

Estimation of genetic parameters for some quantitative traits in large seeded bean (*Phaseolus vulgaris* L.) lines by factorial analysis of generation means

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Abstract Understanding the nature of gene action in the breeding materials is helpful for breeders in formulating breeding strategy. In order to understand the type of gene actions operating in the breeding materials, six generation means (P_1, P_2, F_1, F_2, BC_1 and BC_2) from two crosses among large seeded bean lines grown at Awassa 2002 were used to estimate the genetic effects of some quantitative traits. The result revealed that for seed yield (gm/plant), pods/plant and pod length additive genetic model was not sufficient to explain most of the genetic variation for the expression of these traits. Epistatic effects contributed to the inheritance of these traits in the two crosses used. For seeds/pod and plant height epistatic gene effect was present in one of the two crosses. The nature of epistasis operating in the inheritance of seed yield (gm/plant), pods/plant, pod length, and plant height is duplicate type whereas it is complimentary type for seeds/pod. This indicates that particular allelic combinations at several loci determine the performance of these traits. Thus, population improvement and gamete selection breeding methods may help to improve these traits. Realized heterosis (over mid-parent) was observed for seed yield(gm/plant), pods/plant and plant height in one of the two crosses with no inbreeding effect in F_2 indicating that the heterosis is largely caused by non-allelic interaction even though over dominance was also observed. Pods/plant could be an important trait for plant selection in segregating generations as it revealed a significant positive correlation and high direct effect with seed yield.

Key words: Correlation, epistasis, gene effects, generation mean, large seed bean

Introduction

Improving the yielding potential and related desirable characters is the main objective of common bean (*Phaseolus vulgaris*) breeding program. The efficiency of breeding program increases by careful choice of parents and populations capable of producing progeny with desirable trait combinations (Angela *et al.*, 2002 and Cristina *et al.*, (2002). For a breeding program to be successful, designing appropriate breeding strategy/procedure is *sin qua non*. Understanding the type of gene action operating in breeding materials is helpful for breeders in formulating suitable breeding strategy. Intrinsic genetic properties of breeding populations can be evaluated using genetic designs (Hallauer and Miranda, 1988). Generation mean analysis is used to estimate the component variance which provides information about the predominant type of gene action for the important characters of crop species (Ganesh and Sakila, 1999). Therefore, this study was initiated to determine the relative magnitude of genetic effects contained in the means of some quantitative traits in crosses of large seed bean lines.

