Abstract
In the present investigation, gene action was investigated for six yield contributing traits in Soybean. Six crosses were made between three Kunitz trypsin inhibitor expressing and two Kunitz trypsin inhibitor-free soybean parents during summer 2017. Dominant gene action was found predominant in the inheritance of yield and yield contributing characters like yield per plant and 100 seed weight in cross P. Sangam × NRC 101 and P. Sangam × NRC 102. Both additive and dominance gene effects were significantly involved in the expression of yield per plant in crosses P. Kimya × NRC 101 and P. Kimya × NRC 102 with duplicate epistasis. Biparental mating design is suggested to improve these characters. Complementary epistasis was observed in cross P. Agrani × NRC 101 for days to 50% flowering, plant height and yield per plant and in cross P. Kimya × NRC 101 for plant height, 100 seed weight and pods per plant thereby suggesting that, the selection can be practiced in F3 generation onwards for the improvement of these characters. Trypsin inhibitor-free genotype showed additive gene action.

Key words
Trypsin inhibitor-free, Soybean Gene action, Selection. Dominance, epistasis, Additive gene effects,
The observations were recorded on quantitative carried out regularly as per need and stage of crop growth. In this study, weeding, irrigation and plant protection were M.P.K.V., Rahuri, during Kharif 2017 and Kharif 2018. Sowing was done in rows of 1.5 m. and 30 cm apart at 10 cm distances in a row (medium soil). One row was assigned to P₁, P₂, P₃, F₁, F₂, F₃, F₄, so that each P₁, P₂, P₃, F₁, F₂, F₃, F₄, 30 plants in each of the F₂ and F₃, with three replications in each cross. The fertilizer dose of 50 kg N and 75 Kg P₂O₅/ha for was applied at the time of sowing. Regular operations like thinning, weeding, irrigation and plant protection were carried out regularly as per need and stage of crop growth. The observations were recorded on the quantitative characters in random 5 plants from Parents and F₁s; 20 plants from each of F₂ and F₃ generations of all the six crosses for each replication. The C and D scaling test of Mather (1949) was carried out to have an idea regarding the presence or absence of non-allelic interactions. Further analysis of data was performed according to the method of the “joint scaling test” given by Cavalli (1952), Jinks and Jones (1958) three parameter model and Hayman’s (1958) five parameter model were used. For the computation of gene effects for grain yield and yield attributing character with five generations.

RESULT AND DISCUSSION

The results obtained in the present investigation for, individual and joint scaling test are presented in Table 1. The test revealed significant gene interaction for 30 out of 36 cross traits combination except viz. days to maturity (Cross-P. Agrani × NRC 102 and P. Kimya × NRC 101); pods per plants (Cross-P. Sangam × NRC 101 and P. Sangam × NRC 102) and the seed yield per plant (Cross-P. Agrani × NRC 101 and Cross-P. Sangam × NRC 102), which indicated the only presence of simple additive and dominance model. The results of gene effects are presented in Table 2.

Table 1. Estimates of individual and joint scaling test (, **) for detecting non allelic interaction for yield and yield contributing characters in soybean.

| Sr. No. | Character | Phule Agrani × NRC 101 | Phule Agrani × NRC 102 | Phule Sangam × NRC 101 | Phule Sangam × NRC 102 | Cross name | Phule Kimya × NRC 101 | Phule Kimya × NRC 102 |
|---------|----------|-----------------------|-----------------------|-----------------------|-----------------------|----------------|-----------------------|-----------------------|
|         |          | C-IV                  | C-I                   | C-III                 | C-V                   | IV            | C-IV                  | C-I                   |
| 01      | DF       | 23.00**               | -1.70**               | 90.46**               | -26.93**              | 0.50**        | 1.35**                | 2.33**                |
| 02      | DM       | 23.22**               | -1.00**               | 39.17**               | -26.08**              | 5.05**        | 2.43**                | 8.32**                |
| 03      | PH (cm)  | 18.93**               | 1.70**                | 22.06**               | -26.93**              | 38.90**       | 43.06**               | -11.23**              |
| 04      | 100      | -1.81**               | 6.13**                | 33.99**               | -4.98**               | 5.22**        | 25.46**               | -5.68**               |
| 05      | SYP (g)  | -26.50**              | -9.06**               | 48.96**               | -13.20**              | -23.80**      | 192.18**              | 8.00**                |
| 06      | SYP (g)  | -3.66**               | -3.22**               | 47.05**               | 4.00**                | 2.55**        | 18.71**               | -1.20**               |

