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ASSESSMENT OF GENETIC VARIABILITY FOR AGRONOMIC AND BIOCHEMICAL CHARACTERS IN BARLEY (*HORDEUM VULGARE* L.)

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SUMMARY

In any efficient plant breeding programme for an effective selection of economically plant species, genetic variability plays a pivotal role and an imperative survey of it leads to develop high yielding varieties. The present investigation was carried out during *rabi* 2018-19 at Barley research area, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana. The experiment was conducted to evaluate 45 genotypes of barley and six checks in an Augmented Design. The analysis of variance showed significant differences among experimental material for all traits. High PCV along with high GCV were observed for the characters such as peroxidase, grain yield per plot, biological yield per plot. High heritability coupled with high genetic advance was recorded for the traits namely peroxidase, dehydrogenase, number of grains per spike, spike length, number of effective tillers per meter, harvest index and grain yield per plot. Grain yield per plot discerned significant correlation with number of grains per spike, 1000 grain weight, biological yield per plot, harvest index and dehydrogenase. Path coefficient analysis revealed maximum direct effect on grain yield per plot employed by biological yield per plot followed by harvest index. The combined study of correlation and path coefficients indicated to the characters namely, biological yield per plot, 1000 grain weight, harvest index and dehydrogenase were the major yield attributing traits.

Key words: Barley, correlation, genetic variability, path analysis

Barley is one of the primarily cultivated crops of ancient era. The period of 5000 to 7000 B.C. and before bears its documented antiquity. Due to its high malt content barley is an important crop in brewing industry for production of beer. Its ability to withstand drought makes it the most suitable fit crop in arid and semi-arid regions all around the world (Ghazi *et al.*, 2007). In India, barley occupied an area of 0.59 mha with 1.72 mt production and 2920 kg/ha average productivity (ICAR-IIWBR, 2020). The proximate compounds that are present in barely are full of vitamins and has rich amount of healthy nutrients (Santos *et al.*, 2011).

The extent of genetic variability existing in a material determines the success of a breeding programme. The magnitude of heritability estimates in parts decides the type of selection and progress for a particular character (Ajibade, 2000). The reliability of phenotypic success is attained by heritability (Hamdi and Erskine, 1990). The crop potential to respond positively towards breeding programs relies on the magnitude and nature of variability (Allard, 1960). The knowledge of relationship amongst a wide variety of characteristics affecting grain yield is additionally crucial for the efficacy of selection process (Sharma, 1998).The complex trait grain yield is quite influenced by many genetic elements and environmental fluctuations as well (Smith *et al.,* 1989). Genetic variability gives a wider scope for selection making it the primary requirement for crop improvement.

The mutual relationship among the variables is described by correlation. The extent of affiliation between distinct characters is revealed by both genotypic and phenotypic correlation. The highly variable expression *i.e.* yield is considered as the ultimate goal in most of the breeding programs (Mohammadi *et al.*, 2012).The study of correlation in conjunction with path analysis is important to highly recognize the cause and effect relationship between exclusive pairs of characters. Therefore, the path coefficient evaluation used to be additionally undertaken to apprehend the direct and oblique

consequences of a range of characteristics on seed yield (Wright, 1921).

The present study therefore, proposed with 45 barley genotypes along with 6 checks to figure out genetic variability and to categorise trait specific promising genotypes which may subsidize in combination breeding for future exploitation.

MATERIAL AND METHODS

The present study was carried out during *rabi* 2018-2019 at Barley research area of Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The experimental material for the present study consisted of 45 barley genotypes alongwith 6 check varieties namely BH 946, BH 959, BHS 400, RD 2715, DWRB 101 and HUB 113.The soil of the research farm is primarily sandy loam in nature and received 44.1 mm rainfall with mean monthly minimum and maximum temperatures of 10.43 ? and 26.37 ?, respectively through the crop season of *rabi* 2018-19.

