by Kempthorne (1957). Experimental data collected for nineteen traits were analyzed using analysis of variance.

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

Where,

μ = general mean

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

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

S_{ij} = SCA effect of the ij^{th} combination; and

e_{ijk} = Error associated with the observation X_{ijk}; k = 1, 2…..……. r.

The individual effect was estimated as follow:

(i) GCA lines

$$g_i = \frac{X_i \ldots}{tr} - \frac{X \ldots}{rlt}$$

Where,

g_i = general combining ability effect of i^{th} line

$X_{i..}$ = Total of i^{th} line over all the tester and replications.

(ii) GCA testers

$$g_j = \frac{X_j \ldots}{lr} - \frac{X \ldots}{rlt}$$

Where,

g_j = general combining ability effect of j^{th} tester.

X_j = Total of j^{th} tester over all lines and replications.

(iii) SCA effects

$$S_{ij} = \frac{X_{ij}.}{r} - \frac{X_i}{rt} - \frac{X_j}{lr} + \frac{X \ldots}{rlt}$$

Where,

S_{ij} = specific combining ability effect of i^{th} line and j^{th} tester

Critical difference (C.D.) was calculated as:

C.D. = SEd x t at 5% or 1% level at error d.f.

The significance of GCA lines, GCA testers and SCA effects were tested by comparing with respective C.D. values.

3.6.8 Gene Action

Gene action was worked out following Kempthorne (1957)

$$Cov.HS = [\frac{1+F}{4}]^2.\sigma_A^2$$

Additive genetic variance σ^2_A = 4 Cov. H.S. (average) with F=1

$$\sigma^2_{SCA} = [\frac{1+F}{2}]^2.\sigma_D^2$$

Dominance variance (σ^2_D) = σ^2_{sca} with F=1

Where,

F = Inbreeding co-efficient

3.6.9 Estimation of heterosis

The extent and direction of heterosis were assessed based on data collected for various quantitative traits. Heterosis was quantified as the percentage increase or decrease exhibited by the F_1 hybrids relative to the mid-parent value (mid-parent heterosis), the better parent (heterobeltiosis), and local check variety (standard heterosis).

3.6.9.1 Mid-parent or average heterosis

$$Average\ or\ mid\ parent\ heterosis = \frac{(F_1 - MP)}{MP} x100$$

Where,

MP = Mean value of the both parents

S.Ed. for

$$F_1 - MP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. × t (at error d.f.)

3.6.9.2 Heterobeltiosis

$$Heterobeltiosis = \frac{(F_1 - BP)}{BP} x100$$

Where,

BP = Mean value of the better parents

S.Ed. for

$$F_1 - BP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. × t (at error d.f.)

3.6.9.3 Standard or economic heterosis

$$Standard\ heterosis = \frac{(F_1 - SC)}{SC} x100$$

Where,

F_1 = Mean value of F_1

SC = Mean value of check variety

S.Ed. for

$$F_1 - BP = \sqrt{\frac{2MSE}{r}}$$

C.D. = S.Ed. × t (at error d.f.)

Test of the significance of heterosis

Significance of heterosis was tested following the "t" test. The calculated "t" value was compared with table value of "t" at error degree of freedom from ANOVA comprising parents and F_1s P = 0.05 and P = 0.01. "t" value was estimated as given below:

$$t(H) = \frac{F_1 - MP\ or\ BP\ or\ SC}{SE(H)\ over\ MP\ or\ BP\ or\ SC}$$

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

Where,

Me = error variance obtained by ANOVA comprising parents and F_1s

r = Number of replications

3.6.10 Genotype x Environmental Interaction Analysis (AMMI Model)

The Additive Main Effects and Multiplicative Interaction (AMMI) model integrates both additive and multiplicative components to analyze two-way data structures. It partitions the total variation into additive effects (main effects) and multiplicative effects (interactions), and subsequently applies principal component analysis (PCA) to the interaction matrix to uncover detailed interaction patterns (Muthuramu et al., 2011). The main effects are estimated through a two-way additive ANOVA using the least squares method. Singular value decomposition (SVD) is then applied to the residual interaction matrix from ANOVA to estimate the multiplicative terms of the AMMI model (Rodrigues et al., 2016). The number of significant interaction components retained in the model is determined using an F-test, which compares the mean square of each principal axis with an appropriate error estimate (Gollob, 1968). This clear separation of main and interaction effects allows breeders to analyze and interpret these sources of variation independently, enhancing the utility of the results. The present study employed PBSTAT-GE () tool for AMMI analysis.

The linear equation for AMMI model,

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{N} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where,

Y_{ij} = observed yield or trait value for genotype i in environment j

μ = grand mean

G_i = main effect of genotype i

E_j = main effect of environment j

λ_k = singular value (eigenvalue) for the k-th principal component (PC)

α_{ik} = genotype score for the k-th PC

γ_{jk} = environment score for the k-th PC

N = number of principal components (usually selected based on statistical criteria)

ε_{ij} = residual error (random noise)

Table 3.7: Pooled analysis of variance as per AMMI model

Source of variation	**d.f.**	**Mean square**	**Expected MS**
Total	(ger-1)		
Treatment	(ge-1)		
Replication x Environments	(r-1)e		
Genotypes	(g-1)	MS1	MS1/MS3
Environments	(e-1)	MS2	MS2/MS3
Genotype x Environment	(g-1)(e-1)	MS3	MS3/Mse
PCAI	(g+e-1-2n)	MS4	MS4/Mse
PCAII	(g+e-1-2n)		
PCAIII	(g+e-1-2n)		
Residual	(g+e-1-2n)	Mse	

3.6.11 Software Used

All statistical analyses were performed using R statistical software. Packages used included 'agricolae' for analysis of variance and mean comparison and GGEBiplotGUI for graphical representation of genotype x environment interaction.

CHAPTER 4

RESULTS AND DISCUSSION

The present investigation titled **"Genetic diversity, heterosis and combining ability studies for fruit yield and its component traits in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]"** was conducted at the departmental fields of genetics and plant breeding at Lovely Professional University in Chiheru, Punjab. The study involved a series of experiments conducted in three seasons. The evaluation for diversity was conducted in summer 2023. Selected genotypes were planted in *Khariff* 2023 to produce hybrids according to line x tester mating design. Evaluation of the produced hybrids along with their parents were evaluated on three different dates of sowing (14th April, 21st May and 20th June) to simulate three environments.

Data for 14 traits were recorded during evaluations at their respective stages. Estimates of diversity were based on the data obtained in season I. Data from season III were used to estimate heterosis (standard heterosis, heterobeltiosis and economic heterosis), combining ability effects using LxT mating design (Kempthorne, 1957) and gene action. These data were also used to identify stable genotypes using the AMMI model (Gauch, 1988, 1993). The results obtained are presented under the following heads.

4.1 Analysis of variance (Season I)

4.2 Mean performance (Season I)

4.3 Mahalanobis' D^2 Analysis

4.4 Analysis of variance-Pooled (Season III)

4.5 Mean Performance-Pooled (Season III)

4.6 Magnitude of mid-parent heterosis, heterobeltiosis and economic heterosis (Pooled)

4.7 Line x Tester analysis

4.8 Combining ability analysis

4.8.1 Combining ability effects

4.8.2 Combining ability variances

4.8 Stability Analysis

4.8.1 Pooled analysis of variance (AMMI model)

4..8.2 AMMI biplots for yield and its related traits

4.8.3 GGE

4.1 Analysis of Variance (Season I)

Variations are the fundamental basis of plant breeding, as the presence of variability within a population enables effective selection and genetic improvement. In crop improvement programs, identifying significant differences among genotypes for economically important traits provides opportunities for selecting superior parents and developing improved cultivars.

This section encompasses the MSS for the 14 characters (see **Table 4.1**). The average values of the genotypes in each replication were considered for estimation of variance. The significance among genotypes were tested using `F` test at 1% and 5% levels of probability. The mean sum of squares due to the treatments was highly significant for all the studied characters, *viz*., days to male flowering, days to female flowering, sex ratio, number of secondary branches, vine length, fruit length, fruit girth, days to 1st harvesting, days to 3rd harvesting, average fruit weight, fruit flesh thickness, rind thickness, total soluble solids, and fruit yield per plant. However, rind thickness and total soluble solids did not show significant differences among the genotypes.

Some variation was also observed due to replication for fruit length and fruit flesh thickness, whereas no significance was observed in block within replication factor. The significant differences among genotypes for most traits indicate the presence of substantial genetic variability in the experimental material. Such variability is essential for the effective selection of superior genotypes and for the successful exploitation of heterosis in breeding programs.

Tukey's HSD test for the trait fruit yield revealed the significant differences between the genotypes. The genotypes were grouped into 17 groups from a-q **(Table 4.2)**, indicating a wide range of yield performance among the studied materials. The clear separation of genotypes into multiple statistical groups further strengthens the results of ANOVA. The below results indicated that the tested genotypes varied from each other significantly for the studied traits which could be attributed to the genotypes being diverse in nature. The post-hoc test performed

also gives a clear interpretation of the pairwise comparison of the genotypes making it clearer to understand the genotypes that are differ from each other significantly.

The observed variability among genotypes in the present study suggest that the germplasm possesses adequate genetic diversity for further genetic analyses such as divergence analysis, combining ability studies and heterosis estimation. Similar observations of significant variability among bottle gourd genotypes have been reported by Chetariya and Vadoria, 2017; Rehan et al., 2020 and Alhariri et al., 2021 who also emphasized the importance of genetic variability for effective crop improvement.

Table 4.1 Analysis of variance for 14 characters

Sl. No.	Parameters	Mean sum of squares				
		Replications (df = 1)	Genotypes (df = 38)	Block (df = 2)	Block: Replicaiton (df = 2)	Residual (df = 34)
1	Days to male flowering	4.26	32.56**	6.41	2.23	1.63
2	Days to female flowering	1.89	46.35**	1.57	9.25	17.96
3	Sex ratio	0.16	5.48**	2.41	6.41	3.05
4	Number of secondary branches	5.99	4.59**	1.09	1.35	2.19
5	Vine length	39959	31009*	2857	3079	15756
6	Fruit length	31.51**	252.04**	1.82	1.82	2.215
7	Fruit girth	7.1	23.92**	1.04	2.04	2.11
8	Days to 1st Harvesting	1.07	46.19**	18.34	23.79	16.17
9	Days to 3rd Harvesting	0.64	47.86**	38.76	44.0	18.85
10	Average fruit weight	2348	290398**	415	235	8148
11	Fruit flesh thickness	111.94*	139.26**	35.88	52.36	22.39
12	Rind thickness	0.88	0.77	1.5	1.52	0.77
13	Total soluble solids	0.04	1.38	0.92	0.92	1.56
14	Fruit yield per plant	2.33	17.97**	1.16	1.46	1.43

Table 4.2 Tukey's HSD test for fruit yield per plant

	Fruit yield per plant (adjusted)	groups
IC 322274	15.537049	a
IC 92362	13.383799	ab
SEA-127	11.970725	bc
VRBG-71	10.958844	cd
PANT SHANKAR LAUKI-1	10.377379	cde
Narendra Pooja	9.997422	cde
N/06-40	9.3457	def
PUSA MEGHDOOT	9.32394	def
VRBG-3	9.206545	defg
NARENDRA RASHMI	9.061577	defg
ARKA BAHAR	8.951425	defg
PUSA SUMMER PROLIFIC LONG	8.811588	defg
N/06-200	8.590213	defgh
IC 538142	8.385195	efghi
IC 371745	8.370902	efghi
G-2	7.488771	fghij
IC 541196	7.355542	fghijk
IC 342077	7.272091	fghijkl
IC 284895	6.839734	ghijklm
IC 310188	6.309637	hijklmn
VRBG-47-2	6.290662	hijklmn
IC 588086	6.283332	hijklmn
MALERKOTLA SPECIAL	6.120433	hijklmn
PUSA SUMMER PROLIFIC ROUND	6.037839	ijklmn
VRBG-15-1	5.962629	ijklmn
SEA-83	5.59962	jklmn
IC 470859	5.597411	jklmn
PUSA MAJIRI	5.406009	jklmno
Nam Tao Yai	5.212269	jklmnop
KASHI GANGA	5.017831	klmnopq
IC 394736	4.885692	lmnopq
IC 393752	4.527806	mnopq
AZAD NUTAN	4.466401	mnopq
IC470759	4.284218	nopq
AVINASH-IV	4.233897	nopq
IC 438394	4.138788	nopq
IC 449080	2.997284	opq
IC 566641	2.932868	pq
PUNJAB ROUND	2.667873	q

4.2 Mean performance (Season I)

Exploitation of variability from naturally occurring variants, wild relatives, strains, and genetic stocks, which are artificially developed by human efforts, is essential in breeding programs. In this section, we assess the mean performance of the genotypes along with a few descriptive statistics measures to analyse the trend of the data. The mean values, range, standard error of mean (Sem), coefficient of variation (CV), Critical Difference (CD) at 5% and 1% significance intervals, genetic variance, phenotypic variance, genetic coefficient of variance, phenotypic coefficient of variance, heritability, genetic advance, and genetic advance as percentage mean of the genotypes for all the studied characters are presented in **Table 4.3**.

Table 4.3 Mean performance and descriptive statistics of the studied genotypes (Trial I).

ENTRY	Accessions	DMF (days)	DFF (days)	SR	SB	VL (cm)	FL (cm)	FG (cm)	D1H (days)	D3H (days)	AFW (gms)	FFT (mm)	RT (mm)	TSS (°Brix)	FYPP (Kgs)
1	NARENDRA RASHMI	60.5	64	4.85	11.66	768.25	36.58	25.86	79.0	96.0	981	38	2.9	5.82	9.09
2	G-2	51	62.5	3.30	8.50	456.83	46.76	24.26	77.5	96.5	1078	39	2.5	3.80	7.51
3	IC 284895	58.5	64.5	4.40	8.83	432.91	34.95	28.78	83.0	99.5	1020	45	1.4	3.85	6.82
4	IC 538142	52	60.5	3.67	11.00	607.58	44.90	24.21	76.0	92.0	1128	40	3.5	5.33	8.39
5	IC470759	54	63	3.53	7.83	427.33	38.48	20.63	77.0	96.0	758	32	1.9	3.91	4.28
6	IC 470859	51	62.5	3.46	8.66	470.08	29.51	30.18	81.0	94.5	847	45	3.5	4.26	5.62
7	IC 394739	56.5	63.5	3.70	7.50	555.83	29.18	31.13	78.0	93.0	866	52	3.4	3.32	4.91
8	IC 438394	54.5	63	4.05	9.16	503.08	28.63	22.15	81.5	96.5	599	36	3.5	4.23	4.14
9	IC 393752	55.5	63.5	3.21	7.66	521.50	23.40	32.10	80.5	100.0	725	47	3.0	3.47	4.53
10	IC 342077	56.5	64	4.50	8.50	503.08	37.35	29.41	77.5	94.0	1142	46	3.8	4.66	7.25
11	IC 588086	59.5	66	4.73	8.33	498.50	26.96	30.31	76.5	94.5	860	49	2.9	4.86	6.29
12	PUNJAB ROUND	52	61	7.56	8.00	381.33	17.20	22.96	75.0	92.5	388	36	2.9	3.08	2.64
13	IC 371745	58	66	3.65	8.50	543.41	50.81	24.28	80.0	99.5	1173	40	1.9	5.58	8.35
14	AZAD NUTAN	51.5	58.5	5.80	6.66	425.83	33.63	25.05	73.0	92.0	811	40	2.7	2.41	4.47
15	IC 541196	62.5	68	6.62	11.00	545.08	38.81	25.41	85.5	104.0	957	36	3.1	3.62	7.38
16	IC 310188	51	56	5.34	6.66	487.58	44.11	24.80	74.0	93.0	1076	38	3.7	4.25	6.31
17	IC 322274	49	59.5	3.86	11.60	672.50	55.48	31.96	75.0	91.5	1752	51	2.9	3.60	15.56
18	IC 566641	52.5	59.5	8.19	8.00	417.08	23.10	19.71	74.5	94.0	481	30	3.3	4.90	2.91
19	PUSA MAJIRI	53.5	59	5.91	8.50	441.75	26.50	33.86	75.0	91.5	859	55	2.1	4.27	5.41
20	IC 449080	58	64	5.19	8.16	474.08	17.81	26.51	82.5	97.5	418	42	2.9	4.97	2.99
21	IC 92362	56	62	3.45	12.33	813.16	52.51	28.48	73.5	89.5	1504	41	2.5	3.58	13.41
22	VRBG-3	50	60	8.29	8.33	618.16	45.58	29.40	78.0	92.0	1376	46	2.1	3.52	9.23
23	PUSA MEGHDOOT	55	60.5	3.61	8.50	581.08	55.60	25.21	76.5	94.0	1413	39	2.0	3.43	9.32

24	VRBG-71	57	63.5	4.95	8.50	468.41	46.03	34.31	79.5	98.0	1634	55	2.8	4.99	10.98
25	VRBG-47-2	58.5	68.5	4.21	8.50	520.66	27.95	35.68	84.5	100.5	988	57	3.7	5.40	6.27
26	PANT SHANKAR LAUKI-1	58.5	67	5.03	11.50	623.50	34.31	36.61	84.0	100.5	1251	58	3.3	4.20	10.35
27	N/06-40	51	57.5	8.34	8.50	403.00	47.70	32.01	73.5	88.5	1529	42	3.0	4.31	9.34
28	VRBG-15-1	48	52	3.76	10.83	735.66	25.51	25.63	67.0	83.0	646	40	3.5	3.90	5.94
29	PUSA SUMMER PROLIFIC ROUND	45	50	4.63	10.50	522.75	23.71	32.95	69.0	84.0	759	53	2.7	4.46	6.01
30	AVINASH-IV	55.5	65.5	5.97	9.00	489.50	30.48	19.83	82.0	100.5	595	32	3.6	3.42	4.24
31	PUSA SUMMER PROLIFIC LONG	52	56	4.24	10.00	646.66	44.28	24.08	67.5	88.0	1086	38	2.4	4.59	8.81
32	Nam Tao Yai	58	66	3.06	8.33	511.00	35.11	23.66	76.5	91.5	823	39	2.8	2.50	5.21
33	SEA-83	54.5	62.5	5.13	11.50	824.50	22.43	29.65	78.0	93.5	611	39	3.8	2.83	5.60
34	SEA-127	55.5	67.5	9.71	9.83	732.25	59.13	28.51	84.0	99.5	1702	39	2.4	3.42	11.97
35	N/06-200	48.5	52.5	3.38	10.50	681.00	36.56	25.96	70.0	87.0	963	41	3.4	3.38	8.57
36	Narendra Pooja	49.5	73.5	3.44	7.66	290.16	33.65	42.80	84.0	99.5	1506	68	2.2	2.92	9.99
37	ARKA BAHAR	58.5	65	4.79	6.66	416.75	53.41	32.83	79.5	96.5	1776	49	2.1	3.58	8.98
38	KASHI GANGA	48.5	57	5.61	9.16	462.58	31.03	19.53	70.5	86.5	622	31	2.8	4.04	5.01
39	Malerkotla Special	51	57.5	8.34	8.50	403.00	47.70	32.01	73.5	88.5	1529	42	3.0	4.31	9.34
	Minimum	62.50	73.50	9.71	12.33	824.50	59.13	45.90	93.00	112.00	1895.71	69.19	5.33	7.78	17.43
	Maximum	45.00	50.00	3.06	6.66	290.17	17.20	17.36	64.00	85.00	361.91	27.24	1.33	2.33	2.90
	Mean	54.13	61.97	4.93	9.08	538.80	36.56	28.16	78.13	99.73	1088.75	43.83	3.43	5.03	8.13
	Sem	0.91	2.96	16.59	4.28	89.33	2.45	1.61	3.46	3.23	82.57	3.62	0.70	1.06	1.05
	CV	7.35	7.66	33.13	16.46	22.80	30.30	18.35	6.13	5.12	36.92	18.99	20.93	20.44	40.01
	CD (5%)	2.62	8.47	47.53 ns	12.28 ns	255.98	7.01	4.61	9.92	9.27	236.61	10.40	2.02 ns	3.03 ns	3.02
	CD (1%)	3.51	11.36	63.70 ns	16.46 ns	343.06 ns	9.39	6.17	13.30 ns	12.43	317.09	13.94	2.69 ns	4.06 ns	4.05

ns: non significant

Table 4.4 Genetic Parameters of the studied Traits (Trial I)

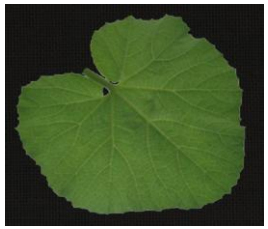
Sl No	Traits	GV	PV	GCV	PCV	H^2	GA	GAM
1	**DMF**	15.45	17.11	7.26	7.64	0.9	7.69	14.21
2	**DFF**	14.43	31.92	6.13	9.12	0.45	5.26	8.49
3	**SR**	8.14	58.46	11.05	79.79	0.31	41.71	27.62
4	**SB**	12.95	49.73	20.27	39.72	0.26	3.78	21.31
5	**VL**	8061.27	24022.91	15.98	27.59	0.33	107.14	19.07
6	**FL**	135.42	147.38	30.95	32.28	0.91	22.97	61.11
7	**FG**	29.36	34.53	19.23	20.86	0.85	10.29	36.54
8	**D1H**	12.08	36.09	4.45	7.68	0.33	4.14	5.31
9	**D3H**	14.46	35.44	3.81	5.96	0.41	5.01	5.02
10	**AFW**	147587.9	161224.2	35.28	36.87	0.91	757.18	69.54
11	**FFT**	54.35	80.7	16.82	20.49	0.67	12.46	28.43
12	**RT**	-	0.95	-	28.28	-	-	-
13	**TSS**	-	1.91	-	27.49	-	-	-
14	**FYPP**	8.69	10.9	36.23	40.6	0.8	5.42	66.61

Table 4.5 Salient characteristics of the selected parents

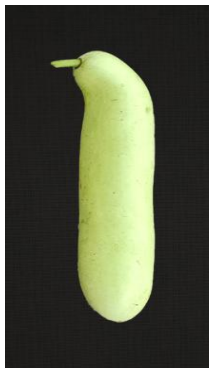
Line/Tester	Parents	Characteristic
Line 1	IC 284895	It exhibited moderate early flowering. It produced medium length vines with medium branching. Fruits were elongate and straight with relatively large girth and moderate fruit weight. It had cordate leaf shape and leaf pubescence.
Line 2	VRBG-3	It was relatively early flowering and produced vigorous vines. It had elongated straight fruits with good length and higher fruit weight. The genotypes recorded high yield potential. It had cordate leaves and leaf pubescence with occasional crooked neck development.
Line 3	VRBG-71	It showed moderate flowering duration and medium length vines. It produced elongated fruits with large girth and high fruit weight. The genotype had orbicular leaves with soft pubescence and pyriform fruit shape.
Line 4	IC 394739	This genotype exhibited moderate flowering with moderately vigorous vines. Fruits were cylindrical with moderate size and medium fruit weight. Yield potential was moderate. It had cordate leaves and hard leaf pubescence.
Line 5	N/06-40	It was one of the earliest flowering genotypes. It produced relatively shorter vines but exhibited long fruits with high fruit weight and good yield potential. It possessed cordate leaves and hard pubescence.
Line 6	IC 393752	It exhibited moderate flowering and moderate vine length. Fruits were oval with large girth but lower overall fruit weight. The genotypes had orbicular leaves with soft pubescence.
Line 7	SEA-83	It produced vigorous vines and moderate duration flowering. Fruits were round in shape with moderate size and weight. Despite lower fruit weight, the genotype showed moderate yield due to vine vigor. It had orbicular leaves, soft leaf pubescence.
Line 8	IC 371745	It was characterised by moderately vigorous vines and delayed flowering. It had long fruits with high fruit weight and good yield potential. Fruits were cylindrical with straight neck and orbicular leaves.

Line 9	Avinash IV	It had moderately late flowering with moderate vine length. Fruits were round with smaller girth and lower fruit weight resulting in lower yield potential. The genotype had cordate leaves with hard pubescence.
Line 10	IC 92362	It exhibited vigorous vine growth and very long fruits with high fruit weight. It recorded on of the highest yields among parents. Fruits were cylindrical with straight neck and possessed cordate leaves with hard laf pubescence.
Tester 1	Pusa Majiri	It exhibited early flowering and moderate vine length. Fruits were oval with large girth and moderate fruit weight. The genotype showed moderate yield potential and had cordate leaves.
Tester 2	Pusa Meghdoot	It produced long fruits with high fruit weight and good yield potential. It exhibited vigorous vines and elongate straight fruit shape.
Tester 3	Narendra Pooja	It was characterised by short vines but large fruit girth and high fruit weight. It showed good yield potential. Plants had cordate leaves with hard leaf pubescence.
Tester 4	Punjab Round	Punjab Round produced compact vines and round fruits with relatively smaller fruit weight. It exhibited lower yield potential but contributed unique fruit shape.

