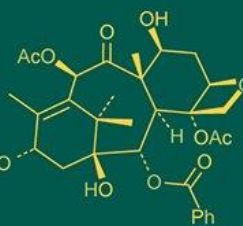
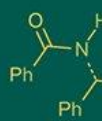


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Estimation of genetic variability and traits association through correlation and path coefficient analysis in guava (*Psidium guajava* L.)

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Abstract

Seven guava (*Psidium guajava* L.) genotypes namely Allahabad Safeda, Lalit, Arka Amulya, Shweta, Lucknow-49, Hisar Surkha and Hisar Safeda, were evaluated during 2018–19 to estimate genetic variability, heritability, genetic advance, correlation and path coefficient analysis for economically important horticultural traits. High genotypic and phenotypic coefficients of variation were observed for seed weight and number of seeds per fruit, indicating substantial genetic variability among the genotypes. Broad-sense heritability was high for all the characters studied, ranging from 66.39 to 98.05%, with the highest value recorded for number of seeds per fruit. High genetic gain was observed for number of seeds per fruit (48.81%), seed weight (44.47%), thickness of outer flesh (24.20%) and total soluble solids (21.23%), indicating the predominance of additive gene action and the effectiveness of phenotypic selection. Correlation analysis revealed that average fruit weight was positively and significantly associated with fruit length and fruit width. Path coefficient analysis showed that seed weight exerted the highest positive direct effect on average fruit weight, followed by fruit width and fruit length. The findings indicate that fruit length, fruit width and seed weight are important selection criteria for improving fruit weight and developing superior guava genotypes in future breeding programmes.

Keywords: Guava, genetic variability, heritability, genetic advance, correlation, path coefficient analysis

Introduction

Guava often called the poor man's apple is a highly valued fruit from the Myrtaceae family, cultivated in over 60 tropical and subtropical countries worldwide. It is a popular choice due to its year-round availability, affordability, ease of transport and general consumer appeal. Beyond its convenience, guava is a nutritional powerhouse. It's packed with Vitamin C, pectin and essential minerals like calcium, phosphorus, and iron. Guava also contains antioxidants and has been linked to controlling systolic blood pressure. These health benefits combined with low cultivation costs make guava an economically significant crop in many regions (Rodriguez *et al.*, 2010) [12]. Since guava is a cross-pollinated crop there is a lot of natural variation among seedling populations in different growing areas (Srivastava, 2005) [14]. This leads to significant differences in fruit quality and yield potential among various guava clones (Deshmukh *et al.*, 2013) [4]. In India many guava cultivars have developed from seedling selection and are widely grown by seed propagation. However, this method has a downside it has led to the emergence of several guava genotypes that are not true to the parent genotype. These new types often differ significantly from their parent plants in various characteristics (Saxena *et al.*, 2007) [13]. Due to high heterozygosity and frequent cross-pollination current guava seedling populations show significant variation allowing for the selection of promising genotypes (Dinesh and Vasugi, 2010) [6]. Studying the genetic variability of leaf and fruit characteristics can reveal wild genotypes with useful traits for improving the crop (Nogueira *et al.*, 2012) [9]. To effectively select and improve the base population it is crucial to assess genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance. Additionally, path analysis based on the genotypic correlation coefficients helps to understand how different traits contribute to average fruit weight.

Therefore, this study aimed to gather information on the genetic variability, heritability, correlation and genetic advance of important guava characteristics. The goal was to identify genetically diverse parents for hybridization programs which could lead to superior offspring with desirable traits.

Materials and Methods

Planting material and site: The investigation was carried out during 2018-19 at the Experimental Farm and Laboratory of the Department of Fruit Science, College of Horticulture and Forestry, Neri, Hamirpur, Himachal Pradesh. It is situated in subtropical climate on geographical coordinates 31°41'47.6" N, 76°28'6.3" E and at an altitude of 650 m above mean sea-level. The research work was conducted on two-year-old trees of seven genotypes viz., Allahabad Safeda, Lalit, Arka Amulya, Shweta, Lucknow-49, Hisar Surkha and Hisar Safeda. The trees were planted during the year 2016 under a High-Density Plantation (HDP) system with a spacing of 2.5 × 2.0 m. Three plants of each cultivar that were uniform in growth characteristics, free from insect pests and diseases and growing under healthy conditions were selected for recording observations on various characteristics.

Genotypic and phenotypic coefficients of variation:

Genetic parameters Genotypic and Phenotypic Coefficients of variability were calculated as per formulae given by Burton and De-Vane (1953) [3].

Heritability (in broad sense): Heritability in broad sense was calculated by the formula as recommended by Allard (1960) [2].

Genetic advance (GA): The expected genetic advance (GA) resulting from selection of five per cent superior individuals and was worked out as suggested by Allard (1960) [2].

