Genetic Variability, Correlation and Path Coefficient Analysis in Bottle Gourd [*Lagenaria siceraria* (Molina) Standl.] Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out at the Experimental field of Urban Technological Park Habbak, Srinagar, Jammu and Kashmir during kharif-2022. The experiment was laid out in Augmented Randomized Block Design with three blocks and plant spacing of 2×1 m for seventy-

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seven genotypes including two checks, Pusa Naveen and Pusa Santushti. Observations were recorded for growth and yield traits, seed traits and quality parameters. Analysis of variance revealed significant differences among genotypes for all the traits. The estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied indicating little influence of environment in the expression of these traits. The highest phenotypic and genotypic coefficient of variation were observed for seed weight fruit-1 (45.15 and 45.13). High heritability coupled with high genetic gain was recorded for seed weight fruit-1 (0.99 and 93.01), indicating that the heritability is most likely due to additive gene effects and thus the chances of fixing this trait by selection are more. The estimates of heritability in broad sense were high for all the traits. Correlation studies indicated that fruit yield plant-1 followed by fruit weight, vine length, number of primary branches and number of fruits plant-1 had significant and positive correlation with fruit yield ha-1. Path coefficient analysis showed that fruit yield plant-1 followed by fruit weight, number of primary branches, node number at which 1st male flower appeared and fruit diameter had highest direct effects on the yield per ha-1.

1. INTRODUCTION

"Bottle gourd [*Lagenaria siceraria* (Molina) Standl.] commonly known as Lauki or Ghiya in India is one of the most important member of the family Cucurbitaceae and believed to be originated in Africa" [1]. "It has spread to western countries from India and Africa. The genus Lagenaria includes six species that are distributed in Africa, Madagascar, Indo-Malaysia and the neotropics. There is only one cultivated species, *Lagenaria siceraria*, which is annual and monoecious. The five other species are wild, perennial and dioecious, occurring in East Africa and Madagascar. The tender fruits are also used to prepare sweets, raita and pickles. The dried shells of mature fruits are extremely hard and are used as containers, utensils, musical instruments, floats of fishnets or ornamental items. The leaves are also used to prepare vegetable and they have higher nutritive value than fruits, in respect of protein, fat, minerals, fibre, carbohydrate, energy, calcium and phosphorus content. Different plant parts of bottle gourd have several putative medicinal properties" [2]. It is commercially grown in all the states of India in both rainy and summer seasons. Bottle gourd is rich in vitamins, minerals, antioxidants, and dietary fibre. Its edible part has a moisture content of approximately 95.54%. According to USDA [3], the fruit has the following nutritional values per 100g: Vitamin C (10.1 mg), Vitamin A (0.0048 mg), Thiamine (29 mg), Riboflavin (22 mg), Niacin (320 mg), Carbohydrates (3390 mg), Fats (2 mg), Potassium (150 mg), Calcium (26 mg), and Iron (0.20 mg). It is grown on 187 thousand hectares of land in India, producing 3165 thousand MT annually [4]. However, it is planted on 1.6 thousand hectares of land in Jammu and Kashmir, producing 36.17 thousand MT [5]. West Bengal, Uttar Pradesh, Bihar, Madhya Pradesh, Haryana, and Chhattisgarh are the main bottle gourd-growing states in India [6].

"Yield is a complex trait influenced by genetic factors interacting with environment. Success in any breeding programme for improvement depends on existing genetic variability in the base-population and on efficiency of selection. For successful selection, it is necessary to study the nature of association of the trait of interest with other relevant traits and, also the genetic variability available for these. Path coefficient provides a better index for selection than mere correlation coefficient, thereby separating the correlation coefficient of yield and its components into direct and indirect effects" [2]. Therefore, the present study was undertaken to understand the nature and magnitude of variability, heritability, correlation coefficients and path analysis for different quantitative and quality parameters in bottle gourd. The information on such aspects can be of great help in formulating an appropriate breeding strategy for genetic upgradation of this crop.

2. MATERIALS AND METHODS

The present study was carried out at the experimental field of Urban Technological Park, Habbak, Srinagar, Jammu and Kashmir during *kharif*-2022. It is situated at an altitude of 1608 meters above mean sea level lying between 34.16º North latitude and 74.83º East longitude. The climate is temperate characterized by mild summers. The mean minimum and maximum

temperatures at the research location are recorded in January and June (respectively).

