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Original Research Article

Estimation of Genetic Variation for Maturity Traits in Eight Genotypes of Bottle Gourd [*Lagenaria siceraria* (Mol.) Standl.]

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ABSTRACT

Keywords

Additive, Dominance, Genetic variation, Samrat, PSPL, Maturity hybridization programmes and also in the choice of appropriate breeding procedure for the genetics improvement of various quantitative characters. The experimental material for the present study consisted of eight distinct genotypes and important varieties collected from Indian Institute of Vegetable Research. These were Samrat (P_1 + Stranded variety), Aditi (P_2), Pusa Summer Prolific Long (P₃), IC 093236 (P₄), TC 092372 (P₅), VRBG 100 (P_6), VRBG VAR - 45 (P_7) and VRBG 444 (P_8). Additive (D) component was lower in magnitude than dominance components of genetic variation for all the maturity characters except node number of first staminate flowers and node number of first pistilate flower which revealed preponderance of both dominant and recessive component of variance. Proportion of genes $(H_2/4H_1)$ in the parents were less than 0.25 for all the maturity traits except node number of first staminate flowers which showed asymmetrical distribution of loci showing dominance in the inheritance of these characters. The ratio of $(4D H_1)^{1/2}$ +F/(4D H₁)^{1/2}-F indicated the excess of dominant as well as recessive genes among the parental strains for most of the maturity characters.

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Introduction

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is synonymously called as Calabash gourd. Bottle gourd is a vigorous, monoecious, annual, climbing or prostrate, branching herb, with angular, ribbed, thick, softly hairy stem and proximally bifid tendrils. The tender edible fruit are also prepared into sweets, pickles, rayata and other delicious preparation. It is one of the most nutritive menu for human and tone up his energy and vigour, because it happens to be valuable source of carbohydrates, proteins, vitamins and minerals.

Knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also in the choice of appropriate breeding procedure for the genetics improvement of various quantitative characters. Hence, insight into the nature of gene action involved in the expression of various quantitative characters is essential to a plant breeder for starting a judicious breeding programme in bottle gourd (Pandey *et al.*, 2004).

The nature of gene action is measured in terms of combining ability variance and effects. The gca is a primarily function of additive genetic variance. On other hand, sca variance is a mainly function of dominance variance. Heterosis is directly proportional to existence of non-additive genetic variance in a population. On other words, presence of significant amount of dominance variance in bottle gourd is a prerequisite for the commercial exploitation of heterosis.

Therefore, for development of effective breeding programme in bottle gourd one need to elucidate the genetic nature and magnitude of quantitative inherited traits and estimated prepotency of parents in hybrid combinations.

Materials and Methods

The experimental material for the present study consisted of eight distinct genotypes and important varieties collected from Indian Institute of Vegetable Research. These were Samrat (P_1 + Stranded variety), Aditi (P_2), Pusa Summer Prolific Long (P₃), IC 093236 (P₄), TC 092372 (P₅), VRBG 100 (P₆), VRBG VAR - 45 (P_7) and VRBG 444 (P_8). experiment conducted The was in Randomized Complete Block Design with three replications to assess the performance of 28 hybrids and their 8 parental lines conducted at Vegetable Research Farm, Department of Horticulture, Banaras Hindu University, Varanasi during the summer season of 2013 and 2014. The crop was planted in rows spaced at 3.0 meters with plant to plant spacing of 0.5 meter apart. All the recommended agronomic package of practices and plant protection measures were followed to raise a good crop. The data were recorded for maturity traits *viz.*, days to first staminate flower anthesis, days to first pistilate flower anthesis, days to first fruit harvest, primary branches per plant, node number of first staminate flowers and node number of first pistilate flowers.

Results and Discussion

Genetic components were used in estimation of average degree of dominance $(H_1/D^1)^{1/2}$, proportion of dominant and recessive genes (KD/KR) in parents i.e. $(4DH_1)^{1/2} + F/(4DH_1)$ -F and number of gene groups, which control the character and exhibit dominance (h^2/H_2) . The coefficient of correlation (r) between parental order of dominance (Wr-Vr) and parental measurements (Yr) was calculated to get an idea about the dominance genes with positive and negative effects. The non significant value of t^2 or 1-b/SEb indicates validity of assumptions pertaining to diallel analysis. However significant value of t^2 showed failure of hypothesis of diallel cross analysis.

