Int.J.Curr.Microbiol.App.Sci (2018) *7*(7): 2007-2019

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 7 Number 07 (2018)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2018.707.237

Variability and Diversity Studies in Exotic and Indigenous Barley (*Hordeum vulgare* L.)

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Keywords

Barley, Variability, heritability, GCV, PCV, D^2 and diversity.

Article Info

Accepted:
15 June 2018
Available Online:
10 July 2018

A B S T R A C T

The present investigation comprising of 101 barley genotypes was conducted at Genetics and Plant Breeding, Banaras Hindu University, during *rabi* of 2016-17. Variability and diversity analysis was carried out based on data collected on 13 various quantitative traits. High Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) was observed for grain yield plant, proline concentration and grain per ear. Medium PCV and low GCV values were displayed for days to heading. High heritability coupled with high genetic advance was observed for plant height, spike length, number of spikelets per spike, number of kernels per spike, kernel weight per spike, thousand kernel-weight and days to 50% flowering. These 101 barley genotypes were grouped into 12 clusters based on relative magnitude of the D^2 values. The intra cluster distance was found minimum for cluster I and maximum distance in cluster VI while it was zero for cluster III, IV, V, VII, VIII, IX, X, XI and XII as these clusters consisted of only single genotype. The maximum inter-cluster distance was recorded between cluster VIII and cluster X. The cluster V had high mean value for flag leaf length, spike length with awn, spike length without awn and grains per ear. Cluster IV had high mean value for plant height, SPAD value; cluster III had high mean value for stomatal conductivity.

Introduction

Hordeum, Triticum and Secale belong to the tribe Triticeae, the Poaceae family. Poaceae is considered to be monophyletic; therefore all grasses belonging to this family may have evolved from a single ancestor. The genus Hordeum consists of 32 species and 45 taxa including diploid (2n = 2x = 14), tetraploid (2n = 4x = 28) and hexaploid (2n = 6x = 42) cytotypes. Barley (*Hordeum vulgare* L.) from eating, the importance even extended to having religious significance and used in Ayurveda in India, and ritual significance in ancient Greece. It is fourth largest cereal crop after maize, wheat and rice in the world with a share of 7 per cent of the global cereal production. It is a major source of food for large population of cool and semi-arid areas of the world, where wheat and other cereals are less adapted.

Barley is an annual cereal grain crop that is consumed as a major feed for the animals. The rest is used as malt in whiskey or sugar as well as health food. Overall India's barley production was estimated to be 1781.4 MT spread over an area of 6.93 lakh ha for the year 2016-17. The average productivity was estimated to be 25.80 q/ha (1). The positive fact about the Barley trade is the growth in the consumption over the years and the consistent increase in the production. If this pattern of consumption continues in the coming years, the exports are bound to maintain a steady uptrend as the supply is always going to lag behind the demand. Even with such a potential to become a commercial crop, in India, it always remained as poor man's crop and mostly grown with minimal inputs in marginal lands where other crops cannot survive/adapt. Hence to overcome the ill treatment it receives in the country and to compensate the minimal inputs, there is a requirement of identifying genotypes which adapt to more adverse conditions where the crop is often grown and yield to the maximum genotypic potential.

Hence, getting the genetic information about existing barley genotypes in connection with better yield and its contributing traits other argonomically important traits is need of the hour. Such information shall provide good support to barley breeders or researcher to develop the superior genotypes of varieties. Genetic variability is the back bone of crop improvement programme, effectiveness of selection depends upon nature and magnitude of genetic variability present in the genetic material. The nature and amount of genetic variability available in the germplasm indicates the scope of improvement of the character by exploiting the genetic variability. The great interest in genetic diversity arises from the possibility of demonstrating that phenotypic mean values express, in a larger or smaller degree, the genotypic value of an individual. Thus, while evaluating the divergence among populations, based on average phenotypic values, the divergence among genotypic values associated with gene frequency in different sample units (populations, varieties, clones, etc.) is also evaluated. The multivariate analysis using Mahalanobis' D2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance. Therefore, the present investigation aimed at studying variability, magnitude of coefficient of variations and diversity among 101 exotic and indigenous barley germplasm collection.