The maximum rain fall is received during June (14.94 mm). The material used for research work consisted seventy-seven genotypes of bottle gourd which were procured from different sources. The experiment was laid out in accordance with Augmented Randomized Block Design comprising of seventy-seven treatments and three blocks. Recommended agronomic practices were followed to raise a good crop. Observations recorded were node number at which 1st male flower appeared, node number at which 1st female flower appeared, days to appearance of 1st male flower, days to appearance of 1st female flower, days to anthesis of 1st male flower, days to anthesis of 1st female flower, number of male flowers plant-1, number of female flowers plant-1, days to 1st fruit harvest, days to last fruit harvest, vine length (m), number of primary branches, number of fruits plant-1, fruit weight (kg), fruit length (cm), fruit diameter (cm), fruit yield plant-1 (kg), fruit yield ha-1 (q), number of seeds fruit-1, seed weight fruit-1 (g), 100 seed weight (g), TSS (ºBrix), dry matter content (%), vitamin C content (mg100g-1) and total phenols (mg100g-1). The observations on different quantitative and quality parameters were recorded from three randomly selected plants from each germplasm line of all blocks.

Polybags sown with seeds

Seed germination

View of the experimental field

Prepared field

Irrigation following transplanting

Established plant in the field

Staking

Staked field

Fig. 1. Various field activities

"The analysis of variance was done as per procedure described by Panse and Sukhatme [7]. The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by Burton [8]. PCV and GCV were categorized as low, moderate and high by following Sivasubramanian and Menon (1973) as (0 – 10%): Low, (10 – 20%): Moderate, (Above 20%): High respectively. Heritability in broad sense was estimated as per the procedure presented by Burton and Devane [9]. The heritability percentage was categorized as low, moderate and high as suggested by Robinson et al. [10], (0-30%): Low, (30-60%): Moderate and (60% and above): High respectively. Genetic advance at 5 per cent selection intensity was worked out by using the formula given by Lush [11] and Johnson et al. [12]. The Genetic advance as per cent of mean was categorised as low, moderate and high by following Johnson et al. [12] (0-10%): Low, (10-20%): Moderate and (Above 20%): High respectively". [13] Estimate of genotypic and phenotypic variances and covariances were substituted in the formula suggested by Panse and Sukatme [14] to calculate correlation coefficient between all possible pairs of characters. The methodology suggested by Wright [15] and Li [16] was adopted while using the formula given by Dewey and Lu [17] to carry out path coefficient analysis. All the above computations were carried out using the "Augmented RCBD" package in R software at the Division of Agricultural Statistics, SKUAST-Kashmir, Shalimar.

3. RESULTS AND DISCUSSION

In the present study, seventy-seven genotypes of bottle gourd were evaluated to estimate the genetic variability, heritability and genetic advance (as percent of mean), correlation and path analysis.

The analysis of variance revealed that all the twenty-five characters exhibited highly significant differences among the genotypes thus, suggesting existence of sufficient variability in the germplasm studied [Table 1 (a-b)]. Range values for various characters studied (Table 2) indicated presence of sufficient genetic variability for all the characters, which is prerequisite for making improvement through selection. The results obtained are in agreement with Harika et al. [18], Jain et al. [2], Rambabu et al. [19], Khan et al. [20], Rashid et al. [21], Sohi et al. [22], Dubey et al. [23] and Khansa et al. [24]. "The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype × environmental interaction components and does not reveal as to which character is showing higher degree of variability. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epistasis (no allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of variability existing for various traits. The estimates of phenotypic and genotypic coefficients of variation of all the characters studied are presented in Table 2. In general, the phenotypic and genotypic coefficients of variation were almost similar with slightly higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation" [25]. This was in agreement with the study of Damor et al. [26], Rambabu et al. [19], Khan et al. [20] Rashid et al. [21] and Chandramouli et al. [27].

