

Inheritance of quality traits in barley (*Hordeum vulgare* L.)

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SUMMARY

Genetic components of variance and related statistics for three quality characters i.e. 1000-grain weight, protein content and tryptophan content were estimated in F_1 and F_2 generations derived from 12x12 diallel cross excluding reciprocals. The results revealed that both additive and non-additive gene effects were important for the traits 1000 grain weight, protein content and tryptophan content in both the generations. Over dominance was also observed for all the traits under study. High heritability estimate coupled with moderate genetic advance were observed for protein content and tryptophan content while it was moderate for 1000-grain weight. Simple selection procedures followed by recurrent selection and diallel selective mating system might be helpful for improvement of these traits in barley.

Key words : *Hordeum vulgare*, Genetic components, Quality traits, Gene action, Diallel analysis.

Barely is one of the oldest cereal crop grown in India and abroad under poor management in marginal and submarginal soils. It is a good quality animal feed. Due to its high digestibility and a rich source of dietary fibres, it is an ideal food for diabetics and heart patients. A large number of research works on genetics of quantitative traits have been reported by several workers but genetic information regarding quality traits are extremely limited. Thus, the present study was carried out to determine suitable breeding methods for quality improvement of this crop and it would provide the clear picture of relative importance of additive and dominance components in the improvement of quality traits.

MATERIALS AND METHODS

Twelve diverse genotypes of barley namely Jagrati, P 528, DL 449, K 370, K 226, K 329, RD 915, BH 164, RS 6, P 482, BH 156 and DL 36 were crossed in a diallel mating system excluding reciprocals. Derived hybrid seeds were advanced in off season nursery at Wellington; (Nilgiri hills) to get F_1 's seeds. The parents, F_1 and F_2 population were grown in a randomized block design with three replications in two rows of 5 m long and 30 cm apart. The observations on 1000-seed weight, protein and tryptophan content were recorded for biometrical analysis. The protein content in each treatment was estimated by Micro-Kjeldahl method while tryptophan content was determined by Calorimetric method. Different genetic components were estimated as per the procedure of Hayman (1954). Heritability estimates in narrow sense (Crumpacker and Allard 1962) and genetic advance as per Robinson *et al.* (1949) were calculated.

RESULTS AND DISCUSSIONS

Genetic components of variation (D, H_1 , H_2 , F, h^2 and E) in F_1 and F_2 generations were estimated (Table 1). The estimates of additive component (D) was significant for all the characters in both the generations except tryptophan content. The dominance components (H_1 and H_2) were

significant in both the generations for all the traits. High magnitude of, H_1 reflected non-additive gene effect for 1000-grain weight, protein content and tryptophan content in both the generations. The higher value of H_1 , over H_2 showed the unequal distribution of genes among the parents. The positive and significant value of F for 1000-grain weight was due to the dominant genes which were more frequently distributed among the parents. The estimates of h^2 were significant for all the characters except protein content in F_2 generation. The non-significant values of E component indicated that the effect of environment was negligible in the expression of quality characters.

The average degree of dominance (H_1/D)^{0.5} in F_1 and ($1/4 H/D$)^{0.5} in F_2 revealed the presence of over dominance for all the traits in both the generations. The value of ($H_2/4H_1$) was less than its expected value i.e. 0.25 for all the traits which indicated the symmetrical distribution of positive and negative genes among the parents in both the generations. The value of $[(4DH_1)^{0.5} + F]/[(4DH_1)^{0.5} - F]$ was observed greater than unity for all the traits in both the generations. The positive value of F indicated that the characters were controlled by more dominant genes (Hayman, 1954).

The low value of h^2/H_2 in both the generations for 1000-grain weight and protein content and in F_2 generation for tryptophan content indicated that all these traits were controlled by at least one gene group while tryptophan content in F_1 generation indicated the presence of two gene groups. Singh and Verma (1979), Gulati and Murty (1979) and Wu and Takeda (1995) were in the view of above findings.

Narrow sense heritability was high for protein content and tryptophan content but moderate for 1000-grain weight in both the generations. An advancement in the tune of 3.41 g in F_1 and 3.57 g in F_2 for 1000-grain weight, 9.81 to 10.47 percent for protein content and 4.80 to 3.22 percent in F_1 to F_2 respectively per cycle of selection was achieved which were very useful for improving the quality parameters. The findings of Phogat *et al.* 1995 were also in

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