Materials and methods

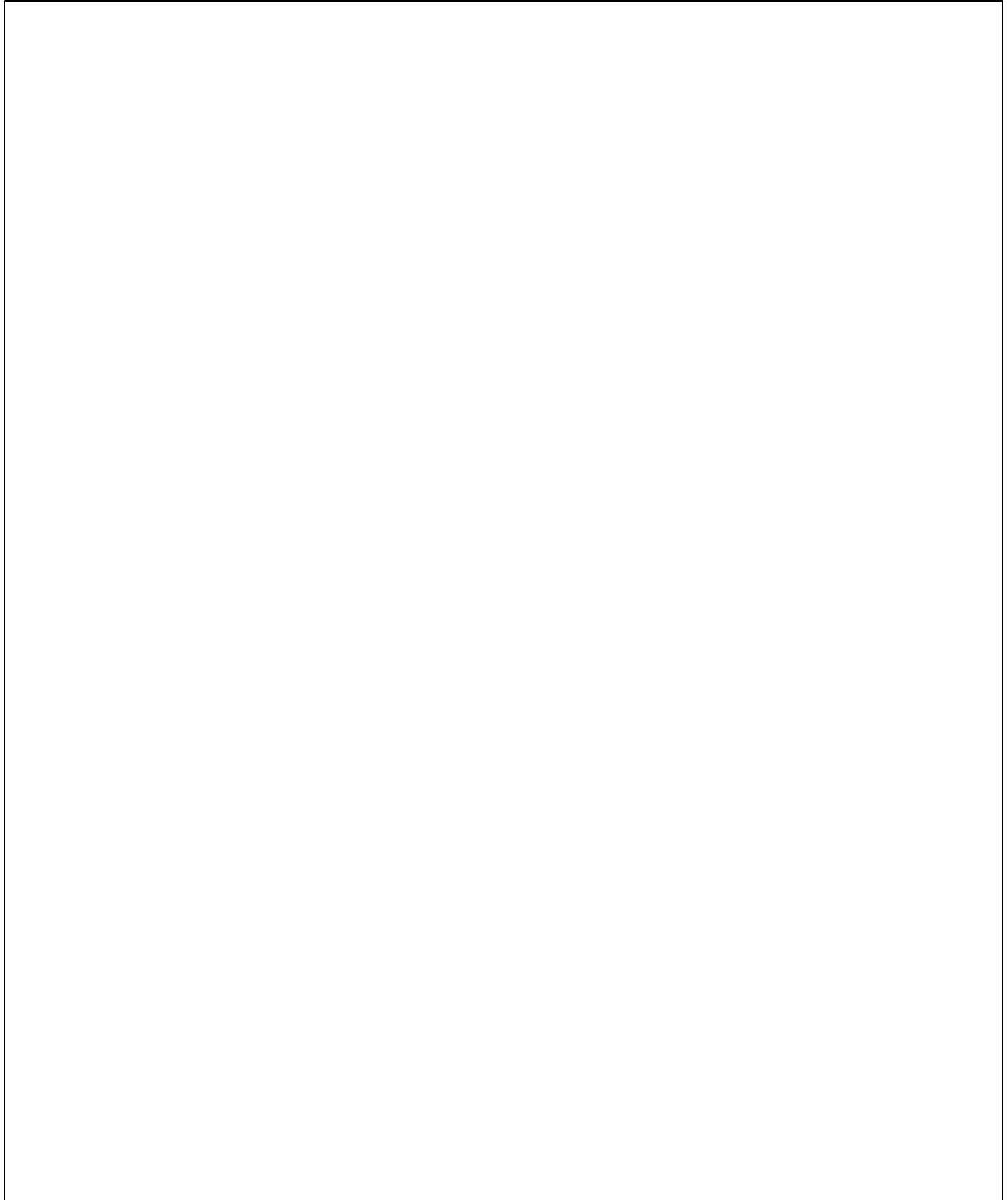
The gene action study for seed yield and its components was conducted on crosses of four large seed bean lines, Omar, DRK-58, Brown speckled and Melke. Omar is white seeded with round seed shape and prostrate growth habit. DRK-58 is dark red kidney shape with upright determinate growth habit. Brown speckled is sugary bean with prostrate growth habit and Melke is calima type with BSM resistance. Single crosses were made between Omar and DRK-58 and between Brown speckled and Melke in 2001 to generate F_1 s. The F_1 s were backcrossed with both parents and advanced to F_2 in 2002 belg (short rain) season. All the six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) in two crosses were grown at Awassa (1700 meters above sea level), Ethiopia in 2002 main season (Mehre) in compact family block design repeated twice. The plot size for non-segregating generations (P_1 , P_2 and F_1) and backcross generations was three rows of 2 meters long each and for F_2 six rows of the same length. The data on seed yield (gm/plant), number of pods/plant, seeds/pod, pod length(cm) and plant height (cm) were collected on individual plant base sampled from middle rows (six plants in P_1 , P_2 and F_1 , 20 plants in F_2 and 10 plants in BC_1 and BC_2 generations). The mean and variance of means of five quantitative traits were computed for each generation of the two crosses. The Hayman (1958) and Mather and Jinks (1971) model were used to determine the type of genetic information obtained in generation means. The significance of scales and gene effects were tested by t-test as described in Sharma (1998). Association between the traits was estimated as described in Singh and Chaudhary (1985).

Results and discussion

The results of scaling tests applied to detect the presence of non-allelic interaction in the parents involved in the crosses are presented in Table 1. At least one of the scale was significant in both of the crosses for seed yield (gm/plant), pods/plant and pod length, and in one of the crosses for seeds/pod and plant height. The significance of any one of the scale reveals the presence of non-allelic interaction. Hence, for seed yield (gm/plant), pods/plant and pod length additive genetic model was not sufficient to explain most of the genetic variation for the expression of these traits. This shows that epistatic effects contributed to the inheritance of these traits in the two crosses used. For seeds/pod and plant height, epistatic gene effect was present in one of the two crosses. In Brown speckled x Melke cross all the scales were non-significant for the characters seeds/pod and plant height indicating a simple additive genetic model was adequate for estimating the genetic components of variance of the traits.