Genetic gain (GG): The Genetic gain expressed in per cent ratio of genetic advance and population mean and it was calculated by the method given by Johnson *et al.* (1955) [8].

Correlations coefficient: The genotypic and phenotypic correlations were calculated by using analysis of variance and covariance matrix suggested by Al-Jibouri *et al.* (1958) [1].

Path Coefficients of analysis: The genotypic correlation coefficient was used to finding out their direct and indirect contribution towards mean fruit weight. The direct and indirect paths were obtained by method suggested by following Dewey and Lu (1959) [5].

Results and Discussion

Phenotypic and genotypic coefficient of variation

The perusal of data presented in Table 1 revealed wide extent of variation for all the characters studied. Phenotypic coefficients of variation for different traits expressed in percentage ranged from 4.42 to 25.45 percent whereas the genotypic coefficient of variation for all the characters ranged from 4.00 to 23.44 % (Table 1). The phenotypic and genotypic coefficients of variability were high for seed weight (25.45 % and 23.44%) and number of seeds per fruit

(24.17 % and 23.93 %). Moderate coefficients of variability both at phenotypic and genotypic level were observed for thickness of outer flesh (13.05 % and 12.38 %) and total soluble solids (11.48 % and 10.88 %), whereas it was low for average fruit weight (8.87 % and 7.29 %), fruit length (7.58 % and 6.18 %), core diameter (7.54 % and 6.41 %) and fruit width (4.42 % and 4.00 %).

The results of present investigation were in close agreement with those of Gupta and Kour (2019) [7] who observed high estimates of PCV and GCV for number of seeds per fruits (37.17% and 35.72%). Moderate estimates of PCV and GCV for total soluble solids (13.88% and 10.92%) while low estimates of GCV for fruit width (8.69). Rajan *et al.* (2005) [11] also reported high estimates of PCV and GCV for number of seeds per fruit (44.49% and 37.14%) and seed weight (37.97% and 28.90%). Rajan *et al.* (2012) [10] reported high estimates of PCV and GCV for number of seeds per fruit (53.67% and 49.37%) and seed weight (50.77% and 46.27%). The high GCV (Genotypic coefficient of variability) and PCV (Phenotypic coefficient of variability) observed for these characters indicates that there is enough genetic variation among the different genotypes and suitability of these attributes for further improvement by selection. Low GCV and PCV estimates suggested that selection based solely on these traits would not be very fruitful. When GCV and PCV are close for certain traits, it means that phenotypic expression of the genotypes is primarily under the genetic control and that these traits are relatively resistant to environmental changes. Indicating low environmental influence in expression of these characters, which implies that phenotypic variability is a reliable measure of genotypic variability. So, selection for improvement of the trait is possible and effective on the phenotypic basis.

Heritability: Heritability is the portion of phenotypic variation that is, transmitted from parent to progeny. Higher the heritable variation, greater will be the possibility of fixing the characters by selection. Hence, heritability studies provide useful estimates to the breeder to judge whether the observed variation for a particular character is due to genotype or due to environment. In the present study, high heritability estimates were obtained for all the characters (Table 1). It ranged from 66.39% to 98.05%. High heritability estimates were recorded for number of seeds per fruit (98.05%) followed by thickness of outer flesh (90.02%), total soluble solids (89.80%), seed weight (84.83%), fruit width (82.00%), core diameter (72.23%), average fruit weight (67.56%) and fruit length (66.39%). These results are in accordance with the findings of Gupta and Kour (2019) [7] who reported high heritability estimates for average fruit weight (91.43%), fruit length (78.33%), fruit width (71.40%), total soluble solids (61.99%) and number of seeds per fruit (92.39%). Rajan *et al.* (2005) [11] also reported high estimates of heritability for average fruit weight (64.10%), number of seeds per fruit (69.70%) and seed weight (72.40%). Rajan *et al.* (2012) [10] reported high estimates of heritability for fruit weight (88.30%), fruit length (85.40%), fruit width (87.10%), seed weight (83.10%) and number of seeds per fruit (84.60%). Burton and Devane (1953) [3] and Rajan *et al.* (2005) [11] also suggested that characters with high heritability linked to high GCV provide greater scope for further selection.

Genetic advance and genetic gain

Genetic advance expressed as percent of population mean is known as genetic gain. Genetic gain is the magnitude of increase in performance of a trait achievable through systematic crop improvement programme. In the present investigation, the estimates of genetic gain varied from 7.46% to 48.81% (Table 1). High estimates of genetic gain were recorded for number of seeds per fruit (48.81) followed by seed weight (44.47%), thickness of outer flesh (24.20%) and total soluble solids (21.23%). Moderate genetic gain was observed for average fruit weight (12.35%) followed by core diameter (11.22%) and fruit length (10.37%) whereas, low genetic gain was recorded for fruit width (7.46%).