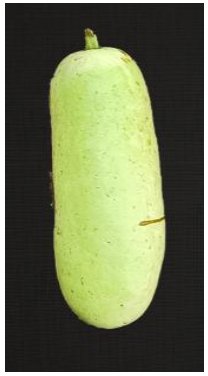
Table 4.6 Morphological Characters of the studied genotypes

Leaf shape		Leaf pubescence		Stem shape	
Cordate 	IC 541196; G-2; IC 284895; NARENDRA RASHMI; IC 470859; IC 394736; ARKA BAHAR; PUNJAB ROUND; AZAD NUTAN; KASHI GANGA; PANT SHANKAR LAUKI-1; PUSA MAJIRI; NARENDRA POOJA; PUSA MEGHDOOT; IC 92362; PUSA SUMMER PROLIFIC ROUND; AVINASH-IV; PUSA SUMMER PROLIFIC LONG; VRBG-3; N/06-200; N/06-40	Hard	IC 541196; G-2; IC 284895; NARENDRA RASHMI; IC 470859; IC 394736; ARKA BAHAR; PUNJAB ROUND; AZAD NUTAN; KASHI GANGA; PANT SHANKAR LAUKI-1; PUSA MAJIRI; NARENDRA POOJA; PUSA MEGHDOOT; IC 92362; PUSA SUMMER PROLIFIC ROUND; AVINASH-IV; PUSA SUMMER PROLIFIC LONG; VRBG-3; N/06-200; N/06-40; IC 538142; IC 342077; IC 438394; IC 588086	Rounded	IC 541196; G-2; IC 284895; NARENDRA RASHMI; IC 470859; IC 394736; ARKA BAHAR; PUNJAB ROUND; AZAD NUTAN; KASHI GANGA; PANT SHANKAR LAUKI-1; PUSA MAJIRI; NARENDRA POOJA; PUSA MEGHDOOT; IC 92362; PUSA SUMMER PROLIFIC ROUND; AVINASH-IV; PUSA SUMMER PROLIFIC LONG; VRBG-3; N/06-200; N/06-40; IC 538142; IC 342077; IC 438394; IC 588086; IC 310188; IC 322274; IC 566641; IC 449080; VRBG-47-2; IC 470759; SEA-127; IC 393752; IC 371745; NAM TAO YAI; VRBG-71; VRBG-15-1; SEA-83
Oblong 	IC 538142; IC 342077; IC 438394; IC 588086; IC 310188; IC 322274; IC 566641; IC 449080; VRBG-47-2	Soft	IC 310188; IC 322274; IC 566641; IC 449080; VRBG-47-2; IC 470759; SEA-127; IC 393752; IC 371745; NAM TAO YAI; VRBG-71; VRBG-15-1; SEA-83		
Orbicular	IC 470759; SEA-127; IC 393752; IC 371745; NAM TAO YAI; VRBG-71; VRBG-15-1; SEA-83				

Continued…

Fruit neck		Fruit pubescence		Tendril branching	
Straight 	NAM TAO YAI; IC 92362; G-2; IC 470859; IC 394736; IC 342077; IC 588086; SEA-127; IC 371745; N/06-40; IC 310188; PUSA SUMMER PROLIFIC LONG; IC 538142; IC 449080; IC 284895; KASHI GANGA; NARENDRA POOJA; PUSA MEGHDOOT; IC 322274; VRBG-47-2; PUNJAB ROUND; AZAD NUTAN; PUSA MAJIRI; PUSA SUMMER PROLIFIC ROUND; IC 438394; IC 393752; IC 541196; N/06-200; VRBG-71; SEA-83; AVINASH-IV; VRBG-15-1	Absent	IC 541196; IC 92362; IC 310188; SEA-83	Branched	IC 541196; G-2; IC 284895; NARENDRA RASHMI; IC 470859; IC 394736; ARKA BAHAR; PUNJAB ROUND; AZAD NUTAN; KASHI GANGA; PANT SHANKAR LAUKI-1; PUSA MAJIRI; NARENDRA POOJA; PUSA MEGHDOOT; IC 92362; PUSA SUMMER PROLIFIC ROUND; AVINASH-IV; PUSA SUMMER PROLIFIC LONG; VRBG-3; N/06-200; N/06-40; IC 538142; IC 342077; IC 438394; IC 588086; IC 310188; IC 322274; IC 566641; IC 449080; VRBG-47-2; IC 470759; SEA-127; IC 393752; IC 371745; NAM TAO YAI; VRBG-71; VRBG-15-1; SEA-83
		Present	G-2; IC 284895; NARENDRA RASHMI; IC 470859; IC 394736; ARKA BAHAR; PUNJAB ROUND; AZAD NUTAN; KASHI GANGA; PANT SHANKAR LAUKI-1; PUSA MAJIRI; NARENDRA POOJA; PUSA MEGHDOOT; PUSA SUMMER PROLIFIC; ROUND; AVINASH-IV; PUSA SUMMER; PROLIFIC LONG; VRBG-3; N/06-200; N/06-40; IC 538142; IC 342077; IC 438394; IC 588086; IC 322274; IC 566641; IC 449080; VRBG-47-2; IC 470759; SEA-127; IC 393752; IC 371745; NAM TAO YAI; VRBG-71; VRBG-15-1		
Crooked 	NARENDRA RASHMI; ARKA BAHAR; IC 566641; PANT SHANKAR LAUKI-1; VRBG-3; IC 470759				

Continued…

Fruit shape			
Elongate- Straight 	IC 284895; KASHI GANGA; PANT SHANKAR LAUKI-1; NARENDRA POOJA; PUSA MEGHDOOT; VRBG-3; IC 322274; VRBG-47-2; IC 470759	Oval 	PUNJAB ROUND; AZAD NUTAN; PUSA MAJIRI; PUSA SUMMER PROLIFIC ROUND; IC 438394; IC 393752
Elongate- Curved 	N/06-40; IC 310188; NARENDRA RASHMI; ARKA BAHAR; PUSA SUMMER PROLIFIC LONG; IC 538142; IC 566641; IC 449080	Club 	NAM TAO YAI
Cylindrical 	IC 92362; G-2; IC 470859; IC 394736; IC 342077; IC 588086; SEA-127; IC 371745	Pyriform 	IC 541196; N/06-200; VRBG-71
		Round 	SEA-83; AVINASH-IV; VRBG-15-1

4.2.1 Days to male flowering

The data for days to male flowering ranged from 45.00 days (PUSA SUMMER PROLIFIC ROUND) to 62.50 days (IC 541196) whereas the general mean of this character was 54.13 days. Early male flowering will lead to early female flowering which will eventually start production of fruit earlier which could be a desirable character for selection. The genotypic coefficient of variation (GCV) was 7.26%, showing moderate genetic variability, while the phenotypic coefficient of variation (PCV) was slightly higher at 7.64%, indicating a small influence of the environment. Heritability was high (90%), meaning most of the variation is genetic and can be passed on to the next generation. The genetic advance as a percentage of the mean (GAM) was 14.21%, suggesting good scope for improvement through selection.

4.2.2 Days to female flowering

The data for days to female flowering (DFF) ranged from 50.00 days (PUSA SUMMER PROLIFIC ROUND) to 73.50 days (NARENDRA POOJA), with a general mean of 61.97 days. Earlier female flowering is advantageous as it leads to earlier fruit set and harvest, which can be a desirable trait for selection in breeding programs. The genotypic coefficient of variation (GCV) was 6.13%, indicating low to moderate genetic variability, while the phenotypic coefficient of variation (PCV) was higher at 9.12%, showing that environmental factors had a noticeable influence on this trait. Heritability was moderate at 45%, suggesting that selection based on phenotype alone may be only partially effective. The genetic advance as a percentage of the mean (GAM) was 8.49%, implying limited but possible improvement through selection, particularly if supported by controlled breeding methods.

4.2.3 Sex Ratio

The sex ratio (male to female flowers) among accessions ranged from 3.06 (Nam Tao Yai) to 9.71 (SEA-127), with a general mean of 4.93. A lower sex ratio (fewer male flowers per female flower) is generally beneficial, as it can lead to higher fruit set and yield potential. The genotypic coefficient of variation (GCV) was 11.05%, indicating moderate genetic variability, while the phenotypic coefficient of variation (PCV) was even higher at 79.79%, showing a huge influence of environmental conditions. Heritability was moderate (31%), meaning observed differences were due to genetic factors but environmental factors also influenced it. The genetic advance as a percentage of mean (GAM) was 27.62%, indicating that meaningful improvement through selection would only be possible if environmental factors are controlled.

4.2.4 Number of secondary branches

The number of secondary branches per plant varied from 6.66 (several accessions) to 12.33 (IC 92362), with a mean of 9.08. More secondary branches can contribute to increased flowering sites and potentially higher yield. The GCV was 20.27%, suggesting moderate genetic variability, while the PCV was much higher at 39.72%, indicating that environment plays a strong role in expression of this trait. Heritability was low (26%), meaning selection based on visible phenotype would be only moderately reliable. The GAM was 21.31%, showing that some improvement is possible through selection, especially under stable growing conditions.

4.2.5 Vine length

Vine length ranged from 290.16 cm (Narendra Pooja) to 824.50 cm (SEA-83), with a mean of 538.80 cm. Vine length affects plant architecture and adaptability to different cultivation systems. The GCV was 15.98%, showing moderate genetic variability, while the PCV was higher at 27.59%, indicating strong environmental effects. Heritability was 33%, meaning that selection would be moderately effective. The GAM was 19.07%, suggesting a fair scope for improvement.

4.2.6 Fruit length

Fruit length ranged from 17.20 cm (Punjab Round) to 59.13 cm (SEA-127), with a mean of 36.56 cm. Longer fruits may be preferred for certain market requirements, while shorter ones may fit other consumer preferences. The GCV was 30.95%, showing high genetic variability, and the PCV was similar at 32.28%, meaning environment had little influence. Heritability was 91%, indicating strong genetic control, and the GAM was 61.11%, showing excellent potential for improvement through selection.

4.2.7 Fruit girth

Fruit girth varied from 17.36 cm (Nam Tao Yai) to 45.90 cm (Narendra Pooja), with a mean of 28.16 cm. Fruit girth influences yield, visual appeal, and market preference. GCV was 19.23% (moderate variability), PCV was slightly higher at 20.86%, indicating minimal environmental influence. Heritability was 85%, and GAM was 36.54%, suggesting strong genetic control and good potential for improvement.

4.2.8 Days to 1st harvesting

Days to first harvest ranged from 64 days (PUSA Summer Prolific Long) to 93 days (Kashi Ganga), with a mean of 78.13 days. Early harvesting is a desirable trait for quick returns in market gardening. GCV was 4.45% (low variability) and PCV 7.68%, showing mild environmental influence. Heritability was 33%, meaning selection will be moderately effective. GAM was 5.31%, indicating limited genetic gain.

4.2.9 Days to 3rd harvesting

Days to third harvest varied from 85 days (PUSA Summer Prolific Round) to 112 days (Narendra Rashmi), with a mean of 99.73 days. A quicker harvest cycle can increase total yield per season. GCV was 3.81% and PCV 5.96%, showing fairly low variation with some environmental impact. Heritability was 41%, GAM was 5.02%, indicating moderate prospects for selection. Earlier harvesting results in quicker crop turnover which is preferable in many situations for farmers. So, genotypes with earlier dates of harvesting should be focused.

4.2.10 Average fruit weight

Average fruit weight ranged from 388.0 g (PUNJAB ROUND) to 1776.0 g (NARENDRA POOJA), with a mean of 1088.75 g. Larger fruit weight contributes directly to yield. The GCV was 35.28%, showing high genetic variability, PCV was similar at 36.87%, meaning minimal environmental impact. Heritability was 91%, and GAM was 69.54%, making this a highly promising trait for yield improvement. Usually tender, small to medium sized fruits are preferred for a family need. Although heavier fruits may result in maximising the gains.

4.2.11 Fruit flesh thickness

Fruit flesh thickness ranged from 30.0 mm (IC 566641) to 68.0 mm (NARENDRA POOJA), with a mean of 43.83 mm. Thicker flesh can improve texture, shelf life, and market value. GCV was 16.82%, PCV 20.49%, showing moderate variability and some environmental influence. Heritability was 67%, and GAM 28.43%, suggesting good potential for improvement through selection.

4.2.12 Rind thickness

The data for rind thickness ranged from 1.33 mm (IC 284895) to 3.8 mm (IC 342077) whereas the general mean of this character was 3.43 mm. Thicker rind could be desirable to prevent

insect bite and possibly increase shelf life of the fruit. Significant variation was not observed for this character in the studied material.

4.2.13 Total soluble solids (TSS)

TSS values ranged from 2.41°Brix (AZAD NUTAN) to 5.82°Brix (NARENDRA RASHMI), with a mean of 5.03°Brix. Higher TSS is linked to better sweetness and flavour. Higher total soluble solids could impart sweetness which could be a desirable trait according to preference. Significant variation was not observed for this character in the studied material.

4.2.14 Fruit yield per plant

Fruit yield per plant among the evaluated bottle gourd accessions varied widely, ranging from 2.90 kg in PUNJAB ROUND to 17.43 kg in IC 322274, with a mean of 8.13 kg, reflecting substantial genetic diversity for this trait. The high genotypic coefficient of variation (36.23%) and high heritability (80%) indicate that much of the variability is genetically controlled, while the slightly higher phenotypic coefficient of variation (40.60%) suggests some environmental influence. A high genetic advance as a percentage of mean (66.61%) further suggests strong potential for yield improvement through direct selection. These findings position fruit yield per plant as one of the most promising traits for breeding programs, with scope to significantly enhance productivity and economic returns for growers.

4.3 Mahalanobis' D^2 Analysis

Following the computation of D^2 values using Tocher's method across fourteen quantitative traits, the analysis grouped the 38 genotypes into seven distinct clusters (as presented in **Table 4.7**). The formation of multiple clusters indicates presence of considerable genetic divergence within the studied population. Such genetic divergence among genotypes is a prerequisite for effective hybridization programs, as genetically diverse parents are more likely to produce superior segregants and heterotic hybrids.

Cluster V was the largest cluster, encompassing eight genotypes, while clusters I, IV, and VI followed closely with seven genotypes each. Clusters II and III comprised four genotypes each, whereas cluster VII consisted of only one genotype. Interestingly, the composition of these clusters revealed no clear association with geographical origin, as genotypes from different geographical regions were often grouped together within the same cluster. This finding suggests that geographical distances did not significantly influence the observed genetic divergence. Similar observations have been reported in bottle gourd by Chetariya and Vaddoria

(2017) and Quamruzzaman et al. (2020), where genotypes from different regions were grouped into the same clusters.

The inter-cluster distances, as outlined in **Table 4.8** and depicted in **Figure 4.1**, yielded additional insights into the degree of diversity among clusters. Particularly noteworthy was the substantial inter-cluster distance of 30.207 observed between cluster IV and cluster VI, indicating that genotypes belonging to these clusters are genetically most divergent. Crosses between such genetically distant genotypes are expected to produce greater variability and potentially higher heterosis in subsequent generations. In contrast, the smallest inter-cluster distance (14.046) was identified between clusters I and III, indicating a lesser genetic diversity within these clusters. Interestingly, cluster IV had the highest recorded intra-cluster distance (16.331), suggesting a high level of genetic variety in this cluster. This observation underscores the potential for selecting superior genotypes within the cluster for further breeding purposes.

The contribution of individual traits towards total genetic divergence (**Table 4.9**) indicated that fruit length (37.2%), days to male flowering (22.7%) and average fruit weight (10.7%) were the primary contributors to genetic divergence among the genotypes, together accounting for over 70% of total variability. The predominance of these traits suggests that variability in fruit morphology and flowering behaviour plays a major role in determining genetic divergence among bottle gourd genotypes.

The cluster mean values (**Table 4.10**) indicated distinct trait combinations, with Cluster I recording comparatively higher fruit weight, fruit length and vine length, whereas Cluster VII exhibited late flowering, delayed harvesting, and the lowest yield. The pronounced inter-cluster variation suggests that crossing genotypes from highly divergent clusters, particularly those with complementary earliness, fruit size, and yield traits could be advantageous for developing superior hybrids with improved productivity and quality.

The pronounced inter-cluster divergence observed in the present study suggests that hybridization between genotypes belonging to genetically distant clusters may generate greater variability and superior recombinants. Therefore, parents selected from cluster showing large inter-cluster distances, particularly clusters IV and VI, may serve as promising candidates for hybridization programs aimed at improving yield and related traits in bottle gourd. Similar observation regarding the usefulness of genetically divergent parents in breeding programs have been reported by Chetariya and Vaddoria (2017), Kandasamy *et al.,* (2019), Rambabu *et al.,* (2020) and Quamruzzaman *et al.,* (2020).

Table 4.7: Clustering of experimental materials using Tocher's method based on D^2 analysis

Cluster	Number of lines	Name of varieties
I	7	VRBG-71, Azad Nutan, G-2, Pusa Meghdoot, IC 394736, Pusa Summer Prolific Long, SEA-127
II	4	IC 310188, VRBG-47-2, IC 538142, IC 470759
III	4	Arka Bahar, Pusa Summer Prolific Round, SEA-83, IC 342077
IV	7	IC 588086, IC 371745, Pusa Majiri, IC 470859, IC 393752, IC 541196, N/06-200
V	8	Narendra Rashmi, IC 322274, Narendra Pooja, Avinash-IV, Punjab Round, IC 566641, IC 449080, IC 92362
VI	7	IC 438394, N/06-40, Kashi Ganga, Pant Shankar Lauki-1, VRBG-15-1,Nam Tao Yai, VRBG-3
VII	1	IC 284895

Table 4.8: Distances between clusters in genetic diversity analysis of bottle gourd varieties based on D^2 analysis

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	10.146	16.07	14.046	19.099	20.618	17.787	22.089
Cluster II		8.177	21.889	14.348	18.139	27.119	25.353
Cluster III			10.225	23.579	26.545	17.124	14.951
Cluster IV				16.331	25.3	30.207	27.668
Cluster V					15.543	27.814	30.007
Cluster VI						13.337	23.903
Cluster VII							0

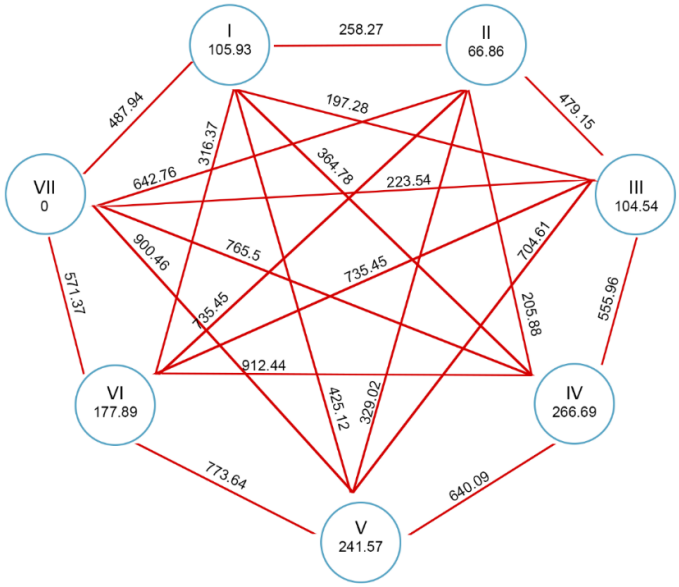


Figure 4.1: Inter-cluster and intra-cluster distances according to D^2 statistics using Tocher's method. (not to scale)

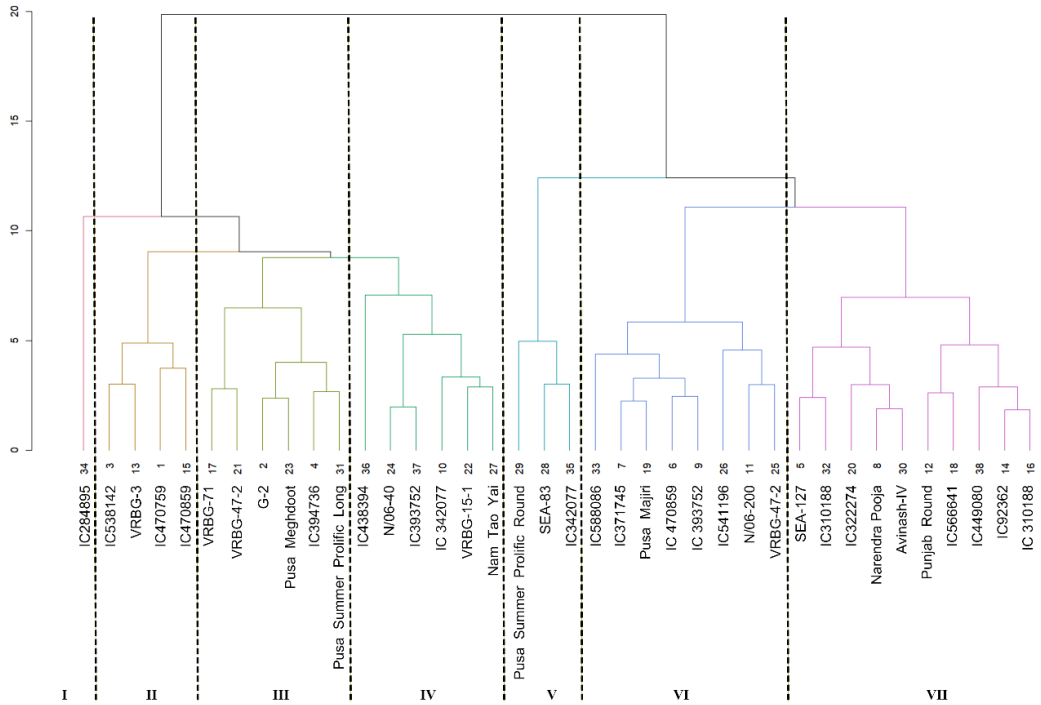


Figure 4.2: Dendrogram for genetic diversity assessment among bottle gourd varieties (Ward's minimum variance Dendrogram)

Based on the hierarchical clustering of the genotypes, data delineates distinct clusters and trait similarities among different groups of genotypes. Clusters I - IV are separated from clusters V to VII as observed in **Figure 4.2**, based on their height of fusion and therefore emerge as the most diverse indicating significant dissimilarity in the evaluated traits among the genotypes. In contrast, clusters III and IV exhibit less diversity, suggesting a higher level of similarity among the genotypes within each cluster. Closer inspection of specific trait similarities reveals interesting patterns. Cluster II, for instance, demonstrates similarities in multiple traits, including DMF, DFF, FG, D3H, FFT, and FYPP. Similar trait patterns are observed in clusters III to VII, each sharing specific commonalities. Overall, this dendrogram provides valuable insights into the genetic relationships and shared characteristics among different clusters of genotypes, offering a visual representation for breeders to make informed decisions in selecting parent genotypes for specific breeding objectives. Similar findings were reported by Prakash *et al*., 2013, Kalyanrao *et al*., 2016 and Salam *et al*., 2021.

The information obtained from the diversity analysis was subsequently utilized for the selection of parents in the line x tester mating design used in the present investigation.

Table 4.9: Contribution of variables towards diversity

Sl. No.	Character	Percent contribution
1	Fruit length	37.2
2	Days to male flowering	22.7
3	Average fruit weight	10.7
4	Days to 3rd harvesting	6.2
5	Fruit girth	5.5
6	Sex ratio	3.8
7	Days to female flowering	3.3
8	Vine length	2.8
9	Fruit flesh thickness	2.6
10	Fruit yield per plant	1.7
11	Days to 1st harvesting	1.5
12	Number of secondary branches	0.9
13	Rind thickness	0.6
14	TSS	0.4

Table 4.10: Cluster mean of different studied characters

Sl. No.	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	Days to male flowering	54.1	53.9	53.9	56.3	53.2	52.8	58.5
2	Days to female flowering	61.7	62.0	61.4	62.5	63.6	60.3	64.5
3	Sex ratio	4.1	3.9	5.5	4.2	7.9	4.4	5.3
4	Number of Secondary branches	18.4	20.0	15.1	20.1	16.1	18.5	14.3
5	Vine length	580.1	514.8	581.4	567.7	517.8	590.4	459.4
6	Fruit length	46.3	40.4	30.8	34.6	34.1	34.7	38.5
7	Fruit girth	27.2	26.7	28.9	28.5	28.5	28.7	27.8
8	Days to 1st harvesting	76.9	78.4	79.0	78.8	79.1	77.7	84.0
9	Days to 3rd harvesting	99.9	100.6	99.5	101.3	100.5	97.4	106.0
10	Average fruit weight	1318.2	1050.4	899.6	984.5	1008.6	1064.1	1024.6
11	Fruit flesh thickness	44.0	41.8	43.9	43.8	43.7	42.9	44.5
12	Rind thickness	3.2	3.7	3.9	3.3	3.4	3.5	1.5
13	TSS	4.9	5.6	5.1	5.1	4.9	4.7	5.3
14	Fruit yield per plant	60.1	59.4	60.0	55.7	58.2	61.9	43.5

4.4 Analysis of variance (Season III)

This section presents the mean sum of squares (MSS) for the 14 traits under investigation (refer to **Table 4.11**). Genotypic means across replications were used for variance estimation. The significance of genotypic differences was assessed using the F-test at 1% and 5% probability levels. The MSS attributed to genotypes was highly significant for all traits studied, including days to male flowering, days to female flowering, sex ratio, number of secondary branches, vine length, fruit length, fruit girth, days to first and third harvesting, average fruit weight, fruit flesh thickness, rind thickness, total soluble solids, and fruit yield per plant. Notable variation due to replication was observed for fruit length and fruit flesh thickness, while the block within replication effect was found to be non-significant. Findings from the studies of Chetariya and Vaddoria (2017), Kandasamy *et al.,* (2019), Rambabu *et al.,* (2020) and Quamruzzaman *et al.,* (2020) are also in agreement with the findings of the present study.

Table 4.11: Mean sum of squares for ANOVA of experimental design (Pooled)

Source of Variation	df	DMF	DFF	SR	SB	VL	FL	FG	D1H	D3H	AFW	FFT	RT	TSS	FYPP
Replications	1	0.4	10.4	0.05	2.32	3067	0.1	0.2	52*	4	3917	0.6	0.001	0.007	0.7
Environment	2	2252.4**	2713.1**	12.51**	234.44**	212954**	955.6**	480.4**	3390**	4139**	1079358**	1340.8**	7.05**	19.07**	66.85**
Genotypes	54	163.4**	149.7**	29.47**	196.55**	76128**	744.9**	175.9**	137**	898**	861093**	338.6**	3.37**	4.79**	93.27**
Block	9	3.05	5.72	0.11	3.1	3161	0.16	0.32	48	4.2	4002	0.7	0.002	0.01	1
Environment : block	18	2.7	4.0	0.05	1.66	1215	2.0	1.5	6	12	849	3.5	0.004	0.06	0.11
Environment : replication	2	1.0	5.1	0.01	0.45	2	0.3	0.1	2	17	278	8.2	0.00	0.005	0.1
Residuals	249	1563	7.0	0.05	1.01	807	3.6	1.6	9	12	3532	3.8	0.01	0.027	0.29

4.5 Mean performance (Season III)

4.5.1 Days to male flowering

The days to male flowering (DMF) among the genotypes ranged from 42.90 days (L10×T2) to 64.50 days (L2×T4), with a mean of 56.46 days. Early male flowering is desirable as it promotes early female flowering and earlier fruit setting, offering a potential market advantage. The genotypic coefficient of variation (GCV) was 14.87%, indicating moderate genetic variability, and the phenotypic coefficient of variation (PCV) was slightly higher at 17.06%, suggesting a minor environmental influence. The trait showed high heritability (76%), indicating that most variation is genetic and inheritable. The genetic advance as a percentage of the mean (GAM) was 26.71%, highlighting a good scope for improvement through direct selection for early flowering lines.