The experiment was planted in Augmented Design with five blocks under normal agronomic practices. The checks were repeated every after 9 genotypes. Each plot comprised of 2 rows of 2.5m length spaced at 30 cm. Five plants from each block were taken for recording of observations on ten morphological characters *viz.,* days to heading, days to maturity, plant height (cm), number of effective tillers per meter, spike length (cm), number of grains per spike, 1000 grain weight (g), grain yield per plot (g), biological yield per plot (g), harvest index (%), and two biochemical traits *i.e.* dehydrogenase activity and peroxidase enzyme. The statistical analyses were carried for the observed data using the standard statistical methods.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance (ANOVA) showed highly significant means sum of squares for all the twelve traits under the present study representing the considerable genetic variation present among all the genotypes (Table 1). This validated further statistical and genetical analyses. Similar results for analysis of variance of different characters were also reported by Joshi *et al.* (2018), Addisu *et al.* (2015), Sunil *et al.* (2017) and Verma and Verma (2011).

TABLE 1

Analysis of variance of twelve characters in barley genotypes

Source of variation	d.f.	Mean Squares												
		DH	DM	PH	NET/M	SL	NG/S	TGW	GY/P	BY/P	HI	DHA	POD
Block (eliminating Check + Var)	4	1.21	1.78	24.19	176.08	5.58	0.88	11.21	6421.66	4411.13	18.42	6.48	9.91
Entries (ignoring Blocks)	50	74.25**	15.15**	120.59**	268.89**	252.65**	569.67**	2604.50**	29541.09**	3313.20**	28.71**	899.96**	1052.85**
Checks	5	155.98**	28.59**	455.55**	221.68*	313.18**	1339.58**	7836.88**	34342.83**	4132.05**	42.22**	5153.45**	1285.64**
Varieties	44	57.61**	13.55*	75.18*	272.84**	211.42**	471.30**	2068.97**	19215.90**	2811.98**	23.10**	366.07**	850.52**
Checks vs. Varieties	1	397.62**	18.40*	444.02*	331.10*	1764.18**	1048.82**	6.00*	459840.50**	21272.96**	208.05**	3123.66**	8791.38**
Error	20	0.79	0.84	9.72	56.16	11.26	4.76	29.23	2966.16	900.25	5.72	2.47	1.93

*, ** Significant at 5% and 1% probability level respectively.

DH: Days to heading, DM: Days to maturity, PH: Plant height, NET/M: Number of effective tillers per meter, SL: Spike length, NG/S: Number of grains per spike, TGW: 1000 grain weight (g), GY/P: Grain yield per plot (g), BY/P: Biological yield per plot (g), HI: Harvest index (%), DHA: Dehydrogenase activity, POD: Peroxidase activity.

Variance components and estimated genetic parameters:

Mean performance

Among all the quantitative and qualitative traits, grain yield per plot possessed highest variance and range, followed by biological yield per plot and 1000 grain weight which indicated that grain yield, biological yield and 1000 grain weight were responsible for wide range of variation in grain yield per plot of different genotypes. Similar results for grain yield were also reported by Hailu *et al.* (2016).

Genetic variability

Estimation of heritable and non-heritable mechanisms is important for acceptance of appropriate breeding programme and this can be evaluated by different biometrical techniques as GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), h^2 (heritability) and GA (genetic advance). Phenotypic coefficients of variation (PCV) resulted greater for all the respective characters in comparison with genotypic coefficient of variation (GCV). It signified the role of different environmental factors on these traits (Krishna *et al.*, 2013; Prasad *et al.*, 2013 and Pratap *et al.*, 2012).

From table 2, it was concluded that high GCV and PCV were detected for number of grains per spike, grain yield per plot and biological yield per plot, moderate values of GCV and PCV were detected for harvest index, number of effective tillers per meter and spike length while lower values were detected for 1000 grain weight, plant height, days to heading and days to maturity. Matin et al. (2019), Lodhi *et al.* (2015), Addisu and Shumet (2015) and Singh *et al.* (2014) also reported similar results for these characters. GCV and PCV outcomes disclosed the chances of further improvement in barley genotypes for different respective traits and also the GCV and PCV differences were minor which exhibited minimum environmental effects (Prasad *et al.*, 2013).

Genotypic coefficient of variation had revealed the full scope to heritable variation so that heritability is valuable for enduring genetic development (Singh, 2000). The GCV along with heritability designate a consistent expected genetic advance as reported by Burton (1952). High heritability for number of grains per spike, days to heading, 1000 grain weight, spike length, days to maturity and plant height designate a higher response to assortment for these characters (Shan and Mishra, 1995; Shadakshari *et al.*, 1995) and these similar findings were in agreement with Matin *et al.* (2019), Singh *et al.* (2014), Ali *et al.* (2012) and Jalata *et al.* (2011). High heritability permits better selection at phenotypic level. This gives a stable improvement in these characters.

