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Genetic variability and correlation between yield and its component characters in brinjal (*Solanum melongena*)

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Abstract
Collection of diverse germplasm and their systematic evaluation assume considerable importance in any crop improvement programme. In the present experiment nineteen genotypes of brinjal (*Solanum melongena* L.) comprising local collections and established varieties were evaluated with the objective of estimating different genetic parameters and genetic associations of yield and yield attributing traits. The experiment was conducted at the Experimental Farm, Department of Horticulture, Assam Agricultural University, Jorhat during the period from October 2009 to March 2010 following Randomized Block Design with three replications.

Analyses of variance revealed substantial variations among the genotypes for the traits under study. The genotype GB-09-05 was the superior performer for yield (1.38 kg/plant), fruit weight (356.0 g) and plant spread (122.33 cm). Some other promising genotypes were JB-3, GB 09-02-02 and GB-09/10-14. Performance of local brinjal genotypes was better than established varieties.

Estimation of genetic parameters indicated high GCV (77.95%) and PCV (78.22%) for fruit-length/diameter ratio. High heritability values of more than 90% were observed for fruit weight (99.55%), fruit-length/diameter ratio (99.17%), plant spread (98.14%), fruit length (97.37%), plant height (96.93%) and number of fruits/plant (96.79%). Expected genetic advance as per cent of mean was highest (89.53%) for number of fruits per plant.

Fruit yield per plant was significantly and positively correlated with fruit weight, leaf length, leaf width, plant height and plant spread. Fruit weight was significantly and negatively correlated to number of fruits/plant.

From the overall performance of genotypes, it is revealed that promising genotypes were GB-09-05, JB-3, GB 09-02-02 and GB-09/10-14 which can be selected directly or utilized in future breeding programmes.

Keywords: Germplasm, genotype, heritability

Introduction
Brinjal (*Solanum melongena* L.) is a widely grown vegetable crop in Asian countries. It is the second major vegetable crop in India. It is grown about throughout the country, covering an area of 4.96 lakh ha with a total production of 78.81 lakh tonnes. It contributes 8.45 and 9 per cent to the area and annual production of vegetables, respectively (Anon., 2007) in India. In Assam it stands 5th among the vegetables covering an area of 12,798 ha with an annual production of 1, 67, 587 mt per year.

Brinjal is cultivated for its immature fruits. It plays an important role in the balanced diet of human being by providing vital nutrients like proteins, carbohydrates, minerals, vitamins etc. On average, 100 g of edible portion contains 1.4 g protein, 0.3 g fat, 0.3 g minerals and 1.3 g fibres, Ca (18 mg), phosphorus (47 mg), Iron (0.9-1.0 mg), vit. A (124 IU), vitamin C (12 mg). Moreover, brinjal fruits have some medicinal values. A brinjal fruit, fried in til (sesamum) oil cures toothache. It has also been recommended as an excellent remedy against liver problem. It has much potential as raw material in pickle making and dehydration industries. Based upon its higher production potential and availability of the produce for consumption, it also termed as poor man's vegetable.

As the cultivable land-man ratio has been declining the factors responsible for achieving higher productivity in any crop per unit area need greater attention. Being an important vegetable, improvement of brinjal through breeding is very much essential. Breeding method for improvement of autogamous crops should be based on the nature and magnitude of genetic variance and the pattern of inheritance of quantitative characters. Hence, for planning an accurate and efficient breeding programme for plant improvement, analysis of the genetic architecture of yield and yield components with the help of different genetic parameters is a prerequisite; such information assist plant breeder to adopt appropriate breeding scheme for achieving maximum progress in the development of varieties. Genetic improvement involves manipulation of genotypes to realize better phenotypic expression in specific environment. A polygenic character like yield is greatly influenced by environment and hence a phenotype is often not indicative of its genotype. Such characters show continuous range of variation and are highly influenced by the environmental fluctuations. The determination of inherent genetic differences among various strains is a major interest to the plant breeder as it offers wide scope for selection.

