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# Genetic basis of quantitative traits in chilli (*Capsicum annuum* L.) multi-parent populations based on skewness and kurtosis

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## Abstract

The effectiveness of breeding and hence rate of genetic gain in chilli relies on understanding the genetics of target traits. Skewness and kurtosis, the third- and fourth-degree statistics, respectively, provide powerful tools to detect and characterize epistasis and the number of genes controlling traits. This study analyzed the genetics of three quantitative traits—average fruit weight (AFW), fruits plant$^{-1}$ (FP), and green fruit yield plant$^{-1}$ (GFY) - in 10 multi-parent (MP)-derived populations. Symmetrical platykurtic distributions in most MP populations indicated the predominance of numerous non-epistatic genes governing AFW, FP, and GFY, suggesting slow genetic gains with mild selection but rapid gains under intense selection. On contrary, positively skewed distributions in three MP populations indicated complementary epistatic genes with decreasing effects on FP and GFY. Additionally, leptokurtic distributions in two MPs indicated fewer genes controlling AFW and GFY, suggesting even mild selection is likely to be effective to improve these traits.

**Keywords:** Genetics, skewness, kurtosis, epistasis

## Introduction

Chilli, also known as hot pepper, is a very important spice-cum-vegetable crop. It is a diploid with chromosome number 2n = 24 and belongs to the family Solanaceae. It is usually regarded as an indispensable ingredient in every Indian kitchen because of its pungent nature (Channabasava *et al.* 2023). The pungency of chilli is mainly due to presence of pepper specific secondary metabolites – capsaicinoids, which also possess various medicinal properties. The fruits contain appreciable quantity of nutrients and other pigments such as lycopene and zeaxanthin which renders anti cancerous properties (Anilkumar *et al.* 2020). Chilli belongs to the genus *Capsicum*. Among the 30 species recognized under the genus *Capsicum*, mainly five species *viz*., *Capsicum annuum* L., *Capsicum frutescens*, *Capsicum pubescens*, *Capsicum chinense* and *Capsicum baccatum* are grown in various regions of the world (Bosland & Votava, 2012). Among these, *Capsicum annuum* and *Capsicum frutescens* are most widely cultivated in India. In southern parts of India, temperature is very favorable for *C. annuum*. However, *C. frutescens, C. chinense* are often grown in specific regions especially in North eastern parts of India and some parts of Karnataka and Kerala. Development and deployment of high yielding cultivars with acceptable fruit quality traits contribute to sustainable and stable chilli production.

Effectiveness of breeding and hence rate of genetic gain in any crop including chilli hinges on comprehensive information on genetics of target traits. Genetics of quantitative traits could be unraveled at first-, second-, third- and fourth-degree statistics levels. The skewness, the third-degree statistic and kurtosis, the fourth-degree statistic are more powerful ones and useful than first (mean) and second degree (variance) statistics and their derivatives, especially for detecting and characterizing the nature of epistasis (Babu *et al.* 2017). Under these premises, the present study was executed to unravel the genetics of three productivity traits.

## Material and methods

The material for the study consisted of 10 multi parent (MP)-derived populations from eight different parents (Table 1). The seeds of these MP populations were procured from the Hot pepper improvement laboratory, Department of Genetics and Plant Breeding (GPB), College of Agriculture (CoA), University of Agricultural Sciences (UAS), Bangalore. The seeds of these populations were sown in a nursery maintained in the net house during 2020-21 pre-monsoon season. Later, well-grown and healthy forty-day old seedlings were transplanted to the main experimental plots at CoA, UAS, Bangalore. The seedlings were planted with an inter-row spacing of 0.75 m and a spacing of 0.45 m within a row of 4.5 m length. All the recommended package of practices were followed to raise a healthy crop. The number of plants within each of these ten MP-derived populations varied from 82 to 155. The data on three quantitative traits

**Table 1.** Pedigree of different eight-parent derived populations

| Sl. No. | MP population code | Pedigree |
|---|---|---|
| 01 | S4 × S2 (119) | [(LG 174×BD) × (Vang×CA14)] × [(PC1×CMS 10B) × (JL×CMS 8B)] |
| 02 | S2 × S1 (112) | [(PC1×CMS 10B) × (JL×CMS 8B)] × [(LG 174×BD) × (Ti×CA14)] |
| 03 | S3 × S2 (82) | [(UA×PJ) × (PS×CMS 6B)] × [(PC1×CMS 10B) × (JL×CMS 8B)] |
| 04 | S5 × S2 (110) | [(LG 174×BK) × (Vang×CA14)] × [(PC1×CMS 10B) × (JL×CMS 8B)] |
| 05 | S1 × S3 (145) | [(LG 174×BD) × (Ti×CA14)] × [(UA×PJ) × (PS×CMS 6B)] |
| 06 | S6 × S3 (155) | [(GB×BK) × (Vang×LG 181)] × [(UA×PJ) × (PS×CMS 6B)] |
| 07 | S5 × S3 (110) | [(LG 174×BK) × (Vang×CA14)] × [(UA×PJ) × (PS×CMS 6B)] |
| 08 | S4 × S3 (99) | [(LG 174×BD) × (Vang×CA14)] × [(UA×PJ) × (PS×CMS 6B)] |
| 09 | S6 × S2 (122) | [(GB×BK) × (Vang×LG 181)] × [(PC1×CMS 10B) × (JL×CMS 8B)] |
| 10 | S7 × S2 (153) | [(GB×CA14) × (Vang×LG 181)] × [(PC1×CMS 10B) × (JL×CMS 8B)] |

**Note**: Values in the parenthesis indicate population size namely, average fruit weight (AFW), fruits plant$^{-1}$ (FP) and green fruit yield plant$^{-1}$ (GFY) were recorded on each plant in each of the MP-derived population.

