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Research Article

Estimation of gene effects for yield attributing traits in mungbean (*Vigna radiata*) and urdbean (*Vigna mungo) for* intra and interspecific crosses

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Abstract

The present investigation was carried out at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar. The experimental material consisted of three genotypes of resistant mungbean and urdbean donor each viz., HUM-16, TMB-37, Samrat and Pant U-31, Uttara, Sekhar, respectively; with a susceptible donor of LGG 450 and Barabanki local for mung and urd, respectively. Six intraspecific and four interspecific crosses were made and P_1, P_2, F_1, F_2 BC_1, BC_2 population were grown in RBD design with three replications. The observations were recorded for thirteen different quantitative as well qualitative traits viz., Days to 50 flowering, Plant height (cm), Number of primary branches, Cluster per plant, pods per cluster, Number of pods per plant, Days to maturity, Pod length (cm), Grains per pod, 100 seed weight (g), Harvest index, Phenol content (mg) and Grain yield per plot (kg).n Basedon the joint scaling test few intraspecific combinations showed the presence of epistasis; whereas in most of the interspecific crosses epistasis was observed. As per the three parameters model additive and/or dominant components seems to play an important role in the inheritance of most of the yield attributing traits in intra and interspecific crosses. As evident from the six parameter model, preponderance of significant reducing (-ve) additive gene effects in intraspecific crosses were observed, whereas additive and dominance components were equally important in interspecific crosses for the expression of most of the yield attributing traits. Among epistatic interactions additive x additive gene effects for days to 50 per cent flowering and dominant x dominant gene effect for 100 seed weight in four intraspecific crosses, whereas in interspecific crosses all three types of epistatic interactions were observed for the expression of most of the yield attributing traits. In most of the intra as well as interspecific crosses, duplicate type of epistasis was observed.

Keywords

Vigna, joint scaling test, generation mean, epistasis, cross. intraspecific and interspecific cross

INTRODUCTION

Pulses are known as grain legumes valued for their protein-rich grain which is two to three times more than cereal. Mungbean is one of the cheapest sources of plant protein, which contains about 22-27 per cent protein. It is also a good source of minerals such as calcium and sodium. Dried mungbean seed are high in vitamin A and B, while the sprouted mungbean is rich in vitamin B and C. Globally, grain legumes are the second most important group of crops. Among pulses, *Vigna radiata* L. (mungbean) and *Vigna mungo* (urd bean) are included in dry beans, which occupy an area of 25.88 million ha and produces 18.13 million tonnes with an average yield of 701 kg/ha at the global level. India a major pulse producing country accounts roughly for 25 per cent of total world production (Indian Statistics at a glance, 2008). In Bihar Mungbean occupy 176.83 thousand ha and produces 95.52 thousand tonnes with a 540 kg/ha productivity; whereas, urd bean occupies only 24.51 thousand hectares with 9.59 thousand productions having 709 kg/ha yield (Directorate of Statistics and Evaluation, Bihar 2010). At the time of independence, National availability of pulse was 70 g per capita per day. But, now availability has declined to 37g while only 20 g per capita per day at the state level (Indian Statistics at a Glance, 2008).

The knowledge of the nature of gene action in the inheritance of yield-related traits would be useful to formulate a suitable breeding programme and develop better cultivars with a higher yield. The major thrust area for genetic improvement would lie in identifying desirable parents for hybridization programme. This would depend to a large extent on the knowledge of gene actions controlling various characters. Scaling test and generation mean analysis is efficient biometrical tools for assessing the importance of epistasis and estimating the gene(s) effects. The reliability of the estimates and genetic gains of selection in segregating population largely depend upon the genetic divergence of the parents involved and the precision of testing. Keeping this in view, in the present study, an attempt has been made to estimate various kinds of gene effects through standard biometrical procedures and to know the relative importance of these gene effects in the control of grain yield and its component characters in *Vigna* species

