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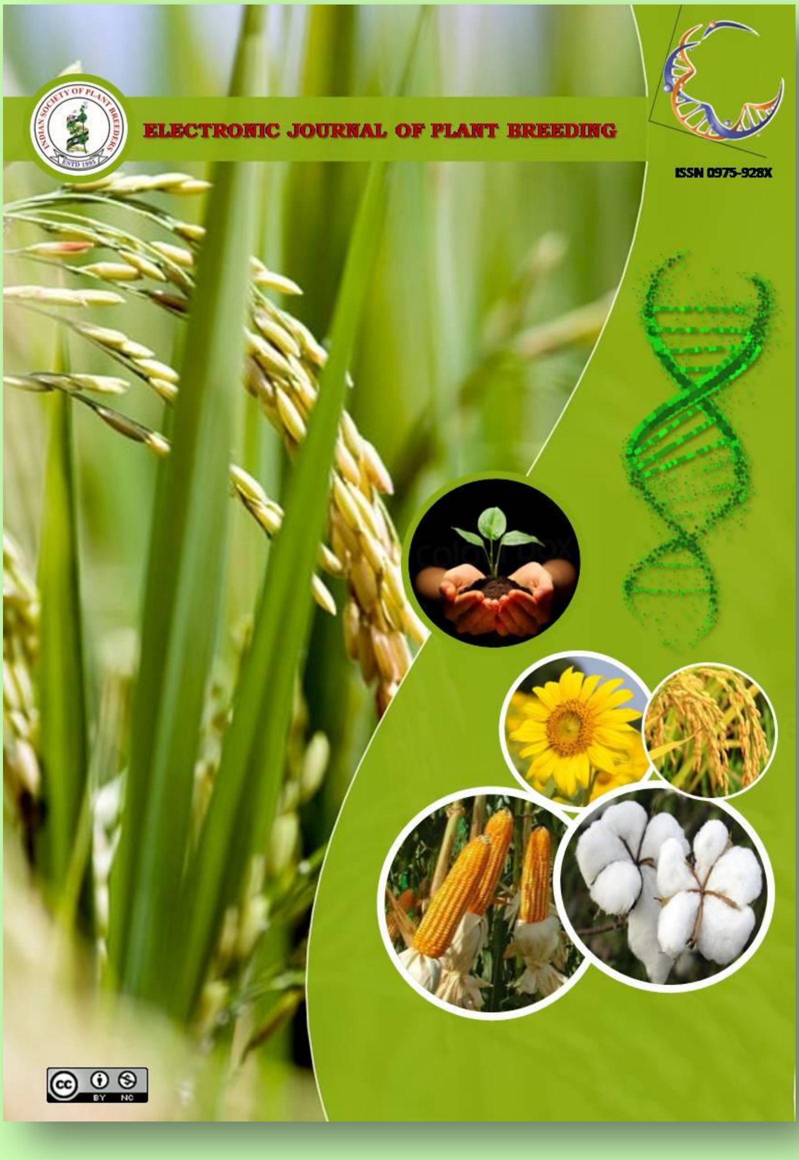

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Research Article

Genetic parameters, character association and path analysis for fruit yield and its component characters in guava (*Psidium guajava* L.)

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Abstract

The present investigation was conducted to estimate genetic parameters, correlations and path coefficients from different traits of nine genotypes in guava. The genotypes exhibited a wide range of variability for all the characters studied. The high estimates of GCV and PCV were recorded for fruit yield per plant, fruit weight, plant height, petiole size, acidity and number of seeds per fruit while low GCV and PCV were expressed by E-W plant spread, leaf length, fruit breadth and N-S plant spread. Heritability estimates revealed that all the characters under study ranged from 99.97 for leaf breadth to 61.99 for TSS. Genetic advance as percent of mean varied from 15.13 (fruit breadth) to 70.73 (number of seeds per fruit). High heritability coupled with high genetic advance as percent of mean was recorded for fruit yield, plant height, fruit weight, acidity and number of seeds per fruit indicating that these traits are under the control of additive gene action and phenotypic selection for their improvement will be effective. Significant positive association of fruit weight with fruit length (0.6134) and fruit breadth (0.7622)indicated the importance of these characters during selection for high yielding genotypes in future breeding programs.