### Statistical analysis

The Quantitative traits (QTs) data on individual plants of each of the MP population were used for statistical analysis. Descriptive statistics such as standardized range (SR) and phenotypic coefficient of variation (PCV) for three QTs were estimated. SR was estimated as, SR = (highest value – lowest value) / population mean. PCV was estimated as, , where, phenotypic standard deviation, population mean. SR and PCV were estimated to assess genetic variability to provide statistical justification for the use of skewness and kurtosis for interpretation on the genetics of three QTs. Coefficients of skewness and kurtosis were estimated using 'R' software version 3.6.3 using package "*Performance Analytics*".

### Interpretation of third- and fourth degree-based statistics

**Skewness:** Skewness describes the degree to which a distribution deviates from symmetrical distribution. The direction of skewed distribution of a population indicates the kind of epistasis among genes with increasing and/or decreasing effects on target trait phenotypes. Positively and negatively skewed distribution indicates involvement of genes that display complimentary epistasis, and duplicate epistasis, respectively controlling target QTs (Kearsey & Pooni, 1996).

**Kurtosis:** Kurtosis indicate the degree of peakedness of a distribution relative to a normal distribution. Positive and high magnitude of kurtosis (>3) known as leptokurtic distribution is characterized by a sharp peak and heavier tails and it suggests that fewer genes control the inheritance of QTs. Negative kurtosis (<3) with high magnitude known as platykurtic distribution, is characterized by a flat distribution with lighter tails and it suggest that a large number of genes control the inheritance of target QTs. Mesokurtic distribution (K = 3) is characterized by symmetric distribution and it indicates that the target QTs are controlled by moderate number of genes (Kearsey & Pooni, 1996).

## Results and discussion

### Variability in MP populations

The involvement of more than two parents in the generation of segregating populations is expected to result in the wide variability in the first filial generation itself as evident by higher estimates of SR and PCV for the three QTs (Table 2). Large variability could be attributed to contribution of different alleles at loci distributed in the founder parents of MP-derived population. Large variability in the MP-derived population could be explained by the following hypothesis and argument. It is hypothesized that each of the eight founder parents of the population harbor at least one different allele resulting a total of eight alleles at each of the loci controlling the three target traits. At each bi-allelic locus, three genotypes are possible. With increase in number of alleles, the number of possible genotypes and hence number of distinct phenotypes also likely to increase. For example, with eight alleles at each locus, 36 distinct genotypes and 36 unique phenotypes are possible at each locus and hence large variability for target traits. Pathy *et al.* (2018) also reported that populations derived from more than two parents display a greater variability compared to those derived from two parent crosses for GFY in chilli.

### Genetics of QTs based on skewness and kurtosis

Theoretical basis for explaining the genetic causes for variation in quantitative traits based on skewness was outlined by Fisher *et al.* (1932). The study of distribution properties such as co-efficient of skewness (third degree statistic)

**Table 2.** Estimates of standardized range and phenotypic coefficient of variation for three quantitative traits in MP populations

| MP populations code | Standardized range (SR) | | | Phenotypic coefficient of variance (PCV) | | |
|---|---|---|---|---|---|---|
| | Average fruit weight (g) | Fruits plant$^{-1}$ | Green fruit yield plant$^{-1}$ (g) | Average fruit weight (g) | Fruits plant$^{-1}$ | Green fruit yield plant$^{-1}$ (g) |
| S4 × S2 | 2.35 | 2.36 | 2.06 | 30.65 | 51.68 | 47.91 |
| S2 × S1 | 1.39 | 2.21 | 2.04 | 23.03 | 41.06 | 41.99 |
| S3 × S2 | 1.35 | 2.52 | 2.18 | 25.92 | 53.8 | 53.75 |
| S5 × S2 | 1.54 | 2.8 | 2.42 | 22.06 | 54.77 | 50.23 |
| S1 × S3 | 1.03 | 2.25 | 2.16 | 22.81 | 45.37 | 43.03 |
| S6 × S3 | 1.23 | 2.8 | 2.74 | 22.03 | 51.56 | 52.92 |
| S5 × S3 | 1.05 | 2.81 | 2.87 | 21.5 | 54.59 | 56.74 |
| S4 × S3 | 1.38 | 2.42 | 2.05 | 24.03 | 53.38 | 48.04 |
| S6 × S2 | 2.09 | 3.29 | 4.63 | 26.58 | 58.51 | 61.29 |
| S7 × S2 | 1.21 | 3.86 | 3.12 | 23.49 | 73.22 | 69.29 |

and kurtosis (fourth degree statistic) provide insight into the nature of gene action (Fisher *et al.* 1932) and number of genes controlling the traits (Robson, 1956), respectively. Skewness and kurtosis are more powerful than first- and second- degree statistics, which reveal interaction genetic effects (Choo & Reinbergs, 1982).

Skewness quantifies the departure of a distribution from symmetry. If there exists greater number of data points to the right and left of the highest ordinate of the frequency curve, the distribution is said to be positively and negatively skewed, respectively. Coefficient of skewness is a function of number of genes and parameters that specify their additive main genetic and digenic additive × additive epistatic interaction effects (Pooni *et al.* 1977; Kimbeng & Bingham, 1999; Roy, 2000).

