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RESEARCH ARTICLE

Assessment of Genetic Diversity in Cultivated and Wild Species Germplasm of Barley based on Morpho-agronomical and Root Architecture Traits

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Genetic variation in a selected set of 213 accessions of wild and cultivated barley germplasm was evaluated for 23 agro-morphological and root traits for two years. Wide range of phenotypic expression was observed for traits such as days to spike emergence (53.50-113.50), plant height (PH) (39.53-141.87 cm), spike length (1.83-13.57 cm), spikelet triplet groups (STG) 10-35.67, 100-grain weight (HGW) (0.12-6.56 g), total root length (RL) (6.96-97.25 cm) and root dry weight (RDW) (0.20-12.84 mg). Wild germplasm grouped under cluster I and cultivated under cluster II with different sub-groups for hull-less, two-rowed and six-rowed germplasm, irrespective of the geographical diversity. Principal component analysis indicated that first five components accounted for 77.23% of the total multivariate variation and it was mainly contributed by grain yield (GY), grain area (GA), STG, RL, total root surface area (RSA), total root volume (RV) and RDW. Correlation coefficients of root traits were positively significant with PH, SL, HGW, GY and grain size, indicating root architecture can play a pivotal role for future yield enhancement in rain-fed crop like barley. Donors for various traits were also identified such as short duration (IC445542, IC542197, IC470019), spike length (IC113052), dwarf plant habit (IC113045), root biomass (EC578716, EC492340).

Key Words: Barley germplasm, Genetic diversity, Root morphology, Wild species.

Introduction

Barley (*Hordeum vulgare* L; 2n=14) is one of the oldest cultivated cereal and has been grown in India since ancient times. It was domesticated in southwest Asia from two-rowed wild progenitor *H. vulgare* ssp. *spontaneum* and Himalayas is considered as it's center of diversification (Badr *et al.,* 2000). Presently, it is the fourth most important cereal crop worldwide after maize, rice and wheat in terms of production (FAO, 2018). Barley provides essential raw material for malting and brewing industries besides being an important feed and fodder crop. It also constitutes traditional staple food and beverage crop in many high altitude regions of world including India. Although, it is an ancient food and feed crop grown in India, its cultivation is presently facing stiff challenge from wheat crop, in terms of area and also fetches less remunerative prices, since green revolution. Further, about 44% area under barley cultivation in India is rain-fed. Therefore, owing to its cultivation as a rain-fed crop in marginal areas or on residual moisture, the increase in the yield of this crop has not been considerable (Ceccarelli *et al.*, 1999; Kumar *et al*., 2013). The rapid spread of improved varieties all over the world has led to narrow genetic base due to replacement of genetic resources and loss of specific alleles. New sources of genetic diversity through evaluation of germplasm collections must be incorporated into plant breeding to diversify the parental material for sustained and continued increase in yield and quality (Dawson *et al.*, 2015; Kaur *et al.*, 2018a, Kaur *et al.*, 2018b). Assessment of genetic diversity in germplasm collections helps breeders to select the accessions for crossing program and broadening the genetic base. Although genetic diversity assessment in barley germplasm assembly from different regions of world *viz*. North Africa (Ben Naceur *et al.,* 2012); Ethiopia (Abebe *et al.*, 2010); Spain (Lasa *et al.,* 2001); North America (Mikel and Kolb, 2008) and India (Manjunatha *et al*., 2007; Sarkar *et al*., 2010, 2014; Kaur *et al*., 2018) have been carried out using above ground agro-morphological traits, there is limited knowledge of genetic variation present in root system architecture and its association with above-ground plant morphology. The root architecture of a crop can influence the efficiency of

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water capture and hence yield and thus are particularly important to study in a rain-fed crop like barley. An advantage of having superior root traits such as root number, branching, root diameter, total root length/ surface area, root length density, and root volume under water scarce conditions have been proved recently in rice and wheat (Henry *et al.*, 2012; Christopher *et al.,* 2013). The present study was therefore, conducted to assess the nature and magnitude of variation in a diverse set of barley germplasm based on agro-morphological and root traits and to identify superior accessions which may have implications in future barley breeding program.

