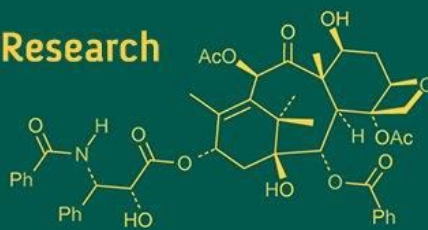
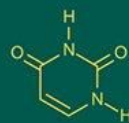


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Frequency distribution and gene action of yield and yield related traits in F₂ populations of Chilli (*Capsicum annuum* L.) derived from varying number of parents

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Abstract

Understanding the nature of variability and gene action governing quantitative traits in segregating generations is crucial for effective selection in crop improvement programmes. The present investigation was undertaken to study the frequency distribution pattern, skewness and kurtosis of yield and yield-related traits in F₂ segregating populations of chilli (*Capsicum annuum* L.) derived from crosses involving varying number of parents. The experimental material comprised nine F₂ populations derived from single, three-way, double and multi-parental crosses. The experiment was conducted during Rabi-summer 2020-21 at the Department of Genetics and Plant Breeding, UAS, Bengaluru. Frequency distribution analysis revealed considerable variation among segregating populations for all traits studied. Predominantly positive skewness coupled with platykurtic distribution was observed for most traits across populations, indicating the involvement of a large number of genes with significant non-additive gene action. Yield and its component traits exhibited differential distribution patterns depending on parental complexity, suggesting enhanced recombination and genetic variability in multi-parental populations. The results indicate that segregating populations derived from higher parental combinations offer greater scope for selection and genetic improvement in chilli breeding programmes.

Keywords: Chilli, F₂ population, frequency distribution, skewness, kurtosis, gene action, multi-parental crosses

Introduction

Chilli (*Capsicum annuum* L.) is one of the most important vegetable and spice crops cultivated extensively across the world for its pungent fruits, nutritional value and economic significance. The crop is widely used in fresh, dried and processed forms and constitutes an essential component of human diets owing to its richness in vitamins, antioxidants and bioactive compounds such as capsaicinoids (Bosland & Votava, 2012; Wahyuni *et al.*, 2013) [1, 16]. In countries like India, chilli plays a crucial role in agricultural income and export earnings, besides supporting the livelihoods of a large farming community (Spices Board of India, 2024; Verma *et al.*, 2025) [14, 15]. Despite its economic importance, improvement of yield and yield-related traits in chilli remains a major breeding objective. These traits are inherently complex, governed by polygenic inheritance and considerably influenced by non-additive gene action and environmental factors, thereby limiting the effectiveness of simple selection strategies (Singh *et al.*, 2025 and Channabasava *et al.*, 2025) [11, 2]. Recent studies have also reported significant genetic variability for yield and other economic traits in chilli germplasm, indicating a rich reservoir of diversity that can be exploited for crop improvement (Singh *et al.*, 2025; Jagtap *et al.*, 2025) [11, 5].

Segregating populations, particularly the F₂ generation, provide an excellent opportunity to study the distribution of quantitative traits and to elucidate the underlying genetic architecture controlling their expression. Frequency distribution analysis, together with estimates of skewness and kurtosis, offers valuable insight into the nature of gene action, the number of genes involved and the extent of epistatic interactions governing quantitative traits

(Wright, 1921; Mather & Jinks, 1982; Falconer & Mackay, 1996) [17, 7, 3]. Fisher *et al.*, (1932) [4] laid the theoretical foundation for using distribution parameters to infer genetic causes of variation, while subsequent studies by Robson (1956) [9] and Pooni *et al.*, (1977) [8] demonstrated the practical usefulness of skewness and kurtosis in understanding polygenic inheritance and gene interactions in segregating populations.

In recent years, the use of crosses involving varying numbers of parents, such as three-way, double and multi-parental crosses, has gained importance in crop improvement programmes due to their greater potential to generate broader genetic variability and transgressive segregants compared to conventional bi-parental crosses. Such crosses facilitate enhanced recombination and allow more effective exploitation of non-additive gene effects. However, information on the frequency distribution patterns and associated gene action of yield and yield-related traits in segregating populations derived from varying parental combinations in chilli is limited.

