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GENETIC ARCHITECTURE OF YIELD TRAITS IN ADZUKI BEAN (*VIGNA ANGULARIS* (WILLD) OHWI & OASHI)

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ABSTRACT

Genetic components of variance were estimated following triple test cross analysis involving 22 pure breeding lines derived from an intervarietal cross (A 1 x HPU 51) of adzuki bean for seed yield, clusters, and pods per plant, pod length, seeds/pod and biological yield/plant. Epistasis was an integral component of genetic variation for all the traits studied. Overall epistasis (i type) was a major component in the cases where all the three types of epistatic interactions were present. Both additive and nonadditive genetic variances were important for most of the traits. Ambidirectional dominance was operative for all the traits except for pods and biological yield/plant for which decreasing alleles were more often dominant than the increasing alleles.

Key words: Triple testcross, *Vigna angularis*, adzuki bean, yield traits.

Information on gene action for yield and its related traits in different populations is pre-requisite for planning effective breeding programme. Several biometrical procedures are available for obtaining information on the nature of genetic variation but, the triple test cross (TTC) of Kearsey and Jinks [1] and its modification [2] is the most efficient for detection and estimation of epistatic variation. It also provides unbiased estimates of additive and dominance components of genetic variation. The present investigation aims to detect epistasis along with precise estimation of additive and dominance components of variation for different traits in adzuki bean, *Vigna angularis*, a genetically unexploited crop.

MATERIALS AND METHODS

The experimental material comprised 22 pure breeding lines derived from the cross A1 x HPU 51 of adzuki bean, namely, HPAB 1, HPAB 2, HPAB 3, HPAB 4, HPAB 5, HPAB 6, HPAB 9, HPAB 12, HPAB 15, HPAB 18, HPAB 19, HPAB 20, HPAB 21, HPAB 22, HPAB 23, HPAB 25, HPAB 27, HPAB 31, HPAB 32, HPAB 35 and HPAB 38; and 3 testers, namely, A1, HPU 51 and their F_1 (A 1 x HPU 51). The 66 triple test cross progeny families (L_{1i}, L_{2i} and

L_{3i}) and 22 parental lines (P_i) were grown in a single plot completely randomized design under rainfed conditions keeping plant to plant distance of 30 cm. Here i represents the cross between $(Pi)^{th}$ inbred line and the three testers P_1, P_2 and L_1. In the L_{3i} progenies, each individual plant has a different genetic constitution. In such a situation, a single plant CRD was preferred against row-plot. Observations were recorded for seed yield, clusters/plant, pods/plant, pod length, seeds/pod, and biological yield/plant.

The variance of comparison ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$) was used for testing the presence of epistasis, following Kearsey and Jinks [1], where $\bar{L}_{1i}$, $\bar{L}_{2i}$, and $\bar{L}_{3i}$ are the means of i-th family in respective tester. The sum squares due to epistasis was partitioned into i (additive x additive), j (additive x dominance) and l (dominance x dominance) types of interactions [3]. The mean squares due to i type interaction were tested as a variance ratio against the mean squares due to j + l types interactions whenever the latter were significantly greater than the corresponding within family variances. An alternative test of epistasis based on the variance of ($\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_i$) was also employed, where $\bar{P}_i$ is the mean of the i-th parent. The simultaneous application of these tests discriminates between the two causes of the failure of simple additive-dominance model, namely, epistasis and inadequacy of testers due to common genes [4]. The significance of the mean squares for these comparisons was tested using χ^2 test against the appropriate within family variances.

The variance of ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and $\bar{L}_{1i} - \bar{L}_{2i}$) were simultaneously computed for the detection and estimation of additive and dominance genetic components. The covariance of ($\bar{L}_{1i} + \bar{L}_{2i}$) on $\bar{L}_{1i} - \bar{L}_{2i}$) for all values of i was calculated which shows the direction of dominance [2].

