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Studies on heritability and genetic advance for fruit yield and its component traits in segregating generations of brinjal (*Solanum melongena* L.)

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Abstract

The present investigation was carried out during *kharif-rabi* 2017-2018, at Main Vegetable Research Station, Anand Agricultural University, Anand. The experimental material for present investigation comprised of six generations *viz.*, P₁, P₂, F₁, F₂, BC₁ and BC₂ of four crosses involving eight diverse cultivars of brinjal (*Solanum melongena* L.) used to study the genetic analysis of various quantitative and qualitative traits. High heritability coupled with high genetic advance were estimated for fruit yield per plant in cross 1 (ABSR 2 × NSP 1), days to first picking in cross 3 (JBGR 1 × GP BRJ 204), number of fruits per plant in cross 1 (ABSR 2 × NSP 1), fruit length in cross 1 (ABSR 2 × NSP 1) and cross 2 (KS 224 × CHBR 1), fruit weight in cross 2 (KS 224 × CHBR 1) and cross 4 (Doli 5 × PN 1) and total soluble sugar in cross 2 (KS 224 × CHBR 1), which indicated preponderance of additive gene action in these traits and for improvement of such a traits, selection will be effective.

Keywords: brinjal, heritability, genetic advance, quantitative and qualitative trait, additive gene action

Introduction

Brinjal or eggplant (*Solanum melongena* L.) is an important commercial vegetable crop in India and having chromosome number $2n = 2X = 24$. It is self-pollinated crop belonging to the family Solanaceae. India considered as the primary centre of origin of brinjal (Vavilov, 1931). Brinjal crop is a versatile crop adapted to different agro-climatic regions and can be grown throughout the year. It is a perennial but grown commercially as an annual crop. The varieties of brinjal exhibit a wide range of fruit size, shapes and colours. Brinjal is a common and popular major vegetable crop in the subtropics and tropics mainly for its immature fruits as vegetables and since ancient time the human society has socio-economic relationship with this crop. Many local cultivars are popular in different locations and cultivated in large area for their qualitative traits but is characterized by very low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions at different parts of country. It is also susceptible to various pests and diseases. As we know, yield is a complex end product of a number of components most of which are under polygenic control. So, all changes in yield must be accompanied by changes in one or more of the components as have been pointed out by Grafius (1959) [8].

The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than their existing ones in one or more traits which produce more economic yield. Sufficient understanding of the inheritance of quantitative traits and information about heritability of fruit yield, its components and quality traits are essential to develop an efficient breeding strategy. The scope for the improvement of the crop plants through proper breeding method depends on the amount of genetic variability available. Luckily a great genetic variation is available in brinjal throughout the country with regard to fruit size, shape, colour, growth habit, canopy fruit bearing habit, yield, diseases and insect-pests resistance as well as quality and adaptability for different localities and for different growing seasons.

Estimate of heritability serves as a useful guide to the plant breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable portion of variation in the first case, and the portion of genetic variation that is fixable in pure lines in the latter case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype.

But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring.

Material and Methods

The material comprising of eight genetically diverse genotypes of brinjal (ABSR 2, NSP 1, KS 224, CHBR 1, JBGR 1, GP BRJ 204, Doli 5 and PN 1) which were selected on the basis of their geographic origin, variation in morphological characters and based on their mineral nutrient content. There were four crosses (ABSR 2 × NSP 1, KS 224 × CHBR 1, JBGR 1 × GP BRJ 204 and Doli 5 × PN 1) obtained by crossing of diverse parents during *Kharif-rabi* 2014-15. Backcrossing was done in *Kharif-rabi* 2016-17 with its respective parents. Selfing of F₁s was done in the same season to get F₂s.

The evaluation trial was conducted in *Kharif-rabi* 2017-18 at Experimental Farm, Main Vegetable Research Station, Anand Agricultural University, Anand. The experimental material consisting of six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) of each of the four crosses were in Compact Family Block Design with three replications. Each replication was divided in four compact blocks. Each cross consisting of six generations were randomly allotted to each plot within a block. Each plot consisted of two rows of parents and F₁, four rows of the backcrosses and eight rows of the F₂ generation of each cross. Inter and intra row spacing was 90 cm and 60 cm, respectively. The standard agronomical practices were followed to raise the good and healthy experimental crop.

In this study, observations for twelve different characters *viz.*, days to first flowering, days to first fruit picking, plant height, number of fruits per plant, fruit length, fruit girth, fruit weight, fruit yield per plant, total phenol content, total soluble sugars, moisture content and total soluble solids were recorded in each experimental unit *i.e.*, generation as five plants in each P₁, P₂ and F₁, ten plants in each BC₁ and BC₂ and twenty plants in F₂. The plants for recording observations were selected randomly from the competitive plants. The selected plants were tagged and numbered for recording different observations. An individual observation of each generation of each family was considered for statistical analysis.