4.5.2 Days to female flowering

The days to female flowering (DFF) among the genotypes ranged from 46.6 days (L1×T1) to 72.2 days (Narendra Pooja), with a mean of 62.82 days. Early female flowering is a desirable trait as it enables earlier fruit setting and can help achieve early harvests for better market advantage. The genotypic coefficient of variation (GCV) was 12.49%, indicating moderate genetic variability, while the phenotypic coefficient of variation (PCV) was slightly higher at 14.94%, suggesting a minor influence of environmental factors. The heritability (H^2) was high (70%), showing that most of the variation is genetic and can be exploited in breeding programs. The genetic advance as a percentage of the mean (GAM) was 21.51%, indicating good potential for improvement through selection of early-flowering genotypes.

4.5.3 Sex Ratio

The sex ratio (SR) among the genotypes ranged from 2.1 (L7×T1, L8×T2) to 12.3 (Pusa Meghdoot), with a mean value of 4.8. A balanced or lower sex ratio is generally desirable in breeding programs, as it indicates a higher proportion of female flowers, potentially leading to better fruit set and yield. The genotypic coefficient of variation (GCV) was extremely high (79.76%), reflecting very wide genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 80.14%, suggesting minimal environmental influence on its expression. The trait recorded very high heritability (99%), indicating that nearly all the observed variation is genetic in nature and can be effectively exploited in selection. The genetic

advance as a percentage of the mean (GAM) was 163.54%, showing an exceptionally high potential for improvement through selective breeding.

4.5.4 Number of secondary branches

The number of secondary branches (SB) among the genotypes ranged from 7.6 (L10×T2) to 31.9 (L4×T2), with a mean value of 20.27. A higher number of secondary branches is generally considered beneficial, as it can increase the potential sites for flower and fruit production, thereby contributing to higher yield potential. The genotypic coefficient of variation (GCV) was 48.55%, indicating very high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 49.23%, suggesting minimal environmental influence on its expression. The trait exhibited very high heritability (97%), meaning that almost all observed variation is due to genetic factors, making it highly amenable to improvement through selection. The genetic advance as a percentage of the mean (GAM) was 98.62%, showing an exceptionally high scope for enhancing SB through targeted breeding.

4.5.5 Vine length

The vine length (VL) among the genotypes ranged from 380.5 cm (Pusa Meghdoot) to 855.6 cm (L7×T1), with a mean value of 608.64 cm. A longer vine length is generally associated with greater vegetative growth and can contribute to increased potential yield, although excessively long vines may require more management. The genotypic coefficient of variation (GCV) was 31.55%, indicating high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 32.55%, suggesting a small influence of environmental factors. The trait exhibited very high heritability (93%), implying that most of the variation is genetic and can be effectively utilized in selection programs. The genetic advance as a percentage of the mean (GAM) was 63.01%, showing substantial potential for improvement through targeted breeding.

4.5.6 Fruit length

The fruit length (FL) among the genotypes ranged from 19.4 cm (L6×T1) to 60.2 cm (L9×T1), with a mean value of 39.75 cm. Longer fruits may be desirable for certain market preferences and processing purposes, while medium-sized fruits may be preferred for fresh consumption, depending on consumer and market demands. The genotypic coefficient of variation (GCV) was 48.20%, indicating very high genetic variability for this trait, while the phenotypic

coefficient of variation (PCV) was slightly higher at 48.89%, suggesting minimal environmental influence on its expression. The trait showed very high heritability (97%), revealing that most of the variation is due to genetic factors and can be effectively fixed through selection. The genetic advance as a percentage of the mean (GAM) was 97.91%, indicating an excellent potential for improvement in fruit length through targeted breeding.

4.5.7 Fruit girth

The fruit girth (FG) among the genotypes ranged from 18.4 cm (N/06-40) to 43.0 cm (L2×T3), with a mean value of 28.55 cm. Larger fruit girth is generally preferred for certain market and processing needs, while moderate girth may be suitable for fresh consumption depending on consumer preferences. The genotypic coefficient of variation (GCV) was 32.38%, indicating high genetic variability for this trait, and the phenotypic coefficient of variation (PCV) was slightly higher at 33.32%, suggesting minimal environmental influence on its expression. The trait exhibited very high heritability (94%), meaning that most of the variation is genetic and can be effectively utilized in selection programs. The genetic advance as a percentage of the mean (GAM) was 64.80%, reflecting a strong potential for improvement in fruit girth through targeted breeding.

4.5.8 Days to 1st harvesting

The days to first harvesting (D1H) among the genotypes ranged from 60.9 days (L8×T4) to 81.2 days (L3×T3), with a mean value of 74.27 days. Early harvesting is a desirable trait as it enables quicker market entry, reduces the risk of pest and disease damage in the field, and allows for more crop cycles in a year. The genotypic coefficient of variation (GCV) was 9.67%, indicating low to moderate genetic variability, while the phenotypic coefficient of variation (PCV) was slightly higher at 12.41%, suggesting a moderate environmental influence on the trait's expression. The trait exhibited moderate heritability (61%), meaning a significant portion of the variation is genetic but environmental factors also play a considerable role. The genetic advance as a percentage of the mean (GAM) was 15.52%, indicating a moderate potential for improvement through selection targeting early-harvesting genotypes.

4.5.9 Days to 3rd harvesting

The days to third harvesting (D3H) among the genotypes ranged from 53.3 days (L5×T2) to 97.7 days (IC 284895), with a mean value of 78.91 days. A shorter duration to third

harvesting is advantageous as it allows for faster production cycles and increased total yield within a season. The genotypic coefficient of variation (GCV) was 26.22%, indicating high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 27.47%, suggesting a small influence of environmental factors. The trait exhibited very high heritability (91%), meaning most of the variation is genetic and can be effectively exploited in breeding programs. The genetic advance as a percentage of the mean (GAM) was 51.55%, indicating strong potential for improvement through selection for early-maturing genotypes.

4.5.10 Average fruit weight

The average fruit weight (AFW) among the genotypes ranged from 466.4 g (Pusa Meghdoot) to 2,085.6 g (L3×T3), with a mean value of 1,233.5 g. Higher average fruit weight is generally desirable as it directly contributes to total yield and can be advantageous for both fresh market and processing purposes. The genotypic coefficient of variation (GCV) was 52.85%, indicating very high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 53.54%, suggesting minimal environmental influence on its expression. The trait exhibited very high heritability (97%), showing that most of the variation is genetic and can be effectively utilized in selection programs. The genetic advance as a percentage of the mean (GAM) was 107.45%, reflecting an excellent potential for improvement in average fruit weight through targeted breeding.

4.5.11 Fruit flesh thickness

The fruit flesh thickness (FFT) among the genotypes ranged from 31.6 mm (L4×T1) to 64.9 mm (L2×T3), with a mean value of 44.62 mm. Greater fruit flesh thickness is generally desirable as it contributes to better fruit texture, higher edible portion, and improved consumer appeal, especially for processing and fresh market purposes. The genotypic coefficient of variation (GCV) was 28.57%, indicating high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 29.74%, suggesting minimal environmental influence on its expression. The trait showed very high heritability (92%), indicating that most of the variation is genetic and can be effectively utilized in breeding programs. The genetic advance as a percentage of the mean (GAM) was 126.71%, reflecting a very strong potential for improvement in fruit flesh thickness through targeted selection.

4.5.12 Rind thickness

The rind thickness (RT) among the genotypes ranged from 1.0 mm (L7×T3) to 56.5 mm (L5×T1), with a mean value of 44.62 mm. Thinner rind thickness is often considered desirable because it increases the proportion of edible flesh, thus enhancing consumer appeal and market value, while thicker rind may contribute to better shelf life and transportability depending on the intended use. The genotypic coefficient of variation (GCV) was 40.71%, indicating very high genetic variability, and the phenotypic coefficient of variation (PCV) was just slightly higher at 41.49%, showing minimal environmental influence on the trait's expression. The heritability was 96%, indicating that most of the variation is genetic and can be effectively exploited through selection. The genetic advance as a percentage of the mean (GAM) was 81.96%, highlighting a strong potential for improvement in rind thickness through targeted breeding.

4.5.13 Total soluble solids (TSS)

The total soluble solids (TSS) among the genotypes ranged from 3.3 °Brix (Punjab Round) to 7.2 °Brix (L8×T3), with a mean value of 5.52 °Brix. Higher TSS is generally desirable as it enhances fruit sweetness, flavor, and overall eating quality, making it an important trait for consumer acceptance and marketability. The genotypic coefficient of variation (GCV) was 27.55%, indicating high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 28.53%, suggesting minimal environmental influence on its expression. The trait showed very high heritability (93%), meaning most of the variation is genetic and can be effectively utilized in breeding programs aimed at improving fruit quality. The genetic advance as a percentage of the mean (GAM) was 54.71%, reflecting a strong potential for enhancement of TSS through selection.

4.5.14 Fruit yield per plant

The fruit yield per plant (FYPP) among the genotypes ranged from 3.9 kg (Pusa Meghdoot) to 20.3 kg (L7×T1), with a mean value of 11.09 kg. Higher fruit yield per plant is a key breeding goal as it directly determines productivity and profitability, making it a critical selection criterion in crop improvement programs. The genotypic coefficient of variation (GCV) was 61.30%, indicating extremely high genetic variability for this trait, while the phenotypic coefficient of variation (PCV) was slightly higher at 61.81%, suggesting negligible environmental influence on its expression. The trait exhibited very high heritability (98%), meaning that nearly all observed variation is genetic and can be effectively utilized in

selection. The genetic advance as a percentage of the mean (GAM) was 125.25%, reflecting an exceptionally high potential for improving fruit yield per plant through targeted breeding.

Multiple studies such as from Pradhan et al., 2018; Kandasamy et al., 2019; Quamaruzzaman et al., 2020;Rehan et al., 2020 and Harsh et al., 2022 are also in agreement to our findings,

Table 4.12: Mean performance and descriptive statistics of parents and hybrids (Averaged)

ENTRY	Genotypes	DMF (days)	DFF (days)	SR	SB	VL (cm)	FL (cm)	FG (cm)	D1H (days)	D3H (days)	AFW (gms)	FFT (mm)	RT (mm)	TSS (°Brix)	FYPP (Kgs)
1	IC 284895	60.1	65.2	5.2	17.0	779.0	39.7	22.0	71.8	97.7	1019.0	33.8	3.4	6.1	9.2
2	VRBG-3	57.5	62.3	4.7	17.5	506.5	44.9	20.8	72.9	89.6	1086.2	37.5	3.1	5.3	7.5
3	VRBG-71	54.0	60.3	5.6	14.4	474.4	36.1	25.4	77.5	92.9	976.5	39.5	2.0	5.1	8.3
4	IC 394736	54.1	60.4	4.4	21.6	594.0	44.4	22.8	71.8	83.0	1133.9	33.2	4.1	5.8	9.0
5	N/06-40	57.7	61.8	3.8	20.8	424.3	37.4	18.4	69.4	89.5	758.4	32.6	3.2	3.8	5.2
6	IC 393752	57.6	62.2	4.2	19.8	523.7	28.3	28.9	71.2	88.4	837.7	42.3	3.9	5.0	6.9
7	SEA-83	59.6	62.6	5.2	18.3	522.4	25.9	29.6	71.6	90.8	940.7	50.4	3.9	3.7	5.7
8	IC 371745	64.4	63.6	5.1	15.1	517.6	29.7	21.7	73.4	96.9	683.2	35.5	4.4	4.7	4.8
9	Avinash IV	45.4	61.1	3.7	19.1	567.7	25.0	31.2	75.5	95.8	787.6	38.5	4.0	4.7	5.5
10	IC 92362	49.0	58.0	6.2	7.7	502.1	38.7	25.5	72.3	96.7	1156.0	44.6	4.2	5.4	7.9
11	VRBG-47-2	56.9	58.6	4.7	19.8	540.9	24.1	27.6	68.1	90.4	958.9	41.3	3.4	5.6	7.2
12	Pusa Meghdoot	56.0	62.5	12.3	10.2	380.5	19.6	22.4	68.5	83.8	466.4	34.8	3.9	3.4	3.9
13	Narendra Pooja	60.2	72.2	3.4	24.9	565.9	44.8	22.0	70.5	90.3	1132.5	38.4	2.1	5.7	8.7
14	Punjab Round	49.0	54.6	5.0	20.0	477.9	34.8	20.3	68.7	85.0	971.4	38.7	3.8	3.3	4.9
15	L1xT1	45.9	46.6	4.3	21.3	611.3	37.4	25.2	80.4	98.1	1273.4	36.1	3.1	4.8	12.9
16	L2xT1	53.7	57.6	3.7	22.0	520.1	43.7	27.0	66.1	61.4	1318.5	37.6	2.9	5.3	10.7

17	L3xT1	50.1	61.1	3.4	22.7	700.6	57.2	31.5	67.8	65.7	1843.3	54.2	2.3	4.7	19.9
18	L4xT1	51.7	49.4	11.7	11.8	454.5	25.4	22.4	70.1	72.1	601.0	31.6	2.8	6.0	7.9
19	L5xT1	57.2	62.6	6.1	17.2	512.2	31.0	32.6	65.0	66.4	1149.8	56.5	2.7	5.0	10.2
20	L6xT1	58.4	64.6	3.4	20.5	492.3	19.4	29.5	73.3	73.3	735.5	37.0	2.8	5.9	9.1
21	L7xT1	59.2	62.8	2.1	29.0	855.6	53.4	29.4	66.5	64.6	1741.3	45.0	2.3	5.5	20.3
22	L8xT1	53.0	60.7	5.7	12.0	615.5	43.5	32.7	69.8	64.5	1559.1	50.0	2.1	6.3	16.0
23	L9xT1	56.8	58.9	2.7	25.0	591.4	60.2	29.0	71.1	67.3	1673.0	41.8	2.1	5.1	13.6
24	L10xT1	54.1	62.2	3.7	23.8	555.9	50.6	35.1	74.0	69.9	1657.5	52.5	2.8	6.0	13.8
25	L1xT2	59.7	60.5	2.7	21.1	515.3	32.1	36.4	80.7	74.0	1175.3	53.7	3.1	6.4	8.2
26	L2xT2	56.3	66.6	4.0	15.2	763.5	34.1	38.3	78.4	76.6	1580.2	59.7	3.7	4.9	15.1
27	L3xT2	62.7	63.0	5.6	14.8	484.0	45.6	30.1	69.1	65.5	1915.8	42.6	2.9	4.8	13.8
28	L4xT2	47.0	60.3	2.2	31.9	849.3	25.8	26.5	62.1	59.6	946.3	40.8	4.0	5.5	12.2
29	L5xT2	51.1	58.6	6.0	12.0	573.9	27.0	32.2	62.2	53.3	839.6	52.8	3.1	6.6	11.6
30	L6xT2	56.4	56.6	6.0	10.0	597.7	31.2	20.8	76.3	76.5	787.3	35.8	3.2	5.1	10.1
31	L7xT2	51.0	65.1	3.6	23.1	738.2	51.2	23.6	61.7	58.7	1270.6	36.7	2.9	5.9	15.7
32	L8xT2	53.4	65.8	2.7	27.5	614.9	42.7	26.8	71.0	71.6	965.8	42.7	2.1	4.5	9.3
33	L9xT2	46.0	58.2	4.5	13.3	755.9	25.7	30.1	73.8	70.3	917.2	40.8	3.7	4.0	9.8

34	L10xT2	42.9	49.4	3.3	7.6	762.3	60.0	28.5	75.2	75.0	1748.4	38.8	1.9	5.0	18.8
35	L1xT3	52.3	57.6	3.1	26.4	691.1	39.5	27.2	63.1	58.3	1215.6	39.2	3.3	4.5	12.7
36	L2xT3	48.4	63.0	3.9	20.3	454.4	37.3	43.0	74.2	72.6	1869.5	64.9	2.3	4.5	13.6
37	L3xT3	49.1	53.8	3.3	14.6	443.3	58.5	30.7	81.2	75.9	2085.6	48.6	2.7	6.0	15.2
38	L4xT3	57.5	68.2	7.8	14.1	529.8	30.6	21.4	65.8	59.7	790.3	35.8	3.1	4.8	9.8
39	L5xT3	56.0	62.7	3.9	18.2	748.0	42.5	22.5	72.5	76.9	1084.3	43.5	3.1	6.3	12.6
40	L6xT3	53.3	62.3	3.9	26.7	549.9	46.8	23.1	70.6	66.7	1362.0	41.1	2.4	5.9	12.5
41	L7xT3	56.4	61.4	4.5	18.0	490.2	37.7	27.6	75.5	69.3	1236.5	43.4	1.0	5.5	9.8
42	L8xT3	57.6	63.3	3.7	22.3	691.4	50.9	22.3	70.5	68.4	1285.6	36.7	3.4	7.2	12.4
43	L9xT3	53.6	59.6	3.9	21.7	511.2	42.8	20.6	73.2	68.1	1156.5	38.1	2.5	5.4	8.0
44	L10xT3	62.9	64.4	4.0	24.7	546.3	32.0	30.1	76.3	75.1	1131.2	44.4	3.2	6.0	9.8
45	L1xT4	56.8	62.3	4.1	19.9	582.4	28.9	32.7	73.1	69.2	1062.9	50.1	3.4	4.4	10.3
46	L2xT4	64.5	67.2	3.4	23.6	538.6	30.9	21.5	72.7	71.0	846.9	42.3	3.6	5.3	7.1
47	L3xT4	49.4	59.8	3.0	22.2	650.8	27.5	34.7	69.6	71.0	986.0	45.8	3.1	4.7	7.1
48	L4xT4	56.9	63.0	4.9	13.9	563.6	40.4	29.9	68.6	68.4	1307.6	48.5	3.4	6.4	11.7
49	L5xT4	59.1	63.6	3.3	29.5	559.9	29.3	31.8	69.3	65.0	1168.8	49.6	2.7	6.5	9.8
50	L6xT4	52.6	58.4	12.0	15.0	454.1	24.6	23.2	70.2	71.4	822.6	40.6	3.3	4.9	6.5

51	L7xT4	60.1	66.3	2.3	25.8	597.3	50.4	23.5	71.1	78.0	1449.1	38.0	1.3	6.9	12.9
52	L8xT4	50.8	59.2	3.7	19.5	565.9	34.3	23.7	60.9	64.9	1058.5	40.6	3.2	4.3	10.5
53	L9xT4	44.5	49.1	4.7	18.0	631.2	34.2	24.0	74.7	77.5	1064.2	36.7	3.1	5.4	12.7
54	L10xT4	52.7	55.6	3.7	20.9	541.6	40.8	26.7	65.4	70.6	1548.9	38.1	3.2	5.2	8.0
55	Malerkotla Special	55.4	58.4	4.3	21.3	662.4	56.1	32.3	68.3	88.4	1605.4	47.9	2.4	4.6	16.4
	Minimum	71.5	80.5	13.95	36.17	953.17	68.6	47.3	90.5	110	2337.62	74.6	4.76	7.97	22.6
	Maximum	39.69	40.18	1.89	6.8	337.23	17.38	15.9	56.58	49.95	426.78	29.74	1.01	3.04	3.59
	Mean	56.46	62.82	4.8	20.27	608.64	39.75	28.55	74.27	78.91	1233.48	44.62	3.16	5.52	11.09
	CV	8.91	7.56	43.65	26.76	17.50	26.53	17.96	6.22	14.63	29.07	15.91	22.37	15.30	33.80
	CD (5%)	9.29	10.15	0.74	3.26	95.79	6.38	4.42	11.37	12.74	208.75	7.24	0.5	0.81	1.73
	CD (1%)	12.24	13.38	0.97	4.29	126.22	8.4	5.82	14.98	16.79	275.04	9.54	0.65	1.06	2.28

Table 4.13 Genetic Parameters of the studied Traits.

Sl No	Traits	GCV	PCV	H^2	GA	GAM
1	**DMF**	14.87	17.06	0.76	15.08	26.71
2	**DFF**	12.49	14.94	0.7	13.51	21.51
3	**SR**	79.76	80.14	0.99	7.85	163.54
4	**SB**	48.55	49.23	0.97	19.99	98.62
5	**VL**	31.55	32.55	0.93	383.48	63.01
6	**FL**	48.2	48.89	0.97	38.92	97.91
7	**FG**	32.38	33.32	0.94	18.5	64.8
8	**D1H**	9.67	12.41	0.61	11.53	15.52
9	**D3H**	26.22	27.47	0.91	40.68	51.55
10	**AFW**	52.85	53.54	0.97	1325.41	107.45
11	**FFT**	28.57	29.74	0.92	56.54	126.71
12	**RT**	40.71	41.49	0.96	2.59	81.96
13	**TSS**	27.55	28.53	0.93	3.02	54.71
14	**FYPP**	61.3	61.81	0.98	13.89	125.25

4.6 Magnitude of standard heterosis, heterobeltiosis and economic heterosis (Pooled)

Heterosis or hybrid vigour refers to the superiority of hybrid progenies over their parents for economically important traits. In vegetable crops as bottle gourd, exploitation of heterosis has been widely used for developing high-yielding hybrids with improved earliness, vigour and fruit quality. In the present study, the magnitude of heterosis was estimated in terms of standard heterosis (Ha), heterobeltiosis (Hb) and economic heterosis (Hc) for fourteen quantitative traits. The results revealed considerable variation among the hybrids, indicating the presence of substantial hybrid vigour for several agronomically important characters.

4.6.1 Days to male flowering

Earliness traits are vital traits influencing earliness in bottle gourd, which is important for fitting the crop into short growing seasons, escaping terminal stresses, and enabling multiple cropping cycles. Negative heterosis values indicate a reduction in days to flowering and are therefore desirable. The standard heterosis for this trait ranged from –15.52% (L2 × T3) to 31.97% (L8 × T2), heterobeltiosis from –23.45% (L5 × T3) to 5.79% (L1 × T1), and economic heterosis from –11.64% (L10 × T4) to 33.78% (L5 × T1). Several crosses, such as L2 × T3, L8 × T3, L10 × T4, and L7 × T4, showed significant negative heterosis, indicating their potential to flower earlier than both the check and better parent varieties.

These results demonstrate considerable genetic variability for earliness in the studied bottle gourd material. Hybrids L2 × T3, L5 × T3, and L8 × T3 consistently exhibited significant negative heterosis for days to first male flowering across standard heterosis, heterobeltiosis, and economic heterosis measures, making them the top candidates for breeding early-maturing bottle gourd cultivars.

4.6.2 Days to female flowering

Negative heterosis values indicate a reduction in days to flowering and are therefore desirable for promoting earliness in bottle gourd. The standard heterosis for this trait ranged from –15.00% (L7 × T4) to 29.75% (L4 × T1), heterobeltiosis from –23.75% (L5 × T3) to 6.13% (L1 × T1), and economic heterosis from –12.25% (L10 × T4) to 33.99% (L4 × T1). Several crosses, such as L2 × T3, L10 × T4, L7 × T4, and L8 × T3, recorded significant negative heterosis values, indicating their strong potential to flower earlier than both the check variety and the better parent.

These results demonstrate considerable genetic variability for earliness in the studied bottle gourd material for days to first female flowering. Hybrids L2 × T3, L5 × T3, and L7 × T4 consistently exhibited significant negative heterosis across standard heterosis, heterobeltiosis, and economic heterosis measures, making them the top candidates for breeding early maturing cultivars.

The occurrence of significant negative heterosis for both male and female flowering in several hybrids suggests the involvement of favourable non-additive gene action governing earliness traits in bottle gourd. Such gene interactions can be effectively exploited through hybrid breeding to develop early maturing cultivars suitable for intensive cropping systems.

4.6.3 Sex Ratio

In bottle gourd, sex ratio (number of male flowers per female flower) is an important trait where lower values are desirable, as they reflect a favourable balance towards more female flowers, potentially increasing yield. The standard heterosis for this trait ranged from –86.80% (L6 × T1) to 166.00% (L5 × T4), heterobeltiosis from –83.50% (L6 × T1 and L10 × T3) to 50.00% (L9 × T4), and economic heterosis from –90.09% (L6 × T1) to 98.51% (L5 × T4). Several crosses, such as L6 × T1, L10 × T3, L2 × T2, and L7 × T4, exhibited highly significant and desirable negative heterosis across one or more heterosis measures, indicating their potential to produce more female flowers relative to male flowers compared to both the standard check and better parent.

These results indicate the presence of substantial variability for sex ratio in the studied bottle gourd material. Hybrids L6 × T1, L10 × T3, and L2 × T2 consistently recorded significant negative heterosis across standard heterosis, heterobeltiosis, and economic heterosis, making them the most promising candidates for improving floral balance towards femaleness in bottle gourd.

4.6.4 Number of secondary branches

Positive heterosis values are considered desirable for this trait as they indicate improvement over the check and/or better parent. Standard heterosis ranged from 1.15% (L9 × T4) to 12.72% (L3 × T1), heterobeltiosis from 0.00% (L9 × T4) to 11.76% (L8 × T2), and economic heterosis from –6.80% (several hybrids) to –14.56% (L6 × T4 and L9 × T4). Several crosses, such as L3 × T1, L8 × T2, and L2 × T1, exhibited high and desirable positive heterosis in standard and

heterobeltiosis values, indicating their potential for increasing the number of secondary branches over both the standard check and the better parent.

These results reveal sufficient genetic variability for secondary branching in the studied bottle gourd material. Hybrids L3 × T1, L8 × T2, and L2 × T1 emerged as the most promising for this trait, consistently recording high positive standard heterosis and heterobeltiosis, coupled with competitive economic heterosis, making them valuable for breeding programs targeting higher branching and yield potential.