Keywords

Correlation, GCV, Genetic Advance, Guava, Heritability, Path Analysis, PCV

Introduction

Guava (*Psidium guajava* L.) also known as poor man's apple is the most valuable cultivated species of the Myrtaceae family and is grown widely in more than sixty countries throughout the tropical and subtropical regions of the world. Guava is a popular tropical fruit due to its year round availability, affordable price, durability in transportation and handling, and overall consumer preference. The fruits are delicious, rich in Vitamin C, pectin and minerals like calcium, phosphorus and iron. Guava fruits contain antioxidant factors and are known to control the systolic blood pressure.Due to these facts, as well as the low cultivation costs, the guava crop is economically important in various tropical and subtropical countries (Rodriguez *et al*.,2010).Being a cross-pollinated species, substantial variability is available in seedling populations in different guava growing regions (Srivastava, 2005). The guava clones are varying greatly with respect to their fruit quality and yield potential (Deshmukh *et al*., 2013).In India, several guava cultivars have emerged as a result of seedling selection and are being commercially exploited through seed propagation and have indirectly given rise to several types which are not true to the commercial type and vary in several characters from the parent population (Saxen *et al*., 2007). High heterozygosity and frequent cross pollination resulted in the present day variability in seedling populations from which promising genotypes have been selected (Dinesh and Vasugi, 2010a).Genetic variability studies based on metrical characteristics of leaf and fruit may indicate genetically divergent wild genotypes with suitable traits for crop improvement (Nogueira *et al*.,2012). The assessment of genetic parameters *viz.*,genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability and genetic advance is a pre-requisite for making effective selection and improvement in the base population. Path analysis based on phenotypic correlation co-efficients further unravels the contribution of different traits towards yield. So the present study was an attempt to gather information on genetic variability, heritability, correlation and genetic advance among the important characters of guava crop, and to identify divergent parents for hybridization program, which would provide superior transgressive segregates.

Material and Methods

The experiment was carried out during 2012-14 on ten year old trees of nine genotypes *viz.*,Allahabad Safeda, Sardar, Red Fleshed, ArkyaAmulya, Behat Coconut, HisarSurkha, Hybrid Baha durgarh, Banglori Seedling and Portugal, grown and maintained in the experimental farm of Punjab Agricultural University, Regional Research Station, Bathinda, Punjab in randomized block design with three replications(one plant per replication). The orchard was laid in square system of plantation (6 m X6 m) and the trees were maintained under uniform cultural operations as per PAU recommended package of practices for cultivation of guava. The climate of the site can be characterized as arid zone with minimum and maximum temperatures ranging from 16 to 32ºC and with average annual rainfall of 480mm. The soil was sandy loam and characterized with 8.31 pH, 0.32 % organic carbon,0.24 dS/m electrical conductivity,216 kg/ha available N, 22.7 kg/ha available P and 368.0 kg /ha available K. Data on vegetative characters like, leaf length (cm), leaf breadth (cm), petiole length (cm), fruit length(cm)and fruit breadth(cm)were recorded from all the four directions of plant using Digital Vernier Caliper. For fruit characters,10 fruits per plant were collected randomly at maturity to optimum ripening stage and observations were recorded. The TSS was measured with the digital refractometer (0-85%) and acidity was estimated by 0.1 N NaOH methods (AOAC,2005).The homogeneity of error of variance, which is an assumption of analysis of variance, was tested using Bartlett's χ^2 test (Snedecor and Cochran 1983). Non significant Bartlett's χ^2 test for all studies characters reveals homogeneity of error of variance therefore combined analysis of three years data was performed. The genotypic and phenotypic coefficients of variation and heritability(in broad sense) were calculated according to Singh and Choudhary(1985), while phenotypic correlation coefficients and genetic advance were estimated as per the procedure described by Johnson *et al.*(1955). The path analysis was carried out according to the method suggested by Dewey and Lu (1959).