The other remaining characters such as plant height (80.89%), grain yield per plot (77.50%), number of effective tillers per meter (70.80%) and harvest index (65.61%) were found to be moderately heritable characters.

Heritability and Genetic Advance

From Table 2, higher genetic advance as per

TABLE 2
Estimates of genetic parameters in barley genotypes

S. No.	Characters	Mean ± SE (m)	Range (Min-Max)	Coefficient of variation (%)		Heritability (bs) (%)	GA as % mean
				PCV	GCV		
1.	Days to heading	94.24±1.04	78-110	6.37	6.30	97.82	12.84
2.	Days to maturity	140.25±0.50	132-148	2.12	2.01	90.45	3.94
3.	Plant height (cm)	106.41±1.23	86-123	6.67	6.00	80.89	11.10
4.	Number of effective tillers/m	93.78±2.31	64-137	14.71	12.38	70.80	21.45
5.	Spike length (cm)	8.72±0.20	5.2-11.2	13.24	12.69	91.78	25.04
6.	Number of grains/spike	51.36±2.94	24-80	34.21	33.93	98.40	69.34
7.	1000 grain weight (g)	41.44±0.62	31.6-52.8	8.74	8.64	97.77	17.59
8.	Grain yield/plot (g)	497.13±18.44	270-850	24.00	21.13	77.50	38.31
9.	Biological yield/plot (g)	2006±73.32	1180-3020	23.33	20.64	57.17	27.46
10.	Harvest index (%)	25.07±0.77	15.00-39.52	16.54	13.40	65.61	25.35
11.	Dehydrogenase	0.39±0.02	0.102-0.978	40.46	40.24	98.93	82.45
12.	Peroxidase	0.87±0.04	0.301-1.517	25.74	25.70	99.64	52.84

Where, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation.

cent of mean were detected for number of grains per spike, spike length, grain yield per plot, biological yield per plot, harvest index, spike length and number of effective tillers per meter suggesting that the above traits can be improved for better performance while adopting selection techniques exploiting additive gene action. Moderate genetic advance was observed for 1000 grain weight, days to heading and plant height and lowest for days to maturity. Matin *et al.* (2019), Sunil *et al.* (2017), Singh *et al.* (2014) and Singh *et al.* (2008) reported the similar results for one or more traits.

Heritability coupled with genetic advance is a better methodology for selecting superior genotypes (Johnson *et al.*, 1955 and Prasad *et al.*, 1980). The estimates of high heritability along with high expected genetic advance indicated additive gene action (Panse and Sukatme, 1957) while lower expected genetic advance indicated non-additive gene action (Singh and Narayanan, 1993). Thus, high heritability coupled with high genetic advance is more reliable. Number of grains per spike, spike length, number of effective tillers per meter, harvest index and grain yield per plot had high heritability coupled with high genetic advance as percent of the mean directed that these traits were simply inherited traits and for these characters selection may be operative in early generations because these traits most likely to be supervised by additive gene effects. Similar conclusions were also stated by different authors like Sunil *et al.* (2017), Singh *et al.* (2014), Akanksha *et al.* (2012), Mishra *et al.* (2008), Begum and Khatun (1997). Though, high heritability together with low genetic advance as percent of mean in case of days to maturity directed towards non-additive gene effects (Sunil *et al.*, 2017) and yet these traits can be developed from combination breeding by intermating better quality genotypes in segregating population (Prasad *et al.*, 2013 and Deb Choudhary and Das, 1998).

Correlation coefficient analysis

To know the suitability of various characters for indirect selection, the study of correlation coefficients is important. Yield is a very complex quantitative trait extremely influenced by different environmental factors, where any direct selection is not realistic. Therefore, the correlation between the grain yield and its associative traits is of meaningful importance for any breeding programme. In Table 3 and Table 4, simple correlations were calculated and presented among twelve characters for different barley genotypes.