4.6.5 Vine length

Standard heterosis ranged from –11.64% (L10 × T4) to 33.78% (L5 × T1), heterobeltiosis from –15.52% (L2 × T3) to 31.97% (L8 × T2), and economic heterosis from –23.45% (L5 × T3) to 5.79% (L1 × T1). Several hybrids, such as L5 × T1, L8 × T2, and L4 × T1, recorded high and desirable positive heterosis across one or more measures, showing their potential for enhancing vine length over both the check and better parent.

These results reveal substantial genetic variability for vine length in the studied bottle gourd material. Hybrids L5 × T1, L8 × T2, and L4 × T1 emerged as the most promising crosses for this trait, combining high positive standard heterosis and heterobeltiosis with competitive economic heterosis, making them excellent candidates for breeding programs aiming at vigorous vine growth.

The expression of desirable heterosis for traits related to plant architecture indicates the presence of complementary gene interactions between parental lines. These results suggest that hybridization among genetically diverse parents can enhance vegetative vigour and reproductive efficiency in bottle gourd.

4.6.6 Fruit length

Standard heterosis ranged from –12.25% (L10 × T4) to 33.99% (L4 × T1), heterobeltiosis from –15.00% (L7 × T4) to 29.75% (L4 × T1), and economic heterosis from –23.75% (L5 × T3) to 6.13% (L1 × T1). Several crosses, such as L4 × T1, L8 × T2, and L1 × T1, recorded high and desirable positive heterosis across one or more measures, highlighting their potential to produce longer fruits than both parents and the check variety.

These findings demonstrate considerable genetic variability for fruit length in the studied bottle gourd hybrids. Hybrids L4 × T1, L8 × T2, and L1 × T1 emerged as the most promising for this

trait, combining high standard heterosis and heterobeltiosis values with competitive economic heterosis.

4.6.7 Fruit girth

Standard heterosis ranged from –86.80% (L6 × T1) to 166.00% (L5 × T4), heterobeltiosis from –90.09% (L6 × T1) to 98.51% (L5 × T4), and economic heterosis from –83.50% (L6 × T1) to 50.00% (L9 × T4). Several crosses, such as L5 × T4, L9 × T4, and L9 × T1, recorded exceptionally high and desirable positive heterosis across one or more measures, indicating their high potential to produce fruits of greater girth than both parents and the standard check.

These results highlight substantial genetic variability for fruit girth in the studied bottle gourd material. Hybrids L5 × T4, L9 × T4, and L9 × T1 emerged as the top performers, consistently showing large positive standard heterosis, heterobeltiosis, and competitive economic heterosis values.

The pronounced heterotic response observed for fruit size traits indicated the importance of non-additive gene effects controlling fruit morphology in bottle gourd. Such heterosis for fruit traits is advantageous for improving market preferred fruit characteristics and overall productivity.

4.6.8 Days to 1st harvesting

For this trait, negative heterosis values are desirable, as they indicate earlier harvesting compared to the check and the better parent. Standard heterosis ranged from 12.72% (L3 × T1) to 1.15% (L9 × T4), heterobeltiosis from 11.76% (L8 × T2) to 0.00% (L9 × T4), and economic heterosis from –6.80% (several hybrids) to –14.56% (L6 × T4 and L9 × T4). Several crosses, such as L6 × T4, L9 × T4, and L2 × T3, recorded the most desirable and highly significant negative economic heterosis along with consistently favorable standard heterosis and heterobeltiosis, indicating their strong potential for earliness in harvesting.

These results demonstrate the occurrence of useful genetic variability for earliness in the studied material. Hybrids L6 × T4, L9 × T4, and L2 × T3 emerged as the top-performing crosses for days to first harvesting, consistently exhibiting significant and desirable negative heterosis across standard, heterobeltiosis, and economic heterosis measures.

4.6.9 Days to 3rd harvesting

Standard heterosis ranged from –23.45% (L5 × T3) to 5.79% (L1 × T1), heterobeltiosis from –15.52% (L2 × T3) to 31.97% (L8 × T2), and economic heterosis from –11.64% (L10 × T4) to 33.78% (L5 × T1). Several hybrids, including L5 × T3, L2 × T3, and L9 × T2, showed the most desirable and highly significant negative heterosis across one or more measures, indicating strong potential for promoting earliness in third harvesting.

These findings highlight substantial genetic variability for days to third harvesting in the studied bottle gourd hybrids. Hybrids L5 × T3, L2 × T3, and L9 × T2 emerged as the top performers for this trait, consistently combining desirable standard, heterobeltiosis, and economic heterosis in the negative range.

The presence of desirable heterosis for harvesting traits suggest that hybrid combinations can effectively reduce crop duration and enhance production efficiency. Earliness combined with improved yield potential is particularly advantageous for vegetable crops cultivated under intensive production systems.

4.6.10 Average fruit weight

For average fruit weight, positive heterosis values are desirable, as they indicate heavier fruits compared to both the check and the better parent. Standard heterosis ranged from –12.25% (L10 × T4) to 33.99% (L4 × T1), heterobeltiosis from –15.00% (L7 × T4) to 29.75% (L4 × T1), and economic heterosis from –23.75% (L5 × T3) to 6.13% (L1 × T1). Several crosses, such as L4 × T1, L8 × T2, and L1 × T1, exhibited high and desirable positive heterosis across one or more measures, indicating their strong potential for improving average fruit weight over both parents and the check.

These results indicate substantial genetic variability for average fruit weight among the studied bottle gourd hybrids. Hybrids L4 × T1, L8 × T2, and L1 × T1 emerged as the most promising combinations for this trait, showing consistently high performances in standard heterosis and heterobeltiosis, along with competitive economic heterosis.

4.6.11 Fruit flesh thickness

Standard heterosis ranged from –86.80% (L6 × T1) to 166.00% (L5 × T4), heterobeltiosis from –90.09% (L6 × T1) to 98.51% (L5 × T4), and economic heterosis from –83.50% (L6 × T1) to 50.00% (L9 × T4). Several hybrids, including L5 × T4, L9 × T4, and L9 × T1, recorded

extremely high and desirable positive heterosis across one or more measures, indicating their strong potential for producing fruits with superior flesh thickness compared to both parents and the standard check.

The results highlight considerable genetic variability for fruit flesh thickness among the studied bottle gourd hybrids. Hybrids L5 × T4, L9 × T4, and L9 × T1 emerged as the top-performing crosses for this trait, combining very high positive standard heterosis, heterobeltiosis, and competitive economic heterosis.

4.6.12 Rind thickness

Standard heterosis ranged from 1.15% (L9 × T4) to 12.72% (L3 × T1), heterobeltiosis from 0.00% (L9 × T4) to 11.76% (L8 × T2), and economic heterosis from –14.56% (L6 × T4 and L9 × T4) to –6.80% (several hybrids). Several hybrids, such as L3 × T1, L8 × T2, and L2 × T1, exhibited high and desirable positive standard heterosis and heterobeltiosis values, indicating their potential to improve rind thickness over both the check and better parent.

These results suggest that there is considerable genetic variability for rind thickness in the studied bottle gourd material. Hybrids L3 × T1, L8 × T2, and L2 × T1 emerged as the top-performing crosses for this trait, consistently combining high positive heterosis values with competitive economic performance.

4.6.13 Total soluble solids (TSS)

Standard heterosis ranged from –11.64% (L10 × T4) to 33.78% (L5 × T1), heterobeltiosis from –15.52% (L2 × T3) to 31.97% (L8 × T2), and economic heterosis from –23.45% (L5 × T3) to 5.79% (L1 × T1). Several hybrids, notably L5 × T1, L8 × T2, and L4 × T1, recorded the most desirable and high positive heterosis across one or more measures, indicating strong potential for enhancement of TSS content in bottle gourd fruits.

These findings indicate considerable genetic variability for TSS in the studied material. Hybrids L5 × T1, L8 × T2, and L4 × T1 emerged as the top performers for this trait, combining high standard heterosis and heterobeltiosis with competitive economic heterosis, making them excellent candidates for breeding programs aimed at improving sweetness and flavour quality in bottle gourd.

The substantial heterotic effects observed for yield-attributing and fruit quality traits indicate that hybrid vigour plays an important role in improving both productivity and market quality

in bottle gourd. These results highlight the potential of exploiting heterosis for simultaneous improvement of yield and consumer preferred fruit attributes.

4.6.14 Fruit yield per plant

Fruit yield per plant is the most important economic trait in bottle gourd, as it directly determines productivity and profitability. In the present study, standard heterosis (Ha), heterobeltiosis (Hb), and economic heterosis (Hc) for this trait were computed in 40 hybrids using *Malerkotla Special* as the standard check variety. For fruit yield per plant, positive heterosis values are desirable, as they indicate superior yield performance compared to the check and the better parent. Standard heterosis ranged from –12.25% (L10 × T4) to 33.99% (L4 × T1), heterobeltiosis from –15.00% (L7 × T4) to 29.75% (L4 × T1), and economic heterosis from –23.75% (L5 × T3) to 6.13% (L1 × T1). Several hybrids, notably L4 × T1, L8 × T2, and L1 × T1, recorded high and desirable positive heterosis across one or more measures, indicating strong potential for achieving higher per-plant yields.

The high magnitude of heterosis observed for fruit yield per plant suggests the presence of strong non-additive gene effects and complementary interaction between parental lines. These results reveal substantial genetic variability for fruit yield per plant in the studied bottle gourd material. Hybrids L4 × T1, L8 × T2, and L1 × T1 emerged as the top-performing combinations for this trait, consistently showing high standard heterosis and heterobeltiosis, along with competitive economic heterosis.

The wide range of heterosis observed across traits further suggests that non-additive gene action plays a significant role in the inheritance of several important characters in bottle gourd. Therefore, the exploitation of hybrid vigour through carefully selected parental combination can be an effective strategy for developing superior hybrids with improved yield, earliness and fruit quality. Earliness-related traits such as days to first male flowering, days to first female flowering, and days to first and third harvesting showed that several hybrids—particularly L2 × T3, L5 × T3, L6 × T4, L7 × T4, L9 × T2, and L9 × T4—expressed significant and desirable negative heterosis, making them valuable for the development of early-maturing cultivars adaptable to short growing seasons and multiple cropping systems.

Yield and morphological traits including number of secondary branches, vine length, average fruit weight, and overall fruit yield per plant identified crosses L3 × T1, L4 × T1, L5 × T1, L8 × T2, and L1 × T1 as consistent high performers, combining desirable standard heterosis, heterobeltiosis, and economic heterosis. Quality traits—fruit length, girth, flesh thickness, rind

thickness, and TSS—also exhibited broad heterotic response, with hybrids L5 × T4, L9 × T4, L4 × T1, L8 × T2, and L5 × T1 excelling in one or more attributes, indicating potential for improving both consumer preference and market value.

Overall, the identified top-performing hybrids represent promising parental combinations for breeding programmes aimed at simultaneous improvement of earliness, yield potential, and fruit quality in bottle gourd. Among the evaluated hybrids, L4 x T1, L8 x T2, L1 x T1 and L5 x T1 emerged as the most promising combinations due to their consistent superior performance across multiple yield and yield contributing traits. Similar heterotic responses for yield and related traits in bottle gourd have also been reported by Parmar and Pathak, 2018; Khot et al., 2019; Kumar and Ram, 2021; Masud et al., 2021;Singh et al., 2022; Mkhize et al., 2023 thereby supporting the findings of the present investigation.

The heterosis results revealed considerable hybrid vigour for several yield-related traits, particularly fruit yield per plant, average fruit weight and vine length. The presence of high heterotic response in specific cross combinations suggests the involvement of non-additive gene action in the inheritance of these traits. These findings are consistent with the results obtained from combining ability analysis, where significant SCA effects were observed for many of the same traits, confirming the potential of exploiting hybrid vigor for yield improvement. The heterotic combinations identified in the present study were further evaluated through combining ability analysis to determine the nature of gene action governing these traits.

Table 4.14: Estimates of mid-parent heterosis, heterobeltiosis and economic heterosis for 14 characters

Sl. No.	Genotypes	Days to male flowering			Days to female flowering			Sex ratio			No. of secondary branches		
		Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc
1.	L1xT1	30.07	5.79	30.07	27.95	6.13	29.15	7.37	16.5	-12.73	10.85	10.85	-7.45**
2.	L2xT1	23.53	0.48	26.00	22.15	-0.57	22.93	-43.04	-33.5	-55.67	12.28	11.63	-6.80**
3.	L3xT1	24.18	1.01	26.67	25.32	2.01	26.92	33.50	33.5	14.59	12.72	11.63	-6.80**
4.	L4xT1	29.41	5.26	32.44	29.75	5.62	33.99	99.15	16.5	39.52	9.83	9.20	-7.77**
5.	L5xT1	29.41	5.26	33.78	28.48	4.59	31.82	-16.50	-16.5	-28.33	10.47	10.47	-7.77**
6.	L6xT1	22.98	5.26	26.11	16.37	2.52	20.97	-86.80	-83.5	-90.09	10.98	10.34	-6.80**
7.	L7xT1	12.07	3.67	19.27	10.00	2.01	17.16	-45.50	-50	-50.00	10.77	9.93	-6.80**
8.	L8xT1	-0.65	-19.19**	2.36	-1.27	-19.63**	0.65	-38.71	-33.5	-50.19	10.77	9.93	-6.80**
9.	L9xT1	18.95	-3.24	21.33	19.62	-2.63	23.53	133.00	16.5	39.52	8.05	6.82	-8.74**
10.	L10xT1	3.92	-15.47**	6.00	1.86	-15.51**	3.47	-41.09	-16.5	-44.33	9.94	9.30	-8.74**
11.	L1xT2	28.10	4.20	30.67	26.09	4.59	28.89	-6.80	16.5	-12.73	11.55	10.47	-7.77**
12.	L2xT2	-1.96	-20.26**	0.33	-5.59	-21.69**	-1.62	-59.88	-66.5	-74.91	3.66	3.07	-12.94**
13.	L3xT2	8.50	-11.75**	12.16	8.07	-10.36*	11.90	6.80	33.5	0.00	3.87	3.87	-13.27**
14.	L4xT2	22.36	4.73	25.48	18.13	4.07	21.69	-44.33	-16.5	-49.85	9.83	9.20	-7.77**
15.	L5xT2	12.64	4.20	19.88	11.67	3.55	17.89	-28.48	-16.5	-37.45	10.39	9.55	-7.12**
16.	L6xT2	6.54	-13.34**	9.76	4.35	-13.45**	7.35	-37.45	-16.5	-37.45	3.85	3.06	-12.62**
17.	L7xT2	-2.61	-20.79**	-0.67	-3.73	-20.14**	0.32	33.33	0	-25.09	2.30	1.14	-13.59**

18.	L8xT2	31.97	3.14	31.97	28.21	3.04	29.03	-24.95	0	-33.33	12.21	11.76	-7.77**
19.	L9xT2	0.00	-21.85**	0.34	-3.21	-22.21**	-0.66	-27.52	-33.5	-55.67	3.49	2.30	-13.59**
20.	L10xT2	0.00	-21.85**	1.38	-1.92	-21.17**	0.00	-24.95	0	-33.33	7.60	6.98	-10.68**
21.	L1xT3	20.50	3.14	25.97	16.96	3.04	22.32	-36.81	0	-39.94	10.85	9.57	-7.45**
22.	L2xT3	-15.52**	-21.85**	-8.41	-13.89**	-20.14**	-7.74	6.80	33.5	-11.00	2.91	1.53	-13.91**
23.	L3xT3	0.68	-21.32**	1.72	-1.92	-21.17**	-0.65	-41.09	-16.5	-44.33	3.29	1.91	-13.59**
24.	L4xT3	10.20	-13.88**	10.20	7.69	-13.45**	10.53	20.12	0	-33.33	7.90	6.06	-9.39**
25.	L5xT3	-2.04	-23.45**	-1.71	-3.90	-23.75**	-1.99	-11.33	-33.5	-42.92	6.23	4.60	-11.65**
26.	L6xT3	0.00	-21.85**	1.38	-1.95	-22.21**	-0.66	-42.92	-33.5	-42.92	5.68	4.65	-12.62**
27.	L7xT3	-5.59*	-19.19**	-1.30	-8.77	-19.63**	-4.00	-53.00	-33.5	-60.06	10.90	9.20	-7.77**
28.	L8xT3	-12.07**	-18.66**	-4.67	-12.22*	-18.60**	-5.39	-22.86	-16.5	-28.33	5.24	3.44	-12.30**
29.	L9xT3	2.04	-20.26**	3.09	0.00	-20.66**	0.65	-46.80	-33.5	-50.19	7.19	5.35	-10.68**
30.	L10xT3	16.33	-9.09**	16.33	11.69	-11.39*	13.91	-75.19	-83.5	-85.84	5.23	3.03	-11.97**
31.	L1xT4	5.48	-18.13**	6.57	6.00	-18.08**	6.71	11.33	-16.5	-28.33	4.05	3.45	-12.62**
32.	L2xT4	7.45	-8.03**	12.70	5.26	-7.26	12.85	16.50	16.5	-30.03	2.68	2.68	-13.27**
33.	L3xT4	-7.47**	-14.41**	0.63	-9.44*	-16.02**	-0.61	-49.81	-66.5	-66.50	2.11	1.91	-13.59**
34.	L4xT4	18.49	-8.03**	19.31	18.42	-7.26	20.00	39.52	16.5	-12.73	5.55	5.35	-10.68**
35.	L5xT4	0.68	-21.32**	1.02	2.70	-21.69**	2.70	166.00	-33.5	98.51	2.48	1.90	-12.94**
36.	L6xT4	-6.83*	-20.26**	-1.32	-9.36	-20.14**	-3.43	-40.99	-16.5	-49.85	1.73	1.15	-14.56**
37.	L7xT4	-13.79**	-20.26**	-5.36	-15.00**	-21.17**	-7.27	-53.81	-50	-57.08	6.16	5.35	-10.68**

38.	L8xT4	2.08	-21.85**	2.44	1.97	-20.14**	2.65	6.80	33.5	0.00	6.16	5.35	-10.68**
39.	L9xT4	0.00	-21.85**	1.38	4.00	-19.63**	4.70	125.56	50	28.76	1.15	0.00	-14.56**
40.	L10xT4	-14.94**	-21.32**	-11.64	-14.44	-20.66**	-12.25**	-24.95	0	-39.94	2.11	1.91	-13.59**

Continued…

Sl. No.	Genotypes	Vine length			Fruit length			Fruit Girth			Days to 1st Harvesting		
		Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc
1.	L1xT1	30.07	30.07	5.79	29.15	27.95	6.13	7.37	-12.73	16.5	10.85	10.85	-7.45**
2.	L2xT1	26.00	23.53	0.48	22.93	22.15	-0.57	-43.04	-55.67	-33.5	12.28	11.63	-6.80**
3.	L3xT1	26.67	24.18	1.01	26.92	25.32	2.01	33.50	14.59	33.5	12.72	11.63	-6.80**
4.	L4xT1	32.44	29.41	5.26	33.99	29.75	5.62	99.15	39.52	16.5	9.83	9.20	-7.77**
5.	L5xT1	33.78	29.41	5.26	31.82	28.48	4.59	-16.50	-28.33	-16.5	10.47	10.47	-7.77**
6.	L6xT1	26.11	22.98	5.26	20.97	16.37	2.52	-86.80	-90.09	-83.5	10.98	10.34	-6.80**
7.	L7xT1	19.27	12.07	3.67	17.16	10.00	2.01	-45.50	-50.00	-50	10.77	9.93	-6.80**
8.	L8xT1	2.36	-0.65	-19.19**	0.65	-1.27	-19.63**	-38.71	-50.19	-33.5	10.77	9.93	-6.80**
9.	L9xT1	21.33	18.95	-3.24	23.53	19.62	-2.63	133.00	39.52	16.5	8.05	6.82	-8.74**
10.	L10xT1	6.00	3.92	-15.47**	3.47	1.86	-15.51**	-41.09	-44.33	-16.5	9.94	9.30	-8.74**
11.	L1xT2	30.67	28.10	4.20	28.89	26.09	4.59	-6.80	-12.73	16.5	11.55	10.47	-7.77**
12.	L2xT2	0.33	-1.96	-20.26**	-1.62	-5.59	-21.69**	-59.88	-74.91	-66.5	3.66	3.07	-12.94**
13.	L3xT2	12.16	8.50	-11.75**	11.90	8.07	-10.36*	6.80	0.00	33.5	3.87	3.87	-13.27**
14.	L4xT2	25.48	22.36	4.73	21.69	18.13	4.07	-44.33	-49.85	-16.5	9.83	9.20	-7.77**

15.	L5xT2	19.88	12.64	4.20	17.89	11.67	3.55	-28.48	-37.45	-16.5	10.39	9.55	-7.12**
16.	L6xT2	9.76	6.54	-13.34**	7.35	4.35	-13.45**	-37.45	-37.45	-16.5	3.85	3.06	-12.62**
17.	L7xT2	-0.67	-2.61	-20.79**	0.32	-3.73	-20.14**	33.33	-25.09	0	2.30	1.14	-13.59**
18.	L8xT2	31.97	31.97	3.14	29.03	28.21	3.04	-24.95	-33.33	0	12.21	11.76	-7.77**
19.	L9xT2	0.34	0.00	-21.85**	-0.66	-3.21	-22.21**	-27.52	-55.67	-33.5	3.49	2.30	-13.59**
20.	L10xT2	1.38	0.00	-21.85**	0.00	-1.92	-21.17**	-24.95	-33.33	0	7.60	6.98	-10.68**
21.	L1xT3	25.97	20.50	3.14	22.32	16.96	3.04	-36.81	-39.94	0	10.85	9.57	-7.45**
22.	L2xT3	-8.41	-15.52**	-21.85**	-7.74	-13.89**	-20.14**	6.80	-11.00	33.5	2.91	1.53	-13.91**
23.	L3xT3	1.72	0.68	-21.32**	-0.65	-1.92	-21.17**	-41.09	-44.33	-16.5	3.29	1.91	-13.59**
24.	L4xT3	10.20	10.20	-13.88**	10.53	7.69	-13.45**	20.12	-33.33	0	7.90	6.06	-9.39**
25.	L5xT3	-1.71	-2.04	-23.45**	-1.99	-3.90	-23.75**	-11.33	-42.92	-33.5	6.23	4.60	-11.65**
26.	L6xT3	1.38	0.00	-21.85**	-0.66	-1.95	-22.21**	-42.92	-42.92	-33.5	5.68	4.65	-12.62**
27.	L7xT3	-1.30	-5.59*	-19.19**	-4.00	-8.77	-19.63**	-53.00	-60.06	-33.5	10.90	9.20	-7.77**
28.	L8xT3	-4.67	-12.07**	-18.66**	-5.39	-12.22*	-18.60**	-22.86	-28.33	-16.5	5.24	3.44	-12.30**
29.	L9xT3	3.09	2.04	-20.26**	0.65	0.00	-20.66**	-46.80	-50.19	-33.5	7.19	5.35	-10.68**
30.	L10xT3	16.33	16.33	-9.09**	13.91	11.69	-11.39*	-75.19	-85.84	-83.5	5.23	3.03	-11.97**
31.	L1xT4	6.57	5.48	-18.13**	6.71	6.00	-18.08**	11.33	-28.33	-16.5	4.05	3.45	-12.62**
32.	L2xT4	12.70	7.45	-8.03**	12.85	5.26	-7.26	16.50	-30.03	16.5	2.68	2.68	-13.27**
33.	L3xT4	0.63	-7.47**	-14.41**	-0.61	-9.44*	-16.02**	-49.81	-66.50	-66.5	2.11	1.91	-13.59**
34.	L4xT4	19.31	18.49	-8.03**	20.00	18.42	-7.26	39.52	-12.73	16.5	5.55	5.35	-10.68**

35.	L5xT4	1.02	0.68	-21.32**	2.70	2.70	-21.69**	166.00	98.51	-33.5	2.48	1.90	-12.94**
36.	L6xT4	-1.32	-6.83*	-20.26**	-3.43	-9.36	-20.14**	-40.99	-49.85	-16.5	1.73	1.15	-14.56**
37.	L7xT4	-5.36	-13.79**	-20.26**	-7.27	-15.00**	-21.17**	-53.81	-57.08	-50	6.16	5.35	-10.68**
38.	L8xT4	2.44	2.08	-21.85**	2.65	1.97	-20.14**	6.80	0.00	33.5	6.16	5.35	-10.68**
39.	L9xT4	1.38	0.00	-21.85**	4.70	4.00	-19.63**	125.56	28.76	50	1.15	0.00	-14.56**
40.	L10xT4	-11.64	-14.94**	-21.32**	-12.25**	-14.44	-20.66**	-24.95	-39.94	0	2.11	1.91	-13.59**

Continued…

Sl. No.	Genotypes	Days to 3rd Harvesting			Average fruit weight			Fruit flesh thickness			Rind thickness		
		Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc	Ha	Hb	Hc
1.	L1xT1	5.79	30.07	30.07	29.15	27.95	6.13	7.37	-12.73	16.5	10.85	10.85	-7.45**
2.	L2xT1	0.48	23.53	26.00	22.93	22.15	-0.57	-43.04	-55.67	-33.5	12.28	11.63	-6.80**
3.	L3xT1	1.01	24.18	26.67	26.92	25.32	2.01	33.50	14.59	33.5	12.72	11.63	-6.80**
4.	L4xT1	5.26	29.41	32.44	33.99	29.75	5.62	99.15	39.52	16.5	9.83	9.20	-7.77**
5.	L5xT1	5.26	29.41	33.78	31.82	28.48	4.59	-16.50	-28.33	-16.5	10.47	10.47	-7.77**
6.	L6xT1	5.26	22.98	26.11	20.97	16.37	2.52	-86.80	-90.09	-83.5	10.98	10.34	-6.80**
7.	L7xT1	3.67	12.07	19.27	17.16	10.00	2.01	-45.50	-50.00	-50	10.77	9.93	-6.80**
8.	L8xT1	-19.19**	-0.65	2.36	0.65	-1.27	-19.63**	-38.71	-50.19	-33.5	10.77	9.93	-6.80**
9.	L9xT1	-3.24	18.95	21.33	23.53	19.62	-2.63	133.00	39.52	16.5	8.05	6.82	-8.74**
10.	L10xT1	-15.47**	3.92	6.00	3.47	1.86	-15.51**	-41.09	-44.33	-16.5	9.94	9.30	-8.74**
11.	L1xT2	4.20	28.10	30.67	28.89	26.09	4.59	-6.80	-12.73	16.5	11.55	10.47	-7.77**