The skewed distribution of a trait in general suggest that the trait is controlled by genes that display non-additive action, especially the epistasis and influenced by environmental variables (Pooni *et al.* 1977 and Roy, 2000). Positive skewness is associated with complementary gene interactions while negative skewness is associated with duplicate (additive × additive) gene interactions. The genes controlling the trait with skewed distribution tend to be predominantly dominant irrespective of whether they exert increasing or decreasing effect on phenotype of the target traits (Roy, 2000). Genetic gain for traits showing negatively skewed distribution is likely to be rapid under mild selection intensity (Roy, 2000). This is because, traits that display negatively skewed distribution contain greater number of individuals with desired phenotypes of the target trait. Hence even with mild selection (large proportion of plants selected), the genetic gain is expected to be greater.

Kurtosis is a measure of the "peakedness" of the probability distribution of a random variable. A distribution with kurtosis equal to 3 is called as mesokurtic. A distribution with <3 kurtosis is called platykurtic. A distribution with >3 kurtosis is called leptokurtic. Kurtosis indicates relative number of genes controlling trait under investigation (Robson, 1956: Snape

& Riggs, 1975). The traits with leptokurtic and platykurtic distribution are controlled by fewer and large number of genes, respectively. Kurtosis of magnitude 3 suggest absence of gene interaction. Genetic gain for the traits that display normal distribution tends to be slow with mild selection (large proportion of plants selected) as the trait mean of the selected plants will be closer to the population mean. However, the genetic gain for the traits that display negatively skewed distribution due to duplicate epistasis tends to be rapid even with mild selection as the trait mean of the selected individuals is far greater than that of population mean. On the other hand, the genetic gain is rather slow with mild selection for the traits that exhibit positively skewed distribution due to complimentary epistasis as the trait mean of the selected plants is very close to the population mean.

In the present study, the magnitude and direction of skewness varied with the population and trait (Table 3). Most of the MP-derived populations showed normal distribution with platykurtic distribution except S5 × S2 (Fig. 4A), which showed mesokurtic distribution for AFW. These results indicate that moderate number of non-epistatic genes control the expression of AFW. Therefore, intense selection in these populations is likely to be effective for rapid genetic gain for AFW. However, two MP populations namely S4 × S2 (Fig. 1A) and S6 × S2 (Fig. 9A) showed exceptionally high magnitude of kurtosis with positive skewness. These results indicated that fewer complimentary epistatic genes which reduces AFW are predominant in these two MP-derived populations. The genetic gain is likely to be slow in response to mild selection (large proportion of the plants selected) while it is likely to be rapid with intense selection (fewer plants selected).

As is true for AFW, most of the MP-derived populations except three populations exhibited normal platykurtic distribution for FP (Table 3). These results indicate that a large number of non-epistatic genes govern the expression of FP. To increase the number of fruits in these populations, intense selection is likely to be effective to realise rapid and desired genetic gain. Three MP-derived populations namely, S5 × S3 (Fig. 7B), S6 × S2 (Fig. 9B) and

**Table 3. Estimates of skewness and kurtosis for three quantitative traits among MP populations**

| MP populations codes | Average fruit weight (g) | | Fruits plant$^{-1}$ | | Green fruit yield plant$^{-1}$ (g) | |
|---|---|---|---|---|---|---|
| | Skewness | Kurtosis | Skewness | Kurtosis | Skewness | Kurtosis |
| S4 × S2 | 2.14 | 7.60 | 0.64 | -0.13 | 0.23 | -0.66 |
| S2 × S1 | 0.49 | 1.02 | 0.31 | 0.05 | 0.08 | -0.55 |
| S3 × S2 | 1.05 | 1.15 | 0.67 | 0.01 | 0.39 | -0.78 |
| S5 × S2 | 0.85 | 2.96 | 0.83 | 0.30 | 0.56 | -0.10 |
| S1 × S3 | 0.15 | -0.54 | 0.52 | 0.07 | 0.41 | 0.00 |
| S6 × S3 | 0.02 | 0.20 | 0.51 | -0.04 | 0.42 | -0.31 |
| S5 × S3 | 0.30 | 0.02 | 1.12 | 1.62 | 1.17 | 1.78 |
| S4 × S3 | 0.56 | 0.73 | 0.75 | 0.34 | 0.28 | -0.35 |
| S6 × S2 | 1.19 | 5.78 | 1.31 | 2.10 | 2.33 | 9.81 |
| S7 × S2 | 0.37 | 0.30 | 1.46 | 2.37 | 1.09 | 0.65 |

