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EVALUATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN THIRTY-FIVE BOTTLE GOURD (*LAGENARIA SICERARIA*) VARIETIES FOR YIELD AND YIELD RELATED TRAITS

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Thirty-five bottle gourd genotypes collected from different geographical locations were utilized for the present study to study genetic variability, genetic diversity and character association among 15 traits. The characters number of primary branches, sex ratio, fruit weight, fruit length, fruit width, number fruit vine⁻¹ and fruit yield vine⁻¹ recorded high amount of genetic variability along with heritability and genetic advance indicating that selection for these characters are simple and easy. The evaluation showed the presence of wide genetic diversity as they formed five gene constellations in genetic divergence analysis. The clustering pattern of genotypes revealed that there was no parallelism between geographical diversity and genetic diversity among the genotypes studied. The cluster III was found to constitute the maximum of nineteen genotypes; while cluster V was mono genotypic. The high inter cluster distance was observed between clusters IV and V which indicated the possibility of getting transgressive segregants in advanced generations by intermating between genotypes belonging to these clusters. Path analysis revealed that the fruit characters such as fruit weight, fruit length and number of fruits vine⁻¹ were considered as important traits which directly or indirectly influenced the yield. The correlation study also confirmed the same.

Key words : Transgressive segregants, Coefficient of variability, Genetic advance, Heritability, Bottle gourd.

Introduction

Bottle gourd is highly valued for its nutrition and medicinal properties. The fruit is rich in moisture (96.1 g), protein (0.2 g), carbohydrate (2.5 g) and have traces of minerals like calcium (20 mg), Phosphorus (10 mg) and iron (0.7 mg) in 100 gm of fruit (Thamburaj and Narendra, 2000). Varietal improvement in bottle gourd confers greater significance considering its economic importance. Being a cross - pollinated crop, it has a wide range of variability for maturity, yield and other fruit attributes, which is useful in exploitation of hybrid vigor.

Success of any breeding programme depends on the amount of variability present in the breeding population. Selection exercised over a period with local varieties has nearly exhausted the natural variability present in this crop. In spite of its high economic importance and existing variability in plant and fruit characters, the genetic potentialities of bottle gourd are practically unexplored and very little attempt has so far been made for its genetic improvement (Verma and Behera, 2007). Genetic variability present in the population is inevitable for the selection process. Hence high heritability coupled with high genetic advance was reported to be more useful in practicing selection in a population. Genetic diversity analysis among the elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctiveness among genotypes (Singh et al, 2013). Since, yield is poly genetically inherited and collectively influenced by various components, the genotypic correlation co-efficient in addition to path coefficient estimates may provide information on relative importance of yield components.

Keeping all these theories in view, the present study was oriented to gain further knowledge on the genetic aspects of yield and its components in bottle gourd for commercial exploitation of heterosis by studying the variability, heritability, genetic advance, genetic divergence, character association and the relative contribution of direct and indirect effects of various traits on fruit yield in the germplasm.

Materials and Methods

The present investigation was carried out in the Farmers field at Karaikal in Puducherry District during 2020-2021, which is situated at 10° 49' and 11°01' N Latitude and 79°52'E Longitude, at an altitude of 4 m above mean sea level. Thirty-five bottle gourd genotypes were collected from different geographical locations and utilized for the present study. Seed materials were from IIHR, Bengaluru, IARI, New Delhi, local types and land races collected from different parts of Tamil Nadu and Northern part of India. The genotypes were raised in a randomized block design with three replications during January, 2021 to May, 2021. The seeds were sown in the pits adopting a spacing of $2 \times 2m$. Recommended cultural practices were followed uniformly to all the genotypes. Observations such as vine length, number of primary branches, node of first male flower appearance, node of first female flower appearance, days to first male flower anthesis, days to first female flower anthesis, sex ratio, days to first harvest, fruit length, fruit width, fruit cavity, fruit flesh thickness, fruit weight, number of fruits vine⁻¹ and fruit yield vine-1 were recorded in ten randomly selected plants in each of the replication.

