

Path analysis (Table 3) revealed that number of pods recorded the highest positive direct effect on seed yield followed by number of clusters per plant. Indirect effect of other characters viz; plant height and number of seeds per pod through number of clusters per plant were also much appreciable indicating that these characters played important role in determining yield. In contrast to these results, Boomikumaran and Rathinam (1981) reported negative direct effects for pods per plant and seeds per pod on seed yield. It is interesting to note that number of pods and number of clusters showed high magnitude of positive genotypic correlations with seed yield.

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COMPONENT ANALYSIS OF SOME METRIC TRAITS IN BARLEY

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ABSTRACT

The performance of the eight genetically diverse varieties of barley and their 28 F₁s was evaluated to assess their genetic architecture for the yield and yield contributing traits in a set of diallel crosses. The component analysis indicated the presence of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) genetic variances for plant height length of main spike and grain yield/plant. \hat{D} component was higher than \hat{H}_1 for plant height, number of grains/main spike and biological yield per plant. For remaining characters \hat{H}_1 was higher than \hat{D} component, indicating the preponderance of dominance genetic variance. Over dominance was observed for days to reproductive phase, number of productive tillers/plants, length of main spike and grain yield/plant. Highly significant values of \hat{F} were observed only for plant height indicating the predominance of dominant alleles. While highly significant values of \hat{h}_2 were recorded for all the traits except days to reproductive phase revealing the predominance of dominant alleles.

KEY WORDS : Component, Analysis, Metric Traits, Barley

Barley is a major cereal crop which can resist drought and does better than other crops under low fertility level and in late sown conditions. The concept of drought resistance in barley has been proved to be boon both for breeders as well as farmers. In order to meet this goal, information in the pattern of inheritance of quantitative characters is essential for the breeder to efficiently plan the breeding procedure. In the present study, an attempt is made to analyse the genetic basis of inheritance of yield and some of the important yield attributes through diallel analysis.

MATERIAL AND METHODS

A diallel set of crosses (excluding reciprocals) involving eight diverse varieties/strains of barley, viz., Jyoti, Azad, K-226, K-329, P-147, P-267, Karan 92 and RD-883 were used in this investigation. All the 28F₁ and eight parents were planted in a randomised block design with three replications during *rabi* 1985-86. The recommended spacings and agronomic practices were followed to raise a good crop. Ten plants were selected at random from each plot and observations

Table 1. Analysis of variance for seven characters in a 8 x 8 diallel cross of barley

Source	df	Plant height	Days to reproductive phase	Number of productive tillers/plant	Length of main spike	Number of grains / main spike	Biological yield/plant	Grain yield/plant
Replications	2	150.38**	5.51*	42.32**	3.27	291.19**	925.36**	97.49*
Progenies	35	95.93**	5.88**	18.18**	1.74**	65.18**	836.97**	119.40**
Error	70	28.31	1.64	4.52	0.75	18.78	163.55	24.03

* Significant at P=0.05 and ** Significant at P=0.01.

were recorded on seven characters (Table 1). Plot mean was used for statistical analysis. The components of variance in diallel cross were computed by the use of equation given by Hayman (1954)

RESULTS AND DISCUSSION

The analysis of variance revealed that the mean squares due to progenies were highly significant for all the traits studied (Table 1). The estimates of genetic parameters \hat{D} , \hat{A}_1 , \hat{A}_2 , \hat{F} , \hat{h}^2 and \hat{E} along with their standard errors are presented in Table 2. The estimated value of the component of variation due to additive effects of the genes (\hat{D}) was significant for all the characters except days to reproductive phase and number of grains/main spike. The estimates of dominance component (\hat{A}_1) was only significant for plant height, length of main spike and grain yield/plant. Whereas, estimates of dominance component (\hat{A}_2) was significant for all the characters except for days to reproductive phase and number of grain/main spike. The value of dominance components were also higher than additive components for all the characters except plant height. Thus component analysis indicated the presence of additive (\hat{D}) and dominance (\hat{A}_1 and

\hat{A}_2) genetic variance for all the characters except days to reproductive phase and number of productive tillers/plant. Additive component of variance was higher than dominance component of variance for plant height, number of grains/main spike and biological yield/plant, indicating the preponderance of dominance genetic variability. Finlay (1964), Verma and Jain (1979) and Singh *et al.* (1982) also observed similar findings in their studies.

The values of average degree of dominance ($(\hat{A}_1/\hat{D})^{0.5}$) revealed over-dominance for days to reproductive phase, number of productive tillers/plant, length of main spike and grain yield/plant while, partial dominance for remaining characters. Complete to over-dominance was also reported for grain yield and most of the characters by Jain and Murti (1971) and Singh and Verma (1979).