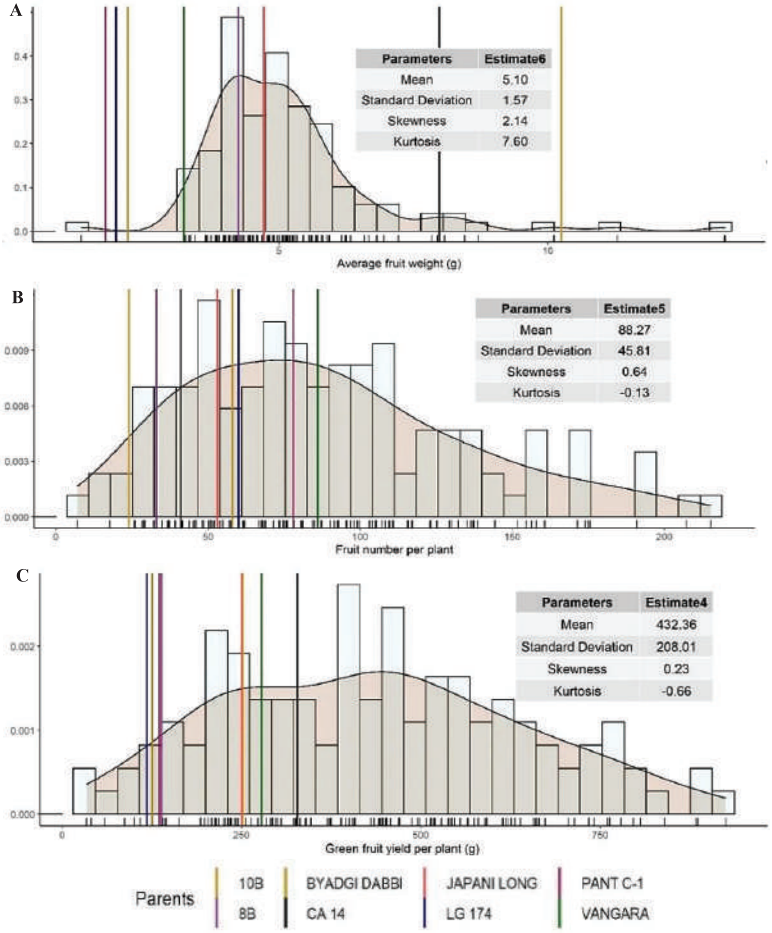


**Fig. 1.** Frequency distribution of S4 × S2 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

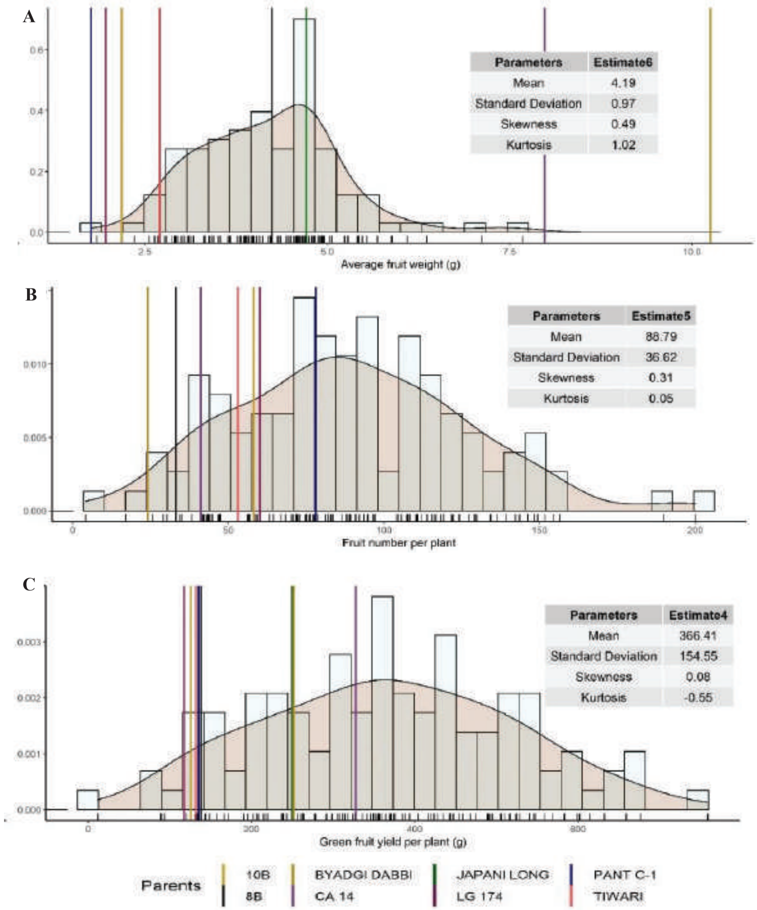


**Fig. 2.** Frequency distribution of S2 × S1 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