Materials and Methods

Plant Materials and Field Experiment

The plant material used in present study comprised of a diverse set of 213 germplasm accessions of spring barley, of which 126 accessions were indigenous collections (IC) and 87 were exotic collections (EC) including seven accessions of wild barley belonging to *Hordeum marinum*, *H. murinum* and *H. vulgare* ssp. *spontaneum*. The germplasm accessions under study were selected from field characterisation of a large collection of 5000 barley accessions conserved at National Gene Bank of ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India. The agro-morphological and phenological data pertaining to this huge set were subjected to diversity analysis using PowerCore (v.1.0) software to select the set of accessions used in present study. Field experiments were carried out during the *Rabi* season consecutively for two years (2016–2017 and 2017–2018) at Issapur experimental farm of ICAR-National Bureau of Plant Genetic Resources located between 28°57′ N, 76°84′ E, altitude 218 m above sea level in south-west of Delhi, India. Issapur has semi-arid sub-tropical climate with around 400 mm average annual precipitation, sandy loam to loamy sand with pH 8.

Phenotyping of Morpho-agronomic Traits and Root System Architecture

Observations were recorded on 23 traits of which field phenotyping was done on 17 agro-morphological traits and six root morphological traits were recorded at seedling stage in laboratory experiment. For field evaluation 11 traits *viz.* days to 75% spike emergence (DSE), days to 80% maturity (DPM), plant height (PH, cm), spike length (SL, cm), spikelet triplet groups (STG), number of grains per spike (NGS), 100-grain weight (HGW, g), and grain yield per meter row (GY, g), grain length (GL, mm), grain width (GW, mm), grain area (GA, mm^2) were recorded quantitatively, while six traits *viz.* growth habit (GH), spike row (SR), awn type (AT); spike density (SD); grain type (GT); grain pericarp color (GPC) were scored qualitatively. Data were recorded on five randomly chosen plants per plot as per minimal descriptors for barley (Mahajan *et al.,* 2000). The grain morphometry (GL, GW and GA) was done using scanner based Grain Analysis software (version 1.3).

For root phenotyping, the surface sterilized seeds were germinated on damp germination paper segment placed in aseptic petri dishes of 90 mm diameter and 15 mm height providing enough moisture for germination. After sprouting for 3 days, uniformly germinated seeds were kept in half strength Hoagland solution (Hoagland and Arnon, 1950) for a period of 10 days in a growth chamber, under a long-day photoperiod (16 h light/ 8 h dark) at 22°C and a relative humidity of 65-75% using germination paper roll method. On 10^{th} day, the roots were washed, cut from root-shoot junction, and were spread out in a root positioning tray (30 × 40 cm) with 1 cm of water. Root samples were then scanned in greyscale at 600 dpi using a desktop scanner (Epson flatbed scanner) and the images obtained in tiff format were analysed using WinRHIZO Pro software (v2009, Regent Instruments, Montreal, QC, Canada), which is an image analysis system specially designed for root measurements. The WinRhizo software provided phenotypic data on total root length (RL; cm), total root surface area (RSA; cm^2), root diameter (RD; µm), root volume (RV; mm^3) and seminal root number (SRN). In addition, root dry weight (RDW; mg) was recorded after drying the root samples in a hot air oven at 70°C for 72 hrs. Ten seedling of each accession were used for recording observations.

Statistical Analysis

The germplasm accessions were evaluated in Augmented Block Design (Federer, 1956) with five standard check varieties *viz.* BH902, RD2552, BH959, BHS352 and DWRB101 in 6 blocks. Each block had 36 accessions and five check varieties which were randomized within blocks. Each accession was sown in two rows of 2 m row length with 30 × 10 cm spacing. The quantitative traits were analysed for various statistical parameters *viz.* mean, range, variances, principal component analysis (PCA)

and Ward's agglomerative hierarchical clustering (Ward, 1963) using SAS (version 9.3, 2009). Before undertaking statistical analysis on the basis of adjusted pooled mean values, homogeneity of variances was tested as per Levene (1960). Phenotypic and genotypic coefficients of variation (PCV and GCV) for each trait were computed as PCV = $\sqrt{V_P}$/mean × 100, GCV = $\sqrt{V_G}$/mean × 100 as per Burton (1952) and the range was categorized as per Sivasubramanian and Madhavamenon (1978). Broad sense heritability was estimated as h^2 (bs) = V_G/V_P × 100 as per Lush (1940) and further classified into low, medium and high (Robinson, 1966). Expected genetic advance was calculated as EGA = k × V_G/V_P × $\sqrt{V_P}$ as per Johnson *et al.* (1955). Here the standard value of k is 2.06 assumed at 5% selection intensity; V_G is genotypic variance; and V_P is phenotypic variance. Genetic advance was expressed as % of mean as GA (%) = EGA/mean × 100. In addition, Pearson correlation coefficients were computed at $P_{0.05}$ for all morpho-agronomic variables including root traits.

