"Studies on Genetic Divergence and Selection Parameters in Barley (Hordeum Vulgare L.)"

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ABSTRACT

The present investigation was conducted with twenty genotypes ofbarley in randomized block design with three replications at the research farm of Janta Mahavidyalaya Ajitmal, Auraiya during Rabi 2021-22. Five plants were selected randomly from each genotype in each replication for recording observations on ten characteristics of barley viz., days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, length of spike, number of grains per spike, 1000- seed weight (g), biological yield per plant (g), harvest index(%) and grain yield per plant. The analysis of variance revealed highly significant difference for all the ten charactersindicated existence of substantial variability among the 20 genotypes of the barley. High estimates of genotypic and phenotypic coefficient of variation were recorded for number of productive tillers per plant, biological yield per plant and grain yield per plant. Moderate phenotypic and genotypic variation were found for length of spike and number of grains per spike. High estimates of heritability were recorded for all the characters. The genetic advance as percent of mean was found to be highest for grain yield per plant, followed by biological yield per plant, number of productive tillers per plant and number of grains per spikes. Highly significant and positive correlation was observed for all the characters. Path coefficient analysis indicated that days to 50% flowering and biological yield per plant had the highest direct effect on seed yield followed by number of productive tillers per plant, plant height and number of grains per spike. The computed D^2 values varied from 7.89 to 28.33. The twenty genotypes were group into three clusters. The greatest inter-cluster distance was found between cluster I and cluster III. It suggested the hybridization possibilities between the genotypes included in these clusters by virtue of their being of wide genetic diversity.

KEYWORDS

Genetic Diversity, High Heritability, Yield-Enhancing Traits, Path Coefficient Analysis.

INTRODUCTION

Among important cereals, barley ranked fourth after wheat, rice, and maize. Barley(*Hordeum vulgare* L.) is a self-pollinated crop belongs to the family Poaceae with diploid chromosome number 2n= 14. Because of its hardiness in many countries around theworld, it is often considered the only possible rainfed cereal crop under low input and stress environments.

Barley is mostly used as a grain diet as well as a cattle and poultry feed. It is easily digestible as compared to wheat because of its lower gluten content. Barley foods have many health enhanced attributes in addition to providingsound nutrition. Beer is also a most essential product produced from barley. Now barley is key ingredientfor beer and wine industry.

Barley is one of the most important cereal crops of the world with 50.90 mha area and 153.47 million tons production (USDA 2021-22). During 2020-21 in India, this crop was grown in an area of 0.61 mha with total production of 1.82 million tonnesand productivity of 2988 kg/ha (directorate of economics and statistics, ministry of agriculture and farmers welfare GoI.)

In the recent years importance of barley increasing as human food due to presence of water-soluble plant fibres essential in human diet to reduce the serum cholesterol(Shimizu et al., 2008).Inthis perspective, barley may be helpful in reducing the sugar of diabetic patient and also to lower the serum cholesterol of heart patient (Pins and Kaur, 2006).Thus, barley is a potential crop and its genetic improvement is needed for high yield, wide adaptation, good quality and resistant to biotic and abiotic stress.

Genetic variability studies offer better scope for selection and help in development of high yielding varieties. Among essential breeding methods, selection is simplest and the foremost method of crop improvement. A comprehensive study and knowledge of genetic variability present in the base population, character association, cause and effect relationship, heritability & genetic advance and genetic divergence help the breeder in making effective selection in a breeding programme.

MATERIAL AND METHODS

The present investigation was conducted during rabi 2021-22 at the research farm of Janta Mahavidyalaya Ajitmal, Auraiya. In this experiment, 20 treatments are grown in a randomized complete block design with three replications. Each plot consisted of two rows of 3-meter length with a spacing 22×5 cm. all the recommended cultural practices were followed to raise a good crop. The data were subjected to analysis of variance via adopting

statistical method given by Panse and Sukhatme (1985). Genotypic, phenotypic coefficient variation and heritability in broad sense were computed by the method given by Burton and Devane, (1953). The expected genetic advance under selection for the different characters was estimated as suggested by the Johanson et al., (1955). The correlation coefficient was calculated by the formula given by Fisher (1918). Using path coefficient direct and indirect effect were calculated by the method given by Wright (1921) and elaborated by Dewey and Lu (1959). Genetic divergence between the genotypes was measured by the technique Suggested by Mahalanobis(1928).

RESULTS AND DISCUSSIONS

The ultimate objective of most of the plant breeding programme is to develop high-yielding superior genotypes/lines better than existing ones through genetic manipulation. Barley is an important rabi cereal grown in India and other countries of the world. Keeping the above aspects in view, the present investigation was undertaken to study genetic variability, heritability and genetic advance, correlation coefficient, path coefficient, and genetic divergence. The results obtained from the present investigation are discussed below.