*, ** Significant at P = 0.05 and 0.01 per cent levels, respectively.
C= Dominance
D= Additive
DF = days to flowering
DM = days to maturity
100SSW= 100 seed weight
PSP= pods per plant
SYP= seed yield per plant

Additive gene effect and additive × additive (i) epistasis were positively significant for days to fifty percent flowering in all the crosses (except cross-II and Cross-V) indicating that the expression of this character was under the influence of an 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 a better response. The result is confirmed with earlier reports of Thakare et al., (2017); Rahangdale and Raut, (2002); Syad et al., (2005) and Bhor et al., (2014). In Cross P. Kimya × NRC 102, an additive gene effect (d) was equally important as non-additive (h) with duplicate epistasis; therefore, for the efficient utilization of fixable and nonfixable components of genetic variation, reciprocal recurrent selection or biparental mating was suggested for this cross. A similar finding was also reported by Halvankar and Patil (1993) Bhor et al., (2014) and Thakare et al., (2017). The positively significant additive × additive non-allelic interaction with duplicate epistasis for days to 50 % flowering was observed in three crosses i.e P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 102 which suggested the possibilities of obtaining transgressive segregants in later generations. Similar results also reported by Bhor et al., (2014) and Thakare et al., (2017).

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Table 2. Estimation of gene effect in six crosses for the quantitative traits in soybean.