MATERIALS AND METHODS

The present investigation was undertaken at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar which is situated at the side of Budhi Gandak river of North Bihar in the humid subtropical zone. It is situated at 25'50^0 N latitude and 85'75^0 E longitude with an altitude of 51 meters above mean sea level. The experimental material consisted of three resistant mungbean donors *viz*., HUM-16, TMB-37 and Samrat with susceptible donor LGG 450 andhree resistant donors of urd bean *viz*., pant U-31, Uttara and Sekhar with a susceptible donor Barabanki local LGG 450 and Barbanki are susceptible donors for mung and urd, respectively. All six genotypes of mung and urd bean were grown in a crossing block in spring 2009 with their respective susceptible donors LGG450 and Barabanki Half of the hybrid seed of three intraspecific crosses of each mung and urd bean as well as interspecific crosses along with parents were raised to obtain F_2 seeds BC_1 and BC_2 seeds. Six F_1 hybrids of intraspecific and four interspecific hybrid F_1 were selfed to obtain F_2 seed as well as backcrossed to both the parent to obtain BC_1 and BC_2. The F_1, F_2, BC_1 and BC_2 Population derived from three intraspecific crosses of each mung and urd bean, as well as four interspecific F1s progenies F2, BC1, BC2 along with their parents, were grown in RBD (Randomized Block Design) with three replications having the plot size of 2.4 m^2 with the row to row spacing at 30 cm and Plant to plant 10 cm, while F_2 populations of each cross were grown in 4.8 m^2 plots having the 10 rows with 4 m length. SML 668 was used as a check. Ten randomly plants were selected, from P_1, P_2, F_1, BC_1, BC_2 and forty plants from F_2 for each cross to recorded the observations for days to 50 per cent flowering plant height (cm), the number of primary branches, the number of cluster per plant, the number of pods per cluster, the number of pods per plant, days to maturity, pod length (cm), the number of grains per pod, 100-seed weight (g), harvest index (hi), phenol content (mg) and grain yield per plot (kg). The individual scaling tests were applied to test the adequacy of additive dominance model as suggested by Mather (1949) and six parameter model (Jinks and Jones 1958). The weighted least square technique was used to estimate the components of different parameters viz., 'm', 'd', 'h', 'i', 'j', and 'l'. The joint scaling test as proposed by Cavalli (1952) was also applied to test the adequacy of the additive-dominance model because the joint scaling test combines, very effectively, several scaling tests into one and offers a more general and informative approach.

RESULTS AND DISCUSSION

The estimation of additive, dominance and presence of epistasis were done by joint sealing test and consequently, the significance of three parameters [m] [d] [h] was evaluated. In intraspecific crosses, few crosses have exhibited the presence of epistasis, and importance of additive components was realized for days to 50 % flowering, plant height, the number of pods per plant, the number of clusters per plant and days to maturity. In contrast, dominance component was found to play an important role in the expression of days to 50% flowering, the number of cluster per plant, the number of pod per plant, days to maturity, the number of grains per pod. However, both additive and dominant component was equally important for the inheritance of days to 50% flowering, plant height, the number of cluster per plant, the number of pod per plant and days to maturity in the crosses namely TMB 37 x LGG 450, HUM 16 x LGG 450, Samrat x LGG 450, Sekhar x Barabanki and Uttara x Barabanki. Days to 50% flowering, the number of cluster per plant and days to maturity in the cross TMB 37 x LGG 450 was observed, whereas, for the trait plant height found in all six crosses except PU 31 x Barabanki. All six crosses were exhibited significant additive as well as dominant components for the expression of the character for the number of pods per plant except in Sekhar x Barabanki. The cross PU 31 x Barabanki also showed the importance of additive and dominant components for days to maturity.