The analysis of variance indicated that highly significant mean differences were observed for all the characters viz., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, length of spike, number of grains per spike, 100-seed weight, biological yield per plant, harvest index and grain yield per plant (Table-1).

IC.	ation	1	Freatment	Erro	r	'F' Cal. (Treatment)
	2		19	3	8	1
_	0.54		1532.22**	18.6	2	13.82
	4.96		1247.11**	11.7	8	17.81
	3.35		132.67**	10.2	6	41.02
	0.23		42.12**	3.1	6	35.25
	0.13		6.42**	0.7	1	11
	0.34		187.67**	4.0	2	25.37
	0.43		49.43**	1.2	7	8.57
	3.46		497.32**	27.1	8	85.38
	0.96		94.96**	1.8	7	14.70
	0.27		224.37**	1.3	6	22.41
	0.27 'F' at	t 5	224.37^{**} % = 2.03. '	 F	1.3 F' at 19	1.36 F' at 1% :

Table 2. Grand mean, SE, CD, heritability, genetic advance, and genetic advance as percent										
of mean for ten characters in barley.										
Character	Grand	SE	CD	GCV	PCV	Heritabilit	Genetic	Genetic		
	Mean					y (broad	Advance	Advance as		
						sense) (%)		% of Mean		
Days to 50% flowering	78.05	0.55	1.11	2.0	2.18	84.0	2.92	3.33		
Days to maturity	120.94	1.02	2.09	1.2	1.33	81.0	2.75	2.27		
Plant height (cm)	86.42	1.22	2.56	7.65	7.87	94.0	13.38	15.49		
Number of productive	5.42	0.27	0.56	23.25	25.22	85.0	2.38	43.91		
tillers per plant										
Length of spike (cm)	9.68	0.13	0.27	7.31	7.85	87.0	1.37	14.16		
Number of grains per spike	39.65	0.37	0.75	9.85	10.57	87.0	7.55	19.05		
1000-seed weight (g)	37.74	0.57	1.15	5.28	5.80	83.0	3.74	9.91		
Biological yield per plant(g)	75.33	1.38	2.82	21.58	23.18	91.0	32.48	<mark>4</mark> 3.10		
Harvest index (%)	38.85	0.42	0.86	8.90	9.17	93.0	6.78	17.44		
Grain yield per plant (g)	25.94	0.91	1.87	18.78	20.89	87.0	9.46	<mark>3</mark> 6.49		

From the inspection of Table2, it is apparent that the estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation. All the traits studied indicating that the apparent variation is not only due to genotypes but also due to the influence of the environment. High estimates of phenotypic coefficient of variation and genotypic coefficient of variation were recorded for grain yield per plant, biological yield per plant, and number of productive tillers per plant. Moderate genotypic and phenotypic coefficient of variation were observed for length of spike, and number of grains per spike. Low phenotypic and genotypic coefficients of variation were observed for days to maturity, days to 50% flowering, 1000-seed weight, harvest index, and plant height.

High estimates of heritability were observed for all the characters. In the present investigation high estimates of heritability coupled with high to moderate genetic advance as percent of mean was recorded for grain yield per plant, biological yield per plant, number of productive tillers per plant, number of grains per spike, length of spike, and plant height. This indicated that these characters might be governed by additive gene effect. The high estimate of heritability with low genetic advance as a percent of mean was found for days to 50% flowering, days to maturity, 1000-seed weight, and harvest index.

Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive correlation both at genotype and phenotype for all the characters. Hence, direct selection for these traits would be most effective in the improvement of barley genotypes (Table-3).

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	Table 3 G	enotypic a	nd phenot	ypic corre	lation for	ten charac	ters in bar	·ley	
Character	2	3	4	5	6	7	8	9	10
Days to	0.998**	0.959**	0.962**	0.998**	0.998**	0.982**	0.998**	0.994**	0.998**
Flowering	(0.915)**	(0.866)**	(0.873)**	(0.861)**	(0.856)*	(0.895)**	(0.924)*	(0.897)**	(0.947)**
					*		*		
Days to		0.950**	0.964**	0.998**	0.997**	0.942**	0.997**	0.933**	0.959**
Maturity		(0.868)**	(0.875)**	(0.855)**	(0.857)*	(0.814)**	(0.921)*	(0.821)**	(0.895)**
					*		*		
Plant Height			0.922**	0.966**	0.954**	0.862**	0.943**	0.934**	0.996**
(cm)			(0.890)**	(0.848)**	(0.863)*	(0.734)**	(0.941)*	(0.810)**	(0.922)**
					*		*		
No. of				0.974**	0.961**	0.862**	0.993**	0.997**	0.996**
Productive				(0.859)**	(0.876)*	(0.734)**	(0.941)*	(0.894)**	(0.852)**
Tillers per Plant			115	South South	*		*		
Length of Spike			1151	0	0.997**	0.934**	0.965**	0.99 <mark>7**</mark>	0.998**
(cm)					(0.895)*	(0.810)**	(0.760)*	(0.838)**	(0.874)**
				5	*		*		
No. of Grains			1AIP	शोध साहित्य	IAIP	0.942**	0.998**	0.99 <mark>9**</mark>	0.998**
per Spike					9//	(0.837)**	(0.855)*	(0.8 <mark>26)**</mark>	(0.887)**
				A CORRECTOR			*		
1000-Seed							0.997**	0.997**	0.998**
Weight (g)		٨	1 1	1	2		(0.897)*	(0.951)**	(0.887)**
		Λ					*	\wedge	
Biological Yield		\square						0.998**	0.997**
(g)								(0.897)**	(0.951)**
Harvest Index									0.998**
(%)									(0.887)**
					Cont				