Grain yield per plot presented significant positive correlation with number of grains per spike, 1000 grain weight, biological yield per plot and harvest index (Sunil *et al.*, 2017; Lodhi *et al.*, 2015; Singh *et al.*, 2014; Pal *et al.*, 2010 and Singh *et al.*, 2008). While, days to maturity and number of effective tillers per plant showed positive but non-significant correlation (Vinesh *et al.*, 2018; Yadav *et al.*, 2014 and Verma and Verma, 2011).These traits appeared to be best for selection projected to positively affect the grain yield because of good grain filling, higher bio-

TABLE 3
Correlation coefficients among twelve characters of barley genotypes

Characters	DH	DM	PH	NET/M	SL	NG/P	TGW	BY/P	HI	DHA	POD	GY/P
DH												
DM	0.802**											
PH	0.217	0.294*										
NET/M	0.261	0.286*	0.364**									
SL	0.127	0.302*	0.666**	0.332*								
NG/S	-0.118	-0.035	0.088	-0.284*	0.086							
TGW	-0.161	-0.150	-0.044	-0.004	0.097	0.507**						
BY/P	0.193	0.326*	0.224	0.469**	0.257	0.288*	-0.135					
HI	-0.405**	-0.344*	-0.416**	-0.401**	-0.389**	0.037	0.024	-0.223				
DHA	-0.110	-0.154	-0.099	0.056	-0.230	0.277*	-0.152	0.146	0.316*			
POD	-0.064	-0.213	0.227	0.145	0.196	-0.182	0.213	0.102	-0.069	-0.296*		
GY/P	-0.069	0.081	-0.060	0.121	-0.020	0.284*	0.278*	0.737**	0.478**	0.360**	0.047	

** Significant at 1% probability level, * Significant at 5% probability level.
DH: Days to heading, DM: Days to maturity, PH: Plant height, NET/M: Number of effective tillers per meter, SL: Spike length, NG/S: Number of grains per spike, TGW: 1000 grain weight (g), GY/P: Grain yield per plot (g), BY/P: Biological yield per plot (g), HI: Harvest index (%), DHA: Dehydrogenase activity, POD: Peroxidase activity.

TABLE 4
Correlation coefficients (Positive and Negative) among different characters

Characters	Type of correlation	Correlation with
DH	+ve	DM**, PH, NET/M, SL, BY/P,
	-ve	NG/S, TGW, HI**, DHA, POD, GY/P
DM	+ve	DH**, PH*, NET/M*, SL*, BY/P*, GY/P
	-ve	NG/S, TGW, HI*, DHA, POD
PH	+ve	DH, DM*, NET/M**, SL**, NG/S, BY/P, POD
	-ve	TGW, HI**, DHA, GY/P
NET/M	+ve	DH, DM*, PH**, SL*, BY/P**, DHA, POD, GY/P
	-ve	NG/S*, TGW, HI**
SL	+ve	DH, DM*, PH**, NET/M*, NG/S, BY/P, POD
	-ve	TGW, HI**, DHA, GY/P
NG/S	+ve	PH, SL, BY/P*, HI, DHA*, GY/P*
	-ve	DH, DM, NET/M*, TGW**, POD
TGW	+ve	SL, NG/S**, HI, POD, GY/P*
	-ve	DH, DM, PH, NET/M, BY/P
BY/P	+ve	DH, DM*, PH, NET/M**, SL, NG/S**, DHA POD, GY/P**
	-ve	TGW, HI
HI	+ve	NG/S, TGW, DHA*, GY/P**
	-ve	DH**, DH**, PH**, NET/M**, SL**, BY/P, POD
DHA	+ve	GY/P**
	-ve	POD**
POD	+ve	GY/P
	-ve	DHA*
GY/P	+ve	DM, NET/M, NG/S*, TGW*, BY/P**, HI**, DHA**, POD
	-ve	DH, PH, SL

DH: Days to heading, DM: Days to maturity, PH: Plant height, NET/M: Number of effective tillers per meter, SL: Spike length, NG/S: Number of grains per spike, TGW: 1000 grain weight (g), GY/P: Grain yield per plot (g), BY/P: Biological yield per plot (g), HI: Harvest index (%), DHA: Dehydrogenase activity, POD: Peroxidase activity.

mass and early maturity leading to higher grain yield (Yadav et al., 2014).However, grain yield also exhibited negative correlation with days to heading (Lodhi *et al*., 2015; Singh *et al*., 2014; Verma and Verma, 2011 and Singh *et al*., 2008), plant height (Yadav *et al*., 2014), spike length (Drikwand *et al*. 2011). Grain yield also exhibited positive association with peroxidase (Kumar *et al*., 2008).