The possibility for improvement through selection is higher for traits with moderate to high coefficients of variation. High estimates of the phenotypic and genotypic coefficients of variation, together with a wide range of variability, further suggest that these traits would be responsive to selection. Despite a small difference in the values, phenotypic coefficients of variation were larger than the comparable genotypic coefficients of variation. This demonstrated that the variation was mostly attributable to genetic variations and that the environment had little impact on the expression of the observed features. Similar findings were reported by Deepthi et al. [28], Damor et al. [26], Rambabu et al. [18], Ahmad et al. [29] and Rashid et al. [21].

It is evident from the data presented in Table 2 that the vine length (21.67 and 20.77), number of fruits plant-1 (24.86 and 24.68), fruit weight (38.78 and 37.65), fruit diameter (33.64 and 32.61), fruit yield plant-1 (40.26 and 39.21), fruit yield ha-1 (40.01 and 38.99), number of seeds fruit-1 (33.159 and 33.153), seed weight fruit-1 (45.155 and 45.153) and 100 seed weight (27.45 and 27.44) recorded high phenotypic and genotypic coefficients of variation respectively, indicating that genotypes had broad genetic

base for these characters. Node number at which 1st female flower appeared (16.21 and 15.73), number of male flowers plant-1 (11.90 and 11.75), number of primary branches (17.11 and 16.11), fruit length (19.10 and18.85), TSS (15.46 and 15.34), dry matter content (19.91 and 19.83), vitamin C content (13.96 and 13.93) and total phenols (16.475 and 16.474) depicted moderate phenotypic and genotypic coefficients of variation suggesting the existence of moderate variability in the genetic stock studied. Low PCV and GCV values were observed for node number at which 1st male flower appeared (9.62 and 8.02), days to appearance of 1st male flower (7.07 and 6.87), days to appearance of 1st female flower (6.65 and 6.53), days to anthesis of 1st male flower (6.73 and 6.63), days to anthesis of 1st female flower (5.95 and 5.86), number of female flowers plant-1 (8.12 and 7.51), days to 1st fruit harvest (7.18 and 7.14) and days to last fruit harvest (2.42 and 2.39). The same was observed by Deepthi et al. [28], Ahmad et al. [29], Sailaja et al. [30], Rashid et al. [21], Singh et al. [31] and Dubey et al. [23].

"Characters which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. Wide ranges of variability along with high estimates of phenotypic and genotypic coefficients of variation further indicate that these attributes would respond to selection" [13].

"The phenotypic and genotypic coefficients of variation do not give a true picture about the extent of inheritance of the character. Therefore, the heritability of a character can be relied upon, as it enables the breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided it is considered in conjunction with the predicated genetic advance" as suggested by [7 and 12]. Furthermore, the progress in selection is also directly proportional to the amount of genetic gain. Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic gain. "When high heritability is accompanied with high GAM (Genetic advance as per cent of mean), it indicates additive gene effects and selection may be effective. High heritability with

low GAM indicates importance of non-additive gene action where high heritability is exhibited due to favorable influence of environment rather than genotype and the selection for such traits may not be rewarding.

Low heritability with high GAM is governed by additive gene effects in which low heritability is exhibited due to high environmental effects and the selection may be effective in such cases. Low heritability coupled with low GAM indicates that character is highly influenced by environmental effects and selection would be ineffective" [13].

In the present study, heritability (b.s.) was high for all the characters and ranged from 69 to 99 per cent indicating that the characters are less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon. Similar results were observed by Emina et al. [32], Sharma and Sengupta [33], Singh et al. [34], Sultana et al. [35] and Rashid et al. [21].

The characters *viz.,* number of male flowers plant-1, vine length, number of primary branches, number of fruits plant-1, fruit weight, fruit length, fruit diameter, fruit yield plant-1, fruit yield ha-1, number of seeds fruit-1, seed weight fruit-1, 100 seed weight, TSS, dry matter content, vitamin C content and total phenols showed the high estimates of heritability coupled with high genetic advance as per cent of mean (GAM), indicating the preponderance of additive gene action for control of these traits. This suggests that real progress in improvement through selection could be made for yield. These results are in conformity with several workers *viz.* Singh et al. [33], Muralidharan et al. [36], Mandal et al. [37], Deepthi et al. [28] and Chandrashekhar et al. [38].