Results and discussion

Guava germplasm across globe as well as within India is highly diverse, so there is an immediate need to explore this wide genetic base in different climatic conditions and environments to bring out good cultivated and promising guava cultivars. The pooled analysis of variance was carried out over three years revealing significant genotypic differences for all the characteristics under study, which signified existence of substantial genetic variability in experimental plant material. The high estimates of GCV(> 15 %) and PCV were recorded for fruit yield per plant, fruit weight, plant height, petiole size, acidity and number of seeds per fruit while low GCV and PCV were expressed by E-W plant spread, leaf length, fruit breadth and N-S plant spread. The high GCV and PCV observed for these characters indicates the presence of adequate genetic variation among the genotypes and suitability of these attributes for further improvement by selection. Similar observations were recorded by Patel *et al.* (2015) for the fruit yield, Thimmappaiah *et al.* (1985) for thickness of primary branches, fruits per tree and yield and Bandopadhyay *et al.* (1992) for leaf dry matter, leaf area and life size. The occurrence of low estimates of GCV and PCV indicated that selection directly based on these traits would not be much rewarding. High GCV and PCV of seeds per fruit, fruit weight, 100-seed weight, fruit length, fruit diameter, acidity and ascorbic acid were noticed (Raghava and Tiwari, 2008). However, Bihari and Suryanarayan (2011) observed the high GCV and PCV values for fruit diameter, fruit weight, seeds per fruit, acidity and sugar in guava. Closeness between GCV and PCV for some traits indicates that the phenotypic expression of all the genotypes is mostly under the genetic control of such traits and those are comparatively stable to environmental variations.

The estimates of heritability (h^2) act as a predictive instrument in expressing the reliability of phenotypic value. Genetic advance is the indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Genetic advance depends upon the heritability of the character under selection, genetic variability of the genotypes and intensity of selection. Heritability along with genetic advance as percent of mean is more reliable than either of these two parameters alone in predicting the resultant effect of selecting the best individual. Heritability estimates revealed that all the characters under study ranged from 99.97 in leaf breadth to 61.99 in TSS (Table 1). Genetic advance as percent of mean varied from 15.13 (fruit breadth) to 70.73 (number of seeds per fruit). Higher percentage of genetic advance was also observed in fruit weight (68.05) and fruit yield per plant (56.45). High heritability coupled with high genetic advance as percent of mean was recorded for fruit yield, plant height, fruit weight, acidity and number of seeds per fruit so it can be considered that these traits are under the control of additive gene action and phenotypic selection for their improvement will be effective. The observations are in accordance with the findings of Patel *et al.* (2015), Thimmappaiah *et al.*(2008) and Suryanarayan *et al.*(2011).These characters also exhibited high GCV, therefore, selection based on phenotypic performance for these traits would be effective in improving these characters directly in the population. High values of GCV and heritability estimates supplemented with greater genetic gains are also indicative of additive gene effects regulating the inheritance of such traits (Narayan *et al.*, 1996).Sirisena and Senanayake (2000) have also reported high magnitude of heritability for fruit weight in several diverse accessions of Musa.

The degree of association of plant characters has always been useful for selection especially in the case of yield which is the multiplicative end product of many factors which jointly or singly influence it and the environment in which the crop has been grown. Positive correlation ensures simultaneous improvement in two or more variables and negative correlation brings out need to obtain a compromise between the desirable characters. The phenotypic correlation coefficients among different characters are presented in Table 2. Fruit yield per plant showed significant positive association with number of seeds per fruit (0.4415) and acidity in fruits (0.4267) and negative association with petiole size (-0.4608). Fruit weight showed significant positive association with fruit length (0.6134) and fruit breadth (0.7622). Plant height showed significant positive association with N-S plant spread (0.6584) and negative association with (-0.5535) fruit length. Fruit length has positive association with fruit breadth (0.6914) and number of seeds per fruit. Marak and Mukunda (2007) recorded that the trunk girth was significantly positively correlated with fruit yield. Patel *et al.* (2015) in guava and Gupta *et al.* (2015) in grapes also observed similar correlation with yield and other characters. Dinesh and Vasugi (2010b) also reported phenotypic coefficient of variance to the tune of 20.93 per cent for fruit weight and moderate values were found for total soluble solids and seed hardness in guava. Raghava and Tiwari(2008) also found significant positive correlation of fruit weight with fruit diameter. Bihari and Suryanarayan (2011) also reported positive correlation of fruit weight with diameter of fruit (0.862) and seed number per fruit (0.176). Correlation studies between fruit weight and its components and their relative contribution to quantitative characters are of great value in planning and evaluating breeding programs.