Statistical Analysis

Heritability in narrow sense: The narrow sense heritability in *per cent* was calculated by using formula suggested by Warner (1952) [29].

$$h^2(\text{ns}) (\%) = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2} \times 100$$

Heritability is a measure of the efficiency of a selection system in separating genotypes. The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al.* 1949) [24].

1. Low heritability : 0 - 30 %
2. Moderate heritability : 30 - 60 %
3. High heritability : > 60 %

Genetic advance: The expected genetic advance at 5 %

selection intensity was estimated by using formula suggested by Allard (1960) [1].

$$G.A. = h^2(\text{ns}) \times K \times \sigma_p$$

Where,

$h^2(\text{ns})$ = Heritability in narrow sense, K = Selection differential ($K=2.06$) at 5% selection intensity and σ_p = Phenotypic standard deviation Expected genetic advance as per cent of population mean was obtained by using following formula

$$\text{Genetic advance } (\%) = \frac{GA}{\bar{X}} \times 100$$

Where,

$$\bar{X} = \frac{\bar{P}_1 + \bar{P}_2}{2} \text{ (Basic population mean)}$$

The value of expected genetic advance for various characters is demarcated into three categories *viz.*, low, moderate and high, as follows (Johnson *et al.* 1955) [9]

1. Low genetic advance : 0 - 10 %
2. Moderate genetic advance : 10 - 20 %
3. High genetic advance : > 20 %

Results and Discussion

Narrow sense heritability may be more helpful in the selection of segregating populations and that is why the genetic advance is calculated on the basis of narrow sense heritability to ascertain more reliable results. In cross 1 (ABSR 2 × NSP 1) high narrow sense heritability was recorded for number of fruits per plant, moisture content, fruit yield per plant, total phenol content, days to first fruit picking, total soluble sugars and fruit length (Table 1). Whereas, in cross 2 (KS 224 × CHBR 1) total soluble sugars, total phenol content, fruit length and fruit weight exhibited high narrow sense heritability. In cross 3 (JBGR 1 × GP BRJ 204) moisture content, first fruit picking, number of fruits per plant and total soluble sugars had recorded high narrow sense heritability. In case of cross 4 (Doli 5 × PN 1) fruit weight and fruit length recorded high narrow sense heritability. The results are in agreement with the findings of Kapadia (1995) [11], Negi *et al.* (2000) [19], Prasad *et al.* (2004) [22], Patel *et al.* (2004) [21], Singh and Kumar (2005) [27], Golani *et al.* (2007) [7], Sharmin *et al.* (2010) [25], Ansari *et al.* (2011) [3], Kafyullah *et al.* (2011) [10], Kumar *et al.* (2011) [14], Dhaka and Soni (2012) [6], Ambade *et al.* (2013) [2], Lokesh *et al.* (2013) [15], Khalil *et al.* (2013) [12], Kumar *et al.* (2013) [13], Mili *et al.* (2014) [17], Chaudhary and Kumar (2014) [5], Madhavi *et al.* (2015), Mistry *et al.* (2016) [18], Balwani *et al.* (2017) [4], Nilakh *et al.* (2017) [20], Ravali *et al.* (2017) [23] and Tripathy *et al.* (2017) [28], who reported high narrow sense heritability for all these trait *viz.*, number of fruits per plant, moisture content, fruit yield per plant, total phenol content, days to first fruit picking, total soluble sugars, fruit length and fruit weight.

In cross 1 (ABSR 2 × NSP 1) moderate narrow sense heritability was recorded for days to first flowering, while total soluble solids had low narrow sense heritability for this cross. In case of cross 2 (KS 224 × CHBR 1) fruit girth and moisture content exhibited moderate narrow sense heritability, while rest of the traits shown low narrow sense heritability in this cross. In cross 3 (JBGR 1 × GP BRJ 204) days to first flowering shown low narrow sense heritability. In

case of cross 4 (Doli 5 × PN 1) total phenol content and total soluble solids exhibited low narrow sense heritability in this cross.