Phenotypic and Genotypic coefficient of variations were estimated using the formula suggested by Burton (1952) and expressed in percentage. Heritability in broad sense (h^2) was calculated according to Lush (1940) and expressed in per cent. The range of heritability was categorized as below as suggested by Johnson *et al.* (1955). Genetic advance was worked out based on the formula suggested by Johnson *et al.* (1955). The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

The D² analysis suggested by Mahalanobis (1936) was used for estimating the divergence among the 35 genotypes. The transformation was done by the pivotal condensation method of Rao (1952). All possible D² values {n(n-1)/2} were worked out by taking the sum of difference between pairs of corresponding 'Y' values taking two genotypes at a time. The D² values were estimated using computer with GENRES statistical package. Based on degree of divergence (D² values)

between any two genotypes, grouping of genotypes was done by using Tocher's method (Singh *et al.*, 1977). The average inter cluster divergence was arrived at by taking into consideration of all the component D² values possible among the members of the two clusters considered. The square root of the average D² values gave the genetic distance D between clusters. Based on the D values (inter cluster distances) the following scale for rating of the distance was adopted (Rao, 1952). Ranking was done as per the method outlined by Singh and Chaudhary (1977). Each character is ranked based on the transformed correlated 'Y' values. The genotypes were ranked based on the method laid out by Zeng *et al.* (2002).

The association between yield and component traits and among themselves was computed based on *per se* performance of the genotypes as genotypic correlation coefficients (Goulden, 1952). The variance and covariance components were utilized to calculate genotypic correlation coefficients as outlined by Aljibour *et al.* (1958). Path coefficient analysis was carried out according to Dewey and Lu (1959) by partitioning the genotypic correlation coefficients into direct and indirect effects. The direct and indirect effects were classified based on the scale given by Lenka and Mishra (1973).

Results and Discussion

Information about the genetic variability in the population is a prerequisite for success of any breeding programme. Presence of high variability offers much scope for improvement and enables the breeders to identify most potential genotypes. Measure of genotypic and phenotypic coefficient of variations is useful in detecting the amount of variability present in the genotypes. In the present study relatively, high estimates of genotypic and phenotypic coefficients of variation were observed for sex ratio, fruit weight and number of fruits vine⁻¹. This is in accordance with the findings of Devi and Mariappan (2013) in snake gourd who observed similar results for fruit weight and number of fruits vine-1 and Maurya et al. (2018) in bitter gourd, Sahoo and Singh (2020) in cucumber also observed cognate results for fruit weight. Kandasmay et al. (2019), Chandramouli et al. (2021) and Sultana et al. (2018) also recorded similar results for number of fruits vine⁻¹ in bottle gourd. Moderate phenotypic and genotypic coefficients of variation (10-19 per cent) were observed for vine length, number of primary branches, fruit flesh thickness and yield vine⁻¹ (Table 1). Selection for these traits may also be given due importance in an improvement programme. In bottle gourd Varalakshmi et al. (2018) also opined the same for vine length. Khan et al. (2020) and Rashid et

S. no.	Traits	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability h ² (broad sense)	Genetic advance
1	Vine length	304.69	202.33-401.12	13.78	14.28	93.00	27.40
2	Number of primary branches	8.04	5.86-11.17	13.43	16.10	69.00	23.07
3	Node of first male flower appearance	8.46	7.23-9.30	4.73	10.33	20.00	4.46
4	Node of first female flower appearance	13.20	11.48-14.98	5.04	7.87	41.00	6.65
5	Days to first male flower anthesis	42.95	40.56-46.47	2.84	4.62	37.00	3.61
6	Days to first female flower anthesis	48.90	47.58-51.29	1.38	2.13	42.00	1.85
7	Sex ratio	0.48	0.19-0.72	24.79	34.19	52.00	37.03
8	Days to first harvest	60.80	58.12-62.91	1.39	2.19	40.00	1.82
9	Fruit length	38.25	33.46-43.03	5.96	6.39	87.00	11.46
10	Fruit width	23.30	20.16-26.89	6.52	7.46	76.00	11.73
11	Fruit cavity	7.75	6.23 - 9.35	9.19	9.78	88.00	17.79
12	Fruit flesh thickness	1.62	1.23-2.33	11.07	18.09	37.00	13.97
13	Fruit weight	1.78	1.40-2.38	13.21	22.19	35.00	16.21
14	Number of fruits vine ⁻¹	2.53	1.96-3.58	15.51	20.20	59.00	24.55
15	Fruit yield vine-1	16.99	11.98-22.35	12.64	18.89	44.00	17.44

Table 1 : Estimates of genetic variability parameters for various quantitative characters in bottle gourd.

al. (2020) have also come out with such results for node of male flower appearance. Shah *et al.* (2018) in cucumber in ridge gourd did observe cognate results for vine length. Rani and Reddy (2017) in bottle gourd reported such results for fruit yield vine⁻¹. The coefficients of phenotypic and genotypic variation in respect to most of the characters did not differ much in their magnitude suggesting that the characters were not much amenable to environmental factors, thus the selection may be executed based very well on the phenotypic values. Such narrow performances were reported by Samadia *et al.* (2011) in ridge gourd.