Materials and Methods

The present investigation was carried out at Genetics and Plant Breeding, Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.) during rabiof 2016-17. Geographically, Banaras Hindu University is situated between 25º18' N latitude, 83º 03´E longitudes and at an altitude of 128.93 meters above the mean sea level in the North Gangetic plain of eastern part of Uttar Pradesh. The experimental materials incorporated 101exotic and indigenous genotypes which were well-kept by BHU under All India Co-ordinated Wheat and Barley Improvement Project. Randomized Block Design with three replications was adopted for laying out the genotypes for the investigation. Each treatment (genotype) was sown in line having 2.75 m length with row to row and plant to plant distance of 25 cm and 10 cm, respectively. All the recommended agronomic practices for respective experimental conditions were followed to raise a healthy crop. Five competitive plants, in each plot were randomly selected and tagged well in advance for recording the observations. Data was recorded on various

yield and yield attributing traits viz.,days to 50 per cent flowering, days to maturity, flag leaf length (cm), number of effective tillers/plant, number of grains/ear, spike length with awns (cm), spike length without awns (cm),stomatal conductivity (m Mol M-2 S-1), SPAD values, proline concentration (µ mol g-1),plant height (cm), 1000-grain weight (gm) and grain yield/plant (gm).

Genotypic, phenotypic and environmental components of variance and their coefficient of variances (Phenotypic: PCV and Genotypic: GCV) were estimated as methods suggested by Lush (1940) and Burton (1952) respectively. The PCV and GCV values were classified as Low: Less than 10%; Moderate: 10 – 20%; High: More than 20% as suggested by Sivasubramanian and Madhavamenon (1973). Heritability in broad sense [h2 (b)] was calculated according to the formulae given by Lush (1940) and categorized as Low: Less than 30%; Medium: 30-60%; High: More than 60% as suggested by Johnson et al. (1955).

From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson et al. (1955).

$$GA = (K)\ (\sigma p)\ h2\ (b)$$

Where, GA = Genetic advance under selection (expected); σp = Phenotypic standard deviation; h2 (b) = Heritability (broad sense); K = Selection differential at 5% selection intensity (2.06)

Genetic advance as per cent of mean was calculated as per the formula.

GA as per cent of mean = ("GA" /¯X)×"\1\0\0"

Where, GA = Genetic advance; ¯X = Grand mean of the character

The range of genetic advance as per cent of mean was classified as Low: Less than 10%; Medium: 10-20%; High: More than 20% as suggested by Johnson et al. (1955).

Genetic diversity between genotypes was estimated by using D2 analysis given by Mahalanobis's (1936).

The D2 value between ith and jth genotypes for P characters was calculated as

$$Dij2 = P\ \Sigma t=1\ (\bar{Y}it - \bar{Y}jt)$$

Where, ¯Yit = uncorrected mean value of ith genotype for t character; ¯Yjt = Uncorrected mean value of jth genotype for t character; Dij2 = D2 value between ith and jth genotype.

Grouping of the genotypes into various clusters was done by using Tocher's method as described by Rao (1952)

Results and Discussion

Analysis of variability

In the present study, ANOVA of traits revealed significant variability for various traits studied in the germplsam (Table 1). Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in (Table 1). Highly significant differences among genotypes (P<0.01) were observed for all 13 characters (days to 50 % flowering, number of productive tillers per plant, spike length, spike without awn, 1000 kernel weight, grain yield plant, SPAD value, grain yield per plant days to maturity, flag leaf length, proline concentration and plant height. This result indicating that there is variability among the genotypes studied and would respond positively to selection. This finding was accordance with (8) while studied on bread wheat genotypes. Thus, it indicated that there was sufficient variability in the material

used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

The values of GCV and PCV were very close which reinforces the greater contribution of genotype rather than environment. So the selection can be operated very well based on the phenotypic values for trait interest. The PCV was higher than the corresponding GCV for all the traits which might be due to the interaction of the genotypes with the environment to some degree or other denoting environmental factors influencing the expression of these characters.

High Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for grain yield plant, proline concentration and grain per ear which were supported by similar reports (20). The present finding is in consonance with the reports made (18); (21); (6). (4).while working with wheat, also reported that the PCV values were higher than GCV values for all the traits studied and medium PCV and GCV were showed for plant height, number of kernels per spike, 1000 kernels weight, grain yield per plot, biomass yield per plot and harvest index. Medium PCV and low GCV values were displayed for days to heading.

Moderate PCV was observed for effective tillers per plant, SPAD value, stomatal conductivity, plant height, 1000 grain weight. These finding are very similar with (3);(4). Lowest magnitude of PCV was observed for days to maturity followed by days to 50% flowering and spike length with awn and other traits exhibits medium values of PCV. The estimates of GCV and PCV were moderate for biological yield per plant, number of effective tillers per plant.