Therefore, the present study was undertaken to assess the frequency distribution, skewness and kurtosis of yield and yield-related traits in F₂ populations of chilli derived from crosses involving varying numbers of parents, with the objective of inferring the nature of gene action governing these traits and identifying the potential of complex crosses for effective selection in chilli breeding programmes.

Materials and Methods

Experimental Material

The experimental material consisted of nine F₂ segregating populations of chilli (*Capsicum annuum* L.) derived from crosses involving different numbers of parents. Details of the parental lines and the cross combinations used for generating the segregating populations are presented in Table 1.

Table 1: Nine Segregating populations derived from Crosses involving varying number of parents

Segregating populations derived from			
Single crosses	Three-way crosses	Double crosses	8-way crosses
GB × Ti	(BK × CMS 8B) × Ti	(PC1 × CMS 10B) × (JL × CMS 8B)	D1 × D2
PC1 × BK	(GB × CMS 7B) × CMS 8B	(CMS 8B × GB) × (Ti × CMS 7B)	D3 × D2
CMS 8B × GB			

Note:

D1 × D2 = [(LG174 × BD) × (vang × CA14)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]

D3 × D2 = [(LG174 × BK) × (vang × CA14)] × [(PC1 × CMS 10B) × (JL × CMS 8B)]

Byadgi Dabbi = BD, Gouribidanur = GB, Tiwari = Ti, Byadgi Kaddi = BK, Japani Long = JL, Vangara = Vang, CMS 7B = 7B, CMS 8B = 8B, CMS 10B = 10B, Pant C1 = PC1

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.

Experimental Design and Crop Management

The field experiment was conducted during the Rabi-summer season of 2020-21 at the experimental fields of the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bengaluru. Forty-day-old seedlings of the nine F₂ segregating populations derived from di-, tri-, tetra- and multi-parental crosses were planted in separate contiguous blocks.

A spacing of 75 cm between rows and 45 cm between plants within rows was maintained. All recommended agronomic practices were followed to raise a healthy crop.

Data Recording and Statistical Analysis

Observations on plant height (cm), primary branches plant⁻¹, secondary branches plant⁻¹, fruits plant⁻¹, green fruit length (cm), green fruit width (cm), average green fruit weight (g) and green fruit yield plant⁻¹ (g) were recorded by selecting five randomly chosen plants from each block. Frequency distribution was worked out for each trait in all segregating populations. The nature of distribution was assessed using coefficients of skewness and kurtosis. Interpretation of skewness and kurtosis was made to infer the nature of gene action and the number of genes controlling the traits, following standard genetic principles.

Coefficients of skewness and kurtosis

Genetic expectations of Skewness ($-3/4 d^2 h$) indicates the nature of genetic control of the traits (Fisher *et al.*, 1932) [4]. Kurtosis reveals the relative number of genes controlling the traits (Robson, 1956) [9]. Coefficients of skewness and kurtosis were estimated (Snedecor and Cochran, 1994) [13] to understand the nature of genetic control of eight quantitative traits using R software version 3.6.3 using libraries Performance Analytics. Further, results obtained for kurtosis and skewness were interpreted as indicated in Table 2 and Table 3, respectively.

Results and Discussion

Skewness and kurtosis are third- and fourth-degree statistical measures that provide valuable insight into the genetic control of quantitative traits. The genetic expectation of the coefficient of skewness is a function of the number of genes and parameters specifying additive main effects and digenic additive × additive epistatic interactions (Pooni *et al.*, 1977) [8]. Kurtosis numerically indicates the number of genes controlling a trait, with leptokurtic, mesokurtic and platykurtic distributions signifying control by fewer, optimum and large numbers of genes, respectively (Robson, 1956) [9]. Fisher *et al.*, (1932) [4] established the theoretical basis for employing skewness to explain genetic causes underlying variation in quantitative traits.