It is advisable to consider the predicted genetic advance as per cent of mean along with heritability estimates as a reliable tool in selection programme (Abhishek *et al.*, 2021). In the present investigation, high heritability coupled with high genetic advance was observed for vine length and number of primary branches which indicated that the selection among the genotypes can bring about significant improvement in the fruit yield and its component characters. This result is in conformity with findings of Varalakshmi *et al.* (2018) and Shah *et al.* (2018) in bottle gourd and Ingole *et al.* (2021) in pumpkin. Further, high heritability combined with medium genetic advance established the existence of additive gene effects for fruit length, fruit width and fruit cavity. Similar findings were reported by (Srikanth et al., 2017) in pumpkin and Damor et al. (2016) in bottle gourd. Sex ratio and number of fruits vine-1 exhibited moderate amount of heritability and high genetic advance which again indicated the prevalence of additive gene action. Therefore, selection might be effective as reported earlier by Shahoo and Singh (2020) in cucumber and Chandramouli et al. (2021) in bottle gourd. Moderate heritability along with medium genetic advance was observed for fruit thickness, fruit weight and fruit yield vine⁻¹ (Table 1). This also indicated the role of additive gene action in determination of these traits. Similar findings were also reported by Maurya et al. (2018) and Kanthasamy et al. (2019) in bottle gourd. Node of first female flower appearance, days to first male flower anthesis and days to first harvest showed moderate heritability and low genetic advance as per cent of mean, which indicated that the expression of these characters are governed by non-additive gene factors. Similar differential performances were reported by Srikanth et

Cluster No	Number of genotypes	Genotypes
Cluster I	10	CO1, Ambrit, Punjab Komal, ArkaBahar, Ajmer Local, Subam, Uttam, Angad, Bahour Local and Vellore Local
Cluster II	2	Paraivai Local and Karaikal Local
Cluster III	19	Peralam Local, Karnal Local, Cuddalore Local, Akkampally Local, Angul Local, Mysore Local, Dharwad Local, Nellore Local, Mannadipet Local, Kumbakonam Local, Vedaraniyam Local, Pusa Naveen, C.B.H.1, Ramapuram Local, Varisurai, Sati surai, Neetu surai, Kuduvaisurai and Vathusurai
Cluster IV	3	Waman, Pachaisurai and Thiruvarur Local
Cluster V	1	Kumbusurai

Table 2 : Distribution of thirty-five bottle gourd genotypes in clusters.

Table 3: Average Inter and intra cluster distances in bottle gourd genotypes. that the genotypes did not resolve according to

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	9.097	9.044	10.502	12.236	9.462
Cluster II		4.493	10.833	9.191	10.029
Cluster III			10.139	13.718	10.434
Cluster IV				9.690	14.407
Cluster V					0.000

al. (2017) in pumpkin and Lal et al. (2021) in bottle gourd.

Quantitative measurement of genetic divergence would enable the plant breeders to understand the racial affinities and evolutionary pattern in various crop species or cultivated plants as well as in decision making for selection of desirable parents in hybridization programme. Among several methods of multivariate analysis, Mahalanobis D^2 statistics is very useful in selecting parents for hybridization. In the present study, thirty-five genotypes formed five gene constellations indicating wide genetic diversity (Table 2). The clustering pattern revealed that the genotypes did not resolve according to their geographical origin. Similar findings were reported by Rambabu *et al.* (2020) and Kumar *et al.* (2021) and Quamruzzaman *et al.* (2020) in bottle gourd. The average intra and inter cluster D² values among the thirty-five bottle gourd genotypes (Table 3) revealed that the cluster III had the maximum intra cluster D²

values, followed by cluster IV, I and II. This is indicative of the fact that the genotypes included in these clusters are very diverse. At inter cluster level, minimum D^2 values was observed between cluster I and II revealing closer relation among the genotypes included in these clusters. The inter cluster D^2 value was found to be maximum between cluster IV and cluster V followed by cluster III and cluster IV. The genotypes belonging to clusters III and IV have greater genetic divergence and hence intermating between the genotypes belonging to them would give more transgressive segregants in advanced

Table 4 : Cluster mean for 15 characters in bottle gourd genotypes.