Path coefficient analysis is important for selection criteria as it is difficult to exploit various yield contributing characters through the knowledge of correlation alone (McGiffen *et al.*, 1994). The coefficients generated by path analysis measure the direct and indirect influence of one variable upon another (Table 3). Phenotypic path coefficient analysis revealed that positive direct effect on yield was exhibited by fruit length (1.950) followed by N-S plant spread (1.273), acidity (0.328), leaf length (0.306), number of seeds per fruit (0.166) and very low magnitude with fruit weight (0.039), plant height (0.075) and petiole size (0.006)indicating good scope for improvement in fruit yield of guava. Fruit length also showed indirect contribution via fruit weight (1.196) and fruit breadth (1.348). Highest direct effect of fruit weight towards fruit yield was also reported by Navjot *et al*. (2009) in ber. Raghava and Tiwari (2008) also recorded that leaf length and maximum leaf breadth showed positive high direct effect on fruit yield in guava. The negative direct effect on fruit yield was imposed by fruit breadth (-1.299), TSS (-0.368) and leaf breadth (-0.180). Among the quality traits, total soluble solids and acidity are the desirable attributes for fruit flavor and taste but these do not affect production.

It is doubtless that many promising varieties in case of guava has been brought to cultivation through introduction and selection however there is still ample scope to exploit this breeding technique for better guava cultivars. Inter varietal hybridization is another successful breeding technique with no crossing barriers. The technique has been widely exploited to develop some well-known guava cultivars such as H1 and H6, Safed Jam and KohirSafeda (Mitra and Bose, 1985; Shanmugavelu *et al*., 1987), ArkaAmulya (Subramanyam and Iyer, 1988), HisarSafeda, HisarSurkha. Interspecific hybridization has focused to develop wilt resistant rootstocks using *P. molle*, P.*guineense*, *P. friedrichsthalianum* (Edward and Shankar, 1964). It is evident from the present studies that fruit yield/ plant, fruit weight and number of seeds/ fruit exhibit highest genotypic and phenotypic variation as well as > 90 heritability. These are some of the important from breeding point of view. Guava has the big challenge of many seeds, seed hardness, so aneuploidy breeding has been employed to develop less seeded and dwarf cultivars. Aneuploids, particularly trisomics, have promising qualities and may be useful in developing plants with reduced seediness and possibly in providing dwarfing rootstocks. This material can also be used to develop auto tetraploids, which have also yielded some promising cultivars with less seed number in earlier studies (Kumar and Ranade, 1952). Mutations have been used in guava to improve some plant characters (Brar and Bal, 2003), however intensive screening is required to standardize the optimum dose to acquire desirable traits. Some physical and chemical mutagens can be evaluated in these cultivars of guava to obtain the desired characters. There is also wide scope of employing latest techniques of tissue culture, micro propagation and marker assisted selection in guava improvement programme. Tissue culture and micro propagation of superior guava cultivars has been reported by many workers (Amin and Jaiswal, 1988; Loh and Rao, 1989; Papadatou *et al*., 1990). Tissue culture occurring somaclonal variation may be useful for selecting guava plants resistant to wilt disease, however this requires an efficient plant regeneration protocol from callus culture. Additionally the plants of haploid origin from anther/pollen culture of guava could offer advantages in breeding. On the basis of present study, it may be concluded that all the characters showed significant variability and provide great opportunity in above discussed breeding program to get desired varieties. Genetic parameters such as heritability, genetic advance, coefficient of variance and correlation coefficient analysis showed encouraging results to transfer desired traits into elite cultivar by employing any of the available breeding technique. Qualitative characters such as fruit weight, fruit breadth and fruit length are the major yield contributing characters and during selection or other breeding techniques, weightage should be given to these characters for the development of high yielding genotypes of guava.