In interspecific crosses, epistasis was evident in most of the crosses for different traits under study. Therefore, the preponderance of additive components were noticed for days to 50% flowering, plant height, the number of pods per plant, days to maturity; whereas, dominance component was found to play an important role in the expression of days to 50% flowering, plant height, the number of primary branches, the number of cluster per plant, the number of pods per plant, days to maturity, pod length. Both additive and dominance components were equally important for the inheritance of days to 50% flowering in the cross Uttara x LGG 450, for plant height in all three crosses except TMB 37 x Barabanki, for the number of pods per plant in all three crosses except Uttara x LGG 450; whereas for days to maturity observed in PU 31 x LGG 450. It is relevant to emphasize the significance of gene interaction involving in the inheritance of yield and yield attributing components in intraspecific and interspecific crosses and epistasis was more frequently found in interspecific crosses as compare to intraspecific crosses. It is indicated that inheritance of yield components become more complex in those crosses having distantly related parents are involved. The relative estimates for two types of gene actions varied from the cross to cross for the same character due to X^2 estimation cannot be compared at zero degree of freedom and sequential elimination technique could not be carried out, and the actual estimation of significant components was through contribution to the traits in the present set of materials.

On the basis of three-parameter model, found that additive and/or dominance components seemed to play an important role in the inheritance of few yield components, such as days to 50% flowering, the number of cluster per plant, the number of pod per plant, days to maturity and pod length, which are expected to be a less complex inheritance. Dominance or additive, epistatic gene interaction was also found to play a significant role in the expression of complex traits likes plant height, number of pods per plant in the majority of the crosses. It indicates that as the inheritance of quantitative character is more complex, the contribution of epistatic gene effects in the inheritance will be greater.

The estimation for the relative magnitude of various gene effects including epistasis has great importance in formulating the most appropriate breeding procedure for further improvement, where the individual cross combination is considered. Linkage effects the epistatic components in generation mean (Hayman, 1958 b); additive and dominance gene effects are likely to be biased in the presence of epistasis (Hayman, 1960 b). The joint scaling test revealed the presence of epistasis in crosses and six parameter model gives reliable estimates of main gene effects as well as epistatic gene interaction. In the present investigation, attempts have been made to examine, whether epistatic gene effect exists in the materials having diverse parents belonging to same species; intraspecific crosses or even to different species i.e. interspecific crosses and their relative importance.

Out of six intraspecific crosses, X^2 value was found to be significant in five crosses for 100 seed weight and harvest index, four crosses for days to 50% flowering, plant height, phenol content and grain yield per plot, three crosses for the number of pods per plant and pod length, two crosses for the number of primary branches and days to maturity and one cross for rest of the characters like the number of cluster per plant, the number of pods per cluster and the number of grains per pod indicating the evidence of epistasis and hence, Joint sealing test was applied to test the adequacy of additive dominance model. Significance of X^2 value indicated the evidence of epistasis in respective crosses for the trait under study. Therefore, data from all the crosses (when X^2 value significant) were further analyzed using six parameter model for their practical application. In intraspecific crosses, the estimation of six parameters for various gene effect revealed the significant reducing (-ve) additive gene effects for the expression of almost all the characters except the number of cluster per plant and the number of pod per cluster; while grain yield per plot exhibited significant enhancing (+ve) additive gene effects. Similar results were also observed by Seenaiah *et al.* (1993), Rasaiah *et al.* (1994) and Manivannan (2002). Significant and positive dominant gene effect was observed for the traits days to 50 % flowering, phenol content, harvest index and grain yield; exhibiting the enhancing (+ve) effects for the inheritance of the traits which was in conformity with an earlier report (Shanmungasundaram and Rangaswamy, 1994; Joseph and Kumar, 2000), while significant reducing (-ve) dominant gene effects were observed for the number of pod per cluster, days to maturity, the number of grains per pod and 100 seed weight for the expression of the traits and similar results were also obtained by Singh *et al.* (2006). The relative magnitude of dominant gene effect was higher than the additive gene effect for the inheritance of all the traits studied, which was in conformity with the earlier reports of Shanmungasundaram and Rangaswamy (1994) and Joseph and Kumar (2000). An epistatic interaction, additive x additive gene effect for days to 50% flowering and dominant x dominant gene effect for 100 seed weight were found in all four crosses except Samrat x LGG 450 and PU 31 x Barabanki, which were exhibited the significant enhancing (+ve) effects for the inheritance of these traits in their respective crosses. In contrast, significant reducing (-ve) additive x additive gene effect for 100 seed weight and dominant x dominant gene effect for days to 50% flowering were observed in four crosses except for Samrat x LGG 450 and PU 31 x Barabanki, which was similar with earlier worker Ammavasai *et al.* (2005).