In general, a skewed distribution indicates the predominance of non-additive gene action, particularly epistasis, and a

considerable influence of environmental factors (Pooni *et al.*, 1977; Roy, 2000; Kimbeng and Bingham, 1999) [8, 10, 6]. Positive skewness is predominantly associated with duplicate gene action acting in the same direction, whereas negatively skewed distribution indicates duplicate gene action irrespective of increasing or decreasing effects on trait expression (Snape and Riggs, 1975) [12]. Positive kurtosis suggests the presence of gene interaction, while negative or near-zero values indicate the absence of significant gene interaction.

Plant Height

Positively skewed and platykurtic distribution was observed across all segregating populations derived from varying numbers of parents for plant height (Table 4). This distribution pattern suggests that plant height is governed by a large number of genes with the predominance of non-additive gene action, particularly complementary epistasis, with most genes exerting decreasing effects on the expression of the trait. The platykurtic nature of the distribution further indicates polygenic control and wide recombination in the segregating populations.

Primary and Secondary Branches per Plant

For primary and secondary branches per plant, positively skewed and platykurtic distribution was observed across most segregating populations derived from varying numbers of parents. This indicates the involvement of a large number of genes governed predominantly by non-additive gene action. However, segregating populations derived from the single cross hybrid CMS 8B × GB exhibited leptokurtic distribution, suggesting control by relatively fewer genes with higher gene interaction. In contrast, three-way [(GB × CMS 7B) × CMS 8B] and double cross hybrids [(CMS 8B × GB) × (Ti × CMS 7B)] showed negatively skewed distribution, indicating the presence of duplicate epistasis influencing trait expression (Table 4). These variations highlight the influence of parental complexity on the genetic architecture of branching traits.

Average Fruit Length

Negatively skewed and platykurtic distribution was observed for average fruit length in most segregating populations, except those derived from the single cross hybrid PC1 × BK, the three-way cross hybrid (GB × CMS 7B) × CMS 8B, and the multi-parent hybrid D1 × D2, which exhibited positively skewed and platykurtic distribution (Table 4). The predominance of negative skewness along with platykurtosis suggests that average fruit length is controlled by a large number of genes, with duplicate epistasis exerting increasing effects on trait expression in most populations. The contrasting distribution in specific crosses indicates differential parental contribution and recombination effects.

Average Fruit Width

Positively skewed and platykurtic distribution was observed for average fruit width across most segregating populations, indicating polygenic control with predominant non-additive gene action. However, the single cross hybrid PC1 × BK showed positively skewed and leptokurtic distribution, suggesting involvement of fewer genes with strong gene

interaction. Negatively skewed and leptokurtic distribution was observed in segregating populations derived from the single cross CMS 8B × GB and double cross hybrids [(CMS 8B × GB) × (Ti × CMS 7B)] and [(PC1 × 10B) × (JL × 8B)], indicating duplicate gene action influencing fruit width (Table 4). These findings reflect the role of parental combinations in modifying gene action patterns.

Average Fruit Weight

Positively skewed and platykurtic distribution was observed for average fruit weight across most segregating populations, suggesting polygenic inheritance governed predominantly by non-additive gene action. However, segregating populations derived from the three-way cross hybrid [(BK × 8B) × Ti] exhibited leptokurtic distribution, indicating control by fewer genes with higher gene interaction. The double cross hybrid [(PC1 × 10B) × (JL × 8B)] showed negatively skewed distribution, reflecting duplicate epistasis influencing fruit weight (Table 4).

Number of Fruits per Plant

For fruits per plant, positively skewed and platykurtic distribution was observed across all segregating populations derived from varying numbers of parents, except the single cross hybrid GB × Ti, which exhibited leptokurtic distribution (Table 4). This indicates that fruits per plant is governed by a large number of genes with predominant non-additive gene action, while the leptokurtic distribution in the single cross population suggests relatively fewer genes with stronger interaction effects.

Green Fruit Yield per Plant

Positively skewed and platykurtic distribution was observed across all segregating populations derived from varying numbers of parents for green fruit yield per plant, indicating polygenic inheritance governed predominantly by non-additive gene action (Table 4). However, segregating populations derived from all single cross hybrids exhibited leptokurtic distribution, suggesting control by fewer genes with significant gene interaction. The positively skewed leptokurtic distribution observed in single cross populations indicates that a majority of genes exert decreasing effects on green fruit yield per plant, implying limited scope for effective early-generation selection. In contrast, the broader platykurtic distribution observed in multi-parental populations suggests enhanced recombination and greater opportunity for isolating superior segregants in later generations.