S. no.	Characters/ Clusters	Ι	I	Ш	IV	V
1	Vine length	299.47	330.30	295.49	383.13	245.10
2	Number of primary branches	7.81	8.10	7.76	10.62	7.75
3	Node of first male flower appearance	8.29	7.76	8.49	9.05	13.03
4	Node of first female flower appearance	12.95	12.57	13.47	9.17	12.27
5	Days to first male flower anthesis	43.86	42.30	42.75	41.27	49.18
6	Days to first female flower anthesis	48.89	48.81	48.75	43.84	51.29
7	Sex ratio	0.42	0.52	0.51	0.45	0.44
8	Days to first harvest	60.25	61.62	60.76	61.66	62.91
9	Fruit length	39.23	39.87	37.46	38.13	40.58
10	Fruit width	23.58	22.42	23.32	22.88	23.01
11	Fruit cavity	7.87	6.84	7.81	7.69	7.54
12	Fruit flesh thickness	1.49	1.58	1.68	1.68	1.54
13	Fruit weight	1.76	2.09	1.73	2.06	1.51
14	Number of fruits vine ⁻¹	2.87	2.22	2.44	2.25	2.30
15	Fruit yield vine ⁻¹	18.72	16.99	15.85	17.93	18.49

generations. Selection of genotypes belonging to clusters with maximum inter cluster distance had also been proposed by Dora et al. (2002) in pointed gourd and Sundaram (2006) in bitter gourd. Cluster mean values for fifteen characters of thirty-five genotypes revealed maximum mean values for fruit width, fruit cavity, number of fruits vine-1 and fruit yield vine-1 and maximum mean values for sex ratio and days to first harvest was represented in cluster I. The maximum cluster mean for fruit weight and minimum mean for node of first male flower appearance was found in cluster II. The maximum cluster mean for fruit flesh thickness was represented by cluster III. The minimum cluster mean for node of first female flower appearance, days to first male and female flower anthesis and maximum cluster for vine length and number of primary branches was found in cluster IV (Table 4). Similar findings were reported by Khatun et al. (2010) in snake gourd and Rashid et al. (2020) in bottle gourd. Such variations in yield and yield attributes among the genotypes differed in their morphological and physiological characteristics and in the translocation of carbohydrates from source to sink (Rani et al., 2014). In addition to the knowledge on the degree of divergence, the study also revealed that the contribution of different characters was responsible for total genetic divergence. The character that appears for maximum number of times ranks first and thus greater is its contribution towards genetic divergence. In the present investigation, an assessment of the contribution of different characters indicated that, fruit yield vine-¹ was the maximum contributor for genetic divergence, followed by fruit cavity, number of fruits vine-1, fruit length, fruit width, vine length and sex ratio. The importance of fruit yield vine⁻¹ in genetic divergence of bottle gourd had been observed by Khatun et al. (2010) and Prabakaran (2010) in chow chow. The relative contribution of node of first male

Table 5 : Genotypic correlation coefficients between vield and vield components in bottle gourd.