In the digenic interactions, additive x additive and dominance x dominance were found equally important for the traits viz. plant height, the number of primary branches, the number of pods per plant, pod length, harvest index, phenol content and grain yield. (Rehman *et al.* 2009) Additive x dominance has significant reducing (-ve) gene effect for days to 50% flowering, plant height and the number of clusters per plant. All the traits except the number of primary branches and the number of pods per cluster showed the expression of these traits.

Duplicate type of epistasis was found in eight traits namely days to 50% flowering, plant height, the number of primary branches, the number of pods per cluster, the number of clusters per plants, days to maturity, the number of grains per pod and 100-seed weight (Khodambashi *et. al.*2012 and Singh *et.al.*2015). Complementary epistasis was observed for one trait number of clusters per plant; whereas, for other four traits viz. pod length, harvest index, phenol content, and grain yield per plot few crosses showed duplicate as well as the complementary type of epistasis. These findings suggested that few cycles of recurrent selection followed by the pedigree method will be effective and useful to utilize all the three types of gene effects. It will create variability in the later generation for effective selection by maintaining considerable heterozygosity through the mating of selected plants in an early segregating generation. Epistasis was mostly of the duplicate type which will reduce variation in F_2 and subsequent generation, consequently, it hinders the pace of progress through selection. The complementary type of non- allelic interaction for the number of clusters per plant was observed and intercrossing of F_2 plants may be recommended to produce superior recombinants having the complex genetic behaviour and selection in the later generation of segregating population for enhancing the number of clusters per plant for the *Vigna* improvement (Payasi *et al* 2010 and Patel *et al.* 2012).

In interspecific crosses, both additive and dominant gene effect (ignoring, sign) were almost equally important and the relative magnitude of dominant gene effect were even higher than the additive gene effects for the inheritance of all the traits under study, which were similar with the earlier reports of Bisht *et al.* (2014), Singh *et al.* (2016) and Jhangirdar (2001). An epistatic interaction positive and significant additive x additive gene effects was observed for the enhancing of the expression of days to 50% flowering, Plant height and Phenol content. Negative and significant additive x additive gene effects were found responsible for reducing (-ve) the expression of the number of pods per cluster, the number of pods per plant, harvest index (HI) and grain yield per plant. Dominant x Dominant gene effects exhibited significant enhancing (+ve) effect for the inheritance of the number of pods per plant, the number of grains per pod and grain yield per plant whereas significant and reducing (-ve) effects for the inheritance of traits days to 50% flowering and phenol content for most of the crosses. Additive x dominance gene effect showed reducing (-ve) effects for the expression of most of the traits except the number of grains per pod and harvest index (HI). For almost all characters duplicate the type of epistasis was observed in Samrat x Barabanki, PU 31 x LGG 450 and Uttara x LGG 450, whereas cross TMB 37 x Barabanki showed the complementary type of gene effect for the traits pod length and phenol content and PU 31 x LGG 450 also showed the complementary type of gene effects for the traits harvest index (HI) and grain yield per plot.

To exploit all the three types of gene action present in most of the crosses for most of the characters, recurrent selection has been suggested followed by modifying pedigree method or and pedigree method as well as intermating of superior selected plants in segregating generation will be useful. It will help in breaking gene constellation and will lead to an effective selection. This is in agreement with the earlier findings of Patil *et al.* (2005,2011), Naidu and Satynaryana (1993), Khattak *et al.* (2002), Sharma and Gupta (1994).

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