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Journal of Applied Horticulture, 7(1):52-54, January-June, 2005

Selection possibilities for seed content— A determinant of fresh fruit quality in guava (*Psidium guajava* L.)

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Abstract

Improvement of guava with regard to less and soft seed content necessitates insight into the magnitude of variability present in the seed characters. Fruit samples were examined for the variability in pulp: seed weight ratio, number and weight of seeds fruit^{-1}, 100-seed weight, number of seeds 100g^{-1} fruit and seed content in fruit in relation with fruit weight during winter seasons of 2003-04 and 2004-05 on sixty-eight genotypes from diverse origin. The differences among the genotypes were highly significant ($P \leq 0.01$) for all the characters studied. A wide range of variation (17.10 to 5905.31) was recorded for the pulp: seed weight ratio with the mean value of 123.36 showing very high (241.59%) coefficient of variation. Highest mean (254.64) was recorded for number of seeds fruit^{-1} (ranging from 2 to 463.0). The high genetic coefficient of variation and heritability estimates associated with greater genetic advance as percent of mean were recorded for pulp: seed weight ratio, 100-seed weight and number of seeds fruit^{-1}, which indicated that these three characters had additive gene effect and therefore effective selections can be made for these characters.

Key words: Guava, *Psidium guajava* L., fruit, seed number, weight, variability.

Introduction

The guava (*Psidium guajava* L.), "Apple of Tropics", was introduced in India in early 17th century and gradually became one of the most important fruit crops of commercial significance (Hayes, 1970). As the extent of cross-pollination in guava is over 35 per cent (Soubihe and Gurgel, 1962), guava grown from the seeds exhibit considerable genetic variability (Shanker *et al.*, 1999) and this has given enough scope for selection of superior genotype. A large number of cultivars are available in India, however, only a few like Allahabad Safeda, Apple colour, Sardar guava and other occupy the major area under its cultivation.

Most of the guava cultivars are diploid and seeded and high seed content reduces the fruit quality (Chohan and Dhaliwal, 1994). But some natural as well as artificial triploids are also known, which produce mostly seedless fruits. Development of a wilt resistant and high yielding cultivar deserves the first priority in guava breeding. Nevertheless, priority should be given to good fruit quality because there is little merit in increasing yield and disease resistance if accompanied with inferior fruit quality. A variety with few soft seeds is still lacking. It is reported that bold seeds in guava were found to be dominant over soft seeds and is governed monogenically. A linkage was also reported between red flesh colour and bold seed size (Subramanyam and Iyer, 1982).

Evaluation of genetic variability among available germplasm helps to identify superior parents to be included for developing new cultivar. Several attempts have been made to select superior types from the seedling population with few numbers of soft seed (Phadnis, 1970 and Rajan *et al*., 1996). In a highly out crossing species like guava, knowledge of the extent of genetic variation for fruit weight and seed characters and its heritability is important. In order to interpret phenotypic values in terms of potential genetic gain, information on quantitative inheritance of seed characteristics is lacking. The objective of this study was to determine the genetic variability and heritability for fruit weight and associated seed characters.

Materials and methods

Guava accessions (68), collected from diverse sources and conserved in a field gene bank situated at Central Institute for Subtropical Horticulture, Lucknow were studied for seed characteristics. The observations were recorded during winter seasons of 2003-04 and 2004-05 on the fruits from the plants maintained under uniform cultural conditions. Each accession was replicated thrice. Three fruits were collected from each tree randomly, fruits were considered as a unit for each replication. Data was collected on fruit weight and seed characters *i.e.* number of seeds fruit^{-1}, seed weight fruit^{-1}, 100-seed weight, number of seeds 100g^{-1} fruit and seed content (%). Seeds from three random fruits were collected in each replication by carefully cleaning and air-drying for 2-3 days. Digital images of uniformly spread seeds (on black background) from each fruit was taken for analysis using ImageJ JavaScript image analysis software. Number of seeds 100g^{-1} fruit was calculated on the basis of fruit weight and seed number. Weight of 100-seed was measured by weighing the seeds and seed content (%) was determined by using weight of the seeds present in 100g fruit.

