GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS IN SOYBEAN [GLYCINE MAX (L.) MERRILL]

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ABSTRACT

The present investigation was undertaken to study the genetics of yield and yield components through generation mean analysis. Dominant gene action was found predominant in inheritance of yield and yield contributing characters like number of primary branches, number of clusters, number of pods and yield per plant. Both additive and non-additive gene effects were significantly involved in the expression of number of clusters and yield per plant with duplicate epistasis. Bi-parental mating design should be used to improve these characters. Complementary epistasis observed for cross NRC 7 x EC 241780 (for days to 50% flowering, maturity, number of clusters and pods per cluster) for cross EC 241780 x Kalitur (primary branches and 100 seed weight) and for Kalitur x NRC 7 (plant height, pods per cluster and 100 seed weight) suggests that selection can be practiced in F₃ generation onwards for improvement of these characters.

Key words: Additive and non-additive gene effects, Bi-parental mating, Complementary epistasis, Gene action, Selection, Inheritance, Soybean

INTRODUCTION

Soybean [Glycine max (L.) Merrill] cultivation is rapidly expanding partly due to its high nutritional value as food for both humans and livestock and as an important industrial crop. It is considered as a “Golden bean” due to its dual qualities viz; high protein (40%) and oil (18 to 20%) content. The protein and oil account for 60% (Nagraj, 1995).

India is the fourth largest producer of soybean in the world. However, India’s share in world production of soybean is only 5%. The current level of soybean yield being around 1.21 ton/ha is about half of the world average productivity. On an average Madhya Pradesh and Maharashtra produce 51 and 33 per cent of total production of soybean respectively.

The classical breeding systems that make use of additive genetic variance will be effective breeding procedures for improving the seed yield. To exploit the existing genetic variability present in breeding material for seed yield as efficiently as possible, the breeder would need the basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection programme. For genetic improvement of the crop, the breeding method to be adopted depends mainly on the nature of gene action involved in the expression of quantitative traits. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately, whether it is complimentary or duplicate at the digenic level. Two genetic models viz; Cavalli (1952) and Hayman (1958) were simultaneously used for determining the nature of gene action involved in the inheritance of yield and yield contributing characters.

The information regarding gene action involved in control of inheritance for yield and yield contributing characters through generation mean analysis is of immense use to the plant breeder to decide suitable breeding strategy for improvement of these characters.
MATERIALS AND METHODS

The present investigation was conducted at Post Graduate Institute, Botany Research Farm, Central Campus and All India Network Research Project on Underutilized Crop, MPKV, Rahuri during the period from 2012-2013 and 2013-2014.

Three crosses viz; NRC 7 x EC 241780 (C-I), EC 241780 x Kalitur (C-II), Kalitur x NRC 7 (C-III) were effected. Crosses were effected in Kharif 2012 and early summer 2013 to produce the F₁ seeds. In early summer 2013 F₁s were sown and F₂s seeds were made. Backcrosses, BC₁s and BC₂s of three crosses were also made in early summer 2013 within the stipulated period.

The experiment was laid out in randomized block design (RBD) with three replications in Kharif 2013. The experimental material consisted of 18 treatments consisting of 6 parents, 3F₁s, 3F₂s, 3B₁s, 3B₂s, of three crosses (NRC 7 x EC 241780, EC 241780 x Kalitur and Kalitur x NRC 7). The parents, F₁s, F₂s, and back crosses were randomized separately in each of the three replications. Sowing was done in rows of 3m length and 30 cm apart accommodating 30 plants at 10 cm distance in a row. One row was assigned to P₁s, P₂s, F₁s, while the two rows to each of the B₁s and B₂s and 10 rows to F₂s. This has permitted for raising of 30 plants in each of P₁s, P₂s, F₁s, 60 plants in B₁s and B₂s, and 300 plants in each of the F₂s, in each of the three replication for each cross. Fertilizer dose of 50 kg N and 75 Kg P₂O₅/ha for irrigated situation was applied at the time of sowing. The experiment was sown on 7th of July 2013. All inter-culturing operations were carried out regularly as per need and stage of crop growth.

The observations were recorded on the nine quantitative characters on 10 random plants from parents and F₁s; 20 plants from backcrosses and 40 plants from F₂s generations of all the three crosses for each replication. Data were first tested for non-allelic interaction by Individual scaling test A, B, C and D given by Mather (1949). Further analysis of data was performed according to the method of “joint scaling test” given by Cavalli (1952). For computation of gene effects for grain yield and its components with six basic generations, Mather (1949) three parameter model and Hayman's (1958) six parameter models were used.