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Table 1.Genetic parameters for fruit yield and its components in guava.

Character	**Mean**	**Heritability (h^2)**	**GA (%)**	**PCV (%)**	**GCV (%)**
Fruit yield/plant (kg)	96.75	91.96	56.45	29.80	28.58
Fruit weight (g)	137.44	91.43	68.05	36.13	34.55
Plant height (m)	3.29	99.87	34.49	16.76	16.75
N-S plant spread (m)	4.03	99.60	22.83	11.13	11.10
E-W plant spread (m)	4.18	99.60	18.74	9.13	9.11
Leaf length (cm)	12.52	99.83	20.08	9.76	9.76
Leaf breadth (cm)	5.91	99.97	24.42	11.86	11.86
Petiole size (cm)	0.68	99.18	32.63	15.97	15.90
Fruit length (cm)	6.10	78.33	26.11	16.18	14.32
Fruit breadth (cm)	5.57	71.40	15.13	10.29	8.69
TSS (%)	10.41	61.99	17.72	13.88	10.92
Acidity (%)	0.18	80.66	32.15	19.35	17.38
Number of seeds/fruit	251.52	92.39	70.73	37.17	35.72

Table 2.Phenotypic correlation coefficients of fruit yield and component characters in guava

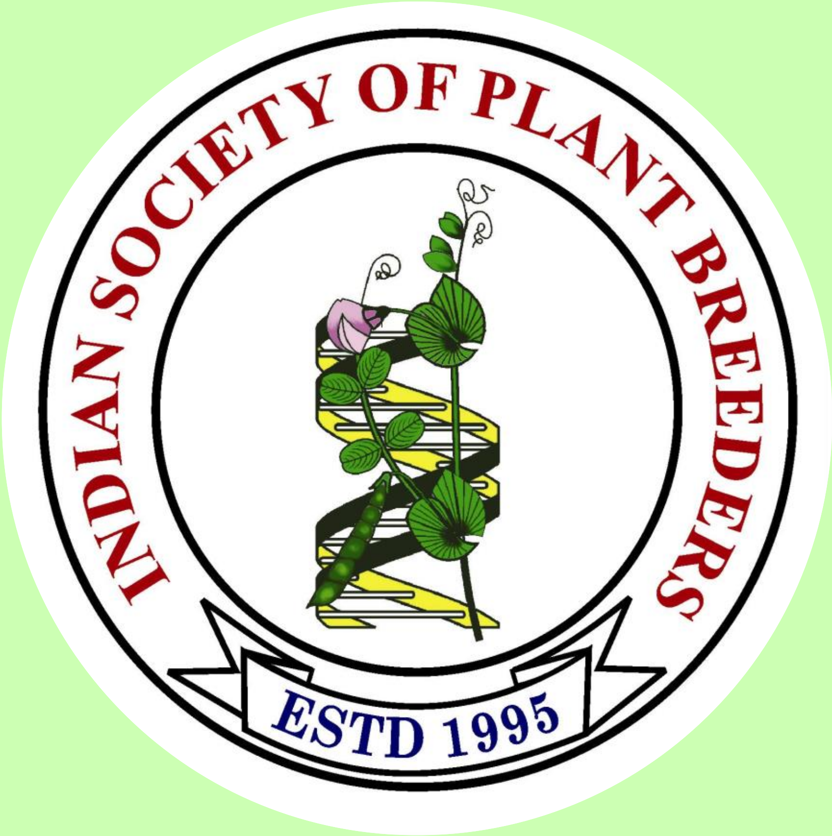
Characters	Fruit yield/plant	Fruit weight	Plant height	N-S plant spread	E-W plant spread	Leaf length	Leaf breadth	Petiole size	Fruit length	Fruit breadth	TSS (%)	Acidity (%)	Seeds/ fruit
Fruit yield/plant	1.000												
Fruit weight	0.2863	1.000											
Plant height	0.2492	-0.3029	1.000										
N-S plant spread	0.2351	-0.0188	0.6584*	1.000									
E-W plant spread	-0.1113	-0.0255	0.3216	0.6419*	1.000								
Leaf length	-0.1605	-0.2147	0.5093*	0.2392	0.5726*	1.000							
Leaf breadth	-0.2353	-0.1560	-0.0182	0.2302	0.5907*	0.6908*	1.000						
Petiole size	-0.4608*	-0.0366	-0.4898*	- 0.5552	0.1083	0.3599	0.4454*	1.000					
Fruit length	0.2458	0.6134*	-0.5535*	-0.6178*	-0.4608*	-0.2362	-0.1480	0.3300	1.000				
Fruit breadth	0.1184	0.7622*	-0.2451	-0.0329	0.1304	0.1157	0.1808	0.2946	0.6914*	1.000			
TSS (%)	-0.0135	-0.4380*	0.4289*	0.6209*	0.2468	0.0813	0.2487	-0.4252*	-0.5720*	-0.3900*	1.000		
Acidity (%)	0.4267*	-0.1010	0.2265	0.6189*	0.0776	-0.3099	-0.0184	-0.5512*	-0.3573	-0.1933	0.4648*	1.000	
Seeds/ fruit	0.4415*	0.2441	-0.4556*	-0.6015*	-0.4065*	-0.2417	-0.1649	0.1014	0.5634*	0.0368	-0.5153*	-0.2610	1.000