The difference between the values of PCV and GCV were high for majority of traits indicating more influence of environment in expression of these traits in both conditions. This statement conformed (20).(2) From analysis of variance found significant differences among entries for all the characters studied. The estimates of GCV and PCV were high for grain yield per plant, biological yield and number of kernels per main spike. (Table 2)

Heritability (h2) and Genetic Advance (GA)

Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to off-spring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. The GCV together with heritability estimates would give reliable indication of the expected progress in a selection programme (15). High heritability percentage coupled with high genetic variability particularly grain yield per plant under normal situation and emerged as an ideal traits for improvement through simple selection in upcoming generations.

In the present investigation, high heritability estimates were obtained for all the thirteen quantitative traits studied (Fig. 1). Broad sense heritability estimate was highest for days to 50% flowering, grain yield per plant, plant height, stomata conductivity and grain per ear. These finding were in accordance with the findings of (13).

However, heritability values alone may not provide clear predictability of the breeding value. Heritability in conjugation with genetic advance over mean is more effective and reliable in predicting the effectiveness of selection. In the present experiment, all the characters studied had exhibited high heritability coupled with high genetic advance

as percentage of mean. Estimates of high heritability and high genetic advance together may be ascribed to the conditioning of the characters by additive effect of the polygene's which could be improved upon by adopting selection without progeny testing.

High heritability coupled with high genetic advance was observed for plant height, spike length, number of spikelet's per spike, number of kernels per spike, kernel weight per spike, thousand kernel-weight and days to 50% flowering, these findings were supported by earlier reports of (14) and (20).

Genetic advance as percentage of mean was highest for grain yield per plant and proline concentration. Similar reports were reported (15). High heritability coupled with high genetic advance as percentage of mean was found for grain yield per plant followed by grain per ear (Fig. 1). These findings were in consonance with earlier reports made (10);(9).

Analysis of genetic diversity

The multivariate analysis using Mahalanobis D2 statistics is a valuable tool for obtaining quantitative estimates of divergence between biological populations. For an effective and informative breeding programme, information concerning the extent and nature of genetic diversity within a crop species is essential to researchers.

Assessment of genetic diversity was made based on the data recorded for thirteen traits on hundred and one barley genotype using Tocher's D2 analysis. Using this method a set of 101 barley genotypes were grouped into 12 clusters based on relative magnitude of the D2 value. Cluster I comprised of 47, Cluster II 29, Cluster VI 16 genotypes each. Cluster such as III, IV, V, VII, VIII, IX, X, XI and XII had one genotype each (Table 3).

Inter and Intra cluster D^2 values:

The intra cluster distance was found minimum for cluster I and maximum distance in cluster VI while it was zero for cluster III, IV, V, VII, VIII, IX, X, XI and XII as these clusters consisted of only single genotype (Table 4). The inter cluster distance was minimum between cluster V and cluster III indicating close relationship and similarity for most of the character of barley genotype falling in these cluster. The maximum inter-cluster distance was recorded between cluster VIII and cluster X followed by cluster V and IX and cluster IV and IX. Suggesting highest genetic divergence existing between the genotypes of these clusters.

Cluster means of various characters studied

The cluster mean values for different characters indicated differences between the clusters for all the traits studied (Table 5). The cluster V had high mean value for flag leaf length, spike length with awn, spike length without awn and grains per ear. Cluster IV had high mean value for plant height, SPAD value; cluster III had high mean value for stomatal conductivity.

Cluster VI had high mean for 1000 grain weight; cluster XI had maximum value for proline concentration. Cluster X had highest value for days to maturity and cluster XII had high value for days to 50% flowering it had lowest value for proline concentration. The result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character. Grain yield per plant, days to 50% flowering, stomatal conductivity, plant height and flag leaf length had highest relative contribution towards divergence followed by days to 50% flowering and stomatal conductivity.