Biological yield per plant had possessed positive significant correlation with days to maturity, number of effective tillers per meter and number of grains per spike. The following literature had also reported the similar results as Sunil et al. (2017), Lodhi *et al*. (2015), Singh *et al*. (2014), Yadav *et al*. (2014), Al-Tabbal *et al*. (2012), Pratap *et al*. (2012) and Yadav *et al*. (2011). While, plant height had possessed positive association with biological yield per plot and similar result has been reported by Tofiq *et al*. (2015) and Verma and Verma (2011).

The present study also presented a negative significant association between number of grains per spike and number of effective tillers per meter which might have been due inter plants competition. These finding are in agreement with Lodhi *et al*. (2015), Singh *et al*. (2014) and Verma and Verma (2011).

Harvest index possessed negative significant correlation with days to heading, days to maturity, plant height, number of effective tillers per meter and spike length. The similar results were also reported by Negash *et al*. (2019), Yadav *et al*. (2014), Al-tabbal *et al*. (2012), Verma and Verma (2011).

5.5 Path coefficient analysis

Considering grain yield per plot as dependent variable (effect) and rest of the characters as independent variables (causes), direct and indirect effects were calculated through partitioning of genotypic correlation coefficients through path coefficient analysis (Table 5). The calculated results depicted that biological yield per plot and harvest index exerted high and positive effect on grain yield per plot

TABLE 5
Path coefficient analysis in barley genotypes

Characters	DH	DM	PH	NET/M	SL	NG/S	TGW	BY/P	HI	DHA	POD	rg with GY/P
DH	0.0556	-0.0042	0.0041	-0.0160	0.0036	0.0006	-0.0065	0.1731	-0.2748	-0.0045	-0.0004	-0.069
DM	0.0446	-0.0052	0.0056	-0.0176	0.0086	0.0002	-0.0060	0.2921	-0.2333	-0.0063	-0.0014	0.081
PH	0.0121	-0.0015	0.0190	-0.0224	0.0190	-0.0004	-0.0018	0.2012	-0.2825	-0.0041	0.0014	-0.060
NET/M	0.0145	-0.0015	0.0069	-0.0614	0.0094	0.0014	-0.0001	0.4207	-0.2725	0.0023	0.0009	0.121
SL	0.0071	-0.0016	0.0126	-0.0204	0.0285	-0.0004	-0.0039	0.2301	-0.2643	-0.0094	0.0012	-0.021
NG/S	-0.0065	0.0002	0.0017	0.0175	0.0024	-0.0051	-0.0204	0.2582	0.0252	0.0113	-0.0012	0.283*
TGW	-0.0049	0.0788	-0.0008	0.0292	-0.0028	0.0596	0.0872	-0.1206	0.0784	-0.0052	0.0786	0.278*
BY/P	0.0107	-0.0017	0.0043	-0.0288	0.0073	-0.0015	-0.0054	0.8965	-0.1512	0.0060	0.0006	0.737**
HI	-0.0225	0.0018	-0.0079	0.0247	-0.0111	-0.0002	0.0010	-0.1996	0.6790	0.0130	-0.0004	0.478**
DHA	-0.0061	0.0008	-0.0019	-0.0034	-0.0065	-0.0014	-0.0061	0.1308	0.2148	0.0410	-0.0019	0.360**
POD	-0.0035	0.0011	0.0043	-0.0089	0.0056	0.0009	0.0086	0.0913	-0.0468	-0.0121	0.0063	0.047

Residual effect = 0.09; rg = genotypic correlation.
DH: Days to heading, DM: Days to maturity, PH: Plant height, NET/M: Number of effective tillers per meter, SL: Spike length, NG/S: Number of grains per spike, TGW: 1000 grain weight (g), GY/P: Grain yield per plot (g), BY/P: Biological yield per plot (g), HI: Harvest index (%), DHA: Dehydrogenase activity, POD: Peroxidase activity.

among all the traits. These findings were also reported by Sunil *et al.* (2017), Pratap *et al.* (2012), Yadav *et al.* (2011) and Jayasudha and Sharma (2010). It proposed that these traits can be considered as the important yield component traits for better selection in breeding programmes for obtaining high grain yield of barley.