Results and Discussion

Amongst qualitative traits, six-row type accessions represented 83% of the total collection under study. Approximately 90% of the accessions were awned. Single accession was recorded as awnless while nine accessions had very short awns and six were with hooded plant type. Spike density was recorded intermediate in 51% of the accessions followed by dense in 44% and lax in 5% accessions only. Seventy seven per cent accessions were hulled types while 23% were naked or hull-less. Grain pericarp color varied widely, *viz*., white, blue, black, red and purple in some accessions, however white/light yellow pericarp was dominant (90%). Wild barley *H. vulgare* ssp. s*pontaneum*, *H. marinum* and *H. murinum* were characterized by awned, two-row spike with brittle rachis form. The spikes were very long and awned in *H. vulgare* ssp. *spontaneum*, while other *Hordeum* sp. were having awnleted short spikes. Our results are in agreement with earlier diversity assessment studies in barley germplasm by Sarkar *et al.* (2010) and Manjunatha *et al.* (2007) who also reported almost similar frequency distribution for major qualitative traits such as row-type, grain type and grain color. Thus in the present study, the most common type of barley germplasm accessions were characterized by semi spreading nature of GH, six-row type spike with intermediate spike density, awned spikes and hulled grains.

Statistical analysis on qualitative traits showed wide range of phenotypic expression for important agro-morphological traits such as PH (39.53-141.87 cm), SL (1.83-13.37 cm), NGS (11.00-83.83), HSW (0.12-6.99 g) and GY (1.11-191.25 g) (Table 1). Mean DSE was 89, but it ranged from 53.50 for accession EC578711

Table 1. Statistical parameters of genetic variability in barley germplasm for various morpho-agronomic and root traits

Traits (n=213)	Range	Mean ± SE	Variance (P)	Variance (G)	PCV (%)	GCV (%)	Heritability	Genetic advance as % of mean
DSE	53.50-113.50	89.03±0.88	159.82	153.86	14.20	13.93	96.27	28.16
DPM	103.00-137.50	123.6±0.41	32.43	20.98	4.61	3.70	64.69	6.14
PH	39.53-141.87	95.94±0.95	172.69	141.70	13.70	12.41	82.05	23.15
SL	1.83-13.57	8.15±0.11	2.52	2.09	19.48	17.74	82.94	33.28
STG	10.00-35.67	23.09±0.33	21.22	15.36	19.95	16.97	72.38	29.75
NGS	11.00-83.83	46.12±1.15	280.72	251.06	36.33	34.36	89.43	66.93
GY	1.11-191.25	83.93±2.70	2226.00	1543.00	47.69	39.71	70.32	68.10
HGW	0.12-6.56	3.98±0.07	1.02	0.99	25.38	25.00	97.06	50.74
GL	6.29-12.43	9.98±0.10	2.04	1.74	14.31	13.22	85.29	25.15
GW	1.76-4.11	2.97±0.05	0.48	0.37	14.23	12.49	77.08	22.59
GA	9.73-34.62	23.80±0.52	56.24	41.88	22.19	19.15	74.47	34.04
RL	6.96-97.25	50.41±0.98	183.33	168.93	26.86	25.78	92.15	50.98
RSA	0.42-15.19	8.64±0.19	6.66	5.97	29.87	28.28	89.64	55.16
RV	2.60-287.60	119.08±3.10	1769.69	1232.03	35.82	29.89	70.62	51.38
RD	265.08-762.35	538.00±4.60	4028.57	2865.24	11.82	9.97	71.12	17.32
SRN	1.50-9.00	5.48±0.07	1.05	0.61	18.70	14.25	58.10	22.38
RDW	0.20-12.84	5.46±0.14	3.86	3.66	35.98	35.04	94.82	70.28

