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Genetic Architecture of Green Fruit Yield and Related Traits in Elite Selections from Multi-Parent Derived Chilli Populations Based on Skewness and Kurtosis

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Understanding the genetic architecture of yield and its component traits is essential for developing effective selection strategies in chilli (*Capsicum annuum* L.). Multi-parent (MP)-derived populations provide opportunities for generating broad genetic variability through the recombination of alleles from several founder parents. The present investigation was undertaken to characterise the frequency distribution and infer the nature of gene action governing yield and yield-related traits in elite selections derived from superior eight-parent MP populations. Five superior MP-derived populations, D4 × D3, D4 × D2, D5 × D2, D6 × D2 and D7 × D2, identified in an earlier assessment of ten MP-derived populations, were used. Observations were recorded for average fruit weight, average fruit number plant^{-1}, average fruit length, average fruit width and green fruit yield plant^{-1}. Skewness and kurtosis coefficients were estimated to assess the nature of the distribution and infer the possible genetic control of the traits. Most traits exhibited relatively low-magnitude skewness, indicating near-symmetrical distributions, although the direction of skewness varied among populations and traits. Negative skewness was predominant for average fruit weight,

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particularly in D4 × D3, D4 × D2, D5 × D2 and D6 × D2, suggesting duplicate-type digenic epistasis involving increasing effects. In contrast, positive skewness predominated for fruit number and green fruit yield, indicating complementary-type epistasis involving decreasing effects. Most trait-population combinations showed platykurtic distributions, suggesting the involvement of a relatively large number of genes. However, fruit width in D5 × D2 and fruit length in D6 × D2 showed leptokurtic distributions, indicating relatively fewer genes contributing to phenotypic variation for these traits in those populations. The results demonstrate that the genetic architecture of yield and its component traits varies among MP-derived populations and highlight the value of elite MP-derived progenies as sources of useful genetic variation for chilli improvement.

Keywords: Chilli; multi-parent populations; green fruit yield; skewness; kurtosis.

1. Introduction

Chilli (*Capsicum annuum* L.) is one of the most important vegetable and spice crops cultivated worldwide and is valued for its fresh and dried fruits, pungency, colour and diverse industrial uses (Ali et al., 2025; Pallerla et al., 2021; Alonso-Villegas et al., 2023). Green fruit yield is a major breeding objective; however, its improvement is challenging because yield is a complex quantitative trait influenced by several component traits and environmental factors (Anilkumar et al., 2019). Fruit weight, number of fruits plant^{-1}, fruit length and fruit width contribute substantially to yield and are themselves quantitatively inherited. Recent evaluation of chilli genotypes likewise reported substantial variability in fruit weight, fruit number and green fruit yield, reinforcing the relevance of these traits to selection for yield improvement (Hulagannavar et al., 2024).

Conventional breeding approaches based on biparental populations provide opportunities for recombination between two parental genomes. However, the genetic diversity captured in such populations is inherently restricted by the alleles contributed by the two parents. Multi-parent populations provide an alternative breeding strategy by combining genetic contributions from several founders and thereby increasing the opportunity for recombination and generation of novel allele combinations (Arrones et al., 2020; Ullah et al., 2026; Scott et al., 2020). Such populations are particularly useful for quantitative trait improvement because they can capture a wider spectrum of alleles and facilitate the generation of transgressive segregants. Recent MAGIC studies in peanut and chickpea further demonstrate the utility of multi-parent designs as genetically diverse resources for dissecting complex agronomic traits (Thompson et al., 2025; Akinlade et al., 2025).

The breeding potential of multi-parent-derived populations in chilli has recently been demonstrated. Siddu et al. (2025) evaluated ten eight-parent MP-derived populations and identified D5 × D2, D4 × D2 and D6 × D2 as populations with high breeding potential. These findings demonstrate the usefulness of MP-derived populations for generating superior segregants and provide a basis for advancing selected plants for further genetic evaluation. A recent chilli segregating-population study likewise reported associations of fruit weight, fruit number and fruit length with yield, indicating their relevance to selection decisions (Nayak et al., 2025).

The frequency distribution of quantitative traits provides useful information about their underlying genetic architecture. Skewness and kurtosis are particularly useful statistical parameters for interpreting deviations from normality in segregating populations. Fisher et al. (1932) demonstrated that skewness can provide information on the nature of epistatic interactions, whereas kurtosis has been used to infer the relative number of genes contributing to quantitative variation (Robson, 1956). Although skewness and kurtosis have been used to characterise genetic architecture in chilli, their application to elite selections derived from superior MP populations can provide additional information for determining which populations and traits may respond favourably to selection. A recent study in chilli demonstrated that MP populations exhibited differential skewness and kurtosis patterns for average fruit weight, fruits plant^{-1} and green fruit yield, emphasising the importance of population-specific genetic architecture in breeding decisions (Channabasava et al., 2025). However, the frequency-distribution-based genetic architecture of yield and its component traits within elite progenies selected from previously identified superior eight-parent chilli MP populations remains insufficiently characterised. Therefore, the present study was undertaken to investigate the frequency distribution and infer the nature of gene action governing yield and yield-related traits in elite selections derived from five superior eight-parent MP-derived populations of chilli.

