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ESTIMATION OF PERCENT CONTRIBUTION OF PARENTS AND THEIR INTERACTION FOR GRAIN YIELD AND ITS CONTRIBUTING TRAITS IN BARLEY (*Hordeum vulgare* L.)

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Barley is most cosmopolitan crop and primary feed crop in semi-arid parts of Asia, Africa, and South America. It has 7% share among world cereal crop production. In India, it occupies around 6.77 mha area that produces 17.88 mt with the productivity of 26.41 q/ha. In India it occupies around 6.77 mha area that produces 17.88 mt with the productivity of 26.41 q/ha. Rajasthan ranks first in barley production (0.86 mt) followed by Uttar Pradesh (0.43 mt) and Madhya Pradesh (0.30 mt) with the productivity level of 30.46 q/ha, 27.74 q/ha and 22.89 q/ha, respectively however highest productivity is in the state of Punjab (35.96 q/ha). In the state of Uttarakhand area under barley is 20 thousand ha, production 26 thousand tons with the productivity of 13 q/ha which is rather low as compared to the national average of 26.41 q/ha (1). In order to achieve the goal, one way for this is the identification of superior parental lines which is an important pre-requisite for the development of high yielding varieties. A wrong choice of parents may undo a meticulously planned and well executed follow-up programme. This study was conducted with the objective to demonstrate a strong cross-breeding advantage of hybrid barley by estimating the percent contribution of parents and their interaction for twelve characters. The parental line(s) which contribute more towards yield can be further evaluated and involve as parents in hybrid barley production.

The present study was conducted at Norman E. Borlaug Crop Research Center of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar during rabi of 2016-17. Ten lines of barley viz., BH 965, DWRUB 64, DWRB 73, BH 976, DWRB 134, RD 2918, RD 2919, BH 902, BH 946, DWRB 140 (female parent) were crossed with three testers i.e., DWRUB 52, DWRB 101, RD 2849 (male parents) in rabi crop season, 2015-16. The F1 seeds of the thirty crosses (10× 3) along with their parents (female and male) were planted in randomized complete block design with three replications. Each replication consisted of 53 treatments consisting of 10 lines, 3 testers and 30 crosses. Each treatment was planted in two rowed plot of two meter long with inter-row and inter-plant distances of 23 and 10 cm, respectively. The experimental plot was kept under normal agronomic care from sowing to maturity. Observations were recorded on proper crop stage on five randomly selected plants for the fourteen traits viz., Days to 75% heading, days to physiological maturity, plant height (cm), peduncle length (cm), spike length (cm), awn length (cm), productive tillers per plant, flag leaf area (cm^2), number of grains per spike, spike weight, 1000 grain weight, biological yield per plant (g), grain yield per plant (g) and harvest index %. The contribution due to parents and F1s was calculated as percent of sum of square due to hybrids.

$$\text{Contribution of lines} = \frac{\text{SS (L)}}{\text{SS (Crosses)}} \quad 100$$

$$\text{Contribution of testers} = \frac{\text{SS (T)}}{\text{SS (Crosses)}} \quad 100$$

$$\text{Contribution of lines and testers (1×t)} = \frac{\text{SS (1} \quad \text{t)}}{\text{SS (Crosses)}} \quad 100$$

Where, SS(L) = Sum of square due to lines,
SS(T) = Sum of square due to testers,
SS(l ×t) = Sum of square due to lines × tester

The perusal of the results of analysis of variance showed that genotypic differences were significant for all agronomic traits studied, indicating that lines possess good amount of genetic variability among them. The present study revealed that the percent contribution of different lines was maximum for plant height (83.24 %) followed by spike length (72.99), awn length (71.98), peduncle length (64.71) and productive tillers per plant (60.24) however, line x tester interaction contributed higher for days to physiological maturity (72.52%) followed by harvest index (61.76%), number of grains per spike (60.22%), grain yield per plant (49.81) and biological yield per plant (47.98). Similar findings have been reported by (2). The male parent (tester) contributed maximum for days to 75% heading. The greatest contribution to the expression of most of the yield traits was found in the lines as well as line × tester interaction than due to testers alone. The findings of the study suggest the selection of parents with high percent contribution for yield and yield enhancing traits for development of potential barley hybrids by involving such parents in the breeding program.

CONCLUSION

A study on estimation of percent contribution of parents and their interaction for fourteen yield traits was conducted

Table-1 : Percent contribution of different components of hybrid sum of squares in barley.

Characters	Due to lines	Due to testers	Due to line and tester
Days to 75% heading	24.67	37.59	37.74
Days to physiological maturity	20.36	7.11	72.52
Plant height (cm)	83.24	0.21	16.55
Peduncle length (cm)	64.71	4.02	31.27
Spike length (cm)	72.99	2.73	24.28
Awn length (cm)	71.98	0.71	27.32
Productive tillers per plant	60.24	1.27	38.5
Flag leaf area (cm^2)	52.82	13.02	34.16
Number of grains per spike	39.58	0.20	60.22
Spike weight	55.47	6.18	38.35
1000 grain weight	45.35	17.96	36.69
Biological yield per plant (g)	50.92	1.10	47.98
Grain yield per plant(g)	48.96	1.23	49.81
Harvest index %	30.73	7.51	61.76

by crossing three testers with ten female parents using line × tester design in barley. The significant differences from parents suggest that material possess good amount of genetic variability for traits studied. The female parents contributed more than the male parents for different traits. For grain yield, the greatest percent contribution was found from line × tester interaction than from line and tester alone.

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