The genotypic and phenotypic coefficient of variation were calculated as per Burton and De Vane (1953), heritability by following Johnson *et al.* (1955) and genetic advance by that of Allard (1960) as follows:

$$\sigma_g^2 = \frac{(Mg - Me)}{r}, \quad \sigma_p^2 = \sigma_g^2 + \sigma_e^2, \quad \sigma^2{}_e = Me$$

$$\text{GCV} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100, \ \text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100, \quad h_b^2 = \frac{\sigma_g^2}{\sigma_p^2}, \ \text{GA} = ih^2 \sigma^2{}_p$$

Where,

GCV = genotypic coefficient of variation
PCV = phenotypic coefficient of variation
Mg = mean sum of square due to genotypes, Me = mean sum of square due to error, r = number of replications, GA = Genetic advance and $\bar{X}$ is the population mean.
h^2_b is heritability in broad sense, σ^2_g, σ^2_p and σ^2_e are the genotypic, phenotypic and environmental variance, respectively, and *i* is the standardized selection differential at selection intensity of 5%.

Table 1. Range, SE, grand mean and coefficient of variation (CV) of fruit weight and seed characteristics

Characters	Minimum	Maximum	SE	Grand Mean	CV (%)
Average fruit weight (g)	41.67	326.33	23.97	144.80	20.27
Pulp: seed weight ratio	17.10	5905.31	243.32	123.36	241.59
Number of seeds fruit^{-1}	2.33	463.33	50.90	254.64	24.48
Seed weight fruit^{-1}(g)	0.025	7.16	0.59	4.02	17.85
100-seed weight (g)	0.859	4.55	0.28	1.77	19.29
Number of seeds 100g^{-1}fruit	1.53	443.32	47.84	185.13	31.65
Seed content	0.019	6.48	0.61	2.96	25.31

Results and discussion

The guava accessions exhibited highly significant difference ($P \leq 0.01$) for fruit weight and their seeds characteristics (Table 1). Pulp: seed weight ratio had a higher range from 17.10 to 5905.31 with population mean value of 123.36. Number of seeds fruit^{-1} ranged from 2 (Seedless) to 463 with mean value of 254.64 and number of seeds 100g^{-1} fruit differed from 1.53 (Seedless) to 443.32 with mean value of 185.13 and average fruit weight varied from 41.67 to 326.33g indicating utmost variability in these traits (Table 1). Highest coefficient of variation was recorded for pulp: seed weight ratio (241.59%), while lowest for the seed weight fruit^{-1} (17.85%). Thus it is clear that pulp: seed weight ratio attributed greater variability in guava population. Wide variation for fruit weight and seed number per fruit was recorded by Chohan and Dhaliwal (1994) and Pandey *et al.* (2002).

Data (Table 2) pertaining to variance components, revealed that pulp: seed weight ratio registered highest genotypic (476921.93), environmental (88809.92), and phenotypic variance (565731.85) followed by number of seeds fruit^{-1}. Number of seeds 100g^{-1} fruit also recorded relatively high magnitude of genotypic, environmental and phenotypic variance. On the other hand, 100-seed weight had low magnitude of genotypic (0.424), environmental (0.117), and phenotypic variance (0.541).

