



Genetic analysis of yield and its components in different environments in wheat (*Triticum aestivum* L.)

Ved Prakash and P. Joshi

Department of Plant Breeding, Agricultural Research Station, Durgapura, Jaipur 302 018

(Received: May 2003; Revised: November 2003; Accepted: November 2003)

Generation means analysis of two crosses, Raj 1482 × HD 2329 and PBW 373 × Raj 3077 involving four varieties of wheat was carried out in respect of grain yield and its components characters. Six generations namely, P₁, P₂, F₁, F₂, B₁ and B₂ of each of two crosses were separately grown in a randomized block design with three replications in 5 M long rows spaced 30 cm apart with plant to plant distance of 10 cm. The whole experiment was planted at three sowing dates, viz. 15th November 30th November and 15th December. Fifteen randomly selected plants each of P₁, P₂ thirty plants of F₁, B₁ and B₂ 60 plants of F₂ generations, were utilized for recording observations on days to heading, plant height, flag leaf area, number of grains per spike, grain yield per spike and grain yield per plant in each environment separately. The data were first subjected to analysis of variance separately of each cross in each environment. The Pooled analysis of variance was done [1]. After that data were subjected to individual scaling tests [2] to detect the presence of epistasis. Further, the data were subjected to joint scaling test [3]. The gene effects of six parameter model and components of heterosis were calculated [4].

The scaling tests were applied only in those characters where generations differed significantly to each other. Out of three scaling tests A, B and C at least one or more scale and joint scaling test were found significant in all the cases, indicating inadequacy of additive - dominance model, except for grain yield per plant in cross PBW 373 × Raj 3077 in E₁ environment, where additive dominance model fitted well. This indicated the presence of epistatic interactions.

The estimates of m, (d), (h), (i) (j) and (1) obtained on the best fit model for the traits studied and presented in Table 1. Both additive (d) and dominant (h) gene effects were significant in respect of days to heading in both the crosses, plant height in cross Raj 1482 × HD 2329, number of grains per spike in cross PBW

373 × Raj 3077 and grain yield per plant in both the crosses over environments. In remaining traits either additive (d) or dominant (h) were non-significant in both the crosses over environments. The dominant component (h) was significant and greater in magnitude than the additive (d) component for most of the traits in both the crosses over environments. This indicated predominant role of dominance gene action in controlling the traits. Importance of the dominance gene effects in wheat has been reported in the inheritance of days to heading and grain yield per plant [5], plant height, flag leaf area, number of grains per spike [6] and grain yield per spike [7].

Among the digenic interaction effects, additive × additive (i) and dominance × dominance (1) were significant for most of the traits in both the crosses over environments.

The signs of (h) and (1) components were screened for these traits, where (h) and (l) omponents were significant. Duplicate gene action was observed for all the traits except plant height in cross PBW 373 × Raj 3077 in E₃ where complementary gene action was observed. This indicated hinderance in selection improvement. In this situation reciprocal recurrent selection is likely to be useful for more effective ultization of both additive and non-additive type of gene actions simultaneously [8].

References

1. **Panase V. G. and Sukhatme P. V.** 1978. Statistical methods for agricultural workers. Indian council of Agricultural Research, New Delhi.
2. **Hayman B. I. and Mather K.** 1955. The description of gene interaction in continuous variation. *Biometrics*, **11**: 69-82
3. **Cavalli L. L.** 1952. An analysis of linkage in quantitative inheritance. *Quantitative inheritance*. H.M.S.O., London, PP, 135-144.
4. **Jinks J. L. and Jones R. M.** 1958. Estimation of components of heterosis, *Genetics*, **43**: 223-234.