Owing to the existence of wide genetic variability, India is considered a primary or secondary centre of diversity of brinjal. A number of different cultivars of brinjal with high variation in production efficiency, fruit colour, shape, size and bearing habit are distributed in different regions. Two main fruit types namely, round and long are cultivated throughout India. Improved varieties of brinjal have been released by different center, while in every state a number of local types are also grown. It is pertinent to investigate the nature and extent of variability and other genetic parameters in the indigenous material of Assam as well as in the improved types of other states.

The interdependence of inherent potentialities and environmental influence has long been recognized. The pattern of growth of a genotype usually reflects not only the characteristics of that genotype but also specific growing conditions. One of the reasons for fluctuation in yield may be differential sensitivity of the varieties to the variable agro-climatic conditions. For evolving better and stable varieties it is important to screen the genotypes over a wide range of environments so as to directly exploit them commercially or utilizing them effectively in breeding programmes. Thus, it becomes necessary to breed varieties with high performance and a low degree of fluctuation when grown over a range of production environments, reflecting lower genotype-environment interaction. Stability of genotypes results from balanced and optimal combination of developmental traits in genotypes.

Keeping these in view, the present investigation was designed to gather information on genetic variability, heritability, genetic advance, genetic association for thirteen quantitative traits. All these information would be considerably helpful in developing high yielding stable genotypes of brinjal.

Materials and methods

Experimental site

The present investigation was conducted during *rabi* season of 2009-2010 at the Experimental Farm of Department of Horticulture, Assam Agricultural University, Jorhat.

Climate and weather

The experimental site is situated at the North-eastern side of the main university campus in the district Jorhat, Assam. The place is situated in the plains of the Upper Brahmaputra Valley Zone of Assam at 24°46'N latitude and 94°14'E longitude of the elevation of 86.56 m from the sea level. The climatic condition of Assam as a whole is subtropical humid, having warm and humid summer and cool dry winter.

Experimental materials

Nineteen genotypes of brinjal (*Solanum melongena* L.) comprising local collections and established genotypes were used as the experimental material.

Genotypic variation and other related parameters

The estimated genotypic variance and other related parameters like phenotypic variance, genotypic and phenotypic coefficient of variation, heritability in broad sense, expected genetic advance and genetic advance as percentage of mean are presented in Table 4.9 and Table 4.10.

The genotypic coefficient of variation ranged from 0.97% for flowering duration to 77.95% for fruit-length/diameter ratio. For GCV estimates, fruit-length/ diameter ratio was followed by number of fruits per plant (44.0%) and fruit length (39.24%). The estimates of GCV were moderately high for leaf length, leaf width, plant height, plant spread, fruit-pedicel length, fruit weight and fruit yield whereas it was low for flowering duration, days to 50% flowering and days to first harvest.

The estimates of PCV was the highest (78.22%) for fruit length/diameter ratio and it was followed by number of fruits per plant (44.92%) and fruit length (39.76%). Whereas PCV was lowest in flowering duration (2.08%) followed by days to 50% flowering (6.09%) and days to first harvest (5.83%).

High heritability value of more than 90% was observed for fruit weight, plant spread, fruit-length/diameter ratio, fruit length, plant height, number of fruits per plant, days to first harvest and days to 50% flowering. The estimates of h^2 were moderately high for fruit yield, leaf length and leaf width while, it was low for fruit-length length (10.14%) and flowering duration (21.91%).

Expected genetic advance as per cent of mean was the highest for number of fruits per plant (89.53%) which was followed by fruit length (79.72%) and plant spread (61.72%). Flowering duration, days to first harvest and pedicel length recorded low magnitude of expected genetic advance.