The results of present investigation were in line with those of Gupta and Kour (2019)^[7] who reported high estimates of genetic gain for number of seeds per fruit (70.73%). Rajan *et al.* (2005)^[11] reported high estimates of genetic gain for number of seeds per fruit (63.89%) and seed weight (50.66%). While, Rajan *et al.* (2012)^[11] reported low estimates of genetic gain for fruit width (2.26%)

Correlation studies

The estimates of correlation coefficients were worked out among different traits which enable the researchers to decide the strategies of simultaneous selection for two or more traits. As many traits of economic importance in the crop plants affect the expression of other traits and the degree of expression of one-character increases or decreases with the increase or decrease in another character and vice-versa.

Genotypic and phenotypic correlation

The perusal of data from Table 2 and Table 3 at genotypic and phenotypic level revealed that average fruit weight had positive and significant correlation with fruit length (0.709 at genotypic level and 0.575 at phenotypic level) and fruit width (0.635 at genotypic level and 0.535 at phenotypic level). Core diameter had positive and significant correlation with fruit width (0.655 at genotypic level and 0.594 at phenotypic level), seed weight (0.766 at genotypic level and 0.604 at phenotypic level) and number of seeds per fruit (0.601 at genotypic level and 0.526 at phenotypic level). Number of seeds per fruit had positive and significant correlation with seed weight (0.920 at genotypic level and 0.866 at phenotypic level). Seed weight had positive and significant correlation with fruit width (0.479 at genotypic level and 0.463 at phenotypic level).

On the other hand, thickness of outer flesh had negative and significant correlation with number of seeds per fruit (-0.634 at genotypic level and -0.581 at phenotypic level). Core diameter had negative and significant correlation for thickness of outer flesh (-0.777 at genotypic level and -0.537 at phenotypic level) and total soluble solids had negative and significant correlation with number of seeds per fruit (-0.494 at genotypic level and -0.455 at phenotypic level) and fruit width (-0.483) at genotypic level.

The results of present investigation are similar in trends of genotypic and phenotypic correlation coefficients with those

of Mahmood (2017). He observed number of seed per fruit had positive and significant correlation with seed weight (0.587) and seed weight had positive and significant correlation with fruit width (0.176). Shiva *et al.* (2017) also reported that average fruit weight had positive and significant correlation with fruit length (0.896) and fruit width (0.941), core diameter showed positive and significant correlation with fruit width (0.815), seed weight (0.719), and number of seed per fruit (0.617), whereas, number of seed per fruit had positive and significant correlation with seed weight (0.986) and seed weight had positive and significant correlation with fruit width (0.591).

Rajan *et al.* (2012)^[11] also reported positive and significant correlation of average fruit weight with fruit length (0.719 and 0.722) and fruit width (0.893 and 0.890), seed weight had positive and significant correlation with fruit width (0.773 and 0.712), while, number of seed per fruit had positive and significant correlation with seed weight (0.892 and 0.859).

Path coefficient analysis

The path coefficients analysis provides a better understanding of the underlying cause of association among different traits which is not revealed by correlation studies alone. The correlation coefficients are partitioned into direct and indirect effects of the traits contributing towards the dependent variable. The results of the present study with respect to direct and indirect effects on average fruit weight are presented in Table 4.

In present investigation, it was found that seed weight (0.814) had highest positive direct effect on average fruit weight followed by fruit width (0.554) and fruit length (0.535) while minimum with total soluble solids (0.161). Further, maximum negative direct effect on average fruit weight was shown by number of seeds per fruit (-0.831) followed by core diameter (-0.342) while minimum was observed for thickness of outer flesh (-0.286). Gupta and Kour (2019)^[7] have reported similar findings who observed fruit weight (0.039), fruit length (1.950) and number of seeds per fruit had maximum positive direct effect on fruit yield.

On the other hand, number of seeds per fruit (0.749) and core diameter (0.623) recorded maximum positive indirect effect via seed weight on average fruit weight. Similarly thickness of outer flesh (0.527) and total soluble solids (0.411) had maximum positive indirect effect via number of seeds per fruit on average fruit weight. Further, fruit length (-0.114) had a maximum negative indirect effect via thickness of outer flesh on average fruit weight. Fruit width (-0.245), seed weight (-0.765) and core diameter (-0.500) had a maximum negative indirect effect via number of seeds per fruit on average fruit weight. Similarly, thickness of outer flesh (-0.349) and total soluble solids (-0.276) had a maximum negative indirect effect via seed weight on average fruit weight. Similar findings have also been reported by Gupta and Kour (2019)^[7] who reported total soluble solids having maximum positive indirect effect via number of seeds per fruit with fruit yield.

Table 1: Estimates of phenotypic and genotypic coefficients of variation, heritability, genetic advance and genetic gain for various characters in Guava.