| Sr. No. | Crosses                  | Days to 50% flowering | Genetic parameters | Type of gene action |
|---------|--------------------------|------------------------|--------------------|---------------------|
|         |                          |                        | m      | d       | h      | i          | l          |                      |
| C-I     | PHULE AGRANI × NRC 101   | 34.51**                | 5.60** | -2.30** | 16.16  | -32.93** | Complementary |
| C-II    | PHULE AGRANI × NRC 102   | 32.91**                | 5.56** | 1.83**  | -       | -         | Absence of inter allelic interaction |
| C-III   | PHULE SANGAM × NRC 101   | 36.15**                | 9.68** | -9.43** | 11.03** | 14.26     | Duplicate    |
| C-IV    | PHULE SANGAM × NRC 102   | 38.15**                | 8.50** | -3.96** | 11.93** | 11.33     | Duplicate    |
| C-V     | PHULE KIMYA × NRC 101    | 35.16**                | 7.50** | 5.00**  | -       | -         | Absence of inter allelic interaction |
| C-VI    | PHULE KIMYA × NRC 102    | 35.48**                | 7.96** | 6.03**  | 21.53** | 18.26**   | Duplicate    |
| C-I     | PHULE AGRANI × NRC 101   | 93.70**                | 10.40** | 6.20**  | 34.00** | -49.60**  | Duplicate    |
| C-II    | PHULE AGRANI × NRC 102   | 91.23**                | 8.83** | 12.02** | 37.32** | -44.97**  | Duplicate    |
| C-III   | PHULE SANGAM × NRC 101   | 94.83**                | 15.40** | 15.62** | 12.67** | 59.67     | Duplicate    |
| C-IV    | PHULE SANGAM × NRC 102   | 93.36**                | 14.10** | 12.42** | 12.67** | 59.67     | Duplicate    |
| C-V     | PHULE KIMYA × NRC 101    | 92.90**                | 12.63** | 1.00ns  | 30.56** | -6.13ns   | Duplicate    |
| C-VI    | PHULE KIMYA × NRC 102    | 93.96**                | 12.00** | 2.91**  | 33.17** | -17.68**  | Duplicate    |
| C-I     | PHULE AGRANI × NRC 101   | 53.51**                | 10.10** | -4.21** | 22.22** | -22.97**  | Complementary |
| C-II    | PHULE AGRANI × NRC 102   | 49.61**                | 9.00** | -21.12**| -10.62**| 87.77**   | Duplicate    |
| C-III   | PHULE SANGAM × NRC 101   | 51.45**                | 14.90** | 7.25**  | 31.95** | 27.68**   | Complementary |
| C-IV    | PHULE SANGAM × NRC 102   | 52.73**                | 12.93** | 3.15**  | 23.08** | 30.22**   | Complementary |
| C-V     | PHULE KIMYA × NRC 101    | 52.98**                | 11.33** | 19.83** | -47.03**| 56.40**   | Duplicate    |
| C-VI    | PHULE KIMYA × NRC 102    | 51.90**                | 11.52** | 28.66** | 44.32** | -23.46**  | Duplicate    |
| C-I     | PHULE AGRANI × NRC 101   | 13.64**                | -0.79** | -1.52ns | -5.99** | 10.60**   | Duplicate    |
| C-II    | PHULE AGRANI × NRC 102   | 12.26**                | -1.56** | -3.34** | -7.44** | 13.61**   | Duplicate    |
| C-III   | PHULE SANGAM × NRC 101   | 13.69**                | -0.83** | 6.67**  | 5.47**  | -5.48m   | Duplicate    |
| C-IV    | PHULE SANGAM × NRC 102   | 15.36**                | 1.55**  | 8.09**  | 10.65** | -11.99**  | Duplicate    |
| C-V     | PHULE KIMYA × NRC 101    | 13.26**                | 0.46**  | 1.74ns  | 3.17**  | 1.44**    | Complementary |
| C-VI    | PHULE KIMYA × NRC 102    | 13.46**                | 1.50**  | -3.17** | 0.26**  | 2.60**    | Duplicate    |
| C-I     | PHULE AGRANI × NRC 101   | 112.10**               | 4.96**  | 6.55ns  | 7.32**  | -77.51**  | Duplicate    |
| C-II    | PHULE AGRANI × NRC 102   | 84.06**                | 5.13**  | 6.84**  | 16.64** | 0.44ns    | Complementary |
| C-III   | PHULE SANGAM × NRC 101   | 103.88**               | 9.70**  | 26.65** | -       | -         | Absence of inter allelic interaction |
| C-IV    | PHULE SANGAM × NRC 102   | 102.38**               | 12.46** | 6.41**  | -       | -         | Absence of inter allelic interaction |
| C-V     | PHULE KIMYA × NRC 101    | 82.71**                | 5.00**  | -49.32**| -48.98**| -154.44** | Complementary |
| C-VI    | PHULE KIMYA × NRC 102    | 108.16**               | 3.70**  | -52.82**| -53.12**| 56.97**   | Complementary |
| C-I     | PHULE AGRANI × NRC 101   | 84.76**                | 4.96**  | 10.77** | 11.54** | 23.37**   | Duplicate    |
| C-II    | PHULE AGRANI × NRC 102   | 16.58**                | -1.16** | -11.28**| -       | -         | Absence of inter allelic interaction |
| C-III   | PHULE SANGAM × NRC 101   | 19.20**                | -0.05ns | 13.85** | 9.77**  | -18.54**  | Duplicate    |
| C-IV    | PHULE SANGAM × NRC 102   | 20.05**                | 0.08ns  | 6.61**  | -       | -         | Absence of inter allelic interaction |
| C-V     | PHULE KIMYA × NRC 101    | 94.83**                | 3.70**  | 7.80**  | 7.50**  | -10.13ns  | Duplicate    |
| C-VI    | PHULE KIMYA × NRC 102    | 16.53**                | 0.55**  | 9.02**  | 8.17**  | -16.57**  | Duplicate    |

*, ** Significant at P = 0.05 and 0.01 per cent levels, respectively.
m = mean effect
d = additive effect
h = dominance effect
i = additive × additive effect
l = dominance × dominance effect

Additive gene effect and additive × additive epistasis was (i) positively significant in all the crosses for days to maturity 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, the selection for days to maturity in this crosses would give a better response. Similar finding was also reported by Bhor et al., (2014); Thakare et al., (2017); Syad et al., (2005). The significant additive × additive (i) non-allelic interaction with duplicate epistasis was observed in all the crosses for days to maturity which suggests the possibilities of obtaining transgressive segregants in later generations which was also reported by Bhor et al., (2014); Thakare et al., (2017); Sharma and Phul, (1994). For plant height, bBoth additive (d) and non-
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additive (h) gene effects were positively significant in the crosses i.e P. Sangam × NRC 101, P. Kimya × NRC 101 and P. Kimya × NRC 102. The similar result were also reported by Bhor et al., (2014); Thakre et al., (2017); Shinde (2010). Among the interaction components, estimates of additive × additive (i) components was positively significant in two crosses i.e. P. Sangam × NRC 101, P. Sangam × NRC 102 with complementary epistasis. In the cross, P. Kimya × NRC 102 positively significant duplicate epistasis was observed. These results are in agreement with earlier report of Bhor et al.,(2014); Thakare et al., (2017) and Maloo and Nair, (2005). Additive gene effect was observed for the trait 100 seed weight in crosses P. Sangam × NRC 102 and P. Kimya × NRC 101 and P. Kimya × NRC 102. Similar results were also reported by Bhor et al., (2014) ; Thakare et al., (2017); Agrawal et al., (1999)