The estimates of \hat{F} parameters were positive and highly significant for plant height only whereas, negative and significant estimates for biological yield/plant. This indicated that dominant alleles were more frequent for plant height. The estimates of \hat{h}^2 were found positive and highly significant for all the characters except days to

Table 2. Estimates of variance components and related statistics for seven characters in a 8-parent-diallel cross of barley

Character	Parameter						Related statistics				
	\hat{D}	\hat{A}_1	\hat{A}_2	\hat{F}	\hat{h}^2	\hat{E}	$\hat{A}_1/0.5$	$\hat{A}_2/4\hat{A}_1$	$\frac{4\hat{D}\hat{A}_1+\hat{F}}{4\hat{D}\hat{A}_1 0.5\hat{F}}$	\hat{h}^2/H_2	r
Plant height	66.44** ± 5.31	66.06** ± 12.22	48.39** ± 10.63	61.73** ± 12.56	36.82** ± 7.13	9.43** ± 1.77	0.99	0.18	2.74	0.76	-0.85
Days to reproductive phase	-2.72 ± 1.14	6.28 ± 2.63	4.83 ± 2.29	3.19 ± 2.70	-0.22 ± 1.53	0.54 ± 0.38	1.51	0.19	2.25	-0.04	-0.52
Number of productive tiller/plant	3.65* ± 1.42	6.99 ± 3.28	8.01* ± 2.85	-4.81 ± 3.37	34.05** ± 1.91	7.53** ± 0.47	1.38	0.29	0.35	4.24	-0.64
Length of main spike	0.50* ± 0.19	1.15* ± 0.45	0.99* ± 0.39	0.43 ± 0.46	3.23** ± 0.26	0.24 ± 0.06	1.50	0.21	1.78	3.23	-0.77
Number of grain/main spike	6.01 ± 9.20	4.56 ± 2.16	33.36 ± 18.41	-6.68 ± 21.75	75.07* ± 12.34	1.81 ± 3.06	0.87	1.82	0.09	2.25	-0.64
Biological yield per plant	145.10** ± 27.44	85.20 ± 63.08	438.90** ± 54.88	-215.30* ± 64.83	2028.79** ± 36.80	37.90** ± 9.14	0.77	1.28	0.02	4.62	-0.20
Grain yield per plant	25.98** ± 8.91	75.28* ± 20.49	69.10** ± 17.83	-40.34 ± 21.06	219.46** ± 11.95	46.68** ± 2.97	1.70	0.23	0.37	3.17	0.18

* Significant at P 0.05 and ** Significant at P 0.01.

reproductive phase indicating the predominance of dominant alleles. The estimates of the ratio $\hat{A}_2/4\hat{A}_1$ was not equal to the theoretical value of 0.25 for the traits. The ratio $(4\hat{D}\hat{A}_1)^{0.5} + F/(4\hat{D}\hat{A}_1)^{0.5} - F$ indicated the excess of dominant genes than recessive genes for plant height, days to reproductive phase and length of main spike while recessive genes for remaining characters. If the genes are dominant in nature, the extent of genetic advance over mean percentage will be high. The ratio (h^2/\hat{A}_2) was higher than unity for all the traits except plant height and days to reproductive phase. This indicated that these characters were governed by more than one gene group. Liang and Walter (1968) reported that complementary gene action depressed the ratio in wheat. Gulati *et al.* (1976) reported in barley that a single recessive gene controlled short plant structure.

The correlation coefficient (r) between the parental order of $(W_r + V_r)$ and parental measurement (Y_r) was negative for all the traits except grain yield/plant indicated that the positive genes were mostly dominant in the expression of these characters.

The choice of the breeding methodology depends upon the nature and magnitude of gene action. It is evident from the present study that both additive and non-additive type of gene action for most of the characters studied. Additive genetic

variance is responsible to extend homozygosity in the population, while non-additive portion of genetic variance which is no doubt desirable an important to maintain the heterozygosity in the population for improvement purposes and recurrent selection could hold promise for genetic improvement of these traits.

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Stylosanthes scabra (Muyal Masal): A PROTEIN RICH DROUGHT TOLERANT FODDER LEGUME

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ABSTRACT

Among the five species of *Stylosanthes*, viz. *S. scabra*, *S. hamata*, *S. humilis*, *S. quianensis* and *S. viscosa* tested for yield potential at the Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore. *S.scabra* was found superior. This species recorded 26.57 tons of green fodder 8.79 tons of dry matter, and 1.48 tons of crude protein per ha per year. It also had maximum dry matter content, plant height, branches and leaves per plant. Based on the desirable traits and high green fodder yield potential, *Stylosanthes scabra* was released under the local name *Muyal masal* by the Tamil Nadu Agricultural University, Coimbatore in January, 1991.

KEY WORDS : *Muyal Masal*, *Stylosanthes scabra*, Fodder Legume

In general, animal productivity in the tropics and sub-tropics is low compared to temperate areas, the primary limitation being poor nutrition quantitatively as well as qualitatively (Pandey,

1990). In our country, more than 60 per cent of the land area for crop production is under rainfed condition. Only about 4 per cent of the cultivated area is under cultivated forages and it is only 1.68