DSE, days to spike emergence; DPM, days to physiological maturity; PH, plant height (cm); SL, spike length (cm); STG, spikelet triplet groups; NGS, number of grains per spike; GY, grain yield per meter row (g); HGW, hundred grain weight (g); GL, grain length (mm); GW, grain width (mm); GA, grain area (mm^2); RL, total root length (cm); RSA, total root surface area (cm^2); RV, total root volume (mm^3); RD, root diameter (μm); SRN, seminal root number; RDW, root dry weight (mg).

to 113.50 for accession EC667569. The early maturing genotypes reached physiological maturity in 103 days and late maturing genotype took 138 days to mature. Similar range for DSE and DPM was also reported by Ebrahim *et al.* (2015) while evaluating genetic diversity in barley. HGW, an important yield character, varied extensively from 0.12 g in accession EC123148 (*H. marinum*) to 6.56 g in DWRB-91 with an average of 3.98 g. The two-rowed accessions showed higher HSW and grain size due to better grain filling than six-row types as also reported by Sarkar *et al.* (2010). Spike emergence and maturity were late in wild accessions. Smallest spike (1.77 cm) and lowest HSW (0.10 g) was recorded in wild EC578252. For root morphological traits, mean RL was 50.41 cm, while the range was 6.95 cm in *H. marinum* accessions to 97.25 cm in EC578523. Accessions EC578821, IC533320 had maximum RSA. Mean SRN was 5.48 while mean RDW was 5.46 g. The wide range of variation observed in this study also corroborated earlier diversity assessment studies in barley by Sarkar *et al.*(2010) for DSE, PH and HSW, Ebrahim *et al.* (2015) for DPM, Sarkar *et al.* (2014) for HSW, SL, NGS and Sun *et al.* (1999) for PH.

The extent of the genetic variability can be better assessed by estimation of GCV in relation to PCV. Small difference between the two indicates underlying genetic factors while larger difference indicates influence of the environment. PCV and GCV were high for GY, NGS, HGW, RL, RSA, RV and RDW and low for rest of the traits. In studied barley germplasm, DSE, SL, NGS, GY, GL, RL, RSA and RDW showed high heritability in broad sense coupled with high genetic advance and are predominantly under additive type of gene action. Accessions IC113052, IC118656, EC578517, IC82573, EC339572, EC578523, EC578821, EC578716 and IC533320 showed high value of these traits and can be exploited further for grain yield through simple phenotypic performance based selection methods using these traits. These traits showed >80% heritability and may be useful for exploiting additive gene action to produce widely adopted genotypes in barley breeding. On the other hand, parameters such as DPM, STG, SRN, GA, SRD, which have low variance, heritability and genetic advance showed the presence of non-additive gene interaction and needed to be improved. Accessions EC328972, IC533203, EC578370, IC445342, IC334463 and EC578653 showed low heritability and genetic advance for above-mentioned traits.

To understand the nature of correlations between traits, data were analysed to determine Pearson simple correlation coefficients among these traits (Table 2). Correlation coefficient between PH, grain yield and yield attributes such as SL, STG, HGW and NGS were significant and positive. Plant height is an important trait directly linked with productive potential of the plant *i.e.* yield. In addition, it is desirable trait for using barley as

Table 2. Correlation coefficients of different quantitative variables for barley germplasm accessions