2. Materials and Methods

2.1 Experimental Material

The experimental material comprised five superior eight-parent multi-parent-derived populations selected from an earlier study that evaluated the breeding potential of ten MP-derived populations (Siddu et al., 2025). The five populations selected for the present investigation were D4 × D3, D4 × D2, D5 × D2, D6 × D2 and D7 × D2. Seeds of the selected MP-derived populations were obtained from the Hot Pepper Improvement Unit, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Bengaluru, India.

Within each of the five superior MP-derived populations, ten elite plants were identified based on their superior performance for yield and yield-related traits. Seeds harvested from these selected plants were advanced and evaluated in the present investigation. Thus, the experimental material represented progenies derived from 50 elite selections, comprising ten selections from each of the five MP-derived populations.

Table 1. Multi-parent derived populations selected based on breeding potential and their parentage

MP-derived population	Parentage
D4 × D3	[(LG 174 × BD) × (Vang × CA14)] × [(UA × PJ) × (PS × CMS 6B)]
D4 × D2	[(LG 174 × BD) × (Vang × CA14)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]
D5 × D2	[(LG 174 × BK) × (Vang × CA14)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]
D6 × D2	[(GB × BK) × (Vang × LG 181)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]
D7 × D2	[(GB × CA14) × (Vang × LG 181)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]

Abbreviations: BD – Byadgi Dabbi; GB – Gouribidanur; UA – Utkal Awa; BK – Byadgi Kaddi; JL – Japani Long; PJ – Phule Jyothi; PS – Pusa Sadabahar; Vang – Vangara; 6B – CMS 6B; 8B – CMS 8B; 10B – CMS 10B; PC1 – Pant C1; CA14 – CA 14; LG174 – LG 174; LG181 – LG 181

2.2 Field Evaluation

Forty-day-old seedlings of each progeny line were transplanted separately in contiguous blocks during the rainy season of 2020 at the experimental farm of the University of Agricultural Sciences, Bengaluru. The progeny rows were planted at a spacing of 75 cm between rows and 45 cm between plants. Recommended agronomic practices were followed throughout the crop growth period to maintain a healthy and uniform crop stand. The progeny blocks were arranged sequentially in the field to maintain the identity of the respective MP-derived populations throughout the evaluation.

2.3 Trait Recording

Observations were recorded on individual plants for five quantitative traits: average fruit weight, average fruit number plant^{-1}, average fruit length, average fruit width and green fruit yield plant^{-1}.

2.4 Estimation and Interpretation of Skewness and Kurtosis

Frequency distributions of the five quantitative traits were characterised using coefficients of skewness and kurtosis. These statistics were used to assess deviations from normality and to infer the probable nature of genetic control of the traits. The genetic expectation of skewness was interpreted according to Fisher et al. (1932) (Table 2). Kurtosis was interpreted following Robson (1956) (Table 3). Coefficients of skewness and kurtosis were estimated using R software, version 3.6.3. The statistical analyses were performed using appropriate statistical functions and libraries, including Performance Analytics, following the procedures described by Snedecor and Cochran (1989).

Table 2. Quantitative genetic interpretation of skewness

Type of skewness	Interpretation
Positive skewness	Complementary type of digenic epistasis between genes with decreasing effects.
Negative skewness	Duplicate type of digenic epistasis between genes with increasing effects.

Table 3. Quantitative genetic interpretation of coefficients of kurtosis

Coefficients of kurtosis	Type of distribution	Interpretation
> 3	Leptokurtic	Fewer number of genes control the trait
3	Mesokurtic	Moderate number of genes control the trait
< 3	Platykurtic	Large number of genes control the trait.

3. Results and Discussion

3.1 Frequency Distribution and Skewness

The estimates of skewness and kurtosis for average fruit weight, average fruit number plant^{-1}, average fruit length, average fruit width and green fruit yield plant^{-1} in the five MP-derived populations are presented in Table 4. The results revealed considerable variation in the shape of frequency distributions among populations and traits, demonstrating that the genetic architecture of quantitative traits was not uniform across the MP-derived populations.

Average fruit weight showed negative skewness in four of the five MP-derived populations, with values ranging from -0.352 in D4 × D3 to -0.753 in D5 × D2. The only exception was D7 × D2, which showed a positive skewness of 0.277. The predominance of negative skewness for fruit weight suggests duplicate-type digenic epistasis involving genes with increasing effects in most of the populations (Kumar et al., 2020; Prasanna et al., 2024). Such distributions indicate that selection for higher fruit weight may involve interactions among favourable alleles rather than simple additive inheritance.