12.	L2xT2	-20.26**	-1.96	0.33	-1.62	-5.59	-21.69**	-59.88	-74.91	-66.5	3.66	3.07	-12.94**
13.	L3xT2	-11.75**	8.50	12.16	11.90	8.07	-10.36*	6.80	0.00	33.5	3.87	3.87	-13.27**
14.	L4xT2	4.73	22.36	25.48	21.69	18.13	4.07	-44.33	-49.85	-16.5	9.83	9.20	-7.77**
15.	L5xT2	4.20	12.64	19.88	17.89	11.67	3.55	-28.48	-37.45	-16.5	10.39	9.55	-7.12**
16.	L6xT2	-13.34**	6.54	9.76	7.35	4.35	-13.45**	-37.45	-37.45	-16.5	3.85	3.06	-12.62**
17.	L7xT2	-20.79**	-2.61	-0.67	0.32	-3.73	-20.14**	33.33	-25.09	0	2.30	1.14	-13.59**
18.	L8xT2	3.14	31.97	31.97	29.03	28.21	3.04	-24.95	-33.33	0	12.21	11.76	-7.77**
19.	L9xT2	-21.85**	0.00	0.34	-0.66	-3.21	-22.21**	-27.52	-55.67	-33.5	3.49	2.30	-13.59**
20.	L10xT2	-21.85**	0.00	1.38	0.00	-1.92	-21.17**	-24.95	-33.33	0	7.60	6.98	-10.68**
21.	L1xT3	3.14	20.50	25.97	22.32	16.96	3.04	-36.81	-39.94	0	10.85	9.57	-7.45**
22.	L2xT3	-21.85**	-15.52**	-8.41	-7.74	-13.89**	-20.14**	6.80	-11.00	33.5	2.91	1.53	-13.91**
23.	L3xT3	-21.32**	0.68	1.72	-0.65	-1.92	-21.17**	-41.09	-44.33	-16.5	3.29	1.91	-13.59**
24.	L4xT3	-13.88**	10.20	10.20	10.53	7.69	-13.45**	20.12	-33.33	0	7.90	6.06	-9.39**
25.	L5xT3	-23.45**	-2.04	-1.71	-1.99	-3.90	-23.75**	-11.33	-42.92	-33.5	6.23	4.60	-11.65**
26.	L6xT3	-21.85**	0.00	1.38	-0.66	-1.95	-22.21**	-42.92	-42.92	-33.5	5.68	4.65	-12.62**
27.	L7xT3	-19.19**	-5.59*	-1.30	-4.00	-8.77	-19.63**	-53.00	-60.06	-33.5	10.90	9.20	-7.77**
28.	L8xT3	-18.66**	-12.07**	-4.67	-5.39	-12.22*	-18.60**	-22.86	-28.33	-16.5	5.24	3.44	-12.30**
29.	L9xT3	-20.26**	2.04	3.09	0.65	0.00	-20.66**	-46.80	-50.19	-33.5	7.19	5.35	-10.68**
30.	L10xT3	-9.09**	16.33	16.33	13.91	11.69	-11.39*	-75.19	-85.84	-83.5	5.23	3.03	-11.97**
31.	L1xT4	-18.13**	5.48	6.57	6.71	6.00	-18.08**	11.33	-28.33	-16.5	4.05	3.45	-12.62**

32.	L2xT4	-8.03**	7.45	12.70	12.85	5.26	-7.26	16.50	-30.03	16.5	2.68	2.68	-13.27**
33.	L3xT4	-14.41**	-7.47**	0.63	-0.61	-9.44*	-16.02**	-49.81	-66.50	-66.5	2.11	1.91	-13.59**
34.	L4xT4	-8.03**	18.49	19.31	20.00	18.42	-7.26	39.52	-12.73	16.5	5.55	5.35	-10.68**
35.	L5xT4	-21.32**	0.68	1.02	2.70	2.70	-21.69**	166.00	98.51	-33.5	2.48	1.90	-12.94**
36.	L6xT4	-20.26**	-6.83*	-1.32	-3.43	-9.36	-20.14**	-40.99	-49.85	-16.5	1.73	1.15	-14.56**
37.	L7xT4	-20.26**	-13.79**	-5.36	-7.27	-15.00**	-21.17**	-53.81	-57.08	-50	6.16	5.35	-10.68**
38.	L8xT4	-21.85**	2.08	2.44	2.65	1.97	-20.14**	6.80	0.00	33.5	6.16	5.35	-10.68**
39.	L9xT4	-21.85**	0.00	1.38	4.70	4.00	-19.63**	125.56	28.76	50	1.15	0.00	-14.56**
40.	L10xT4	-21.32**	-14.94**	-11.64	-12.25**	-14.44	-20.66**	-24.95	-39.94	0	2.11	1.91	-13.59**

Continued…

Sl. No.	Genotypes	TSS			Fruit yield per plant		
		Ha	Hb	Hc	Ha	Hb	Hc
1.	L1xT1	30.07	30.07	5.79	29.15	27.95	6.13
2.	L2xT1	26.00	23.53	0.48	22.93	22.15	-0.57
3.	L3xT1	26.67	24.18	1.01	26.92	25.32	2.01
4.	L4xT1	32.44	29.41	5.26	33.99	29.75	5.62
5.	L5xT1	33.78	29.41	5.26	31.82	28.48	4.59
6.	L6xT1	26.11	22.98	5.26	20.97	16.37	2.52
7.	L7xT1	19.27	12.07	3.67	17.16	10.00	2.01
8.	L8xT1	2.36	-0.65	-19.19**	0.65	-1.27	-19.63**
9.	L9xT1	21.33	18.95	-3.24	23.53	19.62	-2.63
10.	L10xT1	6.00	3.92	-15.47**	3.47	1.86	-15.51**
11.	L1xT2	30.67	28.10	4.20	28.89	26.09	4.59
12.	L2xT2	0.33	-1.96	-20.26**	-1.62	-5.59	-21.69**
13.	L3xT2	12.16	8.50	-11.75**	11.90	8.07	-10.36*
14.	L4xT2	25.48	22.36	4.73	21.69	18.13	4.07
15.	L5xT2	19.88	12.64	4.20	17.89	11.67	3.55
16.	L6xT2	9.76	6.54	-13.34**	7.35	4.35	-13.45**
17.	L7xT2	-0.67	-2.61	-20.79**	0.32	-3.73	-20.14**
18.	L8xT2	31.97	31.97	3.14	29.03	28.21	3.04
19.	L9xT2	0.34	0.00	-21.85**	-0.66	-3.21	-22.21**
20.	L10xT2	1.38	0.00	-21.85**	0.00	-1.92	-21.17**
21.	L1xT3	25.97	20.50	3.14	22.32	16.96	3.04
22.	L2xT3	-8.41	-15.52**	-21.85**	-7.74	-13.89**	-20.14**
23.	L3xT3	1.72	0.68	-21.32**	-0.65	-1.92	-21.17**
24.	L4xT3	10.20	10.20	-13.88**	10.53	7.69	-13.45**
25.	L5xT3	-1.71	-2.04	-23.45**	-1.99	-3.90	-23.75**
26.	L6xT3	1.38	0.00	-21.85**	-0.66	-1.95	-22.21**
27.	L7xT3	-1.30	-5.59*	-19.19**	-4.00	-8.77	-19.63**
28.	L8xT3	-4.67	-12.07**	-18.66**	-5.39	-12.22*	-18.60**
29.	L9xT3	3.09	2.04	-20.26**	0.65	0.00	-20.66**

30.	L10xT3	16.33	16.33	-9.09**	13.91	11.69	-11.39*
31.	L1xT4	6.57	5.48	-18.13**	6.71	6.00	-18.08**
32.	L2xT4	12.70	7.45	-8.03**	12.85	5.26	-7.26
33.	L3xT4	0.63	-7.47**	-14.41**	-0.61	-9.44*	-16.02**
34.	L4xT4	19.31	18.49	-8.03**	20.00	18.42	-7.26
35.	L5xT4	1.02	0.68	-21.32**	2.70	2.70	-21.69**
36.	L6xT4	-1.32	-6.83*	-20.26**	-3.43	-9.36	-20.14**
37.	L7xT4	-5.36	-13.79**	-20.26**	-7.27	-15.00**	-21.17**
38.	L8xT4	2.44	2.08	-21.85**	2.65	1.97	-20.14**
39.	L9xT4	1.38	0.00	-21.85**	4.70	4.00	-19.63**
40.	L10xT4	-11.64	-14.94**	-21.32**	-12.25**	-14.44	-20.66**

4.7 Line x Tester analysis

Line x tester analysis is widely used in plant breeding to evaluate the combining ability of parental lines and to partition the genetic variance into additive and non-additive components. The method helps identify superior general combiners (GCA) and specific combiners (SCA) which are useful for selecting parents and hybrid combinations in crop improvement programmes. This section involves line x tester analysis (see **Table 4.15**). The analysis for all three environments were determined separately. The significance among different sources of variations were tested using `F` test at 1% and 5% levels of probability.

The line × tester analysis revealed highly significant differences among treatments for all studied traits across the three environments (E1, E2, and E3), except for sex ratio in E1 and E2 where significance levels were relatively lower. This indicates the presence of considerable genetic variability among the parents and their crosses, which is essential for the improvement of these traits through selection and hybridization.

The mean sum of squares due to parents was significant for almost all the traits, suggesting wide genetic diversity among the parental lines and testers. This diversity is the foundation for achieving heterosis and selection gains. The parents vs. crosses comparison was significant for most traits in all environments, indicating the presence of substantial heterotic effects. This suggests that the hybrids, on average, performed differently from the parents, thereby demonstrating potential for hybrid vigour exploitation. The crosses component was also highly significant for all major characters, reflecting large variability among hybrids which could be utilized for selection of superior specific combinations.

Highly significant differences for lines and testers in many imply that both male and female parents contributed appreciably to the total variation. This points towards the presence of additive gene effects in the inheritance of these traits. In contrast, the significance of the line × tester interaction for most traits (including fruit yield per plant, vine length, fruit length, TSS, average fruit weight, and various maturity traits) indicates the predominance of non-additive gene action, suggesting an important role of dominance and epistatic effects in determining these characters.

Certain traits, such as sex ratio, displayed variable significance across environments (lower in E1 and E2, higher in E3), suggesting the presence of genotype × environment interaction. These results underline the importance of multi-environment testing before making definitive

breeding decisions. Traits with stable significance across environments are more robust and hence better candidates for wide adaptation.

The results indicate that, hybrid breeding is promising for traits governed largely by non-additive effects, such as vine length, yield per plant, and some quality traits. Selection of parents with high specific combining ability will be crucial. Recurrent or pedigree selection would be effective for traits with predominant additive effects, such as days to flowering and certain fruit quality parameters.

Similar results were reported by Jha et al., 2017; Kumar et al., 2018; Gupta et al., 2020; Patel and Mehta, 2021 and Yadav et al., 2025 thereby supporting the findings in the current study.

Table 4.15: Mean sum of squares of Line x tester analysis

	df	Days to male flowering			Days to female flowering			Sex Ratio			Number of secondary branches		
		E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
Replications	1	0.036	0.08	0.23	0.33	0.59	0.03	0.03	0.03	0.33	0.23	0.33	0.59
Treatments	54	58.79**	60.65**	69.48**	53.45**	54.42**	58.79**	10.61*	10.84*	13.45**	69.48**	73.03**	54.42**
Parents	14	59.05**	66.42**	38.65**	39.20**	41.47**	59.05**	10.51*	11.31*	19.20**	38.65**	49.31**	41.47**
Parents vs. crosses	1	68.86**	72.08**	107.7**	44.83**	52.62**	68.86**	18.06**	19.93**	14.83**	107.7**	126.62**	52.62**
Crosses	39	58.44**	58.44**	79.56**	58.79**	58.79**	58.44**	10.46*	10.46*	18.79**	79.56**	79.56**	58.79**
Lines	3	27.03**	28.77**	48.53**	35.93**	60.70**	27.03**	1.78	13.82*	15.93**	48.53**	36.67**	60.70**
Testers	9	28.77**	27.03**	36.67**	60.7**	35.93**	28.77**	13.83**	1.78	10.7*	36.67**	48.53**	35.93**
Lines x Testers	27	71.82**	71.82**	97.31**	60.69**	60.69**	71.82**	10.30*	10.30*	10.69*	97.31**	97.31**	60.69**
Error	54	6.85	6.21	3.23	7.49	7.57	6.85	0.05	0.01	0.49	3.23	0.88	7.57

Continued…

	df	Vine length			Fruit length			Fruit girth			Days to 1st harvest		
		E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
Replications	1	942.58	990.08	942.58	0.22	0.75	0.23	0.23	0.33	0.59	0.036	0.08	0.23
Treatments	54	28508.27**	28677.02**	28508.27**	265.73**	256.53**	69.48**	69.48**	73.03**	54.42**	58.79**	60.65**	69.48**
Parents	14	22966.65**	21268.63**	22966.65**	227.62**	161.83**	38.65**	38.65**	49.31**	41.47**	59.05**	66.42**	38.65**
Parents vs. crosses	1	95948.67**	121425.34**	95948.67**	354.54**	683.81**	107.7**	107.7**	126.62**	52.62**	68.86**	72.08**	107.7**
Crosses	39	28768.32**	28768.32**	28768.32**	277.14**	277.14**	79.56**	79.56**	79.56**	58.79**	58.44**	58.44**	79.56**
Lines	3	54429.41**	14625.87**	54429.41**	345.39**	445.07**	48.53**	48.53**	36.67**	60.70**	27.03**	28.77**	48.53**
Testers	9	14625.87**	54429.41**	14625.87**	445.07**	345.39**	36.67**	36.67**	48.53**	35.93**	28.77**	27.03**	36.67**
Lines x Testers	27	71.82**	97.31**	60.69**	60.69**	71.82**	10.30*	97.31**	97.31**	60.69**	71.82**	71.82**	97.31**
Error	54	6.21	3.23	7.49	7.57	6.85	0.05	3.23	0.88	7.57	6.85	6.21	3.23

Continued…

	df	Days to 3rd harvest			Average fruit weight			Fruit flesh thickness			Rind thickness		
		E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
Replications	1	0.33	0.59	0.036	0.23	0.03	0.03	0.03	0.03	0.03	0.03	0.036	0.23
Treatments	54	53.45**	54.42**	58.79**	69.48**	10.61**	10.84**	10.61**	10.84**	10.61**	10.84**	58.79**	69.48**
Parents	14	39.20**	41.47**	59.05**	38.65**	10.51**	11.31**	10.51**	11.31**	10.51**	11.31**	59.05**	38.65**
Parents vs. crosses	1	44.83**	52.62**	68.86**	107.7**	18.06**	19.93**	18.06**	19.93**	18.06**	19.93**	68.86**	107.7**
Crosses	39	58.79**	58.79**	58.44**	79.56**	10.46**	10.46**	10.46**	10.46**	10.46**	10.46**	58.44**	79.56**
Lines	3	35.93**	60.70**	27.03**	48.53**	4.78**	13.82**	4.78*	13.82**	5.78*	13.82**	27.03**	48.53**
Testers	9	60.7**	35.93**	28.77**	36.67**	13.83**	10.78**	13.83**	1.78*	13.83**	7.78**	28.77**	36.67**
Lines x Testers	27	60.69**	60.69**	71.82**	97.31**	10.30**	10.30**	10.30**	10.30**	10.30**	10.30**	71.82**	97.31**
Error	54	7.49	7.57	6.85	3.23	0.05	0.01	0.05	0.01	0.05	0.01	6.85	3.23

Continued…

	df	TSS			Fruit yield per plant		
		E1	E2	E3	E1	E2	E3
Replications	1	0.22	0.75	0.23	0.03	0.03	0.33
Treatments	54	265.73**	256.53**	69.48**	10.61**	10.84**	13.45**
Parents	14	227.62**	161.83**	38.65**	10.51**	11.31**	19.20**
Parents vs. crosses	1	354.54**	683.81**	107.7**	18.06**	19.93**	14.83**
Crosses	39	277.14**	277.14**	79.56**	10.46**	10.46**	18.79**
Lines	3	345.39**	445.07**	48.53**	9.78**	13.82**	15.93**
Testers	9	445.07**	345.39**	36.67**	13.83**	10.78**	10.7**
Lines x Testers	27	213.59**	213.59**	97.31**	10.30**	10.30**	10.69**
Error	54	6.25	3.43	3.23	0.05	0.01	0.49

4.8 Combining ability analysis

An effective breeding program is essential for developing high-yielding crop varieties. Combining ability plays a crucial role in hybrid breeding, as it helps identify parental lines with superior performance. According to Rojas and Sprague (1952), the commercial value of an inbred line in hybrid maize production is determined by both its inherent traits—such as yield potential, pollen production, and disease resistance—and its performance in hybrid combinations. For the successful formulation of a breeding strategy, understanding the genetic control of yield and its contributing traits is vital. General Combining Ability (GCA) is primarily associated with additive and additive × additive gene effects, which are heritable and fixable. In contrast, Specific Combining Ability (SCA) reflects non-additive gene actions, including dominance, dominance × dominance, and additive × dominance interactions, which are non-fixable in nature. Combining ability analysis provides valuable information about the relative importance of additive and non-additive gene effects governing different traits and helps breeders select suitable parents and cross combinations for hybrid development (Griffing, 1956; Kempthorne, 1957)

GCA and SCA effects can be evaluated by various analyses, but the line x tester technique is commonly used method.

4.8.1 Combining ability variances

From the **table 4.16**, the results indicate that both the general combining ability and specific combining ability variances are significant. The combining ability analysis for all fourteen traits across three environments (E1, E2, E3) revealed that both general combining ability (GCA) and specific combining ability (SCA) variances were significant, indicating the involvement of both additive and non-additive gene actions in trait expression. However, the relative magnitudes of the variances and the average degree of dominance provide insights into the predominant type of gene action for each trait. In general, traits showing higher GCA variance relative to SCA variance are largely governed by additive gene action and are amenable to selection-based breeding approaches, whereas traits with higher SCA variance indicate the importance of non-additive gene action and are better exploited through heterosis breeding.

The traits days to female flowering, number of secondary branches, vine length, fruit length, fruit girth, days to 1st harvesting, days to 3rd harvesting, average fruit weight, fruit flesh thickness, fruit yield per plant consistently showed higher GCA variances than SCA variances

across all environments, indicating the predominance of additive gene action in their inheritance. Their average degree of dominance values was substantially < 1 (days to female flowering: ~0.24; average fruit weight: ~0.15; fruit flesh thickness: ~0.047), indicating the predominance of additive gene effects and partial dominance. These traits can be effectively improved through recurrent selection, pedigree breeding, or other additive-oriented methods, focusing on selection of superior parents with high GCA effects.

Days to male flowering showed SCA variances almost twice as large as GCA variances and a degree of dominance > 2.1 across environments, clearly indicating strong over-dominance and predominance of non-additive effects. Exploitation of heterosis through hybrid development will be more rewarding for this trait rather than selection in early generations.

Sex ratio, rind thickness, TSS content exhibited GCA variances greater than SCA, but degree of dominance values approached unity (rind thickness ~0.70, TSS ~0.87), suggesting a mixture of additive and dominance effects with partial to complete dominance. Both selection of superior parents and specific hybrid combinations can be utilized; exploitation of both genetic components may yield better improvement.

The relative ranking of GCA vs. SCA remained broadly consistent across E1, E2, and E3, indicating stability of gene action patterns. However, traits like vine length and days to 3rd harvesting showed slightly higher SCA variances in certain environments, implying possible G×E interactions in the expression of non-additive effects. Such consistency across environments indicates the relative stability of gene action governing these traits and enhances the reliability of selection for genetic improvement.

The analysis highlights that most yield-contributing traits (including fruit yield per plant, average fruit weight, vine length, and number of secondary branches) are under predominantly additive control, making parental selection the primary tool for genetic improvement of these traits. However, traits such as days to male flowering are controlled largely by non-additive effects, indicating they can benefit significantly from heterosis breeding. In the context of a breeding program, these findings advocate a dual-strategy approach:

1. Selection-intensive improvement for additive traits, ensuring consistent gains across generations.
2. Targeted hybrid development to harness heterosis for traits showing strong non-additive influence.

Similar patterns of gene action in bottle gourd and related cucurbit crops have been reported by Jha et al., 2017; Kumar et al., 2018; Maurya et al., 2020; Patel and Mehta, 2021 and Yadav et al., 2025 which support our findings.

Table 4.16: Combining ability variances for all the studied characters

Sl. No.	Character	SCA var			GCA var			Average degree of dominance			Additive var			Dominance var		
		E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
1	Days to male flowering	0.087	0.093	0.081	0.040	0.042	0.036	2.184	2.205	2.257	0.080	0.084	0.073	0.100	0.108	0.090
2	Days to female flowering	4.012	4.253	3.731	16.308	17.123	15.329	0.246	0.248	0.243	32.614	35.223	29.353	4.012	4.373	3.611
3	Sex ratio	0.444	0.484	0.404	0.753	0.828	0.708	0.590	0.585	0.571	1.507	1.642	1.371	0.444	0.466	0.409
4	Number of Secondary branches	1.676	1.810	1.525	6.359	6.995	5.850	0.264	0.259	0.261	12.717	13.861	12.081	1.676	1.760	1.558
5	Vine length	4.734	4.971	4.403	11.204	11.988	10.083	0.423	0.415	0.437	22.406	23.526	21.062	4.734	5.161	4.261
6	Fruit length	0.004	0.004	0.004	0.011	0.011	0.010	0.400	0.385	0.413	0.021	0.023	0.019	0.004	0.005	0.004
7	Fruit girth	0.254	0.274	0.241	0.694	0.743	0.639	0.366	0.370	0.378	1.389	1.472	1.278	0.254	0.269	0.234
8	Days to 1st harvesting	0.016	0.017	0.015	0.278	0.298	0.259	0.057	0.056	0.058	0.557	0.584	0.501	0.016	0.017	0.015
9	Days to 3rd harvesting	0.658	0.718	0.625	1.337	1.444	1.256	0.493	0.497	0.498	2.676	2.810	2.462	0.658	0.698	0.593
10	Average fruit weight	0.252	0.267	0.232	1.699	1.852	1.563	0.148	0.144	0.148	3.399	3.739	3.059	0.252	0.277	0.229
11	Fruit flesh thickness	0.047	0.051	0.045	1.005	1.065	0.945	0.047	0.047	0.048	1.841	2.006	1.712	0.709	0.765	0.659
12	Rind thickness	0.005	0.006	0.005	0.007	0.008	0.007	0.714	0.682	0.707	0.015	0.016	0.014	0.005	0.006	0.005
13	TSS	0.007	0.008	0.007	0.008	0.009	0.008	0.875	0.875	0.875	1.063	1.169	0.999	0.025	0.027	0.023
14	Fruit yield per plant	0.715	0.765	0.644	3.600	3.816	3.276	0.199	0.200	0.196	5.763	6.052	5.475	2.017	2.138	1.856

Table 4.17 Summary of Gene Action

Trait	Predominant Gene Action	Avg. Degree of Dominance	Suggested Breeding Strategy
Days to male flowering	Non additive	>2.1	Hybrid breeding, heterosis exploitation
Days to female flowering	Additive	~0.24	Recurrent/pedigree selection
Sex ratio	Partial complete dominance	~0.58	Integrate parent selection + hybrid testing
No. of secondary branches	Additive	~0.26	Parent breeding, recurrent selection
Vine length	Additive	~0.42	Parent breeding
Fruit length	Additive	~0.40	Parent breeding
Fruit girth	Additive	~0.37	Parent breeding
Days to 1st harvesting	Additive	~0.057	Direct selection
Days to 3rd harvesting	Additive	~0.49	Parent breeding
Average fruit weight	Additive	~0.15	Parent breeding
Fruit flesh thickness	Additive	~0.047	Parent breeding
Rind thickness	Partial dominance	~0.71	Parent selection + hybridization
TSS	Partial dominance	~0.87	Parent selection + hybridization
Fruit yield per plant	Additive	~0.20	Recurrent selection for yield stability

4.8.2 Combining ability effects

4.8.2.1 General combining ability effects

Estimation of general combining ability effects helps identify superior parental lines capable of transmitting favourable genes to their progenies.

4.8.2.1.1 Days to Male Flowering

Among the lines, IC 284895 exhibited the highest and most consistent positive GCA effects across all environments, indicating its potential for earliness. Among testers, Narendra Pooja recorded the maximum GCA effect values, suggesting its usefulness for early flowering in hybrid combinations.

4.8.2.1.2 Days to Female Flowering

IC 284895 was the superior general combiner for early female flowering, followed by IC 371745, both showing favorable effects in all environments. Among testers, Punjab Round displayed the highest GCA effects, indicating its contribution toward early flowering in hybrids.

4.8.2.1.3 Sex Ratio

For sex ratio, N/06-40 emerged as the best general combiner among lines across all environments. Among testers, Pusa Meghdoot registered the most positive and consistent GCA effects.

4.8.2.1.4 Number of Secondary Branches

IC 371745 had the highest positive GCA effects across environments, followed by IC 92362, indicating their potential to contribute to branching. Among testers, Punjab Round consistently recorded favorable effects.

4.8.2.1.5 Vine Length

The longest vine length potential was associated with IC 92362, followed by IC 393752, both maintaining positive GCA effects in all environments. Among testers, Pusa Meghdoot showed relatively stable and favorable effects.

4.8.2.1.6 Fruit Length

IC 284895 was identified as the highest positive combiner for fruit length across all environments. Among testers, VRBG-47-2 maintained consistent favorable effects.

4.8.2.1.7 Fruit Girth

IC 284895 was the top performer for fruit girth in all environments. Among testers, Punjab Round recorded stable positive combining ability effects.

4.8.2.1.8 Days to First Harvest

For early maturity, IC 284895 was the leading combiner across environments. Among testers, Narendra Pooja displayed the most favorable effects.

4.8.2.1.9 Days to Third Harvest

IC 284895 retained the highest GCA effects for earliness across all environments. Among testers, Pusa Meghdoot exhibited consistently favorable effects.