Traits	GA	GW	DPM	DSE	GL	PH	SL	STG	GY	HGW	NGS	SRN	RSA	RV	RL	RDW
GW	0.88*															
DPM	-0.04	-0.18*														
DSE	-0.21*	-0.38*	0.61*													
GL	0.83*	0.50*	0.08	-0.02												
PH	0.23*	0.33*	-0.01	-0.03	0.05											
SL	0.45*	0.48*	-0.08	-0.10	0.27*	0.42*										
STG	0.24*	0.29*	0.10	0.18*	0.60	0.40*	0.57*									
GY	0.40*	0.44*	-0.12	-0.22*	0.30*	0.28*	0.18*	0.14*								
HGW	0.66*	0.76*	-0.18*	-0.36*	0.33*	0.33*	0.47*	0.24*	0.45*							
NGS	0.11	0.12	-0.05	-0.02	0.10	0.39*	0.12	0.24*	0.21*	-0.10						
SRN	0.47*	0.59*	-0.28*	-0.35*	0.18*	0.40*	0.53*	0.35*	0.37*	0.57*	0.20*					
RSA	0.58*	0.59*	-0.07	-0.23*	0.40*	0.44*	0.38*	0.31*	0.51*	0.59*	0.10	0.56*				
RV	0.49*	0.48*	-0.03	-0.18*	0.33*	0.40*	0.29*	0.24*	0.41*	0.48*	0.40	0.42*	0.93*			
RL	0.56*	0.57*	-0.06	-0.23*	0.38*	0.47*	0.41*	0.36*	0.48*	0.58*	0.15*	0.57*	0.92*	0.75*		
RDW	0.54*	0.57*	-0.13	-0.27*	0.35*	0.33*	0.35*	0.27*	0.46*	0.55*	0.07	0.56*	0.84*	0.80*	0.76*	
RD	0.37*	0.41*	-0.10	0.17*	0.16*	0.27*	0.24*	0.12	0.19*	0.36*	0.08	0.33*	0.57*	0.75*	0.29*	0.56*

*Correlation is significant at $P_{0.05}$

GA, grain area; GW, grain width; DPM, days to physiological maturity; DSE, days to spike emergence; GL, grain length; PH, plant height; SL, spike length; STG, spikelet triplet groups; GY, grain yield per meter row; HGW, hundred grain weight; NGS, number of grains per spike; SRN, seminal root number; RSA, total root surface area; RV, total root volume; RL, total root length; RDW, root dry weight; RD, root diameter.

fodder crop. Ruzdik *et al.* (2015) also observed significant and positive correlations between grain yield and plant height in barley. DSE was negatively correlated with GA, HGW and GY, which means early spike emergence may lead to more filled bold grains and thus yield in barley. Al-Tabbal and Al-Fraihat (2012), and Sarkar *et al.* (2014) also reported negative correlation of HGW, GY with DSE. DSE and DPM were positively correlated ($r=0.615$, $p_{0.05}$) with each other suggesting accessions showing early spike emergence were also early maturing. All the root traits *viz.* SRN, RSA, RV, RL, RDW and RD were correlated with each other and with GA, GW, GL, PH, SL, GY, HGW. Selection for one trait will cause change in its mean through additive gene effect and simultaneous indirect effect in mean of correlated trait. Therefore, in the present study, positive correlation between root traits and yield components suggests root structure architecture should be paid attention for further yield enhancement in a rain-fed crop like barley.

The clustering pattern based on multivariate analysis of quantitative variables revealed that all the accessions grouped into two main clusters- C1 and CII, constituted by wild and cultivated germplasm, respectively (Fig. 1). Cluster I grouped wild accessions of *H. marinum* and *H. murinum* except *H. vulgare ssp. spontaneum,* which were characterized by late spike emergence and maturity, small PH, SL and small sized grains. *H. vulgare* ssp. s*pontaneum* along with some other two-rowed accessions formed a sub-group under cluster II owing to its more plant height and spike length. It forms the primary gene pool and is fully inter-fertile with cultivated barley and has been known to harbor beneficial sources of genes utilized in breeding for important agricultural traits (Von Korff *et al.,* 2004, Vanhala and Stam, 2006). However, the extent of utilization of other *Hordeum* sp. such as *H. marinum* and *H. murinum* is low because they belong to tertiary gene pool. To depict the genetic relationship among cultivated germplasm, a dendrogram was generated by Ward's agglomerative hierarchical clustering method based on squared Euclidean distances which revealed that CII could be further divided in four sub-groups with 93 accessions in cluster II-A, followed by 21 accessions in cluster II-B, 57 accessions in cluster II-C and 39 accessions in cluster II-D (Table 3). The mean values of accessions grouped under each sub-cluster showed that cluster II-B grouped majority of the two-rowed barley accessions which showed more SL, STG, GY, HSW, RL, RSA, RV, RD, SRN and RDW and were bold seeded. Most of the hull-less barley accessions grouped under cluster II-C which showed late DSE, DPM, lesser yield and small grain size. Cluster II-A and II-D were constituted by hulled six-row barley accessions with a sub-group of two-rowed accessions under both. Manjunatha *et al.* (2007) had also reported separate clustering for hulled barley from hull-less types. Thus, resulting four sub-clusters distinguished hull-less from hulled and two-rowed from six-rowed barley accessions, but failed to separate from different geographical areas in the region. Our results are in congruence with Shekhawat *et al.* (2001) and Mittal *et al.* (2010) who carried out genetic divergence