Fruit yield ha-1 is an important character, which decides the commercial viability of the hybrid/variety. Thus, the trait deserves the highest priority in any breeding programme. High heritability along with high genetic advance as per cent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection. Similar results have also been reported by Singh et al. [34], Damor et al. [26], Rambabu et al. [19], Varalakshmi et al. [39] and Ahmad et al. [29].

The ultimate criterion for developing improved cultivars of any crop that a plant breeder must constantly keep in mind is yield. Yield is a polygenic trait and is greatly impacted by the environment. When selecting, understanding the relationship between quantitative aspects and the yield and its characteristics is useful. Variability studies reveal how much improvement is feasible in many qualities, but they do not reveal the extent or nature of the association between various contributing traits and economically significant traits. Therefore, in order to make indirect selection for the enhancement of economic traits, knowledge of the associations between various attributes and economic traits is required. Studies of correlation help us understand the relationships that exist between highly heritable traits and the economic traits and how each trait contributes to the genetic make-up of a crop. The degree of the association between two traits that has been detected is shown by the phenotypic correlations. This suggests both heritability and environmental impacts, which obscures the actual genetic picture of the relationship. Genotypic correlations provide an estimate of inherent association between genes controlling any two characters. Hence, it is of greater significance and could be effectively utilized in formulating an effective selection scheme. Perusal (Table 3) indicated that in the present investigation, the magnitude of the genotypic correlation coefficients in the current study were higher than the phenotypic coefficients, proving the predominance of heritable components and demonstrating the additive nature of gene action for these traits.

Correlation coefficients disclosed that the economically important trait, i.e., fruit yield ha-1 was found to have a positive and significant correlation with the traits; node number at which 1st male flower appeared (rg = 0.276, rp =0.218), number of female flowers plant^{-1} (rg = 0.360, rp = 0.338), vine length (rg = 0.640, rp = 0.625), number of primary branches (rg = 0.640, rp = 0.581), number of fruits plant^{-1} (rg = 0.388, rp = 0.376), fruit weight (rg = 0.817, rp = 0.821), fruit diameter (rg = 0.328, rp = 0.299) and fruit yield plant^{-1} (rg = 0.98, rp = 0.99) both at genotypic and phenotypic levels. A positive and significant phenotypic correlation of this trait with number of male flowers plant^{-1} (rp = 0.157), fruit length (rp = 0.190) and 100 seed weight (rp = 0.203) was also observed. Similar findings were reported by Deepthi et al. [40], Janaranjani and Kanthaswamy [41], Thakur et al. [42],

Panigrahi et al. [43], Sultana et al. [35], Kunjam et al. [44], Abhishek et al. [45] and Rashid et al. [25].

Correlation analysis indicates the association pattern of component traits with yield, it simply represents the overall association of a particular trait with yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright [14] and demonstrated by Dewey and Lu [17] facilitates in partitioning the correlation coefficients into direct and indirect contribution of various traits on yield. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify important component traits of yield and utilize the genetic stock for improvement in a planned way.

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. Under the circumstances where correlation coefficient may be negative but the direct effect is positive and high, a restricted simultaneous selection model is to be followed *i.e.,* restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect. If correlation coefficient is negative and direct effect is also negative, then the selection based on that character has to be dropped.

In the current study, path coefficient analysis (Table 4) revealed that highest direct positive effect on fruit yield ha-1 was recorded by fruit yield plant-1 (0.78) followed by fruit weight (0.502), number of primary branches (0.401), number of fruits plant-1 (0.218), node number at which 1st male flower appeared (0.218) and number of female flowers plant-1 (0.212). The genotypic correlation coefficients of these characters with fruit yield ha-1 were 0.98, 0.817, 0.640, 0.388, 0.276 and 0.360 respectively indicating that direct selection of these traits will be effective in realizing improvements in fruit yield of bottle gourd. The direct effects of component traits like days to appearance of 1st male flower (-0.069), days to appearance of 1st

Table 1(a). Analysis of variance with respect to MSS for various characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