For days to first staminate flower anthesis, the significance of H_1 and H_2 suggested the role of dominance components for this trait. The positive F value suggested frequency of dominant alleles in the parents. The mean degree of dominance $(H_1/D)^{1/2}$ was more than one, showed over dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was found to be 0.16 denoting asymmetrical distribution of loci showing dominance. The ratio of $(4DH_1)^{1/2}$ +F/ $(4DH_1)^{1/2}$ –F was found more than one which showed excess of dominant genes. The number of group of gene that controls the character (h^2/H_2) and exhibited dominance was 0.06, which indicated that no major gene group was involved in the

inheritance of these traits. The positive value of correlation coefficient (r) between parental order of dominance (Wr+Vr) and parental measurement (Yr) indicated the excess of recessive genes in this population. The value of t^2 for days to first staminate flower anthesis was found non-significant indicating the validity of the hypothesis of assumption of diallel cross analysis.

The value of H_1 was higher than D indicated the major role of dominance component in the expression of days to pistilate flower anthesis. The positive F value suggested frequency of dominant alleles in the parents.

The degree of dominance $(H_1/D)^{1/2}$ was more than one, showed over dominance for this of $H_2/4H_1$ indicated trait. The ratio asymmetrical distribution of dominant and recessive genes in the parent. The number of dominant and recessive genes in parents as indicated by $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was (2.26) showed excess of dominance genes. The estimate of h^2/H_2 was found 0.08 indicated that no major gene group was involved in the inheritance of this trait (Table The positive value of correlation 1). coefficient suggested the preponderance of recessive genes.

The estimates of D, H₁, H₂ and E were significant for this trait while the value of F and h² were found to be non-significant (Table 1). The value of H₁ was higher than the Dvalue indicated the major role of dominance component for days to first fruit harvest. The positive F value suggested frequency of dominant alleles in the parents. The value of average degree of dominance $(H_1 /D)^{1/2}$ showed over dominance for this trait. The ratio of H₂/4H₁ was found to be 0.21 (Table 1) indicating the asymmetrical distribution of positive and negative alleles among the parents. The ratio of $(4DH_1)^{1/2}$ +F/ $(4D/H_1)^{1/2}$ -F was found more than one, which

showed excess of dominant genes. The estimates of h^2/H_2 showed that the number of gene groups control the character and exhibit dominance was 0.20 (Table 1). The positive value of correlation coefficient suggested the preponderance of recessive genes. The value of t^2 for days to first fruit harvest was found non-significant indicating the validity of the hypothesis of assumption of diallel cross analysis.

The greater value of dominance components than D indicated the major role of nonadditive gene in the expression of primary branches per plant. The value of average degree of dominance $(H_1/D)^{1/2}$ was more than one indicated over dominance. The value of $H_2/4H_1$ in the parents was found to be less than 0.25 showing asymmetrical distribution of dominance and recessive genes among the parents. The ratio of $(4D H_1)^{1/2}$ +F/ $(4D H_1)^{1/2}$ -F was found less than one which showed excess of recessive genes. The estimation of (h^2/H_2) was found 0.03 indicated that no major gene group was involved in the inheritance of this characters (Table 1). The positive value of correlation coefficient suggested excess of recessive gene for this character in the population. The value of t^2 for number of primary branches per plant was found nonsignificant.

The significant value of D, H₁, H₂, h² and E indicated the presence of both additives as well as dominance gene effect for the inheritance of node number of first staminate flowers (Table 1). The significance of H₁ and H₂ suggested the role of dominance components for this trait. The positive F value suggested frequency of dominant alleles in the parents. The degree of dominance $(H_1/D)^{1/2}$ was less than one, showed partial dominance for this trait. The ratio of H₂/4H₁ (0.28) indicated symmetrical distribution of dominant and recessive genes in the parent.