RESULTS AND DISCUSSION

The analysis of variance for test I ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$) and test II ($\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_i$) for the adequacy of testers and test of epistasis for different traits is presented in Table 1. Mean squares due to epistasis in both the tests were significant for all the traits, thus, exhibited failure of additive–dominance model in the present material which cannot be due to inadequacy of testers fulfilling all the assumptions required for the model. Therefore, epistasis appears to be an integral component of the genetic architecture of different traits in the present material. Further partitioning of the epistatic term revealed that mean squares due to i type epistasis was significant for clusters/plant, pods/plant, and pod length, whereas j and l types of epistasis were significant for all the characters studied. This clearly showed that all the three types of nonallelic interactions, namely, additive x additive (i), additive x dominance (j), and dominance x dominance (l) with the predominance of the former were associated with clusters/plant, pods/plant, and pod length. For the remaining traits, additive x dominance and dominance x dominance type interactions were present.

Table 1. Analysis of variance (mean squares) for testing epistasis, additive and dominance components for different traits in adzuki bean

Source	Seed yield	Clusters per plant	Pods per plant	Pod length	Seeds per pod	Biological yield per plant
A. Epistasis:						
Test I ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$)	8.2*	6.3*	33.4*	0.6*	0.8*	22.0*
i type	0.0	36.9*	158.8*	2.0*	0.5	25.5
(j+l type)	8.5*	4.8*	27.1*	0.5*	0.8*	21.8*
error	4.6	2.7	1.6	0.2	0.3	12.1
Test II ($\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_i$)	6.6*	4.5*	26.2*	0.5*	0.7*	19.9*
error	3.9	2.8	16.1	0.1	0.3	11.9
B. Additive component:						
($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	10.3*	5.4*	30.5*	0.8*	0.7*	28.5*
error	4.6	2.7	15.6	0.2	0.3	12.1
C. Dominance component:						
($\bar{L}_{1i} - \bar{L}_{2i}$)	7.7*	4.9	37.3*	0.5*	0.7*	30.1*
error	4.7	3.3	19.2	0.1	0.3	14.3
D. Genetic components of variance:						
D	7.6	3.7	20.0	0.8	0.5	21.8
H	6.0		36.1	0.7	0.8	31.6
$(H/D)^{1\backslash 2}$	0.9		1.3	0.9	1.2	1.2
F	NS	NS	-518.2	NS	NS	-654.2

*$P \leq 0.05$. NS—nonsignificant, – not calculated.

Similar findings were obtained by Dahiya and Waldia [5] for pods and clusters/plant in urad bean through generation mean analysis.

The additive and dominance components were worked out for all the traits irrespective of the significance of epistasis in order to assess the relative magnitude of two components. Mean squares due to sums and differences were significant for all the traits except for clusters/plant, for which only mean square due to sums was significant. This shows the importance of both additive and dominance variances for all the traits except for clusters/plant for which only additive variance was present. The relative magnitude of additive (D) and dominance (H) components indicated the predominance of the former component for seed yield/plant and pod length, whereas the reverse was true for pods/plant. These results are in conformity with the findings of urad bean [6–8], mungbean [9, 10], and cowpea [11].

The directional element F was worked out for all the traits where dominance was present. It was significantly negative for pods/plant and biological yield, and nonsignificant for other traits. This means that the decreasing alleles were dominant more often than the increasing alleles for pods and biological yield per plant, whereas ambidirectional dominance was present for the remaining traits.

In this study, the epistasis was an integral component of the genetical structure of the material used and hence detection, estimation, and consideration of this component is important for the formulation of breeding programme.

Additive x additive type epistasis coupled with additive gene action was preponderant for clusters/plant and pod length, and therefore, simple breeding procedures such as pedigree method could be advantageous for improvement in these traits. For other traits additive x dominance and dominance x dominance type interactions coupled with additive or dominance gene action was preponderant. In such a situation, biparental matings may be attempted in F_2 and subsequent generations and selection may be postponed till F_5 generation to allow sufficient epistatic effects to get fixed.

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