Estimates of genetic variance and other related parameters for various characters

Genetic parameters	Leaf length (cm)	Leaf width (cm)	Plant height (cm)	Plant spread (cm)	Flowering duration (days)	Days to 50% flowering	Fruit length (cm)	Fruit-length/ diameter ratio	Pedicel length (cm)	Days to first harvest	Number of fruits/ plants	Fruit weight (g)	Yield (kg/ plant)
σ^2_g	12.34	4.65	131.61	382.78	1.56	58.00	36.33	8.45	2.59	63.61	7.55	717.16	1.70
σ^2_p	13.98	5.70	135.77	390.00	7.12	63.73	37.31	8.52	2.75	69.55	7.80	735.16	7.26
σ^2_e	1.64	1.05	4.16	7.22	5.56	5.73	0.98	0.07	0.16	5.94	0.25	18.00	5.56
GCV (%)	21.91	21.50	22.47	30.25	0.97	5.80	39.24	77.95	14.45	5.58	44.00	17.60	15.47
PCV (%)	23.30	23.80	22.82	30.53	2.08	6.09	39.76	78.22	30.61	5.83	44.92	17.85	32
h^2 (%)	88.26	81.57	96.93	98.14	21.91	91.0	97.37	99.17	10.14	91.45	96.79	99.55	48.34
GA (%) of mean)	42.37	39.90	45.60	61.72	0.94	11.45	79.72	15.94	6.30	11.50	89.53	35.87	26.5

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance
σ^2_e = Environmental variance;
GCV = Genotypic coefficient of variation;
PCV = Phenotypic coefficient of variation;
h^2 = Heritability in broad sense;
GA% of mean = Genetic advance expressed as percentage of mean

Result and discussion

Assessment of genetic variability is a prerequisite for effective selection. The variability in any character is due to cumulative action of hereditary material and environmental factors. The initial analysis of variance (Table 4.9 and 4.10) clearly revealed the existence of sufficient variation among the genotypes for various characters.

The estimates of genetic parameters like genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and expected genetic advance are necessary to understand the magnitude of genotypic variation and genetic value of the material with respect to a particular trait.

The estimates of genotypic and phenotypic coefficient of variation provide a better comparison of the characters for genotypic and phenotypic variation, respectively. In the present investigation, high value of GCV was recorded for fruit-length/diameter ratio, number of fruits per plant and fruit length. Similar results were reported by Singh and Nandpuri (1973) for fruits per plant, fruit length and fruit length/diameter ratio, Gautam and Srinivas (1992) [12]. for fruits per plant and Barik *et al.* (2009) for number of fruits per plant, fruit length and fruit length/diameter ratio. High estimates of GCV for these traits indicated considerable amount of genetic variability, thus suggesting the potentiality of the material for further improvement.

However, it has been suggested that GCV values alone are not sufficient to determine the amount of variation which is heritable. The efficiency of selection for a particular character is best reflected by the extent of its heritability. Burton (1952) [6]. reported that genotypic coefficient of variation together with heritability in broad sense would give the best picture of the extent of advance to be expected from selection.

The present investigation revealed that the heritability estimates were high for fruit weight, plant spread, fruit-length/diameter ratio, fruit length, plant height, days to first harvest and days to 50% flowering, whereas it was relatively low for leaf length, leaf width and yield per plant. High heritability estimates were reported for fruit weight by Gotoh (1953), Dixit *et al.* (1984) [11]. For fruit length, reported high heritability. For fruit-length/diameter ratio, plant spread and plant height heritability was found by Gopimony *et al.* (1984) [13], Singh and Kumar (2005).