High genotypic (GCV) and phenotypic (PCV) coefficients of variation were observed for all the traits under study. However, the genotypic coefficient of variation (GCV) was maximum for pulp: seed weight ratio (559.84%) followed by number of seeds fruit^{-1} (37.14%), 100-seed weight (34.85%) and number of seeds 100g^{-1} fruit (36.12%). The characters showing high GCV indicated that they were highly influenced by the genotypic components. The estimates of phenotypic coefficient of variation (PCV) ranged from 33.85 (average fruit weight) to 609.75% (pulp: seed weight ratio). Number of seeds 100g^{-1} fruit, number of seeds fruit^{-1} and 100-seed weight also exhibited high level of PCV(48.02, 44.49 and 39.83%), respectively. It is worthwhile to mention here that phenotypic coefficient of variation is higher than GCV, which reveals that the apparent variation is not only due to genotypes but also due to the influence of environment. Selection for such traits may not be reliable and in this case estimates of heritability and genetic advance may only help in selection of desirable genotypes from the populations. Apart from this, seed weight fruit^{-1} had comparatively low phenotypic coefficient of variation, among all the characters. This low variation indicates the stable nature of this trait among different genotypes and indicates less scope for improvement. Nevertheless, the difference between GCV and PCV was lowest for 100-seed weight indicating least influence of environment on the trait so this may be valuable trait for crop improvement.

The estimates of heritability in broad sense ranged from 0.558 (seed content) to 0.843 (pulp: seed weight ratio) suggested that all the characters had high magnitude of heritability showing heritable variation among the genotypes. In the present investigation, pulp: seed weight ratio, 100-seed weight, seed weight fruit^{-1} and number of seeds fruit^{-1} had high heritability associated with high GCV indicating less environmental effects on these characters. This suggestes that these four characters may provide greater scope for further selection. These findings are similar to the earlier results reported for fruit weight in guava (Thimmappaiah *et al*., 1985) and in banana (Kulkarni *et al*., 2002).

Burton (1952) suggested that GCV along with high heritability estimates would sketch about the extent of genetic advance for further selection. From Table 2, it is quite clear that estimate of genetic advance as percent of mean ranged from 43.76 (seed percent) to 1058.89 (pulp: seed weight ratio). Genetic advance (GA) as percent of mean for pulp: seed weight ratio, number of seeds fruit^{-1} and 100- seed weight was higher indicating that these parameters were under control of additive gene. This is in

Table 2. Estimates of variance components, GCV, PCV, heritability and genetic advance as percent of mean

Characters	Variance components			GCV	PCV	Heritability (h^2_b)	Genetic advance as percent of mean
	σ^2_g	σ^2_e	σ^2_p				
Average fruit weight (g)	1539.87	861.80	2401.67	27.10	33.85	0.641	44.70
Pulp: seed weight ratio	476921.93	88809.92	565731.85	559.84	609.75	0.843	1058.89
Number of seeds fruit^{-1}	8960.45	3886.97	12847.43	37.14	44.49	0.697	63.89
Seed weight fruit^{-1} (g)	1.36	0.52	1.88	28.90	37.97	0.724	50.66
100-seed weight (g)	0.42	0.11	0.54	34.85	39.83	0.765	62.80
Number of seeds 100g^{-1} fruit	4480.20	3432.31	7912.51	36.12	48.02	0.566	55.97
Seed content (%)	0.71	0.56	1.27	28.44	38.07	0.558	43.76

σ^2_g, σ^2_e and σ^2_p are genotypic, environmental and phenotypic variance, respectively

confirmation with the results of Kumar *et al.* (2002) who noticed additive gene action for 100-seed weight in grape genotypes.

For predicting the effect of selection, heritability estimate in combination with genetic advance is more reliable than study of heritability alone. Panse (1957) pointed out that high heritability accompanied with high genetic advance is mainly attributed to the additive gene action.

The present investigation on winter season guava crop revealed that wide variation exist in fruit weight and associated seed parameters. High GCV and heritability estimate accompanied with greater genetic advance as percent of mean were recorded for pulp: seed weight ratio, number of seeds fruit^{-1} and 100-seed weight therefore these are more reliable seed characters for effective selection.

Acknowledgements

The authors are grateful to Dr R.K. Pathak, Director CISH and Dr Ramesh Chandra, Head, CIP Division for valuable suggestions and facilities.

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