Table.1 Analysis of variance (ANOVA) for thirteen quantitative traits in 101 barley genotypes

Source of variation	Df	Mean Sum of Squares												
		DF	**DM**	**FL**	**ET**	**SPAD**	**SC**	**PC**	**SL**	**SLW/O**	**PH**	**G/E**	**GW**	**GY**
Replication	2	2.08	7.76	0.61	1.57	14.56	75.185	2.40	1.58	0.55	25.78	0.18	0.36	1.70
Treatment	100	137.90**	67.64**	26.54**	6.61**	43.27**	23973.16**	62.60**	5.64**	3.52**	435.42**	398.70**	168.51**	50.55**
Error	200	2.08	3.17	0.73	1.11	10.15	474.33	2.49	2.08	0.28	5.78	9.67	8.01	0.91
Range Min.		62.33	97	6.39	5.96	37.40	313.97	8.61	17.44	5.03	63.11	9.00	25.53	3.53
Max.		97.00	119.33	25.59	13.78	54.33	662.93	27.61	23.16	10.26	117.56	61.00	58.70	24.41
Grand Mean		78.25	113.30	14.75	9.59	45.82	485.35	14.71	20.13	7.35	93.53	39.02	40.24	12.93
SE (±)		0.83	1.03	0.49	0.61	1.84	12.57	0.91	0.83	0.31	1.72	1.80	1.63	0.55

**Significant at p< 0.01.

DF=Days to 50% flowering, FL=flag leaf length, ET=effective tillers/plant, SPAD, SC=stomatal conductivity, PC=proline concentration, SL=splike length with awn, SLW/O=spike length without awn, PH=plant height, G/E=grain per ear, GW=1000 grain yield, DM= days to maturity, GY =grain yield

Table.2 Variability parameters for 13 quantitative characters in 101 barley genotypes. (Early sown condition)

Trait	DF	DM	FL	ET	SPAD	SC	PC	SL	SLW/O	PH	G/E	GW	GY
Range Min.	62.33	97	6.39	5.96	37.40	313.97	8.61	17.44	5.03	63.11	9.00	25.53	**3.53**
Max.	97.00	119.33	25.59	13.78	54.33	662.93	27.61	23.16	10.26	117.56	61.00	58.70	**24.41**
Grand Mean	78.25	113.30	14.75	9.59	45.82	485.35	14.71	20.13	7.35	93.53	39.02	40.24	**12.93**
SE (±)	0.83	1.03	0.49	0.61	1.84	12.57	0.91	0.83	0.31	1.72	1.80	1.63	**0.55**
PCV (%)	8.79	4.38	20.71	17.92	10.03	18.78	32.27	8.99	15.90	13.14	30.25	19.49	**32.31**
GCV (%)	8.60	4.09	19.88	14.12	7.23	18.24	30.43	5.41	14.15	12.75	29.18	18.17	**31.45**
h^2 % (broad sense)	96	87	92	62	52	94	89	36	79	94	93	87	**95**
GA as % of mean (5%)	17.32	7.87	39.31	22.93	10.73	36.48	59.11	6.70	25.94	25.48	57.99	34.92	**63.05**
GA as % of mean (1%)	22.20	10.08	50.38	29.38	13.75	46.75	75.75	8.59	33.24	32.65	74.32	44.75	**80.80**

DF=Days to 50% flowering, FL=flag leaf length, ET=effective tillers/plant, SPAD, SC=stomatal conductivity, PC=proline concentration, SL=splike length with awn, SLW/O=spike length without awn, PH=plant height/E=grain per ear, GW=1000 grain yielded= days to maturity, GY =grain yield

Table.3 Cluster pattern of 101 barley genotypes for thirteen quantitative character (Tocher's Method)