Characters	Coefficients of Variability (%)		Heritability (%)	Genetic advance	Genetic gain (%)
	Genotypic	Phenotypic			
Fruit length (mm)	6.18	7.58	66.39	5.94	10.37
Fruit width (mm)	4.00	4.42	82.00	4.44	7.46
Seed Weight (g)	23.44	25.45	84.83	0.96	44.47
Number of seeds per fruit	23.93	24.17	98.05	119.58	48.81
Thickness of outer flesh (mm)	12.38	13.05	90.02	2.70	24.20
Core Diameter (mm)	6.41	7.54	72.23	3.99	11.22
Total soluble solids (°Brix)	10.88	11.48	89.80	2.51	21.23
Average fruit weight (g)	7.29	8.87	67.56	15.52	12.35

Table 2: Genotypic coefficients of correlation among different traits in Guava.

	FL	FW	SW	NSPF	TOF	CD	TSS	AFW
FL								
FW	0.255							
SW	0.100	0.479*						
NSPF	0.036	0.295	0.920**					
TOF	0.401	-0.357	-0.429	-0.634**				
CD	-0.277	0.655**	0.766**	0.601**	-0.777**			
TSS	0.006	-0.483*	-0.339	-0.494*	0.416	-0.083		
AFW	0.709**	0.635**	0.173	-0.040	0.241	0.205	-0.058	

*Significant at 5% level of significance

**Significant at 1% level of significance

Where,

FL = Fruit length, FW = Fruit width, SW = Seed weight, NSPF = Number of seed per fruit, TOF = Thickness of outer flesh, CD = Core diameter, TSS = Total soluble solids and AFW = Average fruit weight.

Table 3: Phenotypic coefficients of correlation among different traits in Guava.

	FL	FW	SW	NSPF	TOF	CD	TSS	AFW
FL								
FW	0.376							
SW	0.122	0.463*						
NSPF	0.046	0.275	0.866**					
TOF	0.417	-0.273	-0.410	-0.581**				
CD	0.037	0.594**	0.604**	0.526*	-0.537*			
TSS	0.088	-0.365	-0.302	-0.455*	0.393	0.038		
AFW	0.575**	0.535*	0.109	-0.027	0.198	0.213	0.031	

*Significant at 5% level of significance

**Significant at 1% level of significance

Where,

FL = Fruit length, FW = Fruit width, SW = Seed weight, NSPF = Number of seed per fruit, TOF = Thickness of outer flesh, CD = Core diameter, TSS = Total soluble solids and AFW = Average fruit weight.

Table 4: Path coefficient analysis showing the direct and indirect effect of seven fruit characters on average fruit weight at genotypic level

	FL	FW	SW	NSPF	TOF	CD	TSS	AFW
FL	0.535	0.141	0.081	-0.030	-0.114	0.095	0.001	0.709**
FW	0.137	0.554	0.390	-0.245	0.102	-0.224	-0.078	0.635**
SW	0.054	0.265	0.814	-0.765	0.123	-0.262	-0.055	0.173
NSPF	0.019	0.163	0.749	-0.831	0.181	-0.206	-0.080	-0.04
TOF	0.214	-0.198	-0.349	0.527	-0.286	0.266	0.067	0.241
CD	-0.148	0.363	0.623	-0.500	0.222	-0.342	-0.013	0.205
TSS	0.003	-0.267	-0.276	0.411	-0.119	0.028	0.161	-0.058

Residual effect 0.27267

*Significant at 5% level of significance

**Significant at 1% level of significance

Where,

FL = Fruit length, FW = Fruit width, SW = Seed weight, NSPF = Number of seed per fruit, TOF = Thickness of outer flesh, CD = Core diameter, TSS = Total soluble solids and GCCAFW = Genotypic correlation coefficient with average fruit weight

Diagonal figures represent the direct effect.

Conclusion

The study revealed considerable genetic variability among the seven guava genotypes for all the fruit and seed characters evaluated. High heritability along with high

genetic advance and genetic gain for seed weight, number of seeds per fruit, thickness of outer flesh and total soluble solids indicates that these traits are under strong genetic control with limited environmental influence, making them

reliable targets for improvement through simple phenotypic selection. Correlation and path coefficient analyses established that fruit length, fruit width and seed weight are the key contributors to average fruit weight, either through direct positive effects or significant positive association and should therefore be given due emphasis while selecting genotypes for hybridization and varietal improvement. On the other hand, number of seeds per fruit and core diameter, despite their positive correlation with fruit weight, exerted a negative direct effect, underscoring the importance of path analysis in revealing true trait relationships that simple correlation may mask. Overall, the results suggest that simultaneous selection based on fruit length, fruit width and seed weight can be effectively used to develop superior guava genotypes with enhanced fruit weight and yield, offering valuable direction for future guava breeding programmes.

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