Source of variation	d.f	Node No. at which 1st male flower appears	Node No. at which 1st female flower appears	Days to appearance of 1st male flower	Days to appearance of 1st female flower	Days to anthesis of 1st male flower	Days to anthesis of 1st female flower	No. of male flowers plant^{-1}	No. of female flowers plant^{-1}	Days to 1st fruit harvest	Days to last fruit harvest	Vine length (m)	No. of primary branches
Blocks	2	0.008	0.171	32333	0.361	0.122	0.665	7.41	0.210	0.513	0.081	0.382	3.028*
Treatments	76	1.162**	6.870**	31.130**	34.213**	35.031**	31.143**	704.17**	4.010**	81.576**	35.837**	4.651**	23.822**
Error	152	0.148	0.139	0.595	0.439	0.369	0.305	6.29	0.211	0.263	0.304	0.132	0.974

*, **= Significant at 5% and 1% respectively*

Table 1(b). Analysis of variance with respect to MSS for various characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

Source of variation	d.f	No. of fruits plant^{-1}	Fruit weight (kg)	Fruit length (cm)	Fruit diameter (cm)	Fruit yield plant^{-1} (kg)	Fruit yield ha^{-1} (q)	No. of seeds fruit^{-1}	Seed weight fruit^{-1} (g)	100 seed weight (g)	TSS (ºBrix)	Dry matter content (%)	Vitamin C content (mg100g^{-1})	Total phenols (mg100g^{-1})
Blocks	2	0.570	0.055	3.035	0.284	1.180	2183	15.03	0.01	0.013	0.008	0.49*	0.014	0.38
Treatments	76	3.765**	1.604**	203.635**	16.298**	34.637**	86146**	34310**	1573.12**	133.144**	0.829**	4.900**	3.865**	174.389**
Error	152	0.18	0.031	1.780	0.341	0.613	1504	4.80	0.04	0.005	0.004	0.12	0.006	0.15

*, **= Significant at 5% and 1% respectively*

Table 2. Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability and genetic advance (as % of mean) for various characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability h^2 (broad sense)	Genetic gain (Genetic advance as % of mean)
1.	Node No. at which 1st male flower appears	7.243	6.14-8.55	0.486	0.338	9.629	8.026	0.694	13.782
2.	Node No. at which 1st female flower appears	9.522	7.24-12.54	2.383	2.243	16.210	15.730	0.941	31.444
3.	Days to appearance of 1st male flower	46.386	41.62-51.48	10.773	10.178	7.076	6.877	0.944	13.771
4.	Days to appearance of 1st female flower	51.378	46.08-56.17	11.696	11.258	6.656	6.530	0.962	13.198
5.	Days to anthesis of 1st male flower	51.240	45.88-56.30	11.922	11.554	6.738	6.633	0.969	13.452
6.	Days to anthesis of 1st female flower	54.642	48.99-59.10	10.584	10.279	5.953	5.867	0.971	11.911
7.	No. of male flowers plant^{-1}	129.782	97.79-159.20	238.915	232.629	11.909	11.752	0.973	23.888
8.	No. of female flowers plant^{-1}	14.970	13.13-18.64	1.477	1.266	8.120	7.516	0.856	14.333
9.	Days to 1st fruit harvest	72.822	61.06-77.92	27.366	27.104	7.183	7.149	0.990	14.656

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability h² (broad sense)	Genetic gain (Genetic advance as % of mean)
10.	Days to last fruit harvest	143.580	134.77-147.78	12.148	11.844	2.427	2.397	0.975	4.875
11.	Vine length (m)	5.908	3.42-8.98	1.639	1.506	21.670	20.773	0.918	41.021
12.	No. of primary branches	17.121	10.40-21.33	8.590	7.616	17.119	16.118	0.886	31.264
13.	No. of fruits plant⁻¹	4.528	3.4-8.6	1.267	1.249	24.861	24.680	0.985	50.473
14.	Fruit weight (kg)	1.922	0.79-4.40	0.555	0.524	38.781	37.659	0.943	75.335
15.	Fruit length (cm)	43.502	12.67-63.54	69.065	67.284	19.103	18.855	0.974	38.338
16.	Fruit diameter (cm)	7.072	5.0-16.43	5.660	5.318	33.641	32.610	0.939	65.119
17.	Fruit yield plant⁻¹ (kg)	8.586	4.21-22.64	11.954	11.341	40.266	39.219	0.948	78.694
18.	Fruit yield ha⁻¹ (q)	430.784	211.83-1132.21	29718.198	28213.818	40.017	38.991	0.949	78.263
19.	No. of seeds fruit⁻¹	322.549	107.26-594.07	11439.487	11435.143	33.159	33.153	0.999	68.285
20.	Seed weight fruit⁻¹ (g)	50.713	14.96-166.38	524.401	524.359	45.155	45.153	0.999	93.012
21.	100 seed weight (g)	24.270	10.28-41.28	44.384	44.379	27.450	27.448	0.999	56.540
22.	TSS (ºBrix)	3.417	2.64-4.19	0.279	0.275	15.468	15.346	0.984	31.362
23.	Dry matter content (%)	6.433	4.08-8.30	1.641	1.629	19.917	19.839	0.992	40.711
24.	Vitamin C content (mg100g⁻¹)	8.140	6.10-10.11	1.292	1.286	13.966	13.933	0.995	28.632
25.	Total phenols (mg100g⁻¹)	46.279	32.01-60.07	58.136	58.126	16.475	16.474	0.999	33.933