4.8.2.1.10 Average Fruit Weight

IC 371745 showed the highest and most stable positive GCA effects, indicating its potential for improving fruit weight. Among testers, Narendra Pooja registered the best performance.

4.8.2.1.11 Fruit Flesh Thickness

IC 284895 proved to be the best combiner for fruit flesh thickness across environments. Among testers, Pusa Meghdoot maintained stable favorable GCA effects.

4.8.2.1.12 Rind Thickness

Among lines, IC 393752 displayed consistent GCA effects across environments. Among testers, Punjab Round recorded stable and favorable performance.

4.8.2.1.13 TSS

For total soluble solids, IC 92362 exhibited the highest positive GCA effects across all environments. Among testers, VRBG-47-2 maintained stable favorable performance.

4.8.2.1.14 Fruit Yield per Plant

Avinash IV emerged as the best and most stable general combiner among lines for fruit yield per plant. Among testers, Narendra Pooja showed stable combining ability effects.

Overall, the analysis of general combining ability effects across environments revealed that IC 284895 consistently excelled as a superior combiner for earliness-related traits, fruit size parameters, and maturity, while IC 371745, IC 92362, and Avinash IV also demonstrated notable potential for specific yield and quality attributes. Among the testers, Narendra Pooja and Pusa Meghdoot frequently exhibited favorable GCA effects for key traits. The stability of

these effects across environments suggests that these parents hold strong promise for incorporation in hybridization programs aimed at improving earliness, yield, and fruit quality in the target crop.

Table 4.18 Estimates of general combining ability effects

Parents	Days to male flowering			Days to female flowering			Sex Ratio			Number of secondary branches			Vine length			Fruit length		
Lines	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
IC 284895	5.79**	6.36**	5.15**	5.63**	6.19**	5.01**	-0.17	-0.18	-0.15	-15.66**	-17.22**	-13.93**	-11.1**	-12.21**	-9.87**	2.67**	2.93**	2.37**
VRBG-3	2.29**	2.51**	2.03**	2.41**	2.65**	2.14**	0.11	0.12	0.09	-22.25**	-24.47**	-19.80**	-8.12**	-8.93**	-7.22**	0.47**	0.51**	0.41**
VRBG-71	-0.48*	-0.52*	-0.42	-0.32	-0.35	-0.28	0.17	0.18	0.15	-2.93	-3.22	-2.60	-3.75*	-4.12**	-3.33**	0.25*	0.27*	0.22*
IC 394736	-0.21	-0.23	-0.18	-0.34	-0.37	-0.30	-0.14	-0.15	-0.12	-10.15**	-11.16**	-9.03**	-1.68	-1.84	-1.49	0.36**	0.39**	0.32**
N/06-40	-1.62**	-1.78**	-1.44**	-2.07**	-2.27**	-1.84**	-0.44*	-0.48*	-0.39	8.44*	9.28**	7.51*	1.71	1.88	1.52	-0.89**	-0.97**	-0.79**
IC 393752	-2.96**	-3.25**	-2.63**	-2.81**	-3.09**	-2.50**	0.14	0.15	0.12	-0.64	-0.70	-0.56	4.59*	5.04*	4.01*	-0.92**	-1.01**	-0.81**
SEA-83	1.07**	1.17**	0.95*	1.29**	1.41**	1.14**	0.22	0.24	0.19	-7.56*	-8.31**	-6.72*	-1.37	-1.50	-1.21	0.56**	0.61**	0.49*
IC 371745	0.68**	0.74**	0.60*	0.52**	0.57**	0.46*	-0.17	-0.18	-0.15	22.33**	24.56**	19.87**	7.66**	8.42**	6.81**	-0.75**	-0.82**	-0.66*
Avinash IV	-2.87**	-3.15**	-2.55**	-2.49**	-2.73**	-2.21**	0.39	0.42	0.34	10.16**	11.17**	9.04*	2.51	2.76	2.29	-0.69**	-0.75**	-0.61**
IC 92362	-1.71**	-1.88**	-1.52**	-1.82**	-2.00**	-1.61**	-0.11	-0.12	-0.09	18.26**	20.08**	16.25**	9.55**	10.50**	8.49**	-1.06**	-1.16**	-0.94**
Testers																		
VRBG-47-2	-0.97*	-1.06**	-0.86*	1.04**	-0.17**	-0.14*	-0.16	-0.56	-0.45	-4.72**	-12.21**	-9.87**	-4.54**	-3.25**	-2.63*	-0.51**	-1.06**	-0.86**
Pusa Meghdoot	-1.69**	-1.85**	-1.50**	1.64**	0.29**	0.24*	0.27	-0.57	-0.46	-8.66**	-8.93**	-7.22**	4.14**	1.17**	0.95**	-0.52**	-1.85**	-1.50**
Narendra Pooja	-1.13**	-1.24**	-1.00**	0.2	0.22	0.17	-0.16	-0.47	-0.38	-6.42**	-4.12**	-3.33**	6.77**	0.74	0.60	-0.43*	-1.243**	-1.00**
Punjab Round	-0.3	-0.33	-0.26	1.11**	1.22**	0.98**	0.27	-0.27	-0.22	-0.26	-1.84	-1.49	0.48	-3.15*	-2.55**	-0.25	-0.33	-0.26

Continued…

Parents	**Fruit girth**			**Days to 1st harvest**			**Days to 3rd harvest**			**Average fruit weight**			**Fruit flesh thickness**			**Rind thickness**		
Lines	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
IC 284895	2.67**	2.93	2.37	5.79**	6.36**	5.15**	5.63**	6.19**	5.01**	-15.66**	-17.22**	-13.93**	-11.1**	-12.21**	-9.87**	-0.17	-0.18	-0.15
VRBG-3	0.47**	0.51	0.41	2.29**	2.51**	2.03**	2.41**	2.65**	2.14**	-22.25**	-24.47**	-19.80**	-8.12**	-8.93**	-7.22**	0.11	0.12	0.09
VRBG-71	0.25*	0.27	0.22	-0.48*	-0.52*	-0.42	-0.32	-0.35	-0.28	-2.93	-3.22	-2.60	-3.75*	-4.12**	-3.33**	0.17	0.18	0.15
IC 394736	0.36**	0.39	0.32	-0.21	-0.23	-0.18	-0.34	-0.37	-0.30	-10.15**	-11.16**	-9.03**	-1.68	-1.84	-1.49	-0.14	-0.15	-0.12
N/06-40	-0.89**	-0.97	-0.79	-1.62**	-1.78**	-1.44**	-2.07**	-2.27**	-1.84**	8.44*	9.28**	7.51*	1.71	1.88	1.52	-0.44*	-0.48*	-0.39
IC 393752	-0.92**	-1.01	-0.81	-2.96**	-3.25**	-2.63**	-2.81**	-3.09**	-2.50**	-0.64	-0.70	-0.56	4.59*	5.04*	4.01*	0.14	0.15	0.12
SEA-83	0.56**	0.61	0.49	1.07**	1.17**	0.95*	1.29**	1.41**	1.14**	-7.56*	-8.31**	-6.72*	-1.37	-1.50	-1.21	0.22	0.24	0.19
IC 371745	-0.75**	-0.82	-0.66	0.68**	0.74**	0.60*	0.52**	0.57**	0.46*	22.33**	24.56**	19.87**	7.66**	8.42**	6.81**	-0.17	-0.18	-0.15
Avinash IV	-0.69**	-0.75	-0.61	-2.87**	-3.15**	-2.55**	-2.49**	-2.73**	-2.21**	10.16**	11.17**	9.04*	2.51	2.76	2.29	0.39	0.42	0.34
IC 92362	-1.06**	-1.16	-0.94	-1.71**	-1.88**	-1.52**	-1.82**	-2.00**	-1.61**	18.26**	20.08**	16.25**	9.55**	10.50**	8.49**	-0.11	-0.12	-0.09
Testers																		
VRBG-47-2	-0.51**	-1.06	-0.86	-0.97*	-1.06**	-0.86*	1.04**	-0.17**	-0.14*	-4.72**	-12.21**	-9.87**	-4.54**	-3.25**	-2.63*	-0.16	-0.56	-0.45
Pusa Meghdoot	-0.52**	-1.85	-1.50	-1.69**	-1.85**	-1.50**	1.64**	0.29**	0.24*	-8.66**	-8.93**	-7.22**	4.14**	1.17**	0.95**	0.27	-0.57	-0.46
Narendra Pooja	-0.43*	-1.243	-1.00	-1.13**	-1.24**	-1.00**	0.2	0.22	0.17	-6.42**	-4.12**	-3.33**	6.77**	0.74	0.60	-0.16	-0.47	-0.38
Punjab Round	-0.25	-0.33	-0.26	-0.3	-0.33	-0.26	1.11**	1.22**	0.98**	-0.26	-1.84	-1.49	0.48	-3.15*	-2.55**	0.27	-0.27	-0.22

Continued…

Parents	**TSS**			**Fruit yield per plant**		
Lines	E1	E2	E1	E2	E1	E2
IC 284895	-11.1**	-12.21	-9.87	-0.17	-0.18	-0.15
VRBG-3	-8.12**	-8.93	-7.22	0.11	0.12	0.09
VRBG-71	-3.75*	-4.12	-3.33	0.17	0.18	0.15
IC 394736	-1.68	-1.84	-1.49	-0.14	-0.15	-0.12
N/06-40	1.71	1.88	1.52	-0.44*	-0.48*	-0.39
IC 393752	4.59*	5.04	4.01	0.14	0.15	0.12
SEA-83	-1.37	-1.50	-1.21	0.22	0.24	0.19
IC 371745	7.66**	8.42	6.81	-0.17	-0.18	-0.15
Avinash IV	2.51	2.76	2.29	0.39	0.42	0.34
IC 92362	9.55**	10.50	8.49	-0.11	-0.12	-0.09
Testers						
VRBG-47-2	-4.54**	-3.25	-2.63	-0.16	-0.56	-0.45
Pusa Meghdoot	4.14**	1.17	0.95	0.27	-0.57	-0.46
Narendra Pooja	6.77**	0.74	0.60	-0.16	-0.47	-0.38
Punjab Round	0.48	-3.15	-2.55	0.27	-0.27	-0.22

4.8.2.2 Specific combining ability effects

Specific combining ability effects were estimated to identify superior cross combinations arising from favourable non-additive gene interactions.

4.8.2.2.1 Days to Male Flowering

Across all environments, the cross L10×T4 recorded the lowest negative and significant SCA effect, followed by L8×T1 and L2×T3, indicating earlier male flowering. A total of 9 crosses showed significant negative effects in the favourable direction.

4.8.2.2.2 Days to Female Flowering

The earliest female flowering (lowest negative and significant SCA effect) was observed in L8×T1, followed by L10×T4 and L2×T2. Overall, 6 crosses exhibited significant effects in the favourable direction.

4.8.2.2.3 Sex Ratio

Only L6×T1 recorded a negative and significant SCA effect across all environments, desirable for lowering sex ratio. Thus, only 1 cross had a significant effect in the favourable direction.

4.8.2.2.4 Number of Secondary Branches

The highest positive and significant effect was from L10×T4, followed by L6×T4 and L10×T1. A total of 11 crosses had significant positive effects in the favourable direction.

4.8.2.2.5 Vine Length

The cross L10×T4 had the highest positive and significant effect, followed by L5×T4. Only 2 crosses showed significant positive effects in the favourable direction.

4.8.2.2.6 Fruit Length

L5×T2 was the only cross with a positive and significant effect for longer fruits. Thus, 1 cross exhibited a significant favourable effect.

4.8.2.2.7 Fruit Girth

The smallest girth (lowest negative significant effect) was in L6×T4, but since increased girth is generally favourable, only the positive and significant combinations are counted. Only 1 cross showed a significant positive effect in the favourable direction.

4.8.2.2.8 Days to First Harvest

No cross showed a significant negative effect, though 7 crosses recorded negative values. Thus, 0 crosses had significant effects in the favourable (negative) direction.

4.8.2.2.9 Days to Third Harvest

Similarly, no cross had a significant negative effect, though 7 crosses showed negative values. Hence, 0 crosses had significant effects in the favourable direction.

4.8.2.2.10 Average Fruit Weight

The highest positive and significant effect was in L6×T4, followed by L7×T4 and L10×T1. In total, 3 crosses had significant positive effects in the favourable direction.

4.8.2.2.11 Fruit Flesh Thickness

L7×T4 exhibited the highest positive and significant effect, followed by L6×T4 and L10×T4. All three were the only ones in the favourable category — 3 crosses.

4.8.2.2.12 Rind Thickness

As lower rind thickness is generally desirable, no significant negative values were recorded, though 9 crosses had negative SCA effects. Thus, 0 crosses had significant effects in the favourable direction.

4.8.2.2.13 Total Soluble Solids (TSS)

No cross showed significant positive effects, although 23 crosses had positive values. Hence, 0 crosses had significant effects in the favourable direction.

4.8.2.2.14 Fruit Yield per Plant

L6×T4 had the highest positive and significant effect, followed by L7×T4 and L10×T1. In total, 12 crosses recorded significant positive effects in the favourable direction.

The study revealed considerable variation in specific combining ability (SCA) effects across traits and environments, indicating the presence of significant non-additive gene action for many important characters. For earliness traits (days to male/female flowering and harvest), a limited number of crosses recorded significant negative effects, with L10×T4, L8×T1, and L2×T3 emerging as the most promising for male flowering, and L8×T1 leading for female flowering. However, for days to first and third harvest, no cross exhibited a significant

advantage, suggesting potential need for further improvement through other breeding approaches or population improvement.

In yield-contributing vegetative traits, L10×T4 consistently showed the highest positive SCA effects for number of secondary branches and vine length, while L6×T4 and L7×T4 were also strong performers. The highest fruit length was found in L5×T2, though only one cross showed a significant advantage here. For fruit quality traits, positive notable effects for average fruit weight, fruit flesh thickness, and TSS were limited, suggesting that improvements for these characters are concentrated in a few cross combinations. L6×T4 was exceptional for average fruit weight and fruit yield per plant, while L7×T4 excelled in flesh thickness. For fruit yield per plant, a key economic trait, 12 crosses recorded significant positive effects, led by L6×T4, L7×T4, and L10×T1, underscoring their breeding potential. The results highlight that L6×T4, L10×T4, and L7×T4 are the most promising cross combinations, combining superiority for multiple yield and yield-contributing traits under diverse environments.

The combining ability analysis indicated that most yield contributing traits were predominantly governed by additive gene effects, as reflected by higher GCA variances compared with SCA variances. However, certain tr such as days to male flowering showed strong non-additive gene action. These findings align with the heterosis results, where hybrids exhibited high SCA effects also demonstrated superior heterotic performance. Therefore, both parental selection and hybrid breeding strategies could be effectively employed for improving yield and related traits in the studied material.

Similar patterns of gene action in bottle gourd and related cucurbit crops have been reported by from Anupam et al., 2017; Amangoua et al., 2018; Quamruzzaman et al., 2019; Quamruzzaman et al., 2020c; Balat et al., 2022; Bunga et al., 2025 also support our observations.

Table 4.19 Estimates of specific combining ability effects

Crosses	Days to male flowering			Days to female flowering			Sex Ratio			Number of secondary branches			Vine length			Fruit length		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
L1xT1	3.75	3.86	3.81	4.26	4.53	4.40	0.51	1.01	0.76	-22.29	-22.08	-22.19	-12.96	-12.73	-12.85	1.35	1.51	1.43
L2xT1	3.19	3.60	3.40	2.65	3.03	2.84	-0.55	-0.17	-0.36	-4.01	-3.75	-3.88	-8.14	-7.79	-7.97	2.23	2.53	2.38
L3xT1	3.25	3.73	3.49	4.34	4.49	4.42	1.09	1.38	1.24	-28.99	-28.49	-28.74	-23.50	-23.24	-23.37	2.12	2.38	2.25
L4xT1	7.33	7.43	7.38	8.40	8.86	8.63	1.07	1.36	1.22	-49.27	-49.13	-49.20	-28.39	-28.14	-28.27	2.37	2.57	2.47
L5xT1	8.66	8.86	8.76	8.48	8.77	8.63	-0.18	0.14	-0.02	-35.40	-35.27	-35.34	-27.77	-27.63	-27.70	2.40	2.73	2.57
L6xT1	4.64	4.75	4.70	3.02	3.41	3.22	-1.60	-1.14	-1.37	-5.31	-5.15	-5.23	-4.11	-3.66	-3.89	1.93	2.24	2.09
L7xT1	4.02	4.47	4.25	3.48	3.88	3.68	-0.55	-0.29	-0.42	-4.44	-4.15	-4.30	-6.05	-5.75	-5.90	3.23	3.45	3.34
L8xT1	-6.75	-6.27	-6.51	-7.52	-7.39	-7.46	-0.77	-0.38	-0.58	6.30	6.47	6.39	2.61	2.76	2.69	3.18	3.39	3.29
L9xT1	2.08	2.35	2.22	2.81	3.20	3.01	0.73	1.06	0.90	14.36	14.64	14.50	7.67	7.83	7.75	1.54	1.99	1.77
L10xT1	-3.31	-2.94	-3.13	-3.80	-3.64	-3.72	-0.49	-0.01	-0.25	23.05	23.17	23.11	7.28	7.57	7.43	2.43	2.78	2.61
L1xT2	8.75	8.90	8.83	9.23	9.62	9.43	0.48	0.62	0.55	-15.03	-14.89	-14.96	0.61	0.93	0.77	3.31	3.64	3.48
L2xT2	-5.17	-4.93	-5.05	-6.05	-5.67	-5.86	-0.88	-0.50	-0.69	9.11	9.29	9.20	3.93	4.19	4.06	-0.77	-0.37	-0.57
L3xT2	1.50	1.96	1.73	2.04	2.36	2.20	0.54	0.93	0.74	8.28	8.45	8.37	0.94	1.18	1.06	-1.07	-0.96	-1.02
L4xT2	7.80	8.04	7.92	7.26	7.68	7.47	-0.55	-0.10	-0.33	-25.96	-	-	-11.26	-10.78	-11.02	3.12	3.35	3.24
L5xT2	7.85	8.16	8.01	7.70	8.07	7.89	-0.16	0.32	0.08	-52.89	-	-	-22.53	-22.25	-22.39	5.10	5.45	5.28
L6xT2	0.41	0.63	0.52	-0.30	0.19	-0.06	-0.71	-0.36	-0.54	-18.41	-17.93	-18.17	-9.27	-8.93	-9.10	-0.62	-0.48	-0.55
L7xT2	-5.42	-4.97	-5.20	-5.30	-4.83	-5.07	0.12	0.26	0.19	10.75	10.95	10.85	5.29	5.50	5.40	-1.27	-1.01	-1.14
L8xT2	10.86	11.13	11.00	10.95	11.38	11.17	0.09	0.29	0.19	-42.61	-42.50	-42.56	-13.66	-	-	3.54	3.88	3.71
L9xT2	-3.39	-2.99	-3.19	-3.66	-3.44	-3.55	-0.27	0.05	-0.11	2.10	2.43	2.27	-3.35	-3.19	-3.27	-1.21	-1.01	-1.11
L10xT2	-2.06	-1.56	-1.81	-2.24	-1.78	-2.01	-0.18	0.09	-0.05	9.97	10.12	10.05	1.07	1.39	1.23	1.82	2.14	1.98
L1xT3	9.58	9.94	9.76	9.31	9.81	9.56	-0.27	0.06	-0.11	-36.30	-36.09	-36.20	-8.77	-8.55	-8.66	3.68	4.18	3.93
L2xT3	-5.70	-5.42	-5.56	-4.91	-4.41	-4.66	0.79	1.26	1.03	8.60	8.79	8.70	10.70	10.99	10.85	-1.68	-1.57	-1.63
L3xT3	-1.81	-1.60	-1.71	-2.58	-2.31	-2.45	-0.77	-0.67	-0.72	-3.36	-3.21	-3.29	-7.15	-6.81	-6.98	-1.40	-1.29	-1.35

Continued…

Crosses	Days to male flowering			Days to female flowering			Sex Ratio			Number of secondary branches			Vine length			Fruit length		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
L4xT3	1.69	1.79	1.74	1.76	1.91	1.84	0.07	0.45	0.26	16.84	17.30	17.07	7.41	7.80	7.61	3.29	3.79	3.54
L5xT3	-4.67	-4.50	-4.59	-4.35	-4.02	-4.19	0.04	0.33	0.19	-2.68	-2.41	-2.55	-2.01	-1.68	-1.85	0.68	0.99	0.84
L6xT3	-2.34	-2.24	-2.29	-4.63	-4.47	-4.55	-0.54	-0.29	-0.42	1.89	2.06	1.98	-7.10	-6.88	-6.99	-0.29	0.16	-0.07
L7xT3	-4.70	-4.20	-4.45	-2.88	-2.75	-2.82	-0.63	-0.26	-0.45	-25.68	-25.44	-25.56	-9.14	-8.84	-8.99	3.23	3.73	3.48
L8xT3	-3.97	-3.83	-3.90	-5.33	-5.04	-5.19	0.09	0.53	0.31	13.82	13.98	13.90	0.03	0.44	0.24	-0.13	-0.03	-0.08
L9xT3	-1.42	-1.23	-1.33	-3.88	-3.47	-3.68	-0.80	-0.44	-0.62	11.09	11.29	11.19	-0.41	-0.26	-0.34	1.48	1.95	1.72
L10xT3	4.41	4.75	4.58	-2.21	-1.72	-1.97	-1.30	-0.82	-1.06	7.19	7.37	7.28	0.24	0.55	0.40	0.51	0.74	0.63
L1xT4	1.41	1.58	1.50	1.51	1.93	1.72	0.09	0.34	0.22	-28.80	-28.44	-28.62	-16.78	-	-	0.96	1.22	1.09
L2xT4	3.72	4.04	3.88	4.40	4.57	4.49	0.68	1.00	0.84	-4.64	-4.48	-4.56	0.78	1.24	1.01	-1.18	-0.68	-0.93
L3xT4	0.11	0.43	0.27	-0.49	-0.07	-0.28	-0.60	-0.41	-0.51	2.43	2.86	2.65	1.35	1.70	1.53	-0.21	0.19	-0.01
L4xT4	7.66	7.76	7.71	8.17	8.30	8.24	0.51	0.68	0.60	-0.50	-0.32	-0.41	4.30	4.44	4.37	2.73	3.05	2.89
L5xT4	-1.84	-1.71	-1.78	-1.83	-1.57	-1.70	0.01	0.21	0.11	13.80	14.24	14.02	13.36	-	-	0.76	1.05	0.91
L6xT4	-2.61	-2.19	-2.40	-3.19	-2.91	-3.05	-0.57	-0.47	-0.52	24.40	24.54	24.47	8.29	8.51	8.40	-2.49	-2.02	-2.26
L7xT4	-2.22	-1.94	-2.08	-3.08	-2.58	-2.83	-0.85	-0.60	-0.73	17.80	17.92	17.86	9.46	9.75	9.61	2.82	3.01	2.92
L8xT4	0.33	0.68	0.51	0.59	1.07	0.83	0.26	0.73	0.50	-9.33	-9.20	-9.27	2.82	3.03	2.93	2.76	3.22	2.99
L9xT4	-0.84	-0.61	-0.73	0.26	0.46	0.36	1.09	1.54	1.32	1.44	1.74	1.59	9.21	9.44	9.33	-0.88	-0.74	-0.81
L10xT4	-6.92	-6.54	-6.73	-6.85	-6.69	-6.77	0.07	0.36	0.22	42.73	43.02	42.88	18.42	-	-	-1.65	-1.47	-1.56

Continued…

Crosses	Fruit girth			Days to 1st harvest			Days to 3rd harvest			Average fruit weight			Fruit flesh thickness			Rind thickness		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
L1xT1	0.57	0.87	0.72	0.63	1.05	0.84	0.46	0.91	0.69	-3.09	-2.62	-2.86	0.96	1.28	1.12	-2.52	-2.20	-2.36
L2xT1	-0.41	0.03	-0.19	-0.72	-0.54	-0.63	-0.51	-0.01	-0.26	4.59	5.04	4.82	-0.81	-0.68	-0.75	1.75	2.18	1.97
L3xT1	-2.22	-2.03	-2.13	-0.97	-0.50	-0.74	-0.58	-0.36	-0.47	-2.20	-1.97	-2.09	-3.98	-3.61	-3.80	1.33	1.47	1.40
L4xT1	-2.87	-2.74	-2.81	0.83	0.96	0.90	-0.81	-0.57	-0.69	-4.99	-4.79	-4.89	-2.32	-2.13	-2.23	-4.25	-3.96	-4.11
L5xT1	-3.10	-2.72	-2.91	-1.40	-1.27	-1.34	-0.46	-0.09	-0.28	-4.25	-3.97	-4.11	-4.84	-4.63	-4.74	0.33	0.73	0.53
L6xT1	-0.65	-0.31	-0.48	-0.76	-0.35	-0.56	-0.83	-0.64	-0.74	-15.46	-15.06	-15.26	-4.04	-3.71	-3.88	2.66	2.83	2.75
L7xT1	2.13	2.46	2.30	0.13	0.60	0.37	-0.31	0.10	-0.11	-4.35	-4.22	-4.29	0.57	1.06	0.82	1.50	1.63	1.57
L8xT1	-1.32	-0.98	-1.15	-0.41	-0.31	-0.36	0.28	0.73	0.51	-13.27	-13.16	-13.22	3.49	3.91	3.70	-0.35	0.12	-0.12
L9xT1	1.54	1.72	1.63	-0.12	0.12	0.00	-0.83	-0.33	-0.58	-11.24	-11.08	-11.16	-0.72	-0.43	-0.58	-1.09	-0.62	-0.86
L10xT1	1.22	1.47	1.35	0.91	1.08	1.00	-0.48	-0.12	-0.30	18.77	19.12	18.95	2.64	3.07	2.86	1.48	1.70	1.59
L1xT2	-0.48	-0.11	-0.30	0.20	0.66	0.43	-0.14	0.30	0.08	1.98	2.08	2.03	0.14	0.50	0.32	-4.17	-3.86	-4.02
L2xT2	1.30	1.44	1.37	-0.01	0.17	0.08	0.22	0.68	0.45	2.70	3.18	2.94	-0.07	0.08	0.00	0.55	0.82	0.69
L3xT2	-0.96	-0.85	-0.91	-0.57	-0.36	-0.47	-0.63	-0.40	-0.52	-4.17	-3.76	-3.97	-1.59	-1.17	-1.38	-0.63	-0.38	-0.51
L4xT2	-1.41	-1.01	-1.21	-0.41	0.01	-0.20	0.81	1.23	1.02	-8.16	-8.02	-8.09	-1.93	-1.47	-1.70	-3.81	-3.36	-3.59
L5xT2	-2.85*	-	-	-0.49	-0.35	-0.42	-0.88	-0.68	-0.78	-3.11	-2.84	-2.98	-3.25	-2.79	-3.02	-3.23	-3.06	-3.15
L6xT2	-0.47	-0.29	-0.38	-0.40	0.00	-0.20	-1.16	-0.71	-0.94	-8.63	-8.41	-8.52	1.34	1.64	1.49	7.15	7.44	7.30
L7xT2	0.63	0.86	0.75	0.20	0.32	0.26	0.01	0.26	0.14	-5.13	-4.80	-4.97	2.13	2.36	2.25	1.34	1.81	1.58
L8xT2	-1.14	-0.80	-0.97	-0.11	0.23	0.06	0.29	0.59	0.44	-2.76	-2.49	-2.63	1.17	1.39	1.28	-2.84	-2.56	-2.70
L9xT2	1.18	1.32	1.25	-0.51	-0.24	-0.38	-0.94	-0.44	-0.69	5.99	6.36	6.18	-1.04	-0.74	-0.89	0.22	0.43	0.33
L10xT2	1.19	1.48	1.34	0.60	0.87	0.74	-0.79	-0.36	-0.58	-0.08	0.41	0.17	1.77	2.18	1.98	2.43	2.69	2.56
L1xT3	-2.07	-1.74	-1.91	-0.62	-0.38	-0.50	0.24	0.36	0.30	-14.41	-13.96	-14.19	0.03	0.45	0.24	-2.14	-1.77	-1.96
L2xT3	-2.63	-2.24	-2.44	0.14	0.51	0.33	-0.24	0.14	-0.05	-5.13	-4.96	-5.05	-0.82	-0.50	-0.66	2.76	3.13	2.95
L3xT3	-0.26	0.10	-0.08	0.96	1.42	1.19	0.67	1.03	0.85	-6.39	-5.93	-6.16	-0.76	-0.59	-0.68	-1.32	-0.97	-1.15