Moreover, positive and indirect effect was exerted by biological yield per plot on grain yield per plot via number of effective tillers per meter, days to maturity, 1000 grain weight, spike length, plant height and days to heading. While negative and indirect effect was exerted via harvest index. Also, positive and indirect effect on grain yield per plot was exerted by harvest index via number of grains per spike, 1000 grain weight, days to maturity and number of effective tillers per meter. Biological yield per plot and harvest index are significant yield contributing characters which must be taken into account at the time of selection for obtaining high yielding varieties of barley. These were also recognized by Sunil *et al.* (2017), Yadav *et al.* (2014), Carpc and Celk (2012) and Dadashi *et al.* (2010).Improvement in these traits may lead for the betterment of ultimate characters *i.e.* yield.

The residual effect 0.09 indicated that the constituent characters under study were responsible for about 91% of variability in grain yield per plot.

CONCLUSION

(1). Two genotypes *i.e.* IBYT-18-8 and IBYT-18-4 had recorded significantly higher grain yield per plot than the check BH 946, whereas four genotypes namely IBYT-18-8, IBYT-18-4, 5th GSBYT-18-84 and 5th GSBYT-18-7 had significantly higher grain yield per plot than the best check HUB113 with mean value of 687 g. These genotypes formed significant group for higher grain yield per plot. The above stated genotypes also presented better performances for other yield components as well. These genotypes evaluated were found to be very important to be used in different breeding programmes for their further exploitation in barley crossings. Genotypes selected in this study may be utilised into elite barley breeding programmes to have transgressive segregants as well.

(2). Grain yield per plot exhibited positive and significant correlation with number of grains per spike, 1000 grain weight, biological yield per plot, harvest index and dehydrogenase. Strong positive association of these characters discerned that the selection based on these characters would improve grain yield and also suggested that for obtaining desirable high yielding genotypes combination of the above characters be useful for hybridization of genotypes.

(3). The combined analysis of correlation coefficient and path coefficient revealed that the characters, namely, biological yield/ plot, 1000 grain weight and harvest index were the major yield attributing characters and hence

emphasis should be given to these characters while programming any plant breeding program with these genotypes.

REFERENCES

Addisu, F. and T. Shumet, 2015: Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in Ethiopia. *International Journal of Plant Breeding and Genetics*, **9**(2): 68-76.

Ajibade, S.R., 2000: Pedigree selection in Cowpea. *Nigerian Journal of Botany*, **13**: 29-33.

Akanksha, A., S. Kumar, S. Kant, K. Pal, A. Kumar and M. Singh, 2012: Genetic improvement through variability, heritability and genetic advance in barley crop (*Hordeum vulgare* L.). *Environment and Ecology,* **30**(4): 1343-1345.

Ali, Q., M. Elahi, M. Ahsan, M.H.N. Tahir and S.M.A. Basra, 2012: Genetic evaluation of maize (*Zea mays* L.) associations for growth related seedlings traits. *International Journal for Agro Veterinary and Medical Sciences*, **6**(3): 164-172.

Allard, R.W., 1960: *Principles of Plant Breeding*. John Wiley and Sons. Inc. New York.

Al-Tabbal, J.A. and A.H. Al-Fraihat, 2012: Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science,* **4**(3): 193-210.

Begum, S. and F. Khatun, 1997: Genetic parameters and character association in exotic genotypes of two-rowed barley. *Bangladesh Journal of Botany,* **26**(2): 121-126.

Burton, G.W., 1952: Quantitative inheritance in grasses. *6th International Grassland Congress,***1**: 277-283.

Carpc, E.B. and N. Celk, 2012: Correlation and path coefficient analyses of grain yield and yield components in two-rowed of barley (*Hordeum vulgare* var. *distichon*) varieties. *Notulae Scientia Biologicae,***4**: 128-131.

Dadashi, M., A.A. Norinia, M. Morteza-Asghar and S. Azizi-Chakhrchaman, 2010: Evaluate the correlation a number of physiological and morphological characteristics of naked barley varieties with grain yield. *Journal of Eco-Physiology of Crop Plants and Weeds*, **15:** 29-40.