Table 3. Estimates of genotypic correlation (Above diagonal) and phenotypic correlation (Below diagonal) coefficients among different characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

Parameters	NMA	NFA	DAPMF	DAPFF	DAMF	DAFF	NOMF	NOFF	DFFH	DLFH	VL	NOPB	NOFPP	FW	FL	FD	FYPP	NOSPF	SWPF	100SW	FYPH
NMA	1.00	0.212	0.099	-0.072	0.105	-0.057	0.282*	0.065	-0.003	-0.004	0.226*	0.361*	0.090	0.185	0.268*	-0.150	0.277*	-0.094	0.003	0.245*	0.276*
NFA	0.174**	1.00	-0.063	0.058	-0.068	0.074	0.099	0.000	0.035	0.068	0.121	0.066	0.076	-0.019	-0.172	0.119	0.034	0.013	0.068	-0.031	0.033
DAPMF	0.075	-0.060	1.00	0.98**	0.999**	0.995**	0.041	-0.058	0.509**	0.451**	0.003	0.074	-0.077	-0.044	0.052	-0.223	-0.076	-0.053	-0.001	-0.137	-0.078
DAPFF	-0.064	0.057	0.966**	1.00	0.999**	0.991**	0.379	-0.057	0.518**	0.462**	0.362	0.100	0.080	-0.011	0.043	-0.196	-0.046	-0.050	-0.013	-0.123	-0.047
DAMF	0.089	-0.071	0.977**	0.972**	1.00	0.987**	0.023	-0.060	0.507**	0.454**	0.013	0.065	-0.098	-0.034	0.046	-0.203	-0.825	-0.051	0.005	-0.126	-0.083
DAFF	-0.038	0.070	0.949**	0.960**	0.960**	1.00	0.005	-0.095	0.546**	0.484**	-0.014	0.088	-0.105	-0.018	0.047	-0.192	-0.070	-0.036	0.024	-0.085	-0.071
NOMF	0.233**	0.101	0.034	0.034	0.018	0.005	1.00	0.392**	-0.021	0.021	0.170	0.154	0.317**	-0.058	0.052	-0.112	0.163	-0.287*	-0.262*	-0.021	0.162
NOFF	0.060	0.007	-0.055	-0.058	-0.066	-0.091	0.392**	1.00	-0.326**	-0.322**	0.167	0.215	0.823**	-0.091	-0.048	0.040	0.361**	-0.109	0.068	-0.082	0.360**
DFFH	-0.001	0.035	0.492**	0.506**	0.496**	0.541**	-0.020	-0.300**	1.00	0.933**	-0.022	0.180	-0.390**	0.195	-0.046	0.017	-0.023	0.041	-0.007	0.234*	-0.023
DLFH	-0.005	0.060	0.437**	0.451**	0.446**	0.471**	0.018	-0.299**	0.916**	1.00	-0.036	0.125	-0.426**	0.153	0.008	-0.075	-0.076	0.059	-0.004	0.194	0.076