RESULTS AND DISCUSSION

The results obtained in the present investigation for individual and joint scaling test are presented in Table 1. Significant individual and joint scaling tests were observed in all characters for three crosses except number of primary branches/plant in cross Kalitur x NRC 7 and yield/plant in cross NRC 7 x EC 241780. These two characters for the said crosses indicated absence of epistasis and only additive dominance model is adequate to explain the inheritance of these traits. Rest of the characters for all three crosses indicated presence of epistasis. The results of gene effects are presented in Table 2 and 3 and are discussed as below:

Days to 50% flowering: In cross combination NRC 7 x EC 241780 the predominance additive gene effect (negatively significant and desirable direction) with complementary epistasis was observed for the trait 50% flowering and hence it can be exploited effectively by selection for the improvement of the characters (Agrawal et al., 1999; Sayad et al., 2005; Datt et al., 2011). In cross EC 241780 x Kalitur the additive genetic effect (d) was equally important as non-additive (h) with duplicate epistasis, therefore, for efficient utilization of fixable and non-fixable components of genetic variation, reciprocal recurrent selection or biparental mating was suggested for this cross (Halvankar and Patil, 1993; Khattab, 1998).

Additive genetic effect (d) with additive x additive (i) epistasis was positively significant in crosses EC 241780 x Kalitur and Kalitur x NRC 7, indicating that the expression of character was under the influence of additive gene action but for lateness. The additive effects could facilitate fixation of the combination of genes and therefore, selection for days to 50% flowering in this crosses would give better response (Ma et al., 1987; Mehrete et al., 1998; Rahangdale and Raut, 2002; Sayad et al., 2005). The significant additive x additive non-allelic interaction with duplicate epistasis was observed in crosses EC 241780 x Kalitur and Kalitur x NRC 7 for days to 50% flowering suggest the possibilities of obtaining transgressive segregants in later generations. (Talwar et al., 1986; Ghassemi and Yazdi-Samadi, 1987).

Days to maturity: In cross combination NRC 7 x EC 241780, the predominance additive gene effect (negatively significant and desirable direction) with
TABLE 1: Estimation of individual and joint scaling test ($\chi^2$) for yield and yield contributing characters in soybean

<table>
<thead>
<tr>
<th>Cross</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NRC 7 x EC 241780</td>
<td>97.34</td>
<td>449.48</td>
</tr>
<tr>
<td>EC 241780 x Kalitur</td>
<td>-15.19**</td>
<td>25.74**</td>
</tr>
<tr>
<td>Kalitur x NRC 7</td>
<td>-2.20**</td>
<td>6.67**</td>
</tr>
</tbody>
</table>

Additive genetic effect (d) with additive x additive (i) epistasis was positively significant in crosses EC 241780 x Kalitur and Kalitur x NRC 7, indicating that the expression of character was under the influence of additive gene action, but for lateness. The additive effects could facilitate fixation of the combination of genes and therefore, selection for days to 50% flowering in these crosses would give better response (Ma et al., 1987; Rahangdale and Raut, 2002; Sayad et al., 2005). The significant additive x additive non-allelic interaction with duplicate epistasis was observed in crosses EC 241780 x Kalitur and Kalitur x NRC 7 for days to 50% flowering, which suggests the possibilities of obtaining transgressive segregants in later generations (Talwar et al., 1986; Sharma and Phul, 1994).

**Plant height (cm)**: Both additive (d) and non additive (h) gene effects were significant in the crosses NRC 7 x EC 241780 and EC 241780 x Kalitur (Harer and Deshmukh, 1991; Khattab, 1998; Shinde, 2010).

Additive gene effect was significant in negative direction for cross NRC 7 x EC 241780. The positively significant values of additive (d) in cross Kalitur x NRC 7 for height of the plant revealed that selection for this trait would be useful to start from the early segregating generation (Jackovic et al., 1988; Kang, 1990; Triller and Toledo, 1996; Jungyi and Mingan, 1997; Rahangdale and Raut, 2002; Shinde, 2010).