Path coefficient analysis revealed the positive direct effect at genotypic level for days to 50% flowering, plant height, number of productive tillers per plant, number of grains per spike and biological yield per plant.

The indirect effect of all the characters exerted highest positive effect via biological yield per plant on seed yield per plant (Table-4).

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	I	Table-4 I	Direct a	nd indirec	t effect	on mai	n diago	nal		
Traits	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Productive Tillers/ Plant	Length of Spike (cm)	No. of Grains per Spike	1000 - Seed Weight (g)	Biological Yield (g)	Harvest Index (%)	Genotypic Correlation with Yield
Days to 50% Flowering	0.609	-0.107	0.055	0.174	0.052	0.029	0.007	0.363	- 0.063	0.998**
Days to Maturity	0.557	-0.117	0.056	0.179	- 0.053	0.029	- 0.007	0.382	- 0.063	0.998**
Plant Height (cm)	0.531	-0.103	0.057	0.179	0.053	0.029	0.006	0.374	- 0.058	0.998**
No. of Productive Tillers/Plant	0.523	-0.102	0.054	0.171	- 0.062	0.032	- 0.006	0.384	- 0.058	0.996**
Length of Spike (cm)	0.521	-0.100	0.054	0.171	0.062	0.033	0.006	0.368	- 0.062	0.996**
No. of Grains p <mark>er</mark> Spike	0.536	-0.101	0.056	0.186	0.063	0.040	0.007	0.384	- 0.058	0.997**
1000-Seed Weight (g)	0.534	-0.110	0.059	0.188	0.053	0.048	0.039	0.365	- 0.070	0.997**
Biological Yield (g)	0.546	-0.111	0.059	0.188	- 0.053	0.046	- 0.007	0.364	- 0.070	0.998**
Harvest Index (%)	0.546	-0.110	0.059	0.188	- 0.053	0.046	- 0.007	0.364	0.998 **	0.998**
	• 	·	•	Residual	effect: C	.3235			2	
				71		1		10		1

Table 5 Average intra and inter-cluster D2 and D values for 20 genotypes								
Cluster	I	II	III					
	802.89	158.75	208.6					
I	(28.33)	(12.59)	(14.44)					
		134.1	62.39					
II		(11.58)	(7.89)					
			146.96					
II			(12.12)					

On the basis of magnitude of D^2 values, 20 genotypes were grouped into three clusters in the present investigation. Eight genotypes are grouped in cluster I, five in cluster

II and seven in cluster III. The maximum value of inter-cluster distance was observed between cluster I and cluster III followed by cluster I and II suggesting wide diversity between three groups. The lowest value of inter cluster distance was observed between cluster II and III showing close relationship between these groups (Table-5).

Table 6 Contribution of each character toward divergence								
Characters	No. of times appearing	Percent						
	First in Rank	contribution						
Days to 50% flowering	0	0						
Days to maturity	2	1.04						
Plant height(cm)	25	13						
No. of productive tillers per plant	3	1.56						
Length of spike (cm)	0	0						
No. of Grains per spike	21	10.92						
1000- seed weight(gm)	9	4.68						
Biological yield per plant (gm)	। महित्य / 126	65.52						
Harvest index (%)	1	0.52						
Grain yield per plant (gm)	4	2.08						

Contribution of character studied, towards total divergence Table 6 revealed that the biological yield per plant and plant height contributed maximum towards total divergence. These characters were thus, found to be considered suitable in creating variability by hybridization and selecting the desired genotypes while breeding barley for its higher yield.

CONCLUSION

The present investigation on variability, heritability and genetic advance, correlation coefficient and path analysis suggested that the characters viz., biological yield per plant, number of productive tillers per plant, number of grains per spike and grain yield per plant should be taken into consideration while making selection breeding program in order to bring substantial improvement in barley. On the basis of studies made on genetic divergence, it was suggested that crosses between the genotypes of cluster I and III may give fruitful results in the hybridization programme.

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