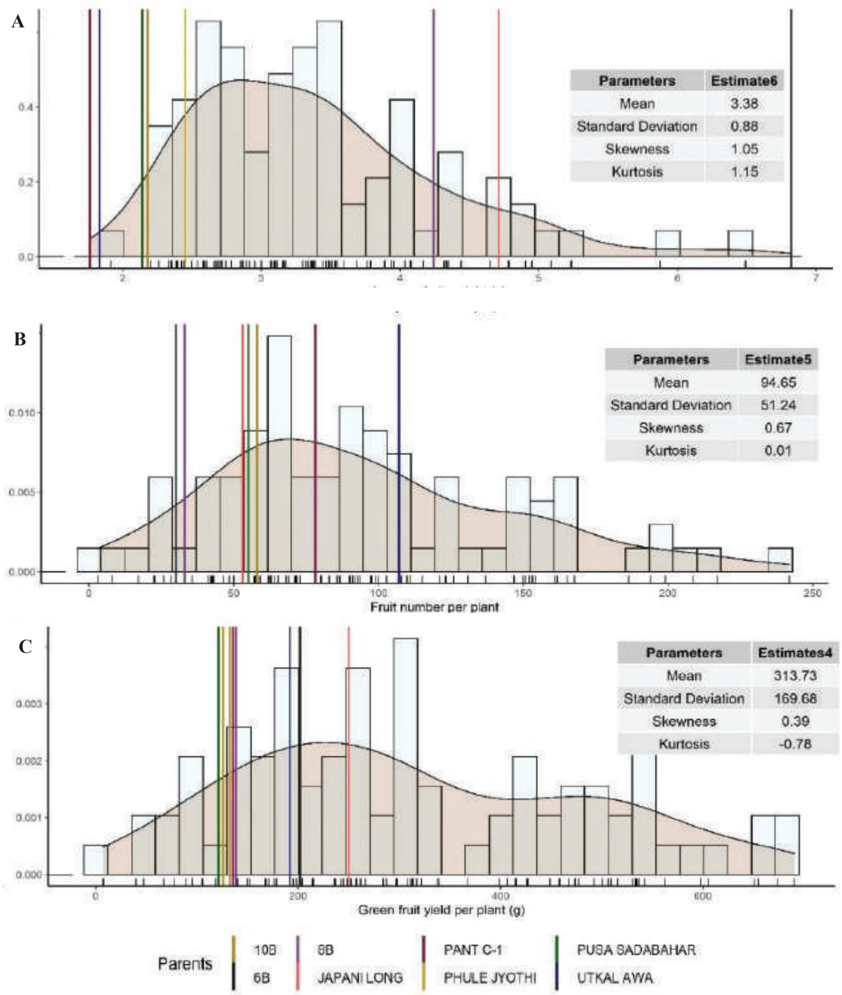


**Fig. 3.** Frequency distribution of S3 × S2 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

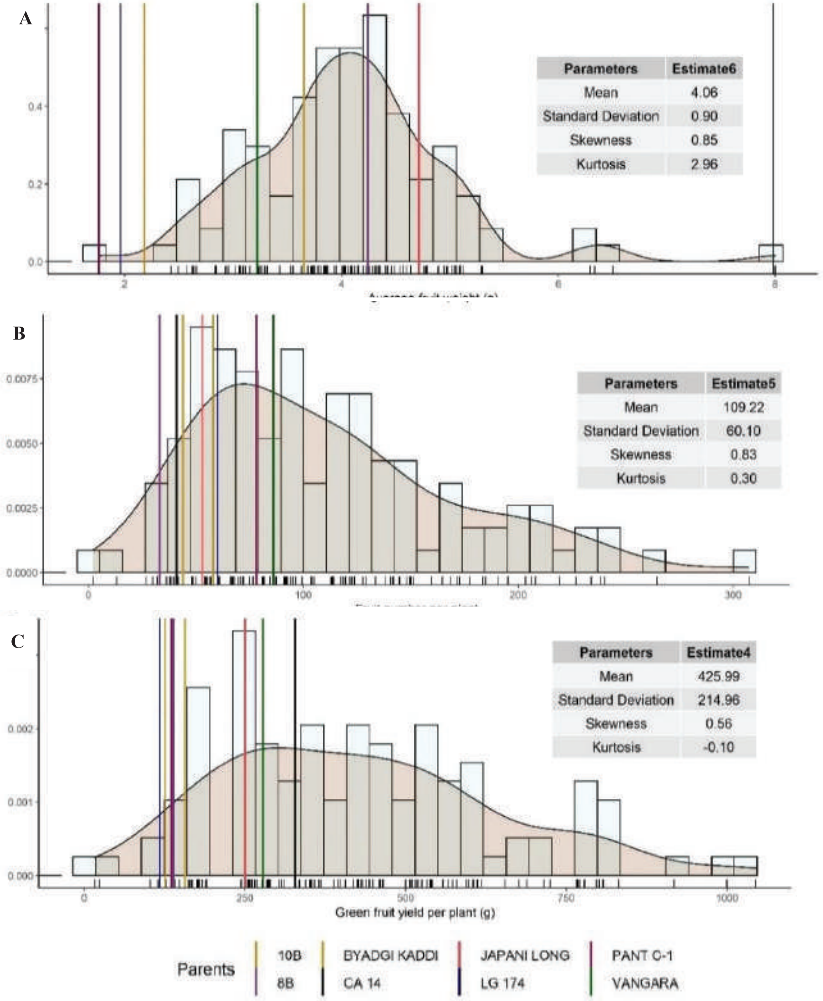


**Fig. 4.** Frequency distribution of S5 × S2 