Among interaction components, values of estimates of additive x additive (i) component was positively significant in crosses NRC 7 x EC 241780 and EC 241780 x Kalitur. The crosses NRC 7 x EC 241780 and EC 241780 x Kalitur recorded complementary epistasis was observed for the trait days to maturity and hence it can be exploited effectively by selection for the improvement of the characters (Zhang et al. 1987; Mehetre et al. 1998; Sayad et al., 2005; Datt et al., 2011). In cross EC 241780 x Kalitur, the additive genetic effect (d) was equally important as non-additive (h) with duplicate epistasis, therefore, for efficient utilization of fixable and non-fixable components of genetic variation, reciprocal recurrent selection or biparental mating was suggested for the cross (Halvankar and Patil, 1993; Sayad et al., 2005; Shinde, 2010).
TABLE 2: Estimation of gene effects in three crosses for days to maturity, plant height number of primary branches and number of clusters/plant

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Genetic parameters</th>
<th>Type of Epistasis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>m</td>
<td>d</td>
</tr>
<tr>
<td><strong>Days to maturity</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>104.24**</td>
<td>-13.20**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>101.90**</td>
<td>4.77**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>98.39**</td>
<td>6.97**</td>
</tr>
<tr>
<td><strong>Plant height</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>50.06**</td>
<td>-21.50**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>74.21**</td>
<td>12.10**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>57.92**</td>
<td>5.40**</td>
</tr>
<tr>
<td><strong>No. of primary branches/plant</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>2.42**</td>
<td>-0.15**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>2.58**</td>
<td>0.04</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>2.52**</td>
<td>-0.04**</td>
</tr>
<tr>
<td><strong>Number of clusters/plant</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>31.80**</td>
<td>-5.43**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>37.22**</td>
<td>7.93**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>34.32**</td>
<td>1.70*</td>
</tr>
</tbody>
</table>

*, ** Significant at 5 & 1% respectively

TABLE 3: Estimation of gene effects in three crosses for number of pods/cluster, number of pods/plant, 100 seed weight and seed yield/plant

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Genetic parameters</th>
<th>Type of Epistasis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>m</td>
<td>d</td>
</tr>
<tr>
<td><strong>Number of pods/cluster</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>2.42**</td>
<td>-0.15**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>2.58**</td>
<td>0.04</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>2.52**</td>
<td>-0.04**</td>
</tr>
<tr>
<td><strong>Number of pods/plant</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>77.07**</td>
<td>-18.87**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>94.41**</td>
<td>21.90**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>86.71**</td>
<td>2.50</td>
</tr>
<tr>
<td><strong>100 seed weight</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>18.12**</td>
<td>2.14**</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>15.85**</td>
<td>1.06**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>17.05**</td>
<td>-2.10**</td>
</tr>
<tr>
<td><strong>Seed yield/plant</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRC 7 × EC 241780</td>
<td>21.14**</td>
<td>-0.71</td>
</tr>
<tr>
<td>EC 241780 × Kalitur</td>
<td>20.94**</td>
<td>5.61**</td>
</tr>
<tr>
<td>Kalitur × NRC 7</td>
<td>22.14**</td>
<td>-2.42**</td>
</tr>
</tbody>
</table>

*, ** Significant at 5 & 1% respectively

significant duplicate epistasis. Insignificant complimentary epistasis observed for cross Kalitur × NRC 7 (Hanson et al., 1967; Ma et al., 1987; Maloo and Nair, 2005). Non additive gene action was predominant for cross II (Croissant and Torrie, 1971; Alam et al., 1984; Talwar et al., 1986; Khattab, 1998).

**Number of primary branches per plant:**
Dominance and dominance x dominance gene actions were found to be predominant in controlling the inheritance of number of primary branches per plant in all crosses (Ghassemi and Yazdi-Samadi, 1987; Kang, 1990; Halvankar and Patil, 1993; Sharma and Phul, 1994; Khattab, 1998). The effect of dominant gene action for the trait should be eliminated through bulk selection method through which homozygosity could be achieved prior to the initiation of selection for the character. The opposite sign of (h) and (l) in duplicate epistasis for cross NRC 7 x EC 241780, while complimentary epistasis with both additive and dominance gene effects for cross EC 241780 x Kalitur and absence of non-allelic interactions for cross Kalitur x NRC 7 was observed. Selection is not desirable in duplicate type of
epistasis, therefore, heterosis breeding would be advantageous. The importance of dominant gene action with duplicate epistasis was reported for this trait (Li-Zenglu et al., 1995; Rahangdale and Raut, 2002; Shinde, 2010; Datt et al., 2011).