The estimate of gene effects, heterosis effect and type of epistasis are presented in Table 2. The estimate of generation mean analysis for grain yield revealed that the additive (d), additive x dominance(j) and dominance x dominance(l) interactions were significant on Omar x DRK-58 cross and only additive x dominance(j) interaction was significant on Brown speckled x Melke cross. In both the crosses, the interaction components ((i) + (j) + (l) = 188.6 for Omar x DRK-58 cross and = 75 for Brown speckled x Melke cross) are greater than the combined main effects (d + h = 56.7 and 27.9 for Omar x DRK-58 cross and Brown speckled x Melke cross, respectively). Among the interactions, dominance x dominance (l) interaction is larger and among main effects, dominance (h) is greater than the additive (d) component in both the crosses. This indicates that heterozygote loci are predominant and more variations are expected in subsequent generations. The (h) and (l) i.e., dominance main effect and dominance x dominance interaction effects are in opposite directions. Hence, the nature of epistasis governing the inheritance of seed yield (gm/plant) in these crosses is duplicate type. The significant interaction component for seed yield indicates that plant selection has to be delayed to advanced generations for the realization of superior segregants. Moreover, population improvement and gamete selection breeding methods may help to improve seed yield.

The additive main effect (d) and dominance x dominance (l) interaction effect in Omar x DRK-58 cross, and dominance (h) main effect, and additive x additive(i) and dominance x dominance(l) interaction effects in Brown speckled x Melke cross were significant for number of pods/plant (Table 2). The interaction components put together i.e., (i) + (j) + (l) are greater than the combined main effects (d+h) indicating epistatic gene action is contributing more in the inheritance of the trait. Among the interactions, dominance x dominance (l) effect and among main effects





dominance (h) component are larger in both the crosses. The nature of epistasis operating in the inheritance of pods/plant is duplicate type. The heterosis effect was present in one of the crosses and it was non-significant. The internal cancellation of (h) and (l) could reduce the heterosis effect in pods/plant.

In seeds/pod, all the main effects and interaction effects were non-significant (Table-2). Epistasis was observed in Omar x DRK-58 cross and it was complementary type. Hence recurrent selection technique could be used for improving seeds/pod.

In pod length, all the interaction effects except additive x dominance (j) were significant in the two crosses (Table-2). The interaction components were greater than the combined main effects. The (h) and (l) are in opposite direction hence the nature of epistasis is duplicate type. The interaction effects account for larger proportion of the variation on pod length and success of selection for pod length could be realized in selection practiced in advanced generations.

All gene effects in Omar x DRK-58 cross and additive and dominance effects in Brown speckled x Melke cross were contributed to the inheritance of plant height (Table-2). All the interaction components were significant in Omar x DRK-58 cross for plant height. The magnitude of interaction effects is greater than the combined main effects. The nature of interaction was duplicate type.

Additive-dominance model was adequate in Brown speckled x Melke cross for seeds/pod and plant height. This indicates that selection could be practiced effectively in F_2 generation for improving these traits on Brown speckled x Melke cross.

In seed yield (gm/plant), pods/plant and pod length, additive x additive (i), additive x dominance(j) and dominance x dominance(l) interaction effects with duplicate nature are contributing in the inheritance of these traits indicating a reciprocal recurrent selection could be employed for genetic improvement of these traits. The method is helpful in breaking up undesirable linkages (Ganesh and Sakila, 1999).

The results of realized heterosis over mid-parental value, inbreeding effect and degree of dominance are depicted in Table 3. The realized heterosis over mid-parental value was observed in the crosses for seed yield (gm/plant), pods/plant and plant height with low inbreeding effects. Over dominance or partial dominance is the cause of heterosis for these traits. But, heterosis in these traits might be caused largely by non-allelic interactions.

The results of phenotypic correlations and path coefficient analysis based on the phenotypic correlations are presented in Tables 4 and 5. Seed yield was positively correlated with pods/plant, plant height and seeds/pod and negatively correlated with pod length. The correlation was highly significant with pods/plant indicating indirect selection using pods/plant could be used in the segregating generation for improving seed yield. The character pods/plant showed high positive direct effect on seed yield. Thus pods/plant is important trait in yield improvement as it revealed a significant positive correlation coefficient and high direct effect as compared to other traits.

Acknowledgements

This research was funded by ECABREN/PABRA. The authors would like to thank Tegene Ayele for his assistance in field works. We are grateful to ECABREN/PABRA/CIAT for sponsoring us to participate in the 6th African Crop Science Conference.

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