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

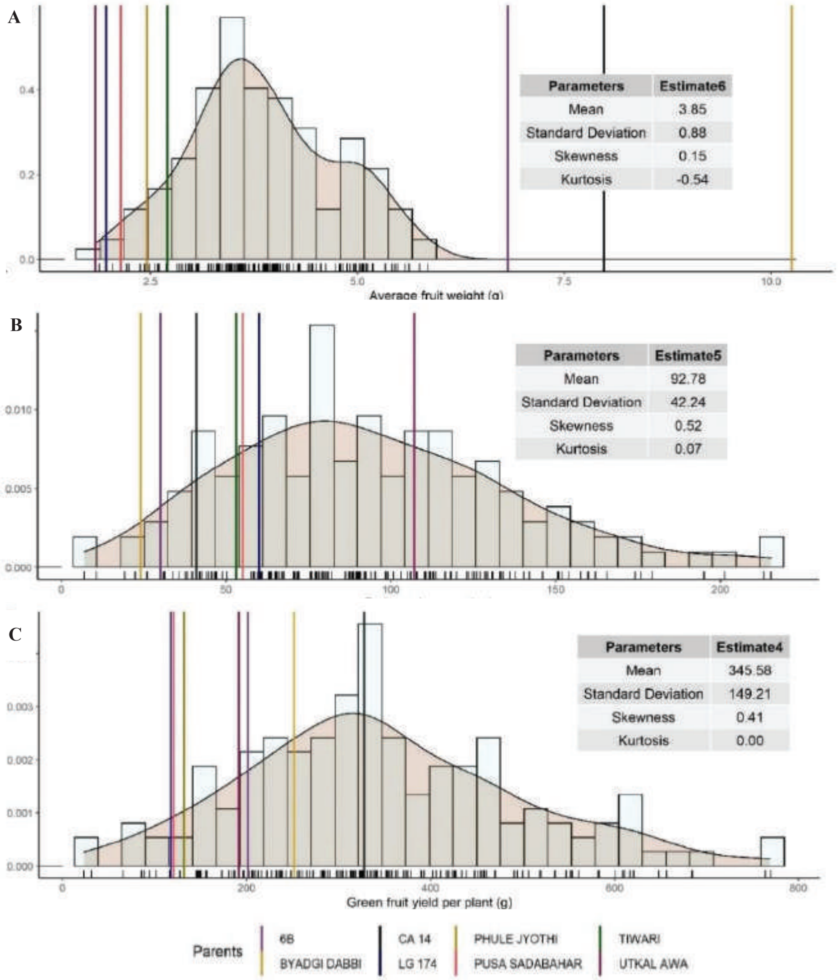


**Fig. 5.** Frequency distribution of S1 × S3 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

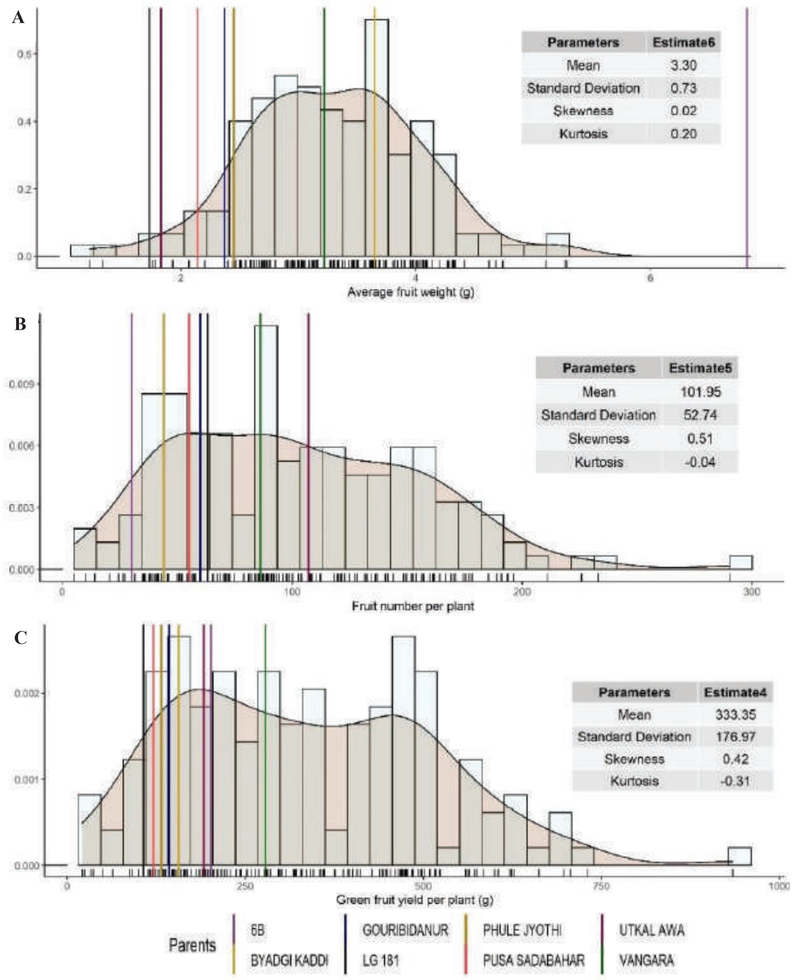


**Fig. 6.** Frequency distribution of S6 × S3 