High expected genetic advance was recorded for number of fruits per plant, fruit yield per plant and fruit length in cross 1 (ABSR 2 × NSP 1); fruit weight, total soluble solids and fruit length for cross 2 (KS 224 × CHBR 1); days to first fruit picking for cross 3 (JBGR 1 × GP BRJ 204) and for fruit yield per plant in cross 4 (Doli 5 × PN 1) (Table 1). However, most of the crosses revealed low to high genetic advance for some more traits. Moderate expected genetic advance was recorded for days to first fruit picking and total phenol content in cross 1 (ABSR 2 × NSP 1); fruit girth for cross 2 (KS 224 × CHBR 1); number of fruits per plant for cross 3 (JBGR 1 × GP BRJ 204) and for fruit length in cross 4 (Doli 5 × PN 1). Low genetic advance was reported for days to first flowering, total soluble sugars, moisture content and total soluble solids in cross 1 (ABSR 2 × NSP 1); total phenol content and moisture content for cross 2 (KS 224 × CHBR 1); days to first flowering, total phenol content and total soluble sugars for cross 3 (JBGR 1 × GP BRJ 204) and for total soluble sugars and total soluble solids in cross 4 (Doli 5 × PN 1). The results of present study are akin with finding of Kapadia (1995) [11], Negi *et al.* (2000) [19], Prasad *et al.* (2004) [22], Singh and Kumar (2005) [27], Ansari *et al.* (2011) [3], Kafyullah *et al.* (2011) [10], Kumar *et al.* (2011) [14], Dhaka and Soni (2012) [6], Ambade *et al.* (2013) [2], Khalil *et al.* (2013) [12], Kumar *et al.* (2013) [13], Mili *et al.* (2014) [17], Madhavi *et al.* (2015) [16], Mistry *et al.* (2016) [18], Balwani *et al.* (2017) [4], Ravali *et al.* (2017) [23] and Tripathy *et al.* (2017) [28], who reported high genetic advance for all these traits *viz.*, days to first fruit picking, number of fruits per plant, fruit yield per plant and fruit length, fruit weight and total soluble solids.

High magnitude of narrow sense heritability coupled with high value of expected genetic advance as per cent of population mean were observed for fruit yield per plant in

cross 1, days to first picking in cross 3, number of fruits per plant in cross 1, fruit length in cross 1 and cross 2, fruit weight in cross 2 and cross 4 as well as total soluble sugar in cross 2, which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be effective. Moderate to high magnitude of narrow sense heritability coupled with moderate value of expected genetic advance as per cent of population mean were observed for days to first picking in cross 1, number of fruits per plant in cross 3, fruit length in cross 4, fruit girth in cross 2 and total phenol content in cross 1, which indicate that heritability of these traits were due to additive gene action, suggesting that these characters can be further improved by adopting selections in succeeding generations. High heritability (narrow sense) associated with moderate to high value of expected genetic advance recorded for days to first picking in cross 1 and cross 3, number of fruits per plant in cross 1, fruit yield per plant in cross 1 and cross 3, fruit length in cross 1, cross 2 and cross 4, fruit girth in cross 2, fruit weight in cross 2 and cross 4, total phenol content in cross 1 and total soluble sugar in cross 2 which indicated that these characters can be further improved through selection in advanced generation. High magnitude of narrow sense heritability associated with low value of expected genetic advance was found for days to first flowering in cross 1, total phenol content in cross 2, total soluble sugar in cross 1 and cross 3 and moisture content in cross 1, which can be improved further by using *inter se* crossing of desirable recombinants keeping adequate size of population. Low magnitude of narrow sense heritability associated with low value of expected genetic advance was estimated for days to first flowering in cross 3, total phenol content in cross 4, total soluble solids in cross 1 and cross 4 and moisture content in cross 2, which indicated that heritability of these traits under the control of non-additive gene action for this cross and selection would be ineffective for this trait.

Table 1: Estimates of heritability [h^2 (ns) %] and genetic advance (GA %) for yield and yield attributing traits in four crosses of brinjal.

Estimates	Days to first flowering	Days to first fruit picking	Plant height	Number of fruits per plant	Fruit length	Fruit girth	Fruit weight	Fruit yield per plant	Total phenol content	Total soluble sugars	Moisture content	Total soluble solids
Cross 1 (ABSR 2 × NSP 1)												
h^2 (ns) %	47.22	112.99	-390.1	154.42	89.38	-138.14	-1908.8	138.87	123.20	102.45	149.04	19.22
GA %	9.42	19.31	-58.71	69.56	32.24	-28.51	1057.7	38.65	13.03	4.77	1.54	0.97
Cross 2 (KS 224 × CHBR 1)												
h^2 (ns) %	-14.3	-14.3	-455.7	-182.7	102.77	46.43	91.56	-84.3	152.6	-108.33	44.88	194.5
GA %	-3.216	-2.86	-85.18	-16.69	47.41	19.12	86.11	-11.42	8.70	-3.52	0.025	53.5
Cross 3 (JBGR 1 × GP BRJ 204)												
h^2 (ns) %	13.64	148.37	-123.3	90.81	-359.7	-89.14	-16.80	-325.20	00.00	79.00	1880.00	-19.48
GA %	3.04	29.72	-33.25	13.13	-102.4	-27.15	-12.49	-46.44	00.00	1.84	-1.02	-1.30
Cross 4 (DOLI 5 × PN 1)												
h^2 (ns) %	-517.8	-888.3	-121.2	-227.6	50.10	-78.27	57.97	-275.00	24.45	-550.00	-16.67	19.22
GA %	-73.36	-64.85	-35.55	-32.51	17.71	-19.17	39.76	-53.62	0.13	-19.58	-0.0095	0.97

Conclusion

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matrix traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate to low estimates of heritability for most of the traits including yield components indicated the preponderance of non-additive variance for yield and yield attributes in the

material under study.

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