Overall Inference on Gene Action

Based on skewness and kurtosis analysis, the inheritance of yield and yield-related traits in the F₂ segregating populations of chilli was predominantly governed by non-additive gene action involving epistatic interactions. Traits in multi-parental and complex crosses exhibited broader platykurtic distributions, indicating polygenic control and enhanced recombination, whereas single cross populations frequently showed leptokurtic distributions, suggesting control by fewer genes. These results emphasize the importance of using multi-parental crosses for generating wider genetic variability and improving selection efficiency in chilli breeding programmes.

Table 4: Estimates of Skewness and Kurtosis for green fruit yield and its attributing traits among F₂ segregating populations derived from crosses involving varying number of parents in chilli

Segregating populations derived from	Trait Parentage	Number of parents involved	Plant height (cm)		Average fruit length (cm)		Average fruit width (cm)		Average fruit weight (g)		Fruits plant ⁻¹		Primary branches plant ⁻¹		secondary branches plant ⁻¹		Green fruit yield plant ⁻¹ (g)	
			Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis
Single cross Hybrids	GB × Ti	2	0.59	0.04	-0.17	-0.37	0.28	-0.33	0.71	0.44	2.60	9.33	-0.20	-0.43	0.01	0.45	2.57	8.05
	PC1 × BK		0.51	0.38	0.03	0.58	1.08	4.15	0.73	1.22	1.41	2.42	0.40	0.06	0.33	0.02	1.70	4.57
	8B × GB		0.49	0.01	-0.25	0.42	-0.31	0.55	0.22	-0.55	1.31	1.70	4.53	34.91	4.38	33.31	2.17	6.54
Three-way cross Hybrids	(BK × 8B) × Ti	3	0.48	0.31	-0.32	-0.45	0.42	-0.43	2.63	13.51	0.53	-0.85	0.50	0.55	0.50	0.54	1.11	0.97
	(GB × 7B) × 8B		0.69	0.5	0.25	-0.46	1.14	2.81	0.74	1.8	0.7	0.45	-0.12	0.42	-0.14	0.3	0.56	-0.67
Double cross Hybrids	(8B × GB) × (Ti × 7B)	4	0.40	-0.57	-0.63	0.92	-1.36	5.99	1.40	2.80	1.65	2.34	-0.23	-0.15	-0.23	-0.15	2.25	4.97
	(PC1 × 10B) × (JL × 8B)		0.49	0.02	-0.41	-0.18	-0.93	2.29	-0.15	0.93	0.96	0.13	0.77	1.32	0.78	1.08	1.19	1.04
Multi parent Hybrids	D1 × D2	8	1.19	2.13	0.09	-0.45	0.82	2.78	1.32	1.95	1.71	3.08	0.82	0.62	1.87	5.6	1.38	0.99
	D3 × D2		0.70	-0.29	-0.16	-0.22	0.58	-0.40	1.28	2.01	1.23	1.03	0.41	-0.08	0.41	-0.08	1.40	1.41

Double cross Hybrids: D1 = [(LG174 × Byadgi Dabbi) × (Vangara × CA14)]

D2 = [(Pant C1 × CMS 10B) × (Japani Long × CMS 8B)]

D3 = [(LG174 × Byadgi Kaddi) × (Vangara × CA14)]

Conclusion

The frequency distribution analysis of yield and yield-related traits in F_2 segregating populations of chilli derived from varying numbers of parents revealed considerable differences in distribution patterns, skewness and kurtosis. Predominantly positive skewness and platykurtic distribution across most traits indicate the involvement of a large number of genes with significant non-additive gene action. Multi-parental and complex crosses exhibited wider and more favourable distribution patterns compared to single crosses, highlighting their potential in generating enhanced variability. The study underscores the usefulness of frequency distribution parameters in understanding genetic architecture and suggests that segregating populations derived from higher parental combinations are promising resources for effective selection and genetic improvement in chilli breeding programmes.

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