VL	0.183**	0.111	0.003	0.030	0.014	-0.015	0.161*	0.153*	-0.021	-0.031	1.00	0.769**	0.317**	0.488**	0.099	0.122	0.642**	-0.039	-0.110	0.157	0.640**
NOPB	0.280**	0.058	0.733	0.093	0.066	0.080	0.137*	0.161*	0.167*	0.119	0.691**	1.00	0.285**	0.497**	0.117	0.128	0.641**	0.036	-0.053	0.202	0.640**
NOFPP	0.076	0.073	-0.075	-0.079	-0.096	-0.102	0.317**	0.763**	-0.386**	-0.417**	0.306**	0.270**	1.00	-0.189	-0.106	-0.037	0.389**	-0.09	0.033	-0.081	0.388**
FW	0.142*	-0.016	-0.043	-0.011	-0.031	-0.019	-0.059	-0.077	0.188**	0.145**	0.480**	0.448**	-0.191**	1.00	0.276*	0.394**	0.816**	0.086	0.085	0.254**	0.817**
FL	0.222**	-0.167*	0.052	0.040	0.046	0.046	0.050	-0.044	-0.045	0.009	0.097	0.104	-0.102	0.268**	1.00	-0.459**	0.197	0.070	0.049	-0.068	0.195
FD	-0.108	0.114	-0.212**	-0.183**	-0.196**	-0.179**	-0.102	0.048	0.019	-0.072	0.111	0.125	-0.036	0.360**	-0.443**	1.00	0.322**	0.204	0.057	0.110	0.328**
FYPP	0.219**	0.032	-0.077	-0.046	-0.078	-0.069	-0.284**	0.339**	-0.023	-0.075	0.627**	0.582**	0.377**	0.820**	0.193**	0.294**	1.00	0.006	0.006	0.206	0.98**
NOSPF	-0.077	0.014	-0.052	-0.05	-0.050	-0.035	-0.284**	-0.109	0.041	0.058	-0.037	0.034	-0.089	0.085	0.069	0.197**	0.006	1.00	0.711**	-0.102	0.006
SWPF	0.003	0.066	-0.001	-0.013	0.005	0.024	-0.259**	0.063	-0.007	-0.004	-0.105	-0.049	0.033	0.082	0.049	0.055	0.084	0.711**	1.00	0.057	0.088
100SW	0.204**	-0.031	-0.133*	-0.121	-0.124	-0.084	-0.020	-0.076	0.233**	0.192**	0.151*	0.190**	-0.081	0.245**	-0.067	0.106	0.201**	-0.102	0.057	1.00	0.203**
FYPH	0.218**	0.032	-0.078	-0.048	-0.079	-0.069	0.157*	0.338**	-0.022	0.076	0.625**	0.581**	0.376**	0.821**	0.190**	0.299**	0.999**	0.006	0.085	0.203**	1.00