| Components of variation and related statistics | Days to first staminate flower anthesis | Days to first pistilate flower anthesis | Days to first fruit harvest | Primary branches per plant | Node number of first staminate flowers | Node number of first pistilate flower |
|---|---|---|--------------------------------|----------------------------------|---|---|
| D (Additive effect) | 13.61* ± 2.29 | 9.72* ± 2.09 | $4.63^{*} \pm 2.01$ | 14.5* ± 2.32 | $1.31^{*} \pm 0.31$ | $1.61^{*} \pm 0.31$ |
| F (Mean Fr over arrays) | $17.20^* \pm 5.40$ | 10.47* ± 4.95 | 3.65 ± 5.11 | 10.3 ± 5.49 | 0.39 ± 0.73 | 0.72 ± 0.73 |
| H ₁ (Dominance effect) | 24.16* ± 5.26 | 18.86* ± 4.81 | $19.52^{\ast}\pm4.97$ | $16.1* \pm 5.34$ | $1.09^{*} \pm 0.71$ | $1.56^{*} \pm 0.71$ |
| H ₂ (Dominance indicating asymmetry of +/-effect of genes | 15.10* ± 4.57 | 12.71* ± 4.19 | 16.49* ± 4.32 | 12.4* ± 4.65 | $1.22^{*} \pm 0.62$ | $1.46^{*} \pm 0.62$ |
| $\frac{g^{2}}{h^2}$ | -0.87 ± 3.07 | -0.96 ± 2.81 | 3.32 ± 2.90 | -0.48 ± 3.12 | $0.59^* \pm 0.42$ | $1.64^* \pm 0.42$ |
| E (Environmental component) | 2.59* ± 0.76 | 3.06* ± 0.70 | $4.42^{*} \pm 0.72$ | 1.46 ± 0.77 | $0.54^{*} \pm 0.10$ | 0.82* ± .010 |
| (H ₁ /D) ^{1/2} (Mean degree of dominance) | 1.33 | 1.39 | 2.05 | 1.05 | 0.91 | 0.99 |
| H ₂ /4H ₁ (Proportion of genes with +/- effects in parents) | 0.16 | 0.17 | 0.21 | 0.19 | 0.28 | 0.23 |
| (4 D H ₁) ^{1/2} +F/(4DH ₁) ^{1/2} -F (Proportion of dominant and recessive genes in parents) | 2.80 | 2.26 | 1.47 | 0.50 | 1.39 | 1.58 |
| h ² /H ₂ (Number of gene groups) | 0.06 | 0.08 | 0.20 | 0.03 | 0.48 | 1.12 |
| r (correlation coefficient) | 0.50 | 0.49 | 0.52 | 0.96 | 0.67 | 0.76 |
| t^2 | 0.24 | 0.38 | 1.89 | 13.8 | 1.18 | 0.57 |

Table.1 Estimates of genetic components of variation and their related statistics for maturity traits of bottle gourd

The number of dominant and recessive genes in parents as indicated by $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}$ –F was (1.39) showed excess of dominance genes. The estimate of h^2/H_2 was found 0.48 indicated that the number of gene group involved in the inheritance of this trait (Table 1). The positive value of correlation coefficient suggested the preponderance of recessive genes. The value of t^2 for node number of first staminate flowers was found non-significant indicating the validity of the hypothesis of assumption of diallel cross analysis.

The significant value of D, H_1 , H_2 , h^2 and E indicated the presence of both additives as well as dominance gene effect for the inheritance of node number of first pistilate flowers(Table 1). The significance of H_1 and H₂ suggested the role of dominance components for this trait. The positive F value suggested frequency of dominant alleles in the parents. The degree of dominance $(H_1 / D)^{1/2}$ was less than one, showed partial dominance for this trait. The ratio of $H_2/4H_1$ (0.23) indicated asymmetrical distribution of dominant and recessive genes in the parent. The number of dominant and recessive genes in parents as indicated by $(4DH_1)^{1/2}$ +F/ $(4DH_1)^{1/2}$ -F was (1.58) showed excess of dominance genes. The estimate of h^2/H_2 was found 1.12 indicated that the major number of gene group involved in the inheritance of this trait (Table 1). The positive value of correlation coefficient suggested the preponderance of recessive genes. The value of t^2 for node number of first pistilate flowers was found nonsignificant indicating the validity of the hypothesis of assumption of diallel cross analysis.

Additive (D) component was lower in magnitude than dominance components of genetic variation for all the maturity characters except node number of first

staminate flowers and node number of first pistilate flower which revealed preponderance of both dominant and recessive component of variance (Rehana and Sharma, 2007). The average degree of dominance $(H_1/D)^{1/2}$ involve in the action of genes was found as partial, complete and over dominance for the traits (Table 1) This suggested that heterosis breeding will be advantageous for improvement of yield and its component traits in bottle gourd (Sharma et al., 2010).

Proportion of genes $(H_2/4H_1)$ in the parents were less than 0.25 for all the traits (Table 1) except node number of first staminate flowers which showed asymmetrical distribution of loci showing dominance in the inheritance of these characters. The ratio of (4D H_1)^{1/2}+F/(4D H_1)^{1/2}-F indicated the excess of dominant as well as recessive genes among the parental strains for most of the characters (Table 1) (Dubey and Ram, 2007). The ratio of h^2/H_2 , provides information about groups of gene exhibiting that minor genes mainly governed the characters except days to first staminate flower anthesis, days to first pistilate flower anthesis and primary branches per plant under study, which may be due to concealing effects of dominant gene with positive and negative effect, which nullify the effects of each other (Quamruzzaman and Ahmad, 2010).

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