**Number of clusters per plant:** Significant non-additive (dominance and epistasis) gene actions with duplicate epistasis in the inheritance of this trait in the crosses II and III, revealed that number of clusters per plant was predominantly under non-additive genetic control. The high magnitude of dominance effect suggested that selection of high yielding genotypes would be postponed till later generation when the dominant effect would have diminished (Rahangdale and Raut, 2002; Shinde, 2010; Datt et al., 2011). In cross I (NRC 7 × EC 241780), complementary epistasis was observed which can help in selection in F₃ onwards for improvement of this trait. Both additive and dominance gene effects were significant in all crosses (Singh et al., 1974).

**Number of pods per cluster:** Significant additive and non-additive (dominance and epistasis) gene actions with complementary epistasis was observed for the inheritance of this trait in the crosses I (NRC 7 × EC 241780) and III (Kalitur × NRC 7), which revealed that the trait number of pods/cluster can be improved by selection in F₃ onwards such that the desired recombinants become available in the population (Singh et al., 1974; Sharma and Phul, 1994; Maloo and Nair, 2005).

**100 Seed weight (g):** Predominance of additive gene effect was observed for the trait 100 seed weight in crosses NRC 7 × EC 241780 and EC 241780 × Kalitur (Zhang et al., 1987; Kang, 1990; Harer and Deshmukh, 1991; Halvankar and Patil, 1993; Junyi and Mingan, 1997; Mehetre et al., 1998; Agrawal et al., 1999), Among non-allelic interaction, all three additive x additive (i), additive x dominance (j) and dominance x dominance (l) effects were significant for the cross Kalitur × NRC 7. Additive x dominance (j) component was significant for all three crosses (Ma et al., 1987; Ghassemi and Yazdi-Samadi, 1987; J ackovic et al., 1988; Sharma and Phul, 1994; Maloo and Nair, 2005).

Duplicate epistasis observed for cross NRC 7 × EC 241780 (Li-ZengLu, 1995; Rahangdale and Raut, 2002; Datt et al., 2011). Biparental mating is suggested for duplicate epistasis.

**Duplicate epistasis observed for cross NRC 7 × EC 241780 (Li-ZengLu, 1995; Rahangdale and Raut, 2002; Datt et al., 2011). Biparental mating is suggested for duplicate epistasis.**

**Yield per plant (g):** Presence of significant dominance component (h) with absence of non-allelic interactions in cross I (NRC 7 × EC 241780) revealed that yield of soybean was predominantly under non-additive genetic control. Predominance of dominance gene effect in cross II (EC 241780 × Kalitur) suggested that selection of high yielding genotypes would be postponed till later generations when the dominance effect would have reduced. Estimates of additive effects can be small due to a high degree of dispersion of increasing alleles.
between parents and dominance can be large due to its bi-directional nature. The presence of duplicate epistasis in crosses II and III for the trait can hinder progress and make it difficult to fix genotypes at a high level of manifestation. Duplicate epistasis may restrict the expression of a trait in early segregating generations. The selection in early generations would not be effective for want of fixable components of variation. Such gene effects can however, be exploited by intermating the selected segregants and delaying the selections to the advanced generations (Rahangdale and Raut 2002; Datt et al. 2011). The predominance of non-additive gene action for this trait was observed (Ghassemi and Yazdi-Samadi, 1987; Jackovic et al., 1988; Halvankar, 1988; Halvankar and Patil, 1993; Sharma and Phul, 1994; Triller and Toledo, 1996; Khattab, 1998; Sayad et al., 2005; Shinde, 2010).

Significant additive x additive gene effects for controlling this trait was observed for cross II (Hanson et al., 1967; Ma et al., 1987). The simple selection procedure in the early segregating generations may not contribute significantly for the improvement of the traits governed by duplicate epistasis. The complex genetic behaviour particularly additive and dominance components could be successfully exploited in later generations. It is, therefore, suggested that the selection for the improvement of all these traits, particularly seed yield should be delayed to the later generations of segregating population in soybean. The bulk method of selection is recommended in which selection is performed after attaining the homozygosity for maximum heterozygous loci. The biparental hybridization between recombinants in early segregating generation ($F_2$) would produce better genetic combination through which the accumulation of desirable genes could be achieved for high yield potential.

In nutshell, the predominant additive gene effects in desirable direction was observed for the days to 50% flowering, days to maturity and plant height in cross NRC 7 x EC 241780 and for 100 seed weight in NRC 7 x EC 241780 and EC 241780 x Kalitur, suggesting that selections can be effectively applied for improvement of these traits. The complementary epistasis observed for all characters, except number of pods and yield per plant for specific crosses, suggests selection can be practiced in $F_3$ generation onwards for improvement of these characters.

**REFERENCES**