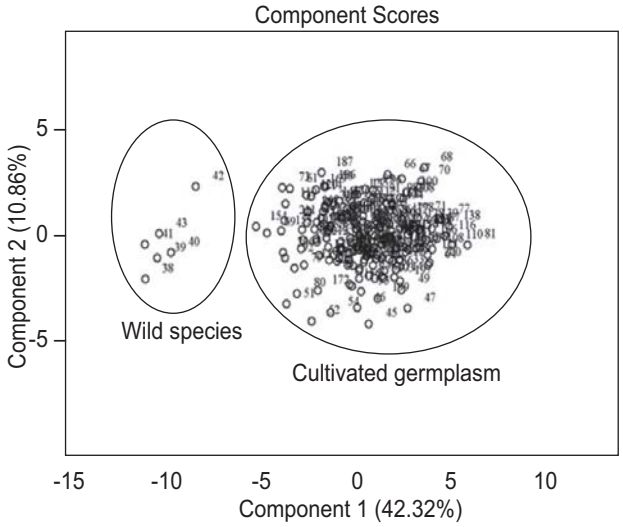

Fig. 1. Principal component biplot showing distribution of 213 barley accessions

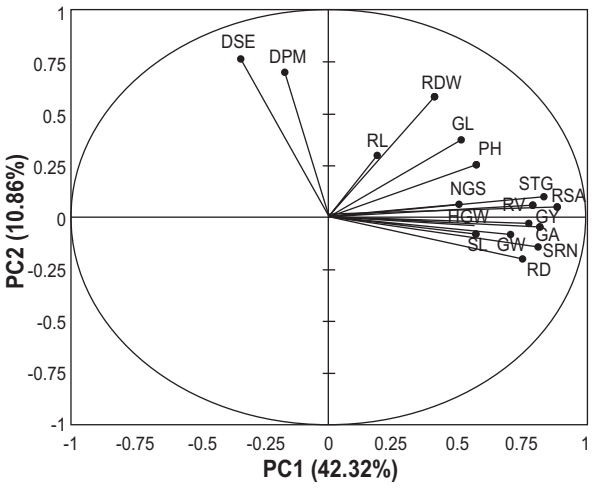

Fig. 2 Scatter plot of different morpho-agronomic and root architecture variables loaded on PC1 and PC2

Table 3. Means of quantitative variables in different clusters of barley germplasm accessions

Cluster variables	C I	C II-A	C II-B	C II-C	C II-D
DSE	111.66	89.63	86.85	93.10	78.31
DPM	129.6	124.99	123.32	125.46	117.71
PH	48.78	100.43	96.13	97.52	90.35
SL	3.11	8.32	9.66	7.78	8.27
STG	13.46	23.19	27.62	23.19	21.80
NGS	16.34	52.17	29.37	45.60	45.85
GY	2.22	97.99	116.68	52.55	82.57
HGW	0.21	4.18	5.00	3.48	4.26
GL	9.50	10.77	10.77	8.45	10.16
GW	2.10	5.11	5.57	4.45	5.05
GA	13.31	37.50	41.25	26.96	35.45
RL	8.72	55.97	65.64	42.98	45.71
RSA	1.18	9.94	11.86	6.83	7.45
RV	7.01	144.21	176.44	88.17	88.59
RD	368.55	565.85	579.07	512.68	510.88
SRN	1.75	5.46	6.49	5.20	5.86
RDW	0.86	6.23	8.11	4.12	4.78
No. of accessions	6	93	21	57	39

DSE, days to spike emergence; DPM, days to physiological maturity; PH, plant height (cm); SL, spike length (cm); STG, spikelet triplet groups; NGS, number of grains per spike; GY, grain yield per meter row (g); HGW, hundred grain weight (g); GL, grain length (mm); GW, grain width (mm); GA, grain area (mm^2); RL, total root length (cm); RSA, total root surface area (cm^2); RV, total root volume (mm^3); RD, root diameter (μm); SRN, seminal root number; RDW, root dry weight (mg).

studies in barley and reported that geographic diversity not necessarily reflect genetic diversity. However, our clustering pattern does not corroborate the studies by Shafaeddin (2002) and Abebe *et al.* (2010) who stated fair relationship between the genetic and geographical classifications among origins of samples, which is not found in our study. Germplasm lines from same geographical regions may fall apart in clusters which may happen due to genetic similarity, selection pressure and environmental influence or due to free exchange of material across different locations. Germplasm belonging to the same cluster are considered similar with respect to aggregate effect of studied traits. Hence, divergent parents can be selected from these clusters as genetic distance among them is due to different genetic constitutions.