	\mathbf{X}_{1}	\mathbf{X}_2	\mathbf{X}_3	\mathbf{X}_4	$\mathbf{X}_{\mathbf{s}}$	$\mathbf{X}_{_{6}}$	\mathbf{X}_{7}	$\mathbf{X}_{\mathbf{s}}$	\mathbf{X}_9	\mathbf{X}_{10}	$\mathbf{X}_{\mathbf{n}}$	\mathbf{X}_{12}	$\mathbf{X}_{_{13}}$	$\mathbf{X}_{^{14}}$	\mathbf{X}_{15}
X	1.000	0.896^{**}	-0.089	0.220*	-0.366**	-0.210*	0.064	0.082	-0.277**	-0.108	-0.264**	-0.054	0.720^{**}	-0.492**	-0.120
\mathbf{X}_2		1.000	0.102	-0.078	-0.436**	-0.408**	0.063	0.044	-0.310**	-0.265**	-0.228*	0.130	0.770^{**}	-0.450**	0.071
X ₃			1.000	0.616^{**}	-0.310**	0.305**	-0.927**	0.273^{**}	-0.360**	0.300**	0.155	0.054	-0.778**	-0.926**	0.072
\mathbf{X}_{4}				1.000	-0.147	-0.393**	0.135	0.067	-0.360**	0.691^{**}	-0.122	0.524**	0.728**	-0.298**	-0.872**
X					1.000	0.593**	0.142	0.227*	-0.047	0.070	-0.054	-0.693**	0.413^{**}	0.798**	0.185**
×°						1.000	-0.289**	0.483**	0.442**	0.260^{**}	0.187	-0.042	-0.476**	0.217^{*}	0.186^{**}
X,							1.000	0.116	-0.186	-0.438**	-0.098	0.304**	-0.643**	-0.210*	-0.500**
X								1.000	0.203*	0.140	0.056	0.428**	0.667^{**}	-0.428**	0.026
X,									1.000	0.188	-0.025	0.253**	0.659**	0.485**	0.170
\mathbf{X}_{10}										1.000	-0.064	0.070	-0.100	-0.002	-0.243*
X											1.000	0.146	-0.946**	0.467**	-0.214*
\mathbf{X}_{12}												1.000	0.092	-0.542**	-0.299**
\mathbf{X}_{13}													1.000	-0.691**	0.209*
\mathbf{X}_{14}														1.000	0.144
$\mathbf{X}_{_{15}}$															1.000
$X_i - V_i$	ne length				$X_7 - Sex$	k ratio		\mathbf{X}_{12} -	-Fruit flesh	thickness					
X ₂ -Nu	umber of pri	imary branc	shes		$X_{s} - Da$	ys to first	harvest	$\mathbf{X}_{13}^{r_2}$	-Fruit weig	ht					
\mathbf{X}_{3}^{-} Nc	de of first r	nale flower	appearanc	e	X ₉ -Frui	it length		$\mathbf{X}_{^{14}-}$	Number fr	uits vine ⁻¹					
$\mathbf{X}_4 - \mathbf{N}_4$	ode of first	female flow	ver appeara	ance	${ m X}_{ m _{10}}$ –Fru	iit width		X_{15} -	Fruit yield	vine ⁻¹					
$X_5 - D_5$	ays to first 1	male flower	r anthesis		X_{11} –Fru	uit cavity									
X - D	avs to first 1	female flow	er anthesis	<i>•</i>											

				-			-		-					
	X ₁	X ₂	X ₃	X4	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄
X ₁	-0.483	-1.432	0.244	-0.833	0.104	-0.043	-0.087	-0.132	0.589	-0.315	-0.596	-0.028	0.793	2.101
X ₂	-0.432	-1.599	-0.280	0.294	0.124	-0.084	-0.085	-0.071	0.658	-0.776	-0.515	0.067	0.848	1.924
X ₃	0.042	-0.162	-2.757	-2.330	0.374	0.063	1.263	-0.444	0.766	0.881	0.350	0.028	-1.959	3.957
X ₄	-0.106	0.124	-1.697	-3.785	0.041	-0.081	-0.183	-0.109	0.764	2.026	-0.276	0.273	0.861	1.275
X ₅	0.176	0.697	3.614	0.555	-0.285	0.123	-0.193	-0.370	0.099	0.204	-0.122	-0.361	0.455	-3.408
X ₆	0.101	0.652	-0.840	1.488	-0.169	0.208	0.394	-0.787	-0.940	0.762	0.422	-0.022	-0.525	-0.927
X ₇	-0.031	-0.100	2.556	-0.509	-0.040	-0.060	-1.363	-0.188	0.395	-1.284	-0.220	0.158	-0.708	0.898
X ₈	-0.039	-0.069	-0.751	-0.253	-0.064	0.100	-0.158	-1.629	-0.431	0.411	0.126	0.223	0.734	1.827
X ₉	0.134	0.495	0.994	1.361	0.013	0.092	0.253	-0.330	-2.126	0.552	-0.055	0.132	0.726	-2.072
X ₁₀	0.051	0.423	-0.828	-2.615	-0.019	0.054	0.597	-0.228	-0.400	2.933	-0.145	0.036	-0.109	0.007
X ₁₁	0.127	0.365	-0.427	0.462	0.015	0.038	0.132	-0.091	0.052	-0.188	2.259	0.075	-1.042	-1.995
X ₁₂	0.026	-0.207	-0.148	-1.983	0.197	-0.008	-0.414	-0.696	-0.538	0.205	0.328	0.521	0.101	2.316
X ₁₃	-0.348	-1.231	4.904	-2.960	-0.117	-0.099	0.876	-1.086	-1.400	-0.292	-2.137	0.048	1.102	2.952
X ₁₄	0.237	0.720	2.553	1.129	-0.227	0.045	0.286	0.696	-1.031	-0.005	1.055	-0.282	-0.761	3.121

Table 6 : Direct and indirect effects of yield components on fruit yield in bottle gourd.