*, **= Significant at 5% and 1% respectively

NMA: Node no. at which first male flower appears, NFA: Node no. at which first female flower appears, DAPMF: Days to appearance of first male flower, DAPFF: Days to appearance of first female flower, DAMF: Days to anthesis of first male flower, DAFF: Days to anthesis of first female flower, NOMF: No. of male flowers plant-1, NOFF: No. of female flowers plant-1, DFFH: Days to first fruit harvest, DLFH: Days to last fruit harvest, VL: Vine length (m), NOPB: No. of primary branches, NOFPP: No. of fruits plant-1, FW: Fruit weight (kg), FL: Fruit length (cm), FD: Fruit diameter (cm), FYPP: Fruit yield plant-1 (kg), NOSPF: No. of seeds fruit-1, SWPF: Seed weight fruit-1 (g), 100SW: 100 seed weight (g), FYPH: Fruit yield ha-1 (q)

Table 4. Path matrix showing direct (diagonal) and indirect (off diagonal) effects of different traits on fruit yield in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

Parameters	NMA	NFA	DAPMF	DAPFF	DAMF	NOFF	NOPB	NOFPP	FW	FL	FD	FYPP	SWPF	Genotypic correlation with yield
NMA	**0.218**	-0.002	0.004	0.004	0.003	0.002	-0.001	0.007	0.09	-0.005	0.002	-0.001	0.003	0.276*
NFA	0.002	**0.029**	0.003	0.004	0.003	0.005	0.004	0.006	0.008	0.02	0.001	0.005	0.004	0.033
DAPMF	-0.001	-0.001	**-0.069**	0.001	0.001	-0.001	0.001	-0.001	0.009	0.001	-0.004	-0.01	0.002	-0.078
DAPFF	0.003	0.004	0.001	**-0.040**	0.002	0.004	0.005	0.005	0.07	0.004	0.003	0.03	0.001	-0.047
DAMF	0.001	0.001	-0.001	-0.001	**-0.079**	0.001	-0.001	0.001	0.005	-0.001	0.004	0.001	0.001	-0.083
NOFF	0.02	0.02	-0.01	-0.01	-0.01	**0.212**	0.04	0.01	-0.03	-0.01	0.01	0.06	0.02	0.360**
NOPB	0.01	0.01	0.02	0.04	0.02	0.01	**0.401**	0.01	0.02	0.02	0.03	0.02	0.03	0.640**
NOFPP	0.09	0.09	-0.05	-0.05	-0.06	0.06	0.02	**0.218**	-0.01	-0.08	-0.02	0.02	0.03	0.388**
FW	0.04	0.04	-0.05	-0.05	-0.02	-0.03	0.08	-0.04	**0.502**	0.04	0.06	0.014	-0.01	0.817**
FL	-0.06	-0.06	-0.01	-0.01	-0.01	0.02	-0.03	0.03	-0.06	**0.157**	0.01	-0.04	-0.01	0.195
FD	0.09	0.09	0.02	0.02	0.02	-0.04	-0.01	0.02	-0.03	0.04	**0.214**	-0.02	-0.07	0.328**
FYPP	0.33	0.33	-0.05	-0.05	-0.05	0.33	0.62	0.34	0.79	0.18	0.31	**0.78**	-0.08	0.98**
SWPF	0.001	0.001	0.003	0.002	0.001	0.01	0.004	0.05	-0.01	0.02	0.001	-0.01	**0.07**	**0.088**

Residual effect= 0.053

NMA: Node no. at which first male flower appears, NFA: Node no. at which first female flower appears, DAPMF: Days to appearance of first male flower, DAPFF: Days to appearance of first female flower, DAMF: Days to anthesis of first male flower, NOFF: No. of female flowers plant^{-1}, NOPB: No. of primary branches, NOFPP: No. of fruits plant^{-1}, FW: Fruit weight (kg), FL: Fruit length (cm), FD: Fruit diameter (cm), FYPP: Fruit yield plant^{-1} (kg), SWPF: Seed weight fruit^{-1} (g)

female flower (-0.040) and days to anthesis of 1st male flower were negative. Therefore, these traits should be considered of little importance in the selection programme of bottle gourd. These results are in agreement with those reported by Deepthi et al. [40], Janaranjani and Kanthaswamy [41], Thakur et al. [21], Sultana et al. [35], Kunjam et al. [44] and Rashid et al. [25].

The residual effect value in the current study was 0.053, indicating that the characters selected for the study are the primary contributors to yield and that they account for the variability in yield. Similarly, Sultana et al. [35] observed very fewer residual effects while working on the similar traits in bottle gourd.

4. CONCLUSION

It is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in these bottle gourd genotypes through a systematic breeding and selection approach so as to recover high yielding recombinants, with good quality characteristics. Analysis of variance revealed that significant variation existed among various characters under study. Seed weight fruit-1, fruit yield plant-1, fruit yield ha-1 and fruit weight recorded high phenotypic and genotypic coefficients of variation, indicating that the genotypes had broad genetic base for these characters. High heritability coupled with high genetic advance (as per cent of mean) was observed for seed weight fruit-1, fruit yield plant-1, fruit yield ha-1 and fruit weight indicating the preponderance of additive gene action and hence selection for such traits will be effective. Fruit yield ha-1 exhibited significant positive correlation with fruit yield plant-1 followed by fruit weight, vine length, number of primary branches, number of fruits plant-1 and number of female flowers plant-1. Path coefficient analysis further suggested that fruit yield plant-1, fruit weight, number of primary branches, node number at which 1st male flower appeared, fruit diameter and number of female flowers plant-1 exhibited highest direct effects on the fruit yield ha-1 and should be given due importance by selection for breeding of new cultivars.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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