Clusters	Germplasm Lines/Genotypes	Number
I	CIHO-7603,K-603,AZAD,RD2552,AMBER,K-551,SONU,RATNA,IBSCGP-05-06, 25th IBON-39-1,HIMANI,ISBCB-02-10,WfBCB-91,NBPGR-07-08, 12thHBSN-7,INBON-05-72,HUB-113,ATHOULPA,29th IBON-6, JAGRATI, ALFA-93,25th IBON-03-11, 11th HBSN-91,25th IBON-45-1, 26th IBYT-16, VIJAY, 11th EMBSN-54, BH-976, HUB-113, GEETANJALI, 13th EMBSN-71, CHIO-6260, 13th EMBSN-46, BCB-W-03-91, CIHO-5924, 22nd IBYT-04-85, HANLEY, INBON-05-79, CIHO-5923, IBRWAGP-04-66, CIHO-3510,25th IBON-46, 24th IBON-1, 26th IBYT-11-1, ISBCB-02-13,22nd IBYT-99-11, WfBCB-88	47
II	BCB-73,22nd IBYT-04-86, 11th HBSN-1, YARDU, 11th EMBSN-26, 22nd IBYT-01-2-2-4, 11th EMBSN-34, KARAN-16, PL-751, 7th HMBSN-15-2, 11th HBSN-127,22nd IBYT-5-1, 22nd IBYT-7-2, 7th HMBSN-1-2-1-1,11th EMBSN-20, 14th HBSN-05-6,12th EMBSN-2, 22nd IBYT-99-14-1, 14th HBSN-05-8, 11th EMBSN-22, ISBCB-02-9, JYOTI, 25th IBON-54-1, 25th IBYT-10-3, 11th EMBSN-40, BCB-W-03-92,LAKHAN, IBGP-03-49, 22nd IBYT-9-2.	29
III	11th HBSN-175	1
IV	CANUT	1
V	MARRIA	1
VI	11th EMBSN-37-1, 25th IBON-11, INBON-07-08-71, HUB-180, 25th IBON-03-6, HARMAL,BEECHER, 24th IBON-40-1, 11th EMBSN-23, HORMAL, MOROC-9-75, PL-825, V-MORALES, INBON-05-50, RD-2715, CIHO-8355.	16
VII	IBGP-03-65	1
VIII	26th IBYT-49	1
IX	11th EMBSN-47-03	1
X	INBON-07-08-8	1
XI	11th EMBSN-21	1
XII	22nd IBYT-7	1

Table.4 Average Intra (bold) & Inter ClusterD^2 Distances of thirteen characters (Tocher's Method)

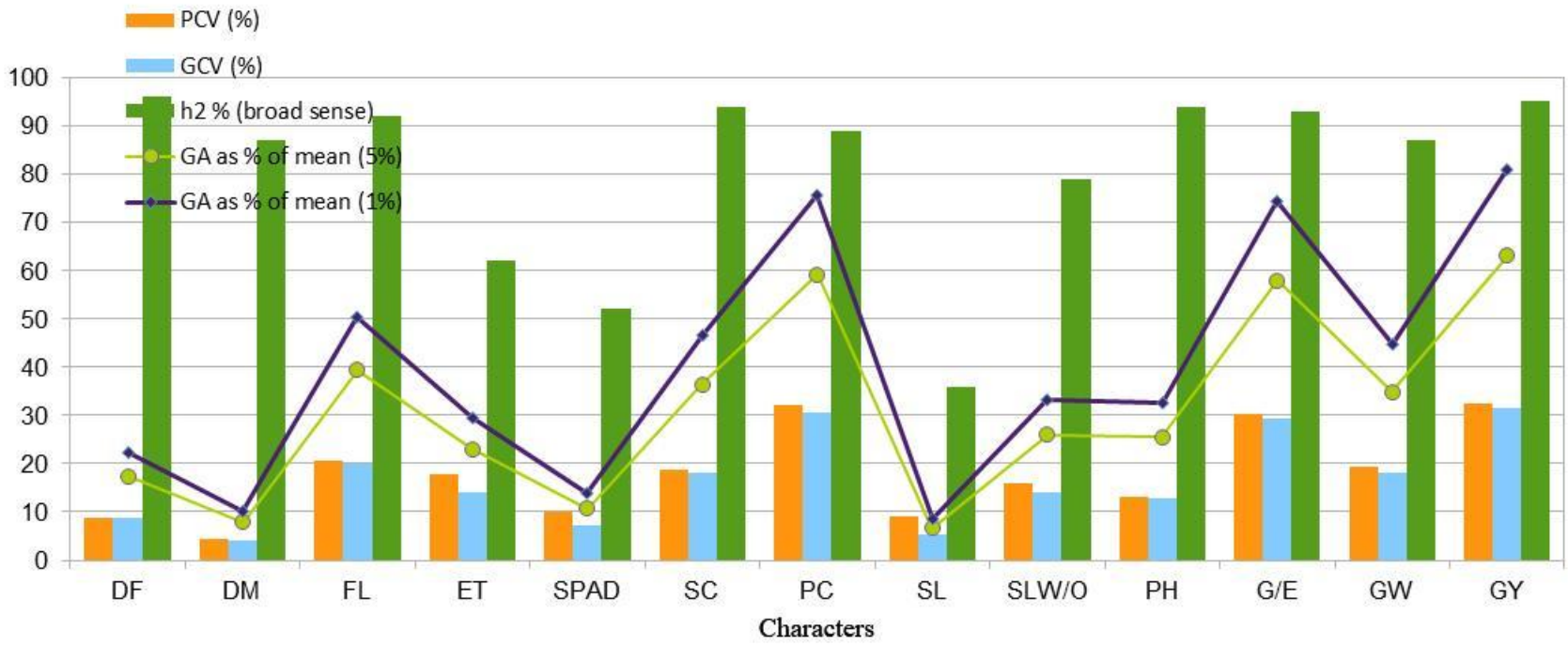
OP	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**45.477**	90.701	67.306	64.000	92.211	87.358	90.789	182.252	208.496	166.689	144.476	182.286
II		**70.133**	167.996	162.819	212.251	149.188	127.813	112.010	118.110	162.185	117.306	143.668
III			**0.000**	42.630	24.249	80.951	169.497	249.191	303.474	292.057	250.860	315.156
IV				**0.000**	55.083	95.300	86.060	301.883	367.418	202.165	193.257	234.050
V					**0.000**	105.183	173.372	318.586	377.955	310.225	316.305	333.909
VI						**72.242**	173.350	240.535	267.430	222.168	202.957	278.204
VII							**0.000**	290.522	334.476	117.031	138.902	101.603
VIII								**0.000**	28.500	389.275	178.244	301.653
IX									**0.000**	353.094	208.906	286.432
X										**0.000**	180.587	80.644
XI											**0.000**	247.391
XII												**0.000**