Average fruit number plant^{-1} exhibited positive skewness in all five populations, ranging from 0.164 in D5 × D2 to 1.027 in D4 × D3. The consistently positive skewness suggests the predominance of complementary-type epistatic interactions (Anu et al., 2022). The relatively consistent direction of skewness across populations indicates that fruit number may be influenced by similar interaction patterns despite differences in founder combinations.

Fruit length showed contrasting distribution patterns among the MP-derived populations. D4 × D3 and D4 × D2 showed negative skewness, whereas D5 × D2, D6 × D2 and D7 × D2 showed positive skewness. The most pronounced skewness was observed in D6 × D2, with a value of 9.235. This exceptionally high positive skewness indicates a highly asymmetric distribution in this population and suggests a strong complementary-type interaction or the presence of a small number of individuals with exceptionally high fruit length (Dinesh et al., 2018).

Fruit width also displayed population-specific patterns. D4 × D3, D5 × D2, D6 × D2 and D7 × D2 showed positive skewness, whereas D4 × D2 showed slightly negative skewness (-0.316). The highest positive skewness was recorded in D5 × D2 (1.398), suggesting a stronger contribution of complementary-type interactions to fruit width in this population (Sumathi et al., 2018).

Green fruit yield plant^{-1} exhibited positive skewness in all five populations, with values ranging from 0.257 in D5 × D2 to 0.893 in D6 × D2. The consistency of positive skewness across populations is particularly important from a breeding perspective because it suggests a similar underlying pattern of complementary epistasis for green fruit yield (Shamini & Selvi, 2022). The presence of positive skewness in yield indicates that favourable combinations of genes may contribute to superior yield expression, and recombination followed by selection may therefore be useful for recovering desirable genotypes.

The predominance of positive skewness for fruit number and green fruit yield is consistent with previous observations in chilli MP populations, where positive skewness was associated with complementary epistatic interactions (Channabasava et al., 2025).

Table 4. Estimates of skewness and kurtosis for yield and yield-related traits in five superior MP-derived populations of chilli

Magic populations	Fruit weight		Fruit number		Fruit length		Fruit width		Green fruit yield	
	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis
D4 D3	-0.352	-1.388	1.027	0.135	-0.867	1.737	0.184	-0.380	0.639	-0.302
D4 D2	-0.652	-0.482	0.828	0.242	-0.314	0.166	-0.316	2.686	0.836	0.627
D5 D2	-0.753	0.076	0.164	-0.836	0.282	1.949	1.398	3.626	0.257	-0.943
D6 D2	-0.530	-0.203	0.955	1.081	9.235	87.730	0.335	0.088	0.893	0.558
D7 D2	0.277	-0.256	1.020	1.190	0.285	-0.280	0.239	-0.282	0.336	-0.470

Abbreviations: BD – Byadgi Dabbi; GB – Gouribidanur; UA – Utkal Awa; BK – Byadgi Kaddi; JL – Japani Long; PJ – Phule Jyothi; PS – Pusa Sadabahar; Vang – Vangara; 6B – CMS 6B; 8B – CMS 8B; 10B – CMS 10B; PC1 – Pant C1; CA14 – CA 14; LG174 – LG 174; LG181 – LG 181

3.2 Kurtosis and the Probable Number of Genes Controlling the Traits

Kurtosis values showed greater variation among traits and populations than skewness. Most of the trait-population combinations recorded kurtosis values below 3, indicating platykurtic distributions and suggesting the involvement of a relatively large number of genes in the inheritance of these traits (Zeng et al., 2026) (Table 4).

For average fruit weight, all five populations exhibited platykurtic distributions, with kurtosis values ranging from -1.388 in D4 × D3 to 0.076 in D5 × D2. This indicates that fruit weight is likely controlled by a relatively large number of genes in the elite selections derived from these MP populations. The absence of a leptokurtic distribution across populations suggests that fruit weight is a highly polygenic trait, and improvement through selection may require the evaluation of larger populations and/or repeated selection cycles.

Average fruit number plant^{-1} also showed platykurtic distributions in all five populations, with kurtosis values ranging from -0.836 in D5 × D2 to 1.190 in D7 × D2. These results indicate that a relatively large number of genes contribute to variation in fruit number. The broad distribution observed for this trait may provide greater opportunity for selection, particularly in populations where favourable allelic combinations have been generated through multi-parent recombination.