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

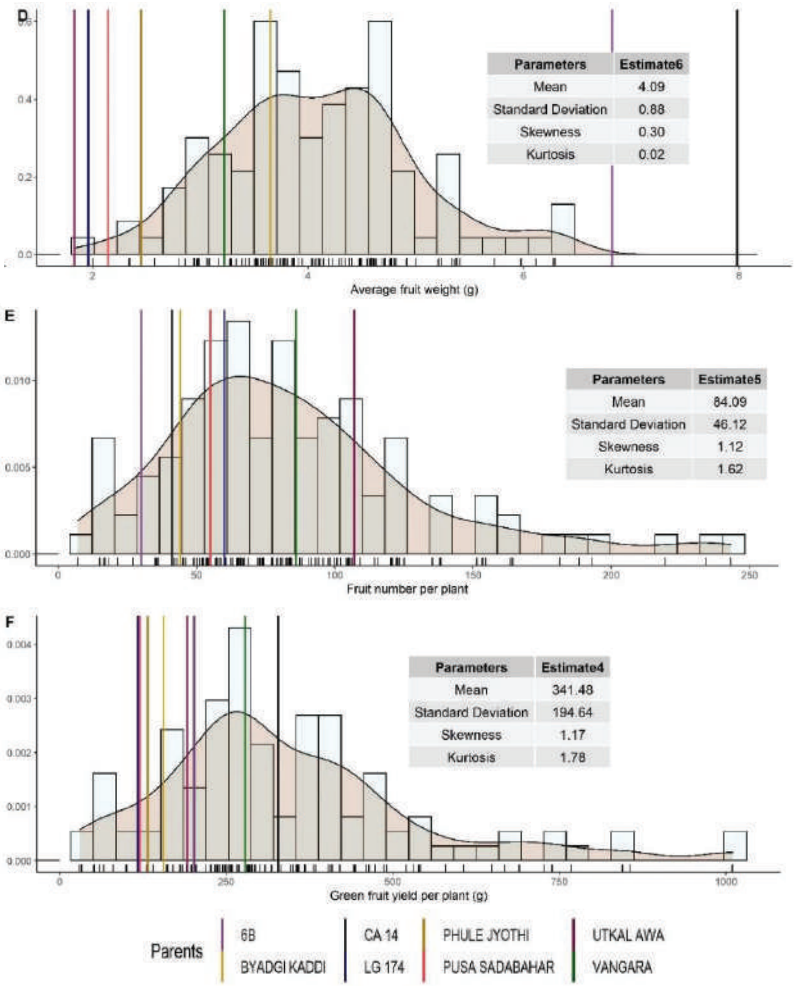


**Fig. 7.** Frequency distribution of S5 × S3 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

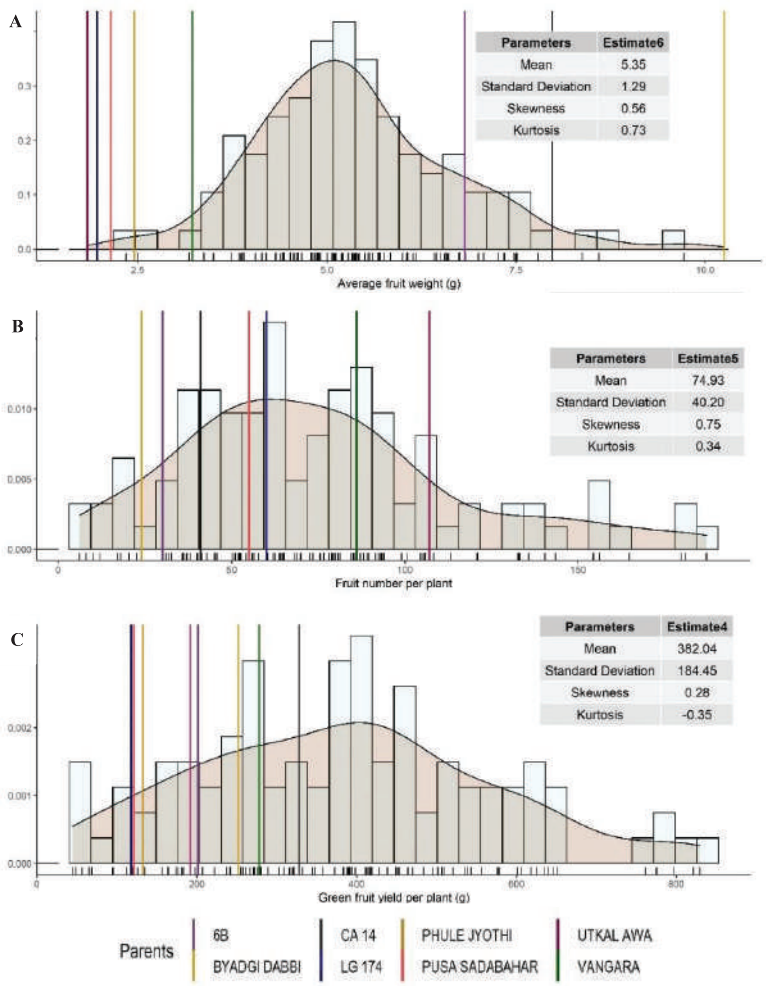
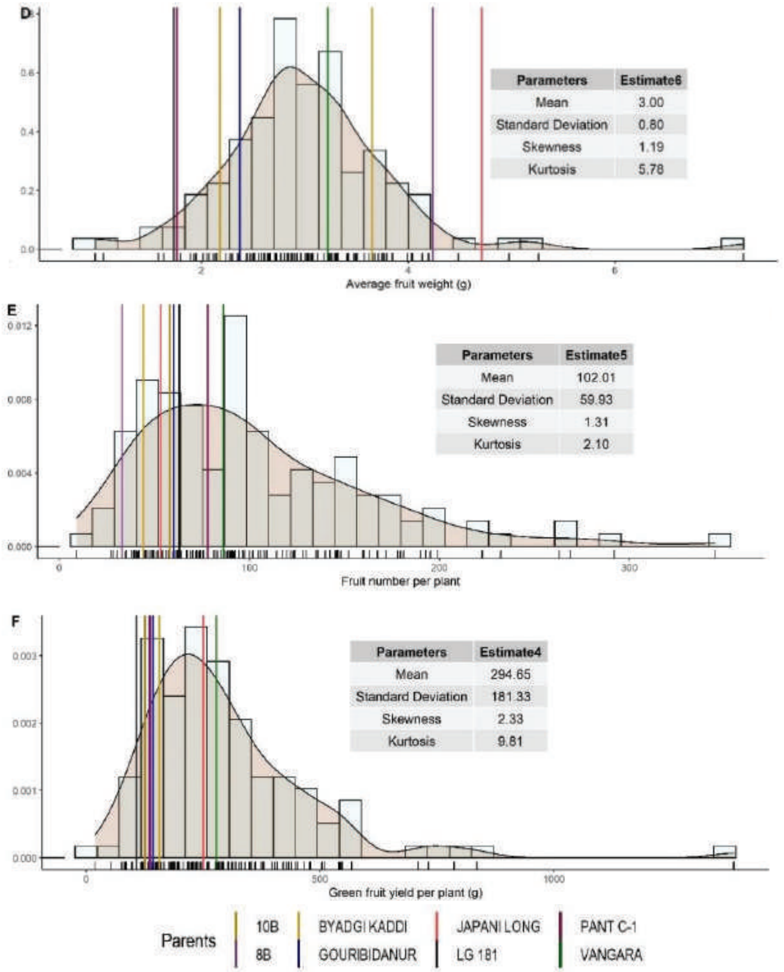