Table 5. Mean values of clusters for thirteen quantitative traits (Tocher's method)

Clusters	DF	DM	FL	ET	SPAD	SC	PC	SL	SLW/O	PH	G/E	GW	GY
I	78.624	115.262	14.832	9.633	45.924	484.035	13.649	20.316	7.605	98.734	42.645	40.290	14.219
II	77.770	110.034	14.110	9.124	44.759	440.594	15.444	19.416	6.730	82.445	30.540	36.048	9.897
III	75.333	116.000	15.220	11.067	46.367	611.533	13.610	19.867	8.177	99.110	58.000	42.333	20.827
IV	87.000	117.333	12.833	9.557	52.233	545.633	15.333	21.333	7.057	105.447	53.000	47.867	19.830
V	77.667	113.333	19.890	9.780	47.567	555.200	15.687	22.333	9.833	104.110	60.667	45.033	23.407
VI	76.083	114.083	15.887	10.322	46.877	578.238	15.968	20.909	7.720	100.481	45.313	49.081	14.664
VII	94.333	117.333	14.787	11.330	50.400	356.333	15.760	18.267	7.643	104.553	41.000	26.900	13.563
VIII	64.000	99.333	10.543	7.887	43.000	365.833	18.207	19.853	5.813	64.557	33.667	34.867	11.510
IX	62.333	98.000	13.603	6.333	40.733	415.667	11.390	20.277	5.623	65.890	18.333	31.933	7.993
X	96.000	118.667	18.500	10.557	49.033	549.180	14.463	19.870	8.213	93.667	20.000	45.410	3.533
XI	82.000	113.333	6.387	9.957	46.833	466.200	26.703	21.230	7.053	104.000	13.333	34.500	6.230
XII	97.000	116.000	17.900	9.387	45.400	375.833	9.573	17.767	6.830	65.777	28.000	31.533	9.537

DF=Days to 50% flowering, FL=flag leaf length, ET=effective tillers/plant, SPAD, SC=stomatal conductivity, PC=proline concentration, SL=splike length with awn, SLW/O=spike length without awn, PH=plant height/E=grain per ear, GW=1000 grain yielded= days to maturity, GY =grain yield

Fig 1. Genetic parameters of 13 quantitative characters in 101 barley genotypes



DF=Days to 50% flowering, FL=flag leaf length, ET=effective tillers/plant, SPAD, SC=stomatal conductivity, PC=proline concentration, SL=splike length with awn, SLW/O=spike length without awn, PH=plant height, G/E=grain per ear, GW=1000 grain yield, DM= days to maturity, GY =grain yield

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How to cite this article:

Banoth Vinesh, L.C. Prasadand Ravindra Prasad. 2018. Variability and Diversity Studies in Exotic and Indigenous Barley (*Hordeum vulgare* L.). *Int.J.Curr.Microbiol.App.Sci.* 7(07): 2007-2019. doi: https://doi.org/10.20546/ijcmas.2018.707.237