*Significant at 5% level of significance

Table 3.**Path analysis coefficient at phenotypic level of fruit yield versus component characters in guava**

Character	Fruit weight	Plant height	N-S plant spread	E-W plant spread	Leaf length	Leaf breadth	Petiole size	Fruit length	Fruit breadth	TSS (%)	Acidity (%)	Seeds/ fruit	PCC with fruit yield
Fruit weight	0.039	-0.022	-0.024	-0.003	-0.066	0.028	-0.000	1.196	-0.990	0.161	-0.033	0.000	0.2863
Plant height	-0.012	0.075	0.838	0.036	0.156	0.003	-0.003	-1.079	0.318	-0.158	0.074	0.000	-0.3039
N-S plant spread	-0.001	0.043	1.273	0.072	0.073	-0.041	-0.003	-1.205	0.043	-0.229	0.203	0.000	0.6584*
E-W plant spread	-0.001	0.024	0.817	0.112	0.175	-0.106	0.001	-0.899	-0.169	-0.091	0.026	0.000	0.6419*
Leaf length	-0.008	0.038	0.305	0.064	0.306	-0.124	0.002	-0.461	-0.150	-0.030	-0.102	0.000	0.5726*
Leaf breadth	-0.006	-0.001	0.293	0.066	0.211	-0.180	0.003	-0.289	-0.235	-0.092	-0.006	0.000	0.6908*
Petiole size	-0.001	-0.037	-0.707	0.012	0.110	-0.080	0.006	0.644	-0.383	0.157	-0.181	0.000	0.4454*
Fruit length	0.024	-0.041	-0.787	-0.052	-0.072	0.027	0.002	1.950	-0.898	0.211	-0.117	0.000	0.3300
Fruit breadth	0.030	-0.018	-0.042	0.015	0.035	-0.033	0.002	1.348	-1.299	0.144	-0.064	0.000	0.6914*
TSS (%)	-0.017	0.032	0.791	0.028	0.025	-0.045	-0.002	-1.116	0.507	-0.368	0.153	0.000	-0.3900*
Acidity(%)	-0.004	0.017	0.788	0.009	-0.095	0.003	-0.003	-0.697	0.251	-0.171	0.328	0.000	0.4648*
Seeds/fruit	0.010	-0.034	-0.766	-0.046	-0.074	0.030	0.001	1.099	-0.048	0.190	-0.086	0.166	-0.2610

Residual effect for phenotypic path = 0.222
Underlined values are direct effect on fruit yield/plant
*Significant at 5% level of significance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