Deb Choudhary, P.K. and P.K. Das, 1998: Genetic variability, correlation and path coefficient analysis in deep water rice. *Annals of Agricultural Research*, **19**(2): 120-121.

Drikvand, R., K. Samiei, and T. Hossinpor, 2011: Path coefficient analysis in hull-less barley under rainfed condition. *Australian Journal of Basic and Applied Sciences*, **5** (12): 277-279.

Federer, W.T., 1977: *Experimental Design: Theory and Application*. Mcmilan, New York.

Ghazi, N., A. Karaki, A. Al-Ajam, and Y. Othman, 2007: Seed germination and early root growth of three barley cultivars as affected by temperature and water stress. *American-Eurasian Journal of Agricultural and Environmental Sciences*, **2**(2): 112-117.

Hailu, A., S. Alamerew, M. Nigussie and E. Assefa, 2016: Correlation and path coefficient analysis of yield associated traits in barley (*Hordeum vulgare* L.) germplasm. *Advances in Crop Science and Technology,* **4**(2): 216-22.

Hamdi, A. and W. Erskine, 1990: Heritability of plant height and lowest pod height in lentil. *Agricultural Research Review*, **68**: 1497-1509.

ICAR-IIWBR, 2020: Director's Report of AICRP on Wheat and Barley 2019-20, Ed: G.P. Singh, ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. P. 94.

Jalata, Z., A. Ayana and H. Zeleke, 2011: Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.) landraces and crosses. *International Journal of Plant Breeding and Genetics*, **5** (1): 44-52.

Jayasudha, S. and D. Sharma, 2010: Genetic parameters of variability, correlation and path coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow low land situation. *Electronic Journal of Plant Breeding*, **1**(5): 1332-1338.

Johnson, H.W, H.E., Robinson and R.E. Comstock, 1955: Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.

Joshi, N., A. Kumar and S.A. Rather, 2018: Determination of extent of variability in wheat germplasm using augmented randomized block design. *International Journal of Chemical Studies,* **6**(3): 1074-1082.

Krishna, A., S. Ahmed, H.C. Pandey and D. Bahukhandi, 2013: Estimates of genetic variability, heritability and genetic advance of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Agricultural Science Research Journals,* **3**(2): 56-61.

Kumar, R. and V.P. Gupta, 2008: Peroxidase activity in relation to plant height and seed yield in Indian mustard (*Brassica juncea* L. Cross).*Journal of Agronomy and Crop Science,* **159**(1): 1-5.

Lodhi, R., L.C. Prasad, A.H. Madakemohekar, S.S. Bornare and R. Prasad, 2015: Study of genetic parameters for yield and yield contributing trait of elite genotypes of barley (*Hordeum vulgare L.*).*Indian Research Journal of Genetics and Biotechnology,* **7**(1): 17-21.

Matin, M.Q., M. Amiruzzaman, M. Billah, M.B. Banu, N. Naher, and D.A. Choudhary, 2019: Genetic variability and path analysis studies in barley (*Hordeum vulgare* L.). *International Journal of Applied Sciences and Biotechnology*, **7**(2): 243-247.

Mishra, C.N., S.K. Singh, P.C. Singh, D.N. Bhardwaj and H.L. Singh, 2008: Studies on genetic variability in barley (H*ordeum vulgare* L.). *International Journal of Plant Sciences*, **3**(1): 220-221.

Mohammadi, M, P. Sharifi, R. Karimizadeh and M.K. Shefazadeh, 2012: Relationships between grain yield and yield components in bread wheat under different water availability (Dry land and Supplemental Irrigation Conditions). *Notulae Botanicae Horti Agrobotanici Cluj*, **40**(1):195-200.

Negash, G., D. Lule, and Z. Jalata, (2019).Correlations and path analysis of some quantitative characters in barley (*Hordeum vulgare* L.) landraces in Western Oromia, Ethiopia. *African Journal of Plant Science*, **13**(2): 34-36.

Pal, S., T. Singh and B. Ramesh, 2010: Estimation of genetic parameters in barley (*Hordeum vulgare* L.).*Crop Improvement*, **37**(1): 52-56.

Panse, V.G. and P.V. Sukhatme, 1957: Genetics and quantitative characters in relation to plant breeding. *Indian Journal of Genetics*, **17**:312-328.