The PCA based on correlation was used to identify determinants of quantitative trait variability. First five PCs having Eigen value >1.0 contributed 77.23% of the total multivariate variation present in the germplasm, 42.32% of which was accounted in the first axis, and 10.86% in the second (Fig. 2). According to Johnson and Wichern (2002), based on Eigen values and vectors, it is possible to identify traits which are mainly responsible to explain the variation. Therefore, a genotype-trait biplot was constructed based on first two principal components revealed that GA, GY, STG, SRN, RSA and RV contributed more positively to PC1, while DSE, DPM and RDW contributed to PC2 which suggests that germplasm accessions could be distinguished by characters associated with PCs having more relative contribution in total variation. PC3, PC4 and PC5 explained 9.11, 8.53 and 6.41% variation, respectively, loaded partially on PH, NGS, GL, GA, SL and HGW. Our results are in congruence with Ebrahim *et al.* (2015) and Manjunatha *et al.* (2007) who reported high contribution of above-mentioned agro-morphological traits while studying diversity assessment in barley.

The superior accessions identified in the first year were planted at two locations during second year evaluation for morpho-agronomic traits. Based on the pooled performance for location and year combination, few trait specific promising germplasm accessions were identified such as hulled barley IC445542 and EC578370 showed early maturity in 103 and 105 days, respectively, compared to checks BH902 (130 days) and BH959 (128 days). Hull-less IC542197 and IC470019 showed short duration/earliness in 107 days compared to check BHS352 (125 days). Early types are essential in most barley producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Early maturity is the main breeding target in India owing

to rain-fed sowing of barley under low input conditions in chief producer states of UP, Rajasthan, Bihar, hilly areas of Uttrakhand and JK and under limited moisture in Punjab and Haryana. Average plant height was 95.94 cm while one accession IC113045 showed dwarf plant habit with 42.51 cm height compared to variety BH959 (91.32 cm) used as check, while EC578707 was recorded to be the tallest attaining the height upto 142 cm. In addition, these accessions also showed early maturity. HGW was more than 5.5 g in accessions EC492340 and IC542206 compared to DWRB101 (4.84 g) used as check for two-row types. For SL, two-rowed accession IC113052 (13.57 cm) and six-rowed IC118656 (12.7 cm) were found promising compared to check DWRB101 (8.15 cm) and BH959 (8.93 cm), respectively. Seed morphometry revealed that accession IC578281 and IC533165 had maximum GL (12.43 mm, 11.28 mm), GW (3.93 mm, 4.11 mm) and GA (34.62 mm^2, 32.05 mm^2), and thus was bold seeded compared to best check BH959. For RDW, accessions EC578716 (12.84 mg) and EC492340 (11.01 mg) were found superior in comparison to best check BH902 (5.8 mg).

In conclusion, present study identified STG, GA, GY, RSA, SRN and RDW as the major traits contributing towards phenotypic diversity based on comprehensive information derived from PCA and cluster analysis. This indicates that yield traits and root morphology have contributed highest genetic variability in barley germplasm under study. The positive significant inter-relationship between the root traits and yield and its attributes suggested that improvement in root architecture could play a pivotal role for future yield enhancement in barley, predominantly sown on residual moisture in India. Moreover, the phenotyping of root traits reported in this study is high throughput, rapid, easy and cost effective technique to screen large number of germplasm accessions for better root structure architecture, which can be further evaluated in field conditions. The trait specific promising germplasm accessions such as EC578711 (early heading), IC445542, IC542197 (short duration), IC533320 (root length) and EC578716, EC492340 (root biomass) identified are likely to be of specific advantage in dry conditions as they represent the best compromise to escape water scarcity, which is main production constraint for rain-fed barley cultivation in India.

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