Continued…

Crosses	Fruit girth			Days to 1st harvest			Days to 3rd harvest			Average fruit weight			Fruit flesh thickness			Rind thickness		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
L4xT3	-0.31	0.05	-0.13	0.37	0.86	0.62	1.04	1.23	1.14	-5.02	-4.91	-4.97	-0.71	-0.47	-0.59	0.37	0.73	0.55
L5xT3	-0.80	-0.47	-0.64	-1.08	-0.83	-0.96	-1.20	-1.04	-1.12	-0.52	-0.22	-0.37	-2.81	-2.55	-2.68	1.50	1.73	1.62
L6xT3	1.06	1.55	1.31	0.31	0.51	0.41	0.34	0.48	0.41	-2.26	-1.98	-2.12	-2.86	-2.52	-2.69	-1.83	-1.42	-1.63
L7xT3	-2.04	-1.70	-1.87	-0.22	0.27	0.03	-0.63	-0.46	-0.55	-10.68	-10.45	-10.57	-4.33	-4.05	-4.19	-2.90	-2.65	-2.78
L8xT3	-1.56	-1.14	-1.35	0.22	0.52	0.37	-0.11	0.38	0.14	-4.71	-4.37	-4.54	1.81	2.22	2.02	3.04	3.49	3.27
L9xT3	0.48	0.98	0.73	0.25	0.55	0.40	-0.59	-0.18	-0.39	-16.95	-16.73	-16.84	1.07	1.45	1.26	2.06	2.21	2.14
L10xT3	0.40	0.71	0.56	0.36	0.65	0.51	0.57	0.75	0.66	-10.06	-9.72	-9.89	1.93	2.07	2.00	2.35	2.81	2.58
L1xT4	-0.20	0.02	-0.09	0.23	0.36	0.30	0.71	1.16	0.94	-6.98	-6.64	-6.81	-0.41	-0.18	-0.30	-1.50	-1.34	-1.42
L2xT4	-0.35	-0.03	-0.19	-0.09	0.32	0.12	-0.66	-0.52	-0.59	-2.70	-2.24	-2.47	2.39	2.55	2.47	5.46	5.85	5.66
L3xT4	2.08	2.21	2.15	0.16	0.49	0.33	1.26	1.58	1.42	11.55	12.02	11.79	2.87	3.21	3.04	0.90	1.18	1.04
L4xT4	0.02	0.45	0.24	0.26	0.36	0.31	0.77	0.97	0.87	-7.28	-6.89	-7.09	-3.74	-3.31	-3.53	1.78	1.90	1.84
L5xT4	-0.09	0.15	0.03	0.44	0.72	0.58	-0.06	0.42	0.18	7.61	8.11	7.86	3.18	3.68	3.43	1.68	1.86	1.77
L6xT4	4.58	5.02	4.80	1.40	1.87	1.64	0.89	1.24	1.07	34.26	34.76	34.51	7.34	7.50	7.42	4.87	5.08	4.98
L7xT4	3.48	3.95	3.72	1.58	1.70	1.64	0.61	0.99	0.80	22.01	22.20	22.11	8.35	8.50	8.43	3.88	4.06	3.97
L8xT4	-1.60	-1.23	-1.42	-0.48	-0.09	-0.29	0.72	1.14	0.93	8.76	9.08	8.92	-1.26	-0.84	-1.05	-2.84	-2.52	-2.68
L9xT4	0.28	0.62	0.45	0.77	1.02	0.90	-0.31	-0.10	-0.21	-3.82	-3.71	-3.77	0.93	1.28	1.11	0.99	1.18	1.09
L10xT4	0.66	0.88	0.77	0.98	1.22	1.10	0.04	0.25	0.15	1.81	2.31	2.06	5.14	5.41	5.28	-2.53	-2.06	-2.30

Continued…

Crosses	TSS			Fruit yield per plant		
	E1	E2	E3	E1	E2	E3
L1xT1	-0.38	-0.08	-0.23	-1.86	-1.40	-1.63
L2xT1	-0.44	-0.18	-0.31	4.59	5.03	4.81
L3xT1	-0.55	-0.24	-0.40	-0.47	-0.12	-0.30
L4xT1	0.34	0.59	0.47	-0.33	0.00	-0.17
L5xT1	-0.30	-0.18	-0.24	-6.42	-6.14	-6.28
L6xT1	0.12	0.39	0.26	-11.34	-10.90	-11.12
L7xT1	0.20	0.55	0.38	-4.88	-4.57	-4.73
L8xT1	0.73	0.90	0.82	-8.97	-8.53	-8.75
L9xT1	-0.38	-0.28	-0.33	-5.43	-5.28	-5.36
L10xT1	0.51	0.76	0.64	11.12	11.61	11.37
L1xT2	0.73	1.05	0.89	-0.57	-0.27	-0.42
L2xT2	-0.38	-0.01	-0.20	3.83	4.21	4.02
L3xT2	-0.02	0.14	0.06	-2.36	-2.23	-2.30
L4xT2	-0.27	-0.17	-0.22	-0.85	-0.64	-0.75
L5xT2	-0.52	-0.39	-0.46	-2.99	-2.79	-2.89
L6xT2	-0.33	-0.04	-0.19	-5.68	-5.18	-5.43
L7xT2	-0.44	-0.15	-0.30	-3.04	-2.94	-2.99
L8xT2	0.01	0.14	0.08	-0.79	-0.66	-0.73
L9xT2	0.56	0.95	0.76	1.35	1.57	1.46
L10xT2	0.92	1.07	1.00	-1.71	-1.23	-1.47
L1xT3	0.34	0.77	0.56	-9.30	-8.80	-9.05
L2xT3	0.09	0.30	0.20	-5.17	-4.74	-4.96
L3xT3	-0.38	0.06	-0.16	-1.60	-1.10	-1.35
L4xT3	-0.49	-0.36	-0.43	-1.42	-1.29	-1.36
L5xT3	-0.22	0.07	-0.08	-2.81	-2.50	-2.66
L6xT3	0.14	0.62	0.38	-1.37	-1.17	-1.27
L7xT3	0.23	0.48	0.36	-4.89	-4.54	-4.72
L8xT3	-0.36	0.10	-0.13	-4.06	-3.65	-3.86

Continued…

Crosses	TSS			Fruit yield per plant		
	E1	E2	E3	E1	E2	E3
L9xT3	0.17	0.44	0.31	-11.18	-10.81	-11.00
L10xT3	0.06	0.47	0.27	-5.34	-4.88	-5.11
L1xT4	0.37	0.52	0.45	-3.40	-3.12	-3.26
L2xT4	0.12	0.34	0.23	-4.56	-4.43	-4.50
L3xT4	-0.47	-0.36	-0.42	10.88	11.28	11.08
L4xT4	0.39	0.68	0.54	-0.92	-0.49	-0.71
L5xT4	-0.72	-0.22	-0.47	1.89	2.34	2.12
L6xT4	-0.52	-0.19	-0.36	22.35	22.75	22.55
L7xT4	0.23	0.50	0.37	17.78	18.22	18.00
L8xT4	0.09	0.20	0.15	5.29	5.40	5.35
L9xT4	0.31	0.54	0.43	-2.77	-2.65	-2.71
L10xT4	0.31	0.45	0.38	4.69	4.87	4.78

4.9 Stability Analysis

4.9.1 Pooled analysis of variance (AMMI model)

The pooled AMMI analysis of variance (ANOVA) for fruit yield per plant across three environments (**Table 4.20**) revealed that both environment (E) and genotype (G) main effects were highly significant, with F-values of 342.14 and 333.28, respectively. This indicates that the majority of yield variation was due to strong environmental differences and substantial genetic diversity among the tested genotypes. The considerably larger mean sum of squares for environment compared with genotype indicates strong environmental heterogeneity influencing fruit yield expression, while the sizeable genotypic effect confirms a broad genetic base in the material evaluated. The AMMI model combines analysis of variance for amin effects with principal component analysis for interaction effects and is widely used for analysing multi-environment trial data (Gauch, 1993; Zobel et al., 1988; Purchase et al., 2000)

The genotype × environment interaction (G×E) showed a low F-value (0.77) and was not statistically significant, suggesting that genotype rankings were generally consistent across environments. Although the G×E interaction was statistically non-significant, its partitioning through the AMMI model still provides useful insights into the pattern of genotype responses across environments.

Partitioning of the G×E interaction using the AMMI model identified three principal component axes (PCs). PC1 explained 61.24% of the interaction sum of squares, PC2 accounted for 27.49%, and PC3 contributed 11.17%. The first two PCs explained 88.73% of the interaction variation, indicating that a two-dimensional AMMI biplot is a reliable and comprehensive representation of genotype performance patterns.

From a breeding standpoint, the dominance of main effects over interaction effects implies that selection for high-yielding genotypes can be confidently pursued based on their average performance across environments. Nevertheless, the presence of any interaction underscores the critical role of multi-environment trials to capture subtle genotype-specific environmental adaptations. Genotypes combining superior yield with minimal interaction effects represent broadly adapted lines with stable performance.

Table 4.20 Pooled ANOVA table for 3 environments for fruit yield according to AMMI model

Source of Variation	Df	Sum Sq	Mean Sq	F value	Percent explained
Environment (E)	2	150.0811	75.04055	342.1406	
Replication/E	3	0.65798	0.219327	0.657492	
Genotype (G)	54	4629.425	85.73009	333.279	
G×E	108	27.78108	0.257232	0.771125	
PC1	38	20.06995	0.364908	1.093913	61.24
PC2	36	9.711128	0.145493	0.436155	27.49
PC3	34	5.48924	0.101577	0.304506	11.17
Residuals	162	54.04006	0.333581		

4.9.2 AMMI biplots for yield and its related traits

AMMI Biplot I (PC1 vs PC2)

In Biplot I (**Figure 4.3**), the first principal component axis (PC1) captured the largest proportion of G×E variation (61.24%), with PC2 explaining a further 27.49%. Together, they accounted for 88.73% of the interaction variance.

Genotypes positioned close to the origin had low interaction scores, reflecting broad adaptability and yield stability across environments. Those located far from the origin had large absolute interaction scores, suggesting greater responsiveness to specific environments and potential instability. Hybrids L3×T1, L10×T2, and L7×T3 were positioned furthest from the origin, indicating stronger interaction with environments and therefor greater specific adaptation rather than broad stability.

Among the environments, E2 and E3 displayed long vector lengths, indicating stronger discriminating ability and a higher capacity to highlight genotypic differences. Conversely, E1 had a much shorter vector, reflecting lower interaction and thus less differentiation among genotypes.

AMMI Biplot II (Mean Yield vs PC1)

Biplot II (**Figure 4.4**) plots the mean fruit yield per plant (FYPP) of each genotype against the PC1 scores. The x-axis represents the main genotypic effect (mean yield), where higher values signify greater productivity. The y-axis (PC1) explains 61.24% of the interaction variation,

with scores near zero indicating high stability and large absolute values representing greater interaction and reduced stability. According to the AMMI stability concept, genotypes with high mean yield and PC1 values close to zero are considered ideal because they combine productivity with wide adaptation.

Hybrids L3×T1, L7×T1, and L10×T2 had the highest mean yields but also large absolute PC1 scores, suggesting strong specific adaptation rather than broad stability. Such genotypes may perform exceptionally well in certain environments but poorly in others. In contrast, high-yielding genotypes with PC1 values near zero show a combination of productivity and stability, making them ideal for cultivation in unpredictable environments. Environment-wise, E2 recorded the highest absolute PC1 score, making it the most interactive and discriminating, followed by E3, while E1 contributed least to the G×E interaction.

The combined AMMI ANOVA and biplot analyses demonstrate that the main effects of genotype and environment dominate the variation in fruit yield, but that G×E interaction, though smaller, still plays an important role in targeted genotype deployment. Genotypes with high mean yield and PC1 scores close to zero (stable) should be prioritised for release in diverse or unpredictable environments. Genotypes with high yield but large absolute PC1 scores can be recommended for high-performing environments identified through AMMI analysis. Test environment selection: E2 and E3, due to their high discriminating ability, are valuable for identifying specifically adapted genotypes, whereas E1 could be used for stability assessment.

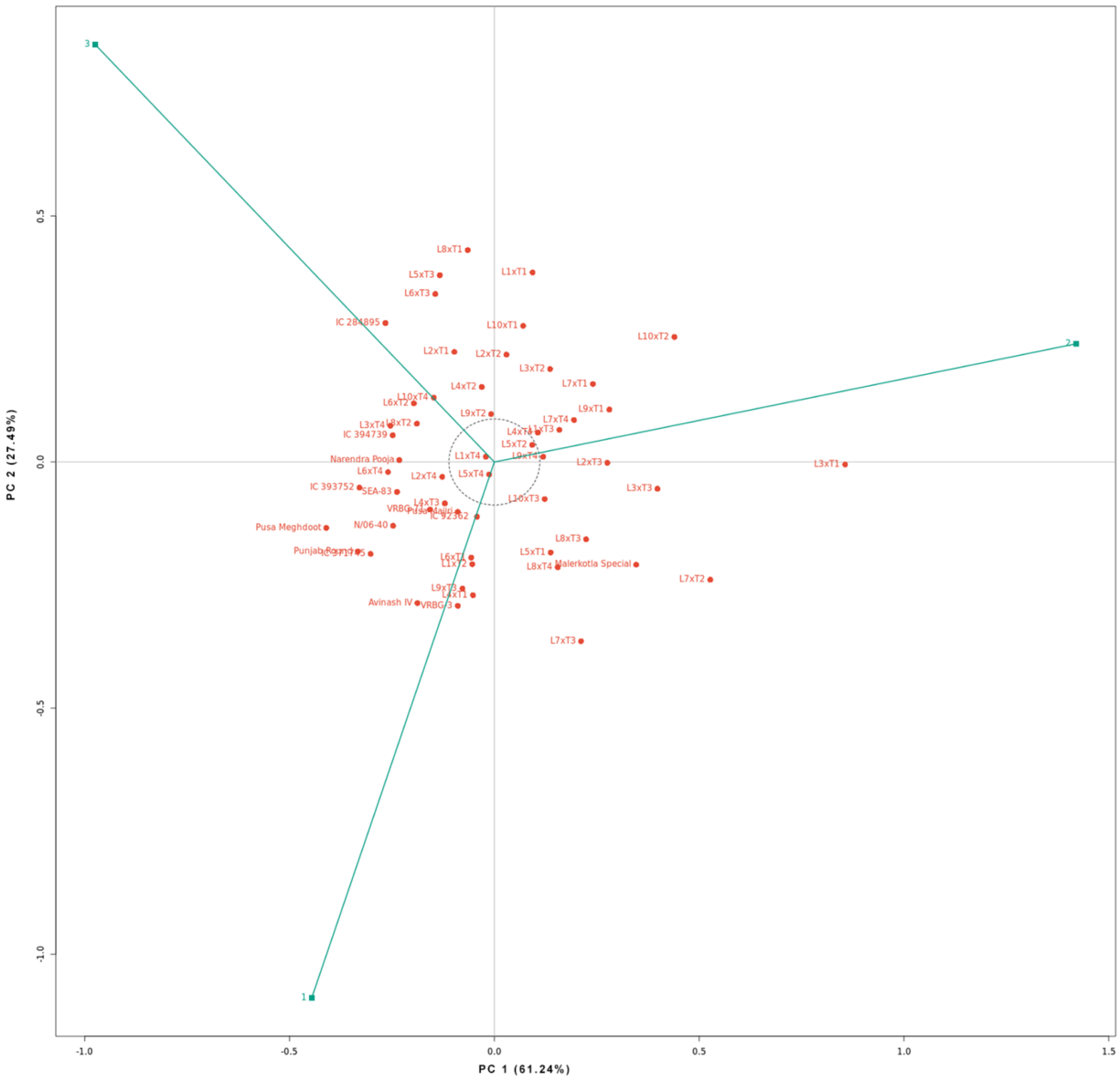


Figure 4.3: AMMI biplot 1 (PC1 vs PC2)

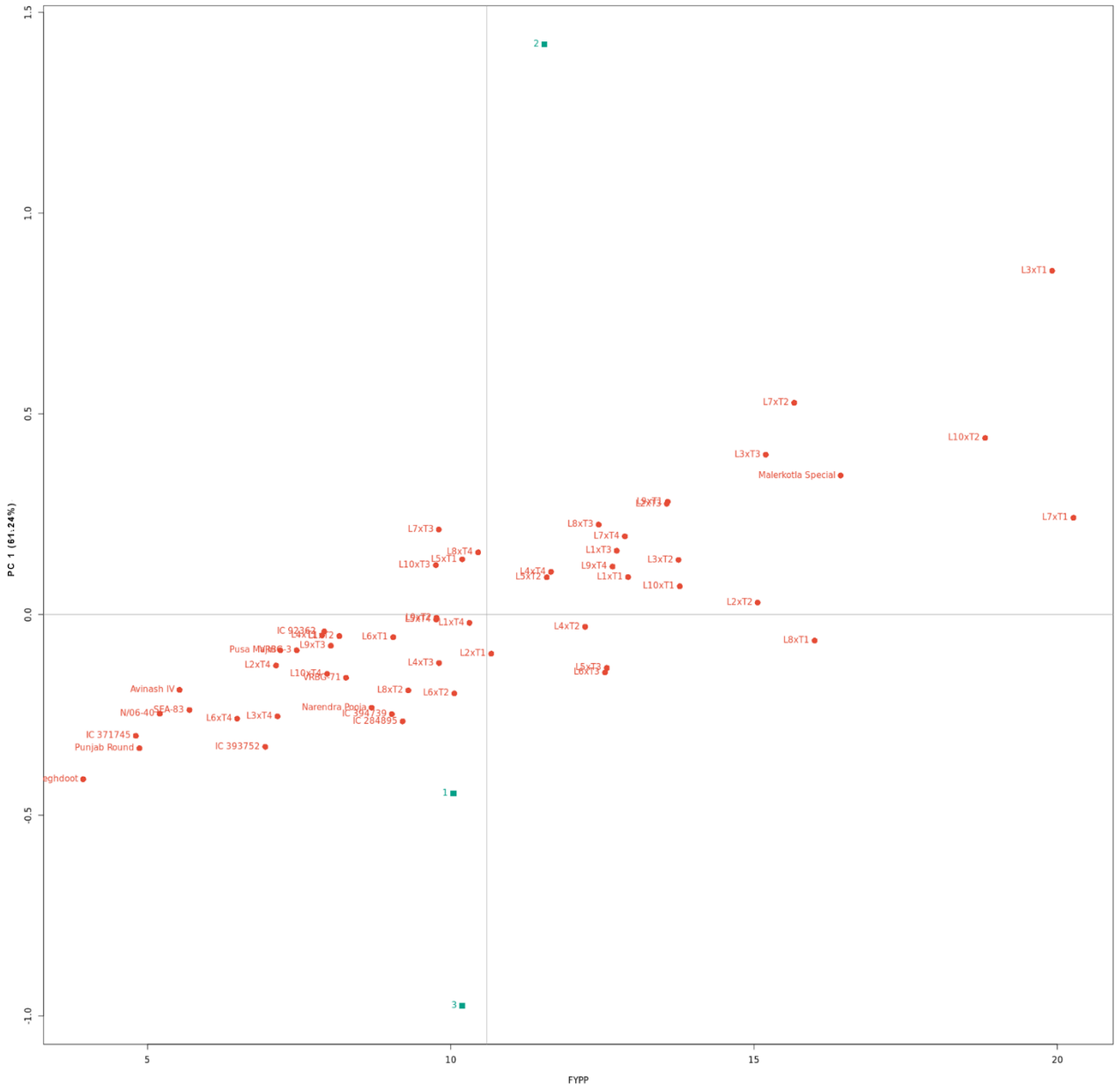


Figure 4.4: AMMI biplot 2 (PC1 vs FYPP)

4.9.3 Genotype + Genotype-by-Environment interaction

The GGE biplot, Which-won-where, (**Figure 4.5**) provides a comprehensive visual assessment of genotype performance and genotype-by-environment interactions across the tested environments. The biplot is constructed using the first two principal components (PC1 and PC2), which jointly explain a substantial proportion of the total variation in fruit yield attributed to genotype and genotype-environment interaction.

A large proportion of genotypes cluster near the origin, suggesting broad adaptation and relatively stable performance across environments. Their proximity to the plot centre indicates minimal interaction effects; these genotypes are likely to perform consistently regardless of environmental variation.

In contrast, the three environments are plotted far from the origin, at the vertices of the polygon in the upper right of the biplot. This separation signifies high discriminating ability and strong capacity for expressing genotypic differences. The environments' distance from the origin reflects their role in amplifying genotype-by-environment interaction; they are the main contributors to identifying specifically adapted genotypes.

The pattern shows that despite thorough testing, most genotypes exhibited broad rather than specific adaptation, as very few were positioned near the environments' sectors. No genotype is located near or directly associated with these discriminating environments—suggesting that none showed pronounced specific adaptation, or that those environments distinguish genotypes with greater G×E, but the genotypes themselves are generally stable.

Genotypes clustered near the origin are recommended for general cultivation due to their high and consistent fruit yield performance across diverse environments. Selection of these genotypes is suitable for unpredictable or variable growing conditions. Environments 1, 2, and 3 are highly interactive and effective for discriminating genotypic yield differences. They should be prioritised in multi-environment testing to reliably identify G×E effects and to validate stability. If any genotypes shift toward the sector closest to a discriminating environment in future trials, those would merit consideration for specific adaptation and targeted release. The absence of genotypes near the edges (environment vertices) in this biplot confirms stability among tested lines.

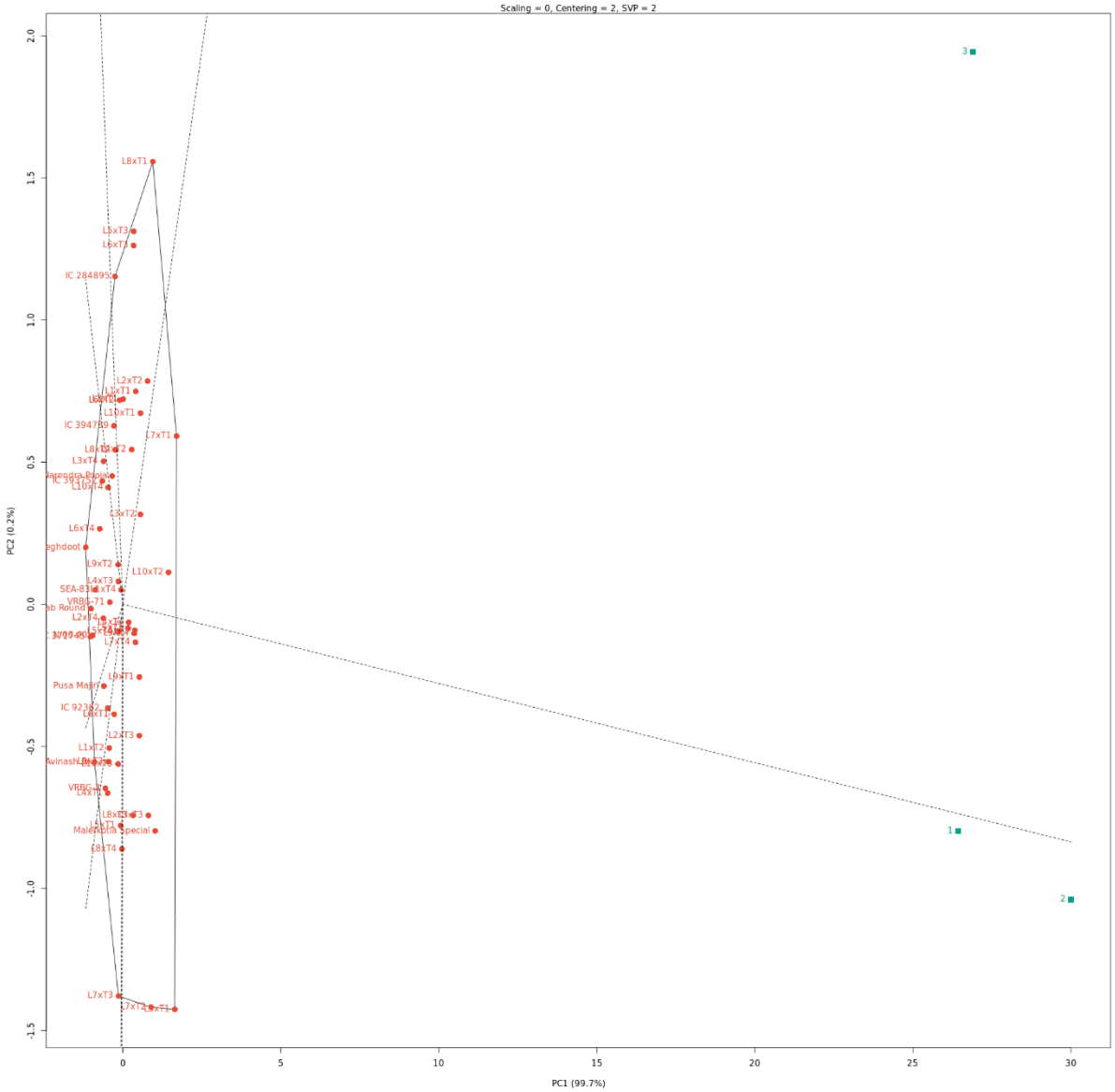


Figure 4.5: Which-won-where biplot

Discriminating Ability: Environments with longer vectors (farther from the origin) possess stronger discriminating capacity, meaning they are more effective in expressing differences among genotype performances. In this plot, Environment 3 displays the longest vector, indicating it is the most discriminating among all environments. It can best distinguish genotypic differences in fruit yield. Environment 2 also has a substantial vector length, signifying good discriminating power. Environment 1 (with the shortest vector) is less discriminating; differences among genotypes are less amplified in this setting.