Residual effect - 0.462

 $X_1 - Vine length$

 X_2 –Number of primary branches

- $\tilde{X_{2}}$ –Node of first male flower appearance
- X_4 Node of first female flower appearance

 X_{5}^{*} – Days to first male flower anthesis

flower appearance, node of first female flower appearance, days to first male flower anthesis and days to first female flower anthesis for divergence among the genotypes was found to be meager, while the number of primary branches, days to first harvest exhibited very less contribution. The study also indicated that the characters such as yield vine-1, number of fruits vine-1, fruit cavity, fruit width, fruit length, vine length, sex ratio, fruit weight and fruit flesh thickness should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence. In the present investigation the clusters I, II and III indicated high yield potential, earliness and market quality which registered wider inter and intra cluster distance. The genotypes of these clusters were placed high based on their mean performance with regard to the characters of preference. Thus, twelve lines and three testers were selected from the clusters I, II and III. They were crossed to obtain thirty-six hybrids.

Yield is a polygenic complex character (Grafius, 1964) and it is influenced by number of economic traits that are in turn interrelated. The correlation coefficients indicate inherent association between various characters. An estimate of genotypic and phenotypic correlation coefficients gives a measure of genotypic association since it has an inherited relationship between the traits. The greater the magnitude of correlation coefficient, the stronger is the association. Results of the present

 $X_7 - Sex ratio$

 X_{8} – Days to first harvest

X₉-Fruit length

X₁₀ –Fruit width

 X_{11}^{--} -Fruit cavity

 X_{12} –Fruit flesh thickness X_{13} –Fruit weight

 X_{14}^{15} – Number fruits vine⁻¹

investigation, on association of observed traits with fruit yield revealed that only three characters viz., fruit weight, days to first male flower anthesis and days to first female flower anthesis recorded significant association with fruit yield both at phenotypic and genotypic levels indicating that fruit yield in bottle gourd could be improved by direct selection for fruit weight. Such kind of positive association was quoted by Ahmed et al. (2005) for average fruit weight and fruit length in bottle gourd, Pandey et al. (2006) for number of fruit vine⁻¹ and average fruit weight in sponge gourd. The characters like node of first male flower appearance, sex ratio, fruit width, fruit cavity and fruit flesh thickness showed negative and highly significant correlation with fruit yield vine⁻¹ both at genotypic and phenotypic levels. Negative correlation observed through sex ratio implies that fruit yield plant⁻¹ increased with decrease in sex ratio. Similar findings were reported by Khatoon et al. (2016) in ridge gourd and Parvatiand Reddy (2006) in bottle gourd. Sex ratio exhibited significant and positive correlation with fruit flesh thickness. The fruit cavity had positive and highly significant correlation with number of fruit vine⁻¹ (Table 5).

Selection of superior genotypes based on yield as such may not be effective for the enhancement of yield and hence selection should be made for the component traits as well. Path coefficient analysis provides an effective means of partitioning direct and indirect causes of association; it permits a critical look to recognize the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. The path analysis revealed that the residual effect (0.462)indicating the adequacy of the traits chosen for the study. The results indicated existence of positive direct effect on fruit weight, number of fruit vine⁻¹, fruit flesh thickness and days to first female flower anthesis. Therefore, plants having a greater number of fruits with average fruit weight could be considered in selection for increasing fruit yield. Directly or indirectly all characters showed positive effect on fruit yield. This was in confirmation with the findings of Husna et al. (2011) and Janaranjani and Kanthaswamy (2015) who reported that number of fruits vine⁻¹ had maximum direct effect on yield followed by fruit weight in bottle gourd. The negative direct effect on yield was recorded by all other characters viz., vine length, number of primary branches, node of first male and female flower appearance, days to first male flower anthesis, days to first harvest, fruit width and fruit cavity (Table 6).

Conclusion

In conclusion, the present study revealed that the characters number of primary branches, sex ratio, fruit weight, fruit length, fruit width, number fruit vine⁻¹ and fruit yield vine⁻¹ recorded high amount of genetic variability along with heritability and genetic advance. Hence, selection for these characters are simple and easy. The study on D^2 analysis revealed that the cluster mean for fruit yield vine⁻¹ was the highest in cluster I and III. The high inter cluster distance was observed between clusters IV and V, which indicated the possibility of getting transgressive segregants in advanced generations by internating between genotypes belonging to these clusters. Path analysis revealed that the fruit characters such as fruit weight, fruit length and number of fruits vine⁻¹ were considered as important traits which directly or indirectly influenced the yield. The correlation study also confirmed the same.

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