Additive × additive (i) interaction was positively significant in the crosses P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 101. The result are in conformity with earlier reports of Thakare et al., 2017; (1988) Sharma and Phul, (1994) and Bhor et al., (2014).

Duplicate epistasis was observed in crosses P. Agrani × NRC 101, P. Agrani × NRC 102, P. Sangam × NRC 101, P. Sangam × NRC 102 and P. Kimya × NRC 102. Similar findings were also reported by Bhor et al., (2014); Thakare et al., (2017); Datt et al., (2011). Biparental mating is suggested for duplicate epistasis to improve the traits. Complimentary epistasis was observed for crosses P. Kimya × NRC 101 which suggests that improvement in the character of seed weight is possible by selection in F3 generation onwards such that the desired recombinants become available in the populations as reported by Sharma and Phul, (1994).

The additive gene effect was positively significant observed for the pods per plant in all the crosses. Similar results were also reported by Bhor et al., (2014); Harer and Deshmukh, (1991); Halvankanr and Patil. (1993) ; Mehetre. et al., (1998); Agrawal et al., (1999).Dominance (h) gene effect was positively significant in two crosses P. Agrani × NRC 102 and P. Sangam × NRC 101. These results are in agreement with earlier reports of Sayad et al., (2005); Mallo and Nair, (2005) Bhor et al., (2014) ; Thakre et al., (2017).

The additive and dominance gene effects were positively significant in crosses, P. Sangam × NRC 101 and P. Agarani × NRC 102. Among inter-allelic interactions, positively significant additive × additive component was observed in the cross P. Agrani × NRC 102 and dominance × dominance in cross P. Kimya × NRC 102. A similar result was also reported by Datt et al., (2011) Bhor et al.,(2014); Thakre et al., (2017). The positively significant values of additive gene effect (d) were higher as compared to non-additive and this helps for the selection of the traits. For seed yield per plant the presence of significant dominance component (h) with the absence of non–allelic interactions in cross P. Sangam × NRC 102 revealed that yield of soybean was predominantly under non-additive genetic control as reported by Bhor et al.,(2014). The presence of duplicate epistasis in cross P. Sangam × NRC 101, cross-P. Kimya × NRC 101 and cross P. Kimya × NRC 102 for the yield 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 yield trait in early generations would not be effective for want of fixable components of variation. Such gene effects can however, be exploited by intermaxing the selected segregants and delaying the selections to the advanced generations. The results are confirmed with earlier reports of Rahangdale and Raout (2002); Datt et al., (2011) Bhor et al., (2014).

Significant additive × additive gene effects for controlling this trait was observed in cross-P. Agrani × NRC 101, Cross-P. Sangam × NRC 101 Cross-P. Kimya × NRC 101 and Cross-P. Kimya × NRC 102. Bhor et al., (2014) are also reported similar gene effects for yield traits. Duplicate epistasis was observed in Cross-P. Sangam × NRC 101 Cross-P. Kimya × NRC 101, and Cross-P. Kimya × NRC 102; hence, the simple selection procedure in the early segregating generations may not contribute significantly for the improvement of the traits governed by duplicate epistasis and dominance components could be successfully exploited in the later generations. It is, therefore, suggested that the selections for the improvement of all these traits, particularly seed yield should be delayed to the later generations of segregating populations in soybean.

It can be concluded that predominant additive gene effects in desirable direction were observed Cross P. Sangam × NRC 102 , Cross P. Kimya × NRC 101 and P. Kimya × NRC 102 for traits pods per plant. In cross P. Kimya × NRC 102 predominance of additive gene effects was observed for the trait 100 seed weight. In crosses P. Sangam × NRC 101, P. Kimya × NRC 101 and P. Kimya × NRC 102 predominance of additive × additive effect was higher as compared to dominance × dominance gene interaction for seed yield traits suggesting that the selections can be effectively applied for improvement of these traits.

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