**Fig. 8.** Frequency distribution of S4 × S3 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

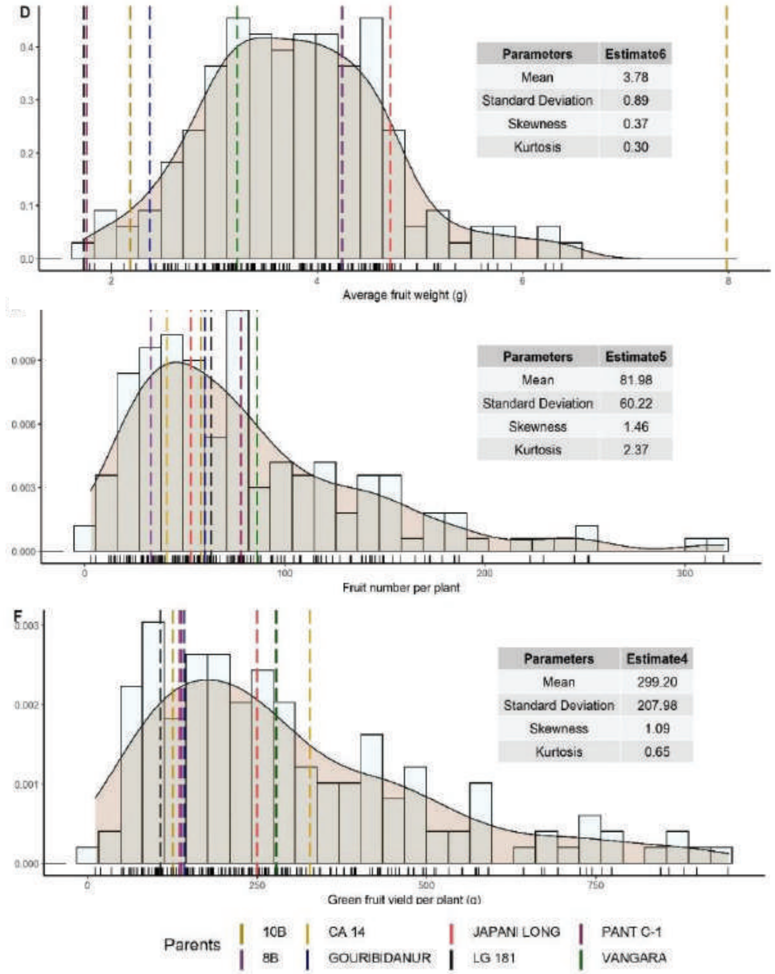


| Parameters | Estimate6 |
|---|---|
| Mean | 3.00 |
| Standard Deviation | 0.80 |
| Skewness | 1.19 |
| Kurtosis | 5.78 |

| Parameters | Estimate5 |
|---|---|
| Mean | 102.01 |
| Standard Deviation | 59.93 |
| Skewness | 1.31 |
| Kurtosis | 2.10 |

| Parameters | Estimate4 |
|---|---|
| Mean | 294.65 |
| Standard Deviation | 181.33 |
| Skewness | 2.33 |
| Kurtosis | 9.81 |

**Fig. 9.** Frequency distribution of S6 × S2 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli



| Parameters | Estimate6 |
|---|---|
| Mean | 3.78 |
| Standard Deviation | 0.89 |
| Skewness | 0.37 |
| Kurtosis | 0.30 |

| Parameters | Estimate5 |
|---|---|
| Mean | 81.98 |
| Standard Deviation | 60.22 |
| Skewness | 1.46 |
| Kurtosis | 2.37 |

| Parameters | Estimate4 |
|---|---|
| Mean | 299.20 |
| Standard Deviation | 207.98 |
| Skewness | 1.09 |
| Kurtosis | 0.65 |

**Fig. 10.** Frequency distribution of S7 × S2 MP population for (A) Average fruit weight (g), (B) Fruits plant$^{-1}$ and (C) Green fruit yield plant$^{-1}$ (g) in chilli

S7 × S2 (Fig. 10B) showed positively skewed platykurtic distribution. These results indicate that a large number of complimentary epistatic genes which reduces the number of fruits is predominant in these three MP-derived populations. Intense selection is likely to result in the rapid genetic gain for the number of fruits.

As expected, for GFY, most of the MP-derived populations except three exhibited normal platykurtic distributions except S6 × S2 (Fig. 9C) which displayed high kurtosis (Table 3). These results suggest intense selection from these populations is likely to be effective to improve GFY. However, as is true for FP, MP-derived populations such as S5 × S3 (Fig. 7C), S6 × S2 (Fig. 9C) and S7 × S2 (Fig. 10C) also showed positively skewed distribution for GFY. These results indicate that a large number of complimentary genes with decreasing effect alleles control the expression of GFY. Therefore, intense selection in these three MP populations is likely to be effective for enhancing GFY.

## Summary

The magnitude and direction of skewness and degree of kurtosis (peakedness/flatness) varied with the population. Most of the MP derived populations displayed normal and platykurtic distribution for all the three traits. However, at least two populations exhibited exceptionally high magnitude of kurtosis and positive skewness for all the three traits. Intense selection is likely to result in rapid genetic gain for these three traits in these exceptional populations showing positive skewness.

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