For fruit length, four populations—D4 × D3, D4 × D2, D5 × D2 and D7 × D2—showed platykurtic distributions. In contrast, D6 × D2 exhibited an exceptionally high kurtosis value of 87.730, indicating a strongly leptokurtic distribution. This result suggests that phenotypic variation for fruit length in D6 × D2 was concentrated around a narrow portion of the distribution with a limited number of extreme observations (Owusu et al., 2022). Under the genetic interpretation adopted here, this may indicate the contribution of relatively fewer genes of larger effect in this population. The extremely high kurtosis in D6 × D2 should, however, be interpreted cautiously. Such a large value may also arise from extreme observations, a restricted sample size or other distributional characteristics. Therefore, the inference of a smaller number of genes should be considered as a genetic indication rather than direct evidence of a specific number of loci.

Fruit width showed predominantly platykurtic distributions. D4 × D3, D4 × D2, D6 × D2 and D7 × D2 recorded kurtosis values below 3, whereas D5 × D2 recorded a value of 3.626 and therefore exhibited a leptokurtic distribution. The result for D5 × D2 suggests that relatively fewer genes may be contributing to the observed variation for fruit width in this population compared with the other MP-derived populations.

Green fruit yield plant^{-1} exhibited platykurtic distributions in all five populations, with kurtosis values ranging from -0.943 in D5 × D2 to 0.627 in D4 × D2. This consistent pattern indicates that green fruit yield is controlled by a relatively large number of genes. The result agrees with the quantitative nature of yield and emphasises the importance of exploiting broad recombination and selecting superior individuals from large segregating populations.

The predominance of platykurtic distributions observed in the present investigation is in agreement with previous studies in chilli MP populations, in which broad, platykurtic distributions were reported for important quantitative traits and interpreted as evidence for the involvement of numerous genes (Channabasava et al., 2025).

3.3 Population-specific Genetic Architecture

An important feature of the present investigation was the clear population-specific nature of skewness and kurtosis. Although all five populations originated from eight-parent combinations, the specific founder combinations differed considerably. Consequently, the frequency distributions of individual traits differed among populations.

D4 × D3 showed negative skewness for fruit weight and fruit length, but positive skewness for fruit number, fruit width and green fruit yield. All traits showed platykurtic distributions. This combination indicates the presence of broad genetic variation and trait-specific epistatic effects, providing opportunities for simultaneous selection for yield and its components.

D4 × D2 exhibited negative skewness for fruit weight, fruit length and fruit width, whereas fruit number and green fruit yield showed positive skewness. The relatively high positive skewness for green fruit yield (0.836) suggests the presence of complementary interactions that may favour the accumulation of desirable alleles for yield.

D5 × D2 showed negative skewness for fruit weight and positive skewness for the remaining four traits. Notably, fruit width exhibited a leptokurtic distribution (3.626), while the other traits were platykurtic. The combination of positive skewness and leptokurtosis for fruit width suggests a relatively restricted genetic architecture in this population for this particular trait, potentially making selection for fruit width comparatively more straightforward than for highly polygenic traits.

D6 × D2 was particularly distinctive because of the extremely high positive skewness (9.235) and kurtosis (87.730) for fruit length. This indicates a highly non-normal distribution and suggests that fruit length in this population may be governed by a distinct genetic architecture compared with the other populations. The same population showed positive skewness for fruit number, fruit width and green fruit yield, while fruit weight showed negative skewness. Thus, D6 × D2 combines different types of gene action across component traits.

D7 × D2 showed positive skewness for all five traits, although the magnitude of skewness was relatively moderate. All traits were platykurtic. This consistent positive skewness suggests that complementary-type epistatic interactions may be particularly important in this population. The broad, platykurtic distributions further suggest the involvement of numerous genes, providing scope for recombination and selection.

4. Conclusion

The five elite eight-parent MP-derived chilli populations displayed distinct frequency-distribution patterns for green fruit yield and related traits, indicating that the probable genetic architecture was population- and trait-specific. Negative skewness for average fruit weight in most populations was consistent with duplicate-type digenic epistasis involving increasing effects, whereas the uniformly positive skewness for fruit number and green fruit yield indicated complementary-type epistatic interactions involving decreasing effects. The predominance of platykurtic distributions across trait–population combinations suggested that most traits were influenced by relatively large numbers of genes. In contrast, the leptokurtic distributions for fruit width in D5 × D2 and fruit length in D6 × D2 indicated relatively fewer contributing genes for these specific combinations. The exceptionally high skewness and kurtosis recorded for fruit length in D6 × D2 should be interpreted cautiously because the distribution was strongly non-normal. Overall, the observed variation among MP-derived populations supports their continued evaluation as sources of useful recombination and genetic variation for selection of yield and yield-related traits in chilli improvement.

5. Limitation

The study evaluated progenies from 50 elite selections under a single rainy-season field evaluation at one experimental location. Consequently, the observed distribution patterns may be specific to the evaluated material and environment. In addition, inferences regarding gene action and the probable number of contributing genes were derived from skewness and kurtosis rather than direct genetic or molecular mapping.

Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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