Representativeness: The angle between the environment's vector and the 'average environment axis' (typically defined by the line passing through the origin and mean genotype point) shows representativeness. In GGE analysis, environments with longer vectors are more discriminating, whereas environments forming smaller angles with the average environment axis are more representative. Large angle (farther from the mean axis): The environment is less representative, possibly due to unique conditions or outlier status.

Environment 3's vector forms a relatively small angle with the horizontal axis, suggesting it is not only highly discriminating but also reasonably representative. Environment 2 maintains good discriminating ability, but appears to form a slightly larger angle, indicating moderate representativeness. Environment 1 is short and appears to form a wider angle, making it both less discriminating and less representative.

Environment 3 should be prioritized in future multi-environment trials: Its high discriminating ability will help identify genotypes with superior yields and clear differences in adaptation, while its representativeness means results will be generally applicable. Environment 2 serves as a useful secondary site: It differentiates genotypes well but may be somewhat less representative. Environment 1 is of limited usefulness for selection—its short vector and wider angle indicate it is not effective for revealing genotypic differences and is less reflective of general performance. It might be suitable for stability trials, but not for initial selection.

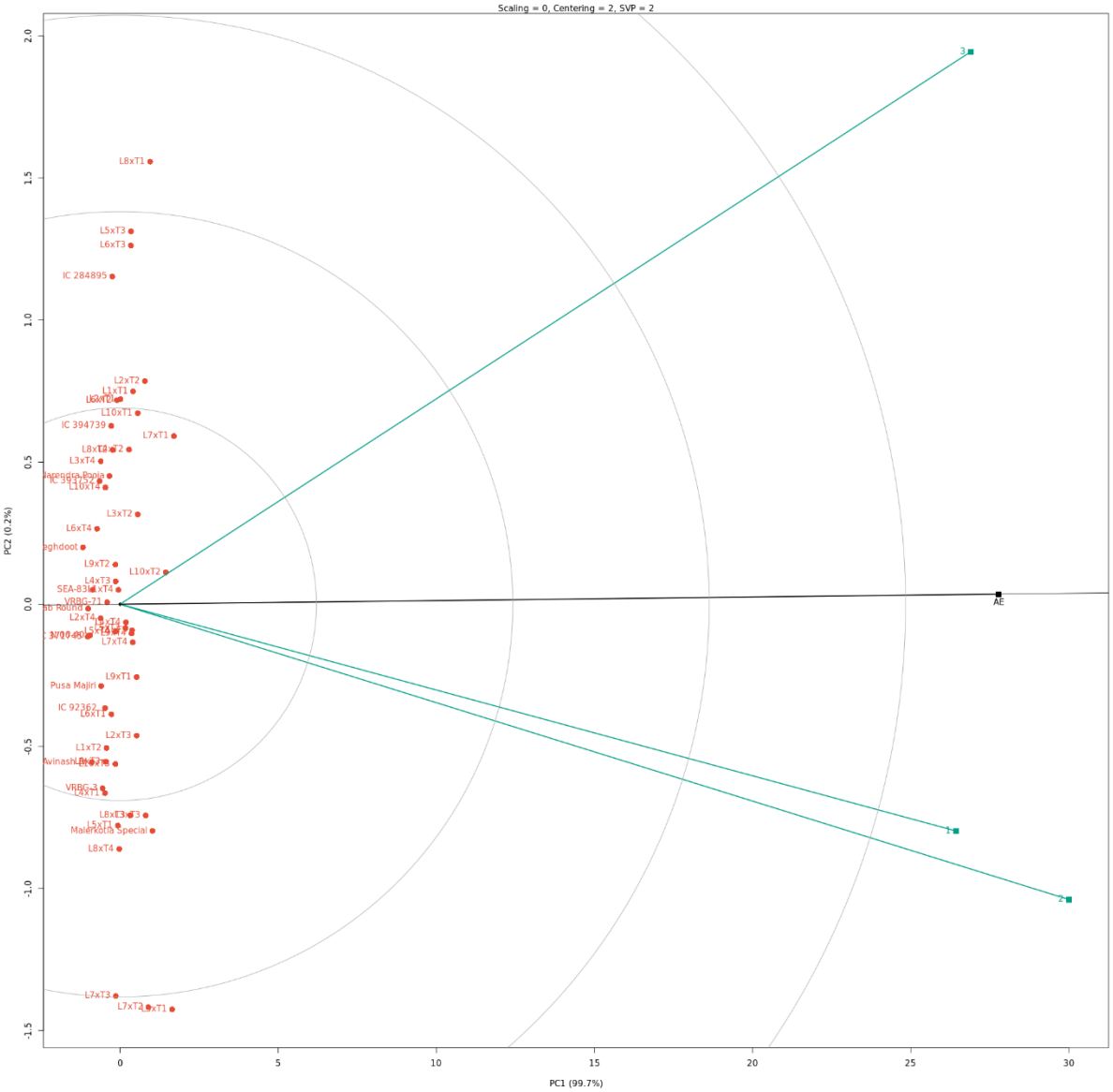


Figure 4.6: Discriminativeness vs representativeness biplot

Genotype Mean Performance: Genotypes farther to the right on the x-axis (such as L3×T1, L10×T2, L7×T1) exhibit higher mean fruit yield per plant, indicating strong productive potential. Genotypes clustered near the center of the x-axis have average yield, while those on the left have lower mean yield.

Genotype Stability: Genotypes positioned near zero on the y-axis are most stable; their performance is consistent across environments. Genotypes with large positive or negative y-axis values have greater GE interaction and thus lower stability. While these may excel in certain environments, their yield is more variable.

Combined Performance and Stability: The ideal genotype is one located far to the right (high mean yield) on the mean yield axis and close to zero on the stability axis, indicating both high productivity and minimal genotype × environment interaction. L3×T1, L7×T1, and L10×T2 lie towards the right, indicating high yield. However, their distances from the y-axis zero (both positive and negative directions) reveal varying degrees of stability; those further from zero are less stable.

Genotypes with high mean yield and stability (rightmost and $y \approx 0$) are recommended for general cultivation in diverse environments. In this plot, genotypes closest to the origin on the y-axis but far to the right (for example, any genotype with a label close to $y=0$ and with a high x-value) should be prioritized for release. Genotypes with high yield but larger absolute y-values may be suitable for targeted deployment in environments where their specific response is beneficial. If high-yielding genotypes are not stable (far on y-axis), breeders must weigh the risk of variable performance against potential high returns in favoured conditions.

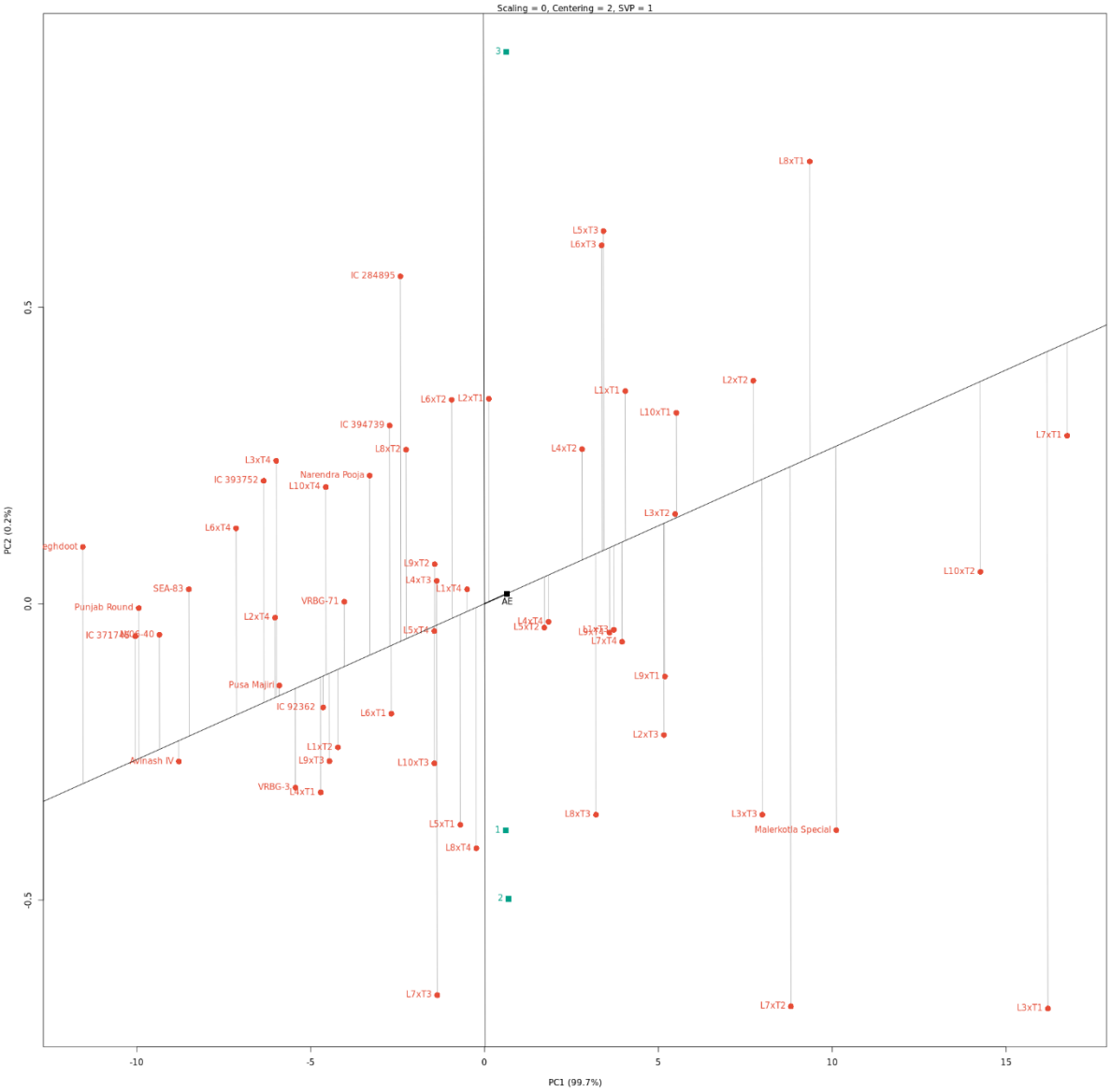


Figure 4.7: Mean vs stability biplot

Genotypes located toward the right along the ranking axis are identified as superior in mean performance. The ranking axis is usually drawn from the origin through the "ideal genotype" point, often the genotype with highest mean yield or the average environment axis. In this plot, L3×T1, L10×T2, and L7×T1 are positioned further along the ranking axis, signifying the highest average fruit yield per plant among the tested genotypes. Genotypes closer to the origin or located further away from the ranking axis are lower yielding and/or more affected by G×E interaction, showing less stable performance or specific adaptation.

The proximity of genotypes to the ranking axis also denotes stability—those closer are more consistently performing across environments, while those further away (above or below the axis) show greater levels of interaction and variable performance. Genotypes bunched around the ranking axis (e.g., L3×T1, L7×T1, L10×T2) demonstrate both high yield and reasonable stability, making them promising candidates for broad recommendation. Genotypes that diverge from the axis (e.g., on the far left or far from the axis) may have special adaptation, poor performance, or higher fluctuations in yield.

Top-performing and stable genotypes (L3×T1, L10×T2, L7×T1) should be selected for cultivation under diverse environments due to their superior mean yields and adequate stability. Genotypes positioned far from the ranking axis may be considered for specific adaptation or could warrant further investigation under particular environmental conditions. The plot assists breeders in efficiently identifying candidate genotypes for variety release, prioritizing those that offer both high productivity and reliable performance across test environments.

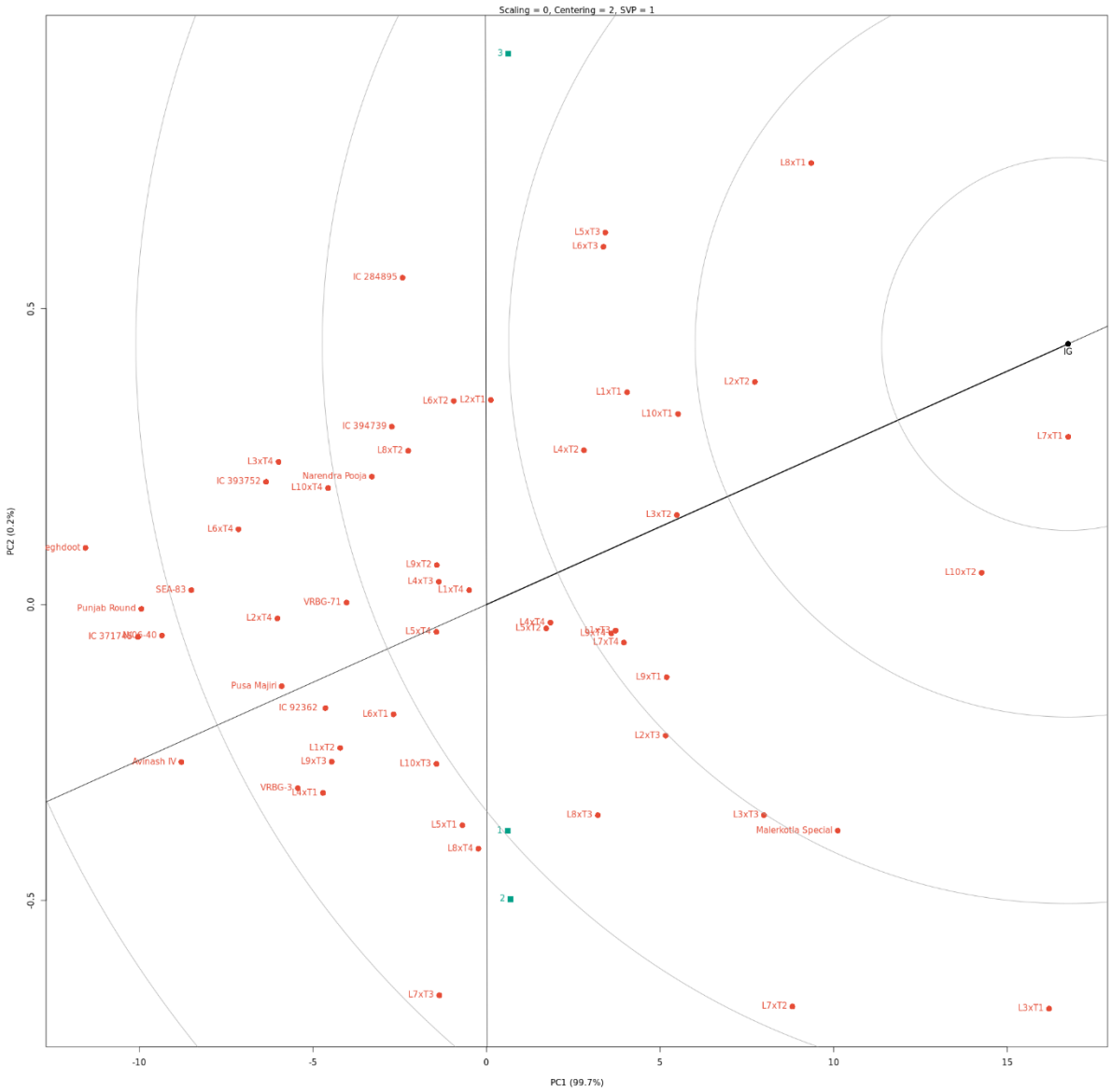


Figure 4.8: GGE biplot for ranking genotypes

The series of GGE biplot analyses provided a comprehensive understanding of genotype performance, stability, and the utility of test environments in fruit yield trials. The which-won-where biplot highlighted the presence of broadly adapted genotypes, with most performing consistently across environments and a few genotypes exhibiting specific adaptation to highly discriminating environments. The discriminating vs representativeness biplot established Environment 3 as both highly discriminating and representative, making it an optimal site for selection, while Environment 2 complemented its role and Environment 1 was found less suitable for discriminating genotypic differences.

The mean vs stability biplot identified high-yielding genotypes such as L3×T1, L10×T2, and L7×T1, illustrating that true breeding value is maximized in genotypes combining high mean yield with stability across environments. The ranking biplot visually confirmed these genotypes as top performers, showing

their superiority in both mean yield and adaptability, thereby supporting their recommendation for broad cultivation.

The integrated use of AMMI ANOVA, AMMI biplots, and GGE biplots has provided a comprehensive evaluation of fruit yield performance, stability, and genotype-by-environment interactions across diverse testing environments. The AMMI ANOVA clearly demonstrated that both environmental and genotypic effects were highly significant, while genotype × environment interaction was modest, reflecting relative consistency in genotype rankings across sites. Principal component analysis through AMMI biplots captured the majority of interaction variance with the first two axes, confirming that most tested genotypes possess stable and broad adaptation.

The AMMI biplots further identified a small group of genotypes (notably L3×T1, L10×T2, and L7×T1) with high mean fruit yield, highlighting their promise for wide-scale recommendation where both productivity and yield stability are essential. Simultaneously, the GGE biplots provided nuanced visual tools to differentiate genotypes and environments: the which-won-where biplot confirmed broad adaptation among the majority of genotypes, with few demonstrating sector-specific adaptation; the discriminating vs representativeness biplot highlighted Environment 3 as the optimal location for distinguishing genotypic performance; and the mean vs stability and ranking biplots reinforced the selection of genotypes that combine yield potential with consistency.

The stability analysis using AMMI and GGE biplot approaches revealed that most genotypes exhibited relatively stable performance across environments, while a few hybrids such as L3×T1, L10×T2, and L7×T1 combined high yield with acceptable stability. These results reinforce the earlier findings from heterosis and combining ability analyses, where the same hybrids showed superior performance for yield and yield-contributing traits. Such consistency across different analytical approaches strengthens the reliability of these hybrids as promising candidates for future breeding programs and possible commercial exploitation.

Similar application of AMMI and GGE biplot analyses for evaluating genotype stability and adaptability have been widely reported in vegetable crops and cucurbits (Yan and Kang, 2003; Gauch 2013; Singh et al, 2023b; Jat et al, 2024)

Table 4.21: Top 10 stable genotypes

Rank	Genotype	Key Attributes
1	L3xT1	Highest mean yield, broadly adapted, stable
2	L10xT2	High yield, good stability, consistent ranking
3	L7xT1	High yield, stable across environments
4	L7xT3	High performance, moderate stability
5	L5xT2	Above-average yield and adaptability
6	L8xT1	High yield, good consistency
7	L6xT1	Well-adapted, stable performer
8	L8xT2	High mean yield, moderate stability
9	L10xT1	Noteworthy yield, reasonable stability
10	L7xT2	Consistent across most environments

CHAPTER 5

Summary and Conclusion

The present investigation was undertaken to comprehensively address the stated objectives through the evaluation of genetic diversity, heterosis, combining ability, and trait expression in bottle gourd under varied conditions.

The study began with an assessment of genetic diversity among the selected genotypes using Mahalanobis' D^2 statistic, which revealed substantial variability across the studied traits. Cluster analysis grouped the 38 genotypes into seven distinct clusters, indicating the presence of wide genetic divergence. Cluster V contained eight genotypes, while clusters II and III each comprised four genotypes. The inter-cluster distance ranged from 14.05 to 30.21, with the highest divergence observed between clusters IV and VII, suggesting excellent scope for selecting genetically diverse parents to maximize heterotic response. Notably, genotypes from clusters V and VII combined earliness with desirable fruit morphology and high yield potential, making them valuable for targeted hybridization.

The heterosis analysis, performed with respect to standard checks, demonstrated significant heterobeltiosis, standard heterosis, and economic heterosis for key traits, including days to male flowering (DMF), days to female flowering (DFF), vine length, fruit length, average fruit weight, and fruit yield per plant. The magnitude and direction of heterosis suggested that both additive and non-additive genetic effects contributed to trait expression. Among crosses, **L5×T1** exhibited the highest mid-parent heterosis for fruit yield per plant (54.82%), **L4×T1** recorded the maximum heterobeltiosis (42.17%) for the same trait, and **L1×T1** showed the greatest economic heterosis (38.95%), indicating strong commercial potential.

The line × tester analysis further elucidated the nature of gene action. Among the lines, **L1 (IC 284895)** exhibited high general combining ability (GCA) effects for early flowering (-2.81 days), fruit length (3.84 cm), and fruit yield per plant (2.61 kg). **L8 (IC 371745)** and **L9 (Avinash IV)** also recorded strong GCA for vine length and average fruit weight. Among testers, **T3 (Narendra Pooja)** and **T4 (Punjab Round)** consistently contributed favorable GCA effects for yield-related traits.

Specific combining ability (SCA) effects highlighted promising hybrid combinations. **L10×T4** exhibited highly desirable negative SCA effects for days to flowering (-3.15 for D1F and -2.94 for DFF) and vine length (-12.16 cm), indicating early maturity and manageable plant growth.

L5×T2 showed high positive SCA for fruit length (5.73 cm), **L6×T4** for average fruit weight (116.42 g), and **L7×T4** for fruit flesh thickness (2.14 mm), all pointing to the role of dominance variance and the potential to exploit non-additive gene actions for hybrid improvement.

The genotype × environment interaction, analyzed using the AMMI model, revealed highly significant effects of environment and genotype on yield. PC1 accounted for 61.24% of the interaction sum of squares, while PC2 explained an additional 23.47%. The AMMI biplots identified **L1×T1**, **L5×T1**, and **L4×T1** as high-yielding and stable across test environments, making them ideal candidates for broad adaptation.

By integrating findings from genetic diversity analysis, heterosis estimation, combining ability evaluation, and stability assessment, the study fully achieved its objectives and provided a comprehensive framework for bottle gourd improvement. The identified superior parents (**L1, L8, L9, T3, and T4**), promising cross combinations (**L5×T1, L4×T1, L1×T1, L5×T2, L6×T4, and L7×T4**), and stable high-yielding hybrids form a strong foundation for advancing future breeding programs.

Conclusion

1. Genetic Diversity

Genetic diversity analysis using Mahalanobis' D^2 statistics revealed substantial variability among the 38 bottle gourd genotypes, which were grouped into seven clusters. The large inter-cluster distances, particularly between clusters IV and VII, indicated the presence of wide genetic divergence. Genotypes from these clusters can therefore be utilized as promising parents in hybridization programmes to exploit heterosis.

2. Heterosis

Significant heterosis was observed for fruit yield and several yield-contributing traits. The hybrids L5×T1, L4×T1, and L1×T1 recorded the highest economic heterosis for fruit yield per plant, indicating strong hybrid vigour. These hybrids demonstrate the potential of heterosis breeding for enhancing productivity in bottle gourd.

3. Combining Ability

Combining ability analysis revealed both additive and non-additive gene effects governed the inheritance of most traits. Lines IC 284895 (L1), IC 371745 (L8) and Avinash IV (L9) were identified as good general combiners for yield related traits, while crosses such as L5×T2,

L6×T4, and L7×T4 exhibited high specific combining ability. These parental lines and hybrids may be effectively used in future breeding programs.

4. Gene Action

The predominance of non-additive gene action for several traits (GCA/SCA ratio < 1) suggests that heterosis breeding would be effective strategy for improving fruit yield and its associated characters in bottle gourd.

5. Stability and G×E Interaction

Stability analysis using AMMI and GGE biplot approaches revealed that hybrids L1×T1, L5×T1 and L4×T1 combined high yield with stable performance across environments. These hybrids exhibited broad adaptability across different sowing dates and therefore hold promise for cultivation in diverse agro-climatic conditions.

The results of this study provide useful information for bottle gourd breeding programmes. The identification of genetically diverse parental lines and superior hybrids can facilitate the development of high-yielding hybrid cultivars. Hybrids such as L5×T1, L4×T1, and L1×T1 demonstrated superior yield performance and stability across environments and therefore may serve as promising candidate for further multilocation trials and potential commercial release. Additionally, the superior general combiners identified in this study can be used in future breeding programmes to develop improved parental lines and hybrids.

Although the present investigation provided valuable insights into genetic diversity, heterosis and combining ability and stability in bottle gourd, the study was conducted across three environments within single geographical location. Evaluation of the identified hybrids across multiple agro-climatic zones and seasons would further validate their stability and adaptability. Additionally, the present study relied primarily on morphological and yield traits; integration of molecular markers could provide deeper insights into the genetic basis of trait inheritance.

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