Prasad, G.S., K.V. Radha Krishna, L.V. Subba Rao and U. Chaithanya, 2013: Quantitative analysis of rice genotypes (*Oryza sativa* L.).*International Journal of Innovative Research and Development*, **2**(9): 14-17.

Prasad, G.S.K. and R.S. Singh, 1980: Genotypic correlation and path coefficient analysis in barley under saline alkaline condition. *Plant Breeding Abstracts*, **2**: 147-158.

Pratap, N., P.K. Singh, R.S. Shekhar, K. Soni and A.K. Mall, 2012: Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.). *SAARC Journal of Agriculture,* **10**(2), 83-94.

Santos, C.A.F., L.C. Correa and S.R. Costa, 2011: Genetic divergence among Psidium accessions based on biochemical and agronomic variables. *Crop Breeding and Applied Biotechnology*, **11**: 149-156.

Shadakshari, Y. G., K. Virupahshappa and G. Shivasharikar, 1995: Genetic variability studies in the germplasm collections of sesamum (*Sesamum indicum* L.). *Mysore Journal of Agricultural Science,* **29**: 133 -137.

Shan, G.S. and R.S. Mishra, 1995: Genetic divergence in tomato. *Mysore Journal of Agricultural Science,* **29**: 5-8.

Sharma, J.R., 1998: *Statistical and Biometrical Techniques in Plant Breeding*. New Age International (P) Limited, publishers. New Delhi. 432p.

Singh, B.D., 2000: *Plant Breeding: Principles and Methods*. Kalyani Publishers, New Delhi.

Singh, J., L.C. Prasad, A.H. Madakemohekar and S.S. Bornare, 2014: Genetic variability and character association in diverse genotypes of barley (*Hordeum vulgare* L.).*The Bioscan,* **9**(2):759-761.

Singh, P. and S.S. Narayanan, 1993: Biometrical techniques in plant breeding. Kalyani Publishers, New Delhi.

Singh, S.K., A. Sirchi, S.A. Kerkhi, O. Singh, V. Kumar, A. Singh, S.P. Singh and R.P. Singh, 2008: Genetic variability in components for grain yield in barley (*Hordeum vulgare* L.). *Environment and Ecology*, **26**: 2379-2381.

Smith, J.H.C. and O.S. Smith, 1989: The description and assessment of distances between inbred lines of maize: The utility of morphological, biochemical and genetic descriptors and a scheme for testing of distinctiveness between inbred lines. *Maydica*, **34**: 151-161.

Sunil, K.D. Sehrawat and M. Khan, 2017: Investigation of genetic variability for yield and yield related traits in Barley (*Hordeum vulgare* L.) genotypes. *Indian Journal of Ecology*, **44**(4): 869-72.

Tofiq, S., S.S. Abdulla and D.A. Abdulkhaleq, 2015: Correlation and path coefficient analysis of grain yield and yield components in some barley genotypes created by full diallel analysis in Sulaimani region for F_2 generation. *International Journal of Plant, Animal and Environmental Sciences*, **5**(4): 76-79.

Verma, I. and S.R. Verma, 2011: Genotypic variability and correlations among morpho-physiological traits affecting grain yield in barley (*Hordeum vulgare L.*). *Journal of Wheat Research,* **3**(1): 37-42.

Vinesh, B., R. Prasad, and K. Madhukar, 2018: Association studies of yield and its attributing traits in indigenous and exotic Barley (*Hordeum vulgare* L.) germplasm. *Journal of Pharmacognosy and Phytochemistry,* **7**(5): 1500-1502.

Wright, S., 1921: Correlation and causation. *Journal of Agricultural Research*, **20**: 557-585.

Yadav, S.K., K.K. Pawar, S.S. Baghel, M. Jarman and A.K. Singh, 2014: Genetic analysis for grain yield and its components in barley (*Hordeum vulgare* L.). *Journal of Wheat Research*, **6**(2): 163-166.

Yadav, S.K., P. Pandey, B. Kumar and B.G. Suresh, 2011: Genetic architecture, interrelationship and selection criteria for yield improvement in rice (*Oryza sativa* L.). *Pakistan Journal of Biological Sciences*, **14**: 540-545.