Heritability estimates obtained from uni-environmental experiment could be biased as variance due to genotype x environment is inseparable from the genetic variance. Such a possibility existed in the present investigation, heritability value alone is not an ideal one for predicting the genetic progress that would result from selecting the best individuals. Heritability and genetic advance when estimated together are more useful for predicting the genetic progress in selection, as high heritability coupled with high genetic advance reflect preponderance of additive gene action. From this consideration, number of fruits per plant in the present investigation which had the highest heritability coupled with highest genetic advance as per cent of mean revealed preponderance of additive gene action. The other characters showing high heritability with moderate to high genetic advance were leaf length, leaf width, plant height, plant spread, fruit length and single fruit weight. Therefore simple mass selection for these characters would be more effective. High heritability estimates along with high genetic advance were also reported by Singh and Singh (1996), Rai *et al.* (1998) and Kumar *et al.* (2010) for fruit length. Vadivei and Bapu (1989), Kumar *et al.*(1998), Prasad *et al.* (2004) and Dhameliya and Dobariya (2007) reported for number of fruits per plant. Relatively moderate heritability accompanied with low genetic advance were observed for flowering duration, fruit length/ diameter ratio and days to 50% flowering indicating predominant role of non-additive gene actions for these traits. Selection with progeny testing would be appropriate in exploitation of such characters.

Association studies

Fruit yield is a complex quantitative trait and is influenced by environment. Therefore, direct selection for yield as such may not be effective in a plant breeding programme. Breeders aim at improving a population for yield by exercising simultaneous selection on some yield attributing traits which have been found to be correlated with yield.

In the present investigation, it was found that yield per plant had high positive correlation with fruit weight (Rajput *et al.*, 1996 and Ashwani and Khandelwal, 2003) [1]. and with plant spread (Gautam and Srinivas, 1992) [12]. at both genotypic and phenotypic levels. Yield was positively correlated with leaf length, leaf width, plant spread and plant height. Fruit length, fruit-length/diameter ratio flowering duration, days to 50% flowering and days to first harvest exhibited no relationship with yield at any level. Number of fruits was negatively correlated with fruit weight at genotypic level only. High genetic correlation of yield with its important attributes such as fruit weight and plant spread might have resulted due to pleiotropy or linkage or both. Selection may be exerted in secondary traits that have greater heritability than the primary traits. The present study indicated that selection for plant spread and fruit weight might result in positive correlated response for yield.

The association among different component characters exhibited some important relationship which would indirectly help in improvement of yield. Positive and high significant correlations were observed between fruit weight and fruit length. The above results suggested that varieties producing heavier and large fruits associated with higher fruit length, fruit-length/diameter ratio and plant spread would give higher yield.

Correlation was found positive and significant between days to first flowering and days to first harvest. As most, it not all, of the genes governing days to first flowering and days to first harvest are expected to be common, the genetic correlation between these two traits could be the reflection of such a possibility. Similarly, the possibility of increased fruit pedicel length, leaf length, leaf width with increasing height of the plant was also supported by their high positive genetic correlations.

The ultimate aim of selection in self-pollinated crops is to obtain a true breeding type. Therefore, the fixable types of gene action assume all the significance. The present investigation revealed the importance of both additive and non-additive gene effects for yield and its important attributes. Faster rate of improvement in these traits will be possible by simultaneous exploitation of both additive and non-additive genetic components.

The results of these studies on variability and association clearly reflected fruit weight, and fruit length as the most potent yield attributing characters for incorporation in brinjal improvement programme.

Conclusions

1. The analysis of variance revealed a wide range of variation among the genotypes for all the characters except fruit-pedicel length
2. Estimation of genetic parameters indicated high genotypic and phenotypic coefficient of variation for fruit-length/diameter ratio and number of fruits/plant. High heritability along with high genetic advance was observed for plant spread, fruit length and number of fruits/plant
3. Yield/plant was significantly and positively correlated with fruit weight, leaf length, leaf width, plant height and plant spread. Association of days to 50% flowering with days to first harvest and flowering duration was highly significant and positive. Significant negative correlation existed between fruit weight and number of fruits/plant. Correlation coefficient was positive and highly significant between fruit length and fruit-length/diameter ratio. Highly significant and positive correlations of fruit-pedicel length with fruit length, leaf width and plant height were observed in the study

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