

RELATIVE PERFORMANCE AND GENETIC ANALYSIS OF DUAL PURPOSE BARLEY GENOTYPES FOR GREEN FODDER AND GRAIN YIELD

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SUMMARY

The current study aimed at genetic assessment of 14 dual purpose barley genotypes for their relative performance and identification of component traits based on eleven agro-morphological characters. The experiment was conducted at CCS Haryana Agricultural University, Hisar during 2023-24 crop season under timely sown irrigated conditions. The experiment was laid in Randomized Block Design (RBD) with four replications where each genotype occupied a plot size of 6.9 m². The results indicated highly significant differences among the genotypes with wide range for all the traits that offered score for selection of desirable types. The number of tillers per meter row, number of grains per spike, biological yield and grain yield indicated high estimates of GCV and PCV, whereas, plant height, spike length and 1000-grain weight exhibited medium; and days to heading and maturity were recorded with lower estimates of GCV and PCV. The study also revealed high heritability coupled with genetic advance for grain yield, number of tillers per meter row, number of grains per spike, biological yield, green fodder yield, 1000-grain weight and spike length. The association analysis showed significant positive correlation of grain yield with number of tillers per meter row, plant height, 1000-grain weight, biological yield, harvest index and green fodder yield. The findings of path coefficient analysis depicted positive direct effect of biological yield, harvest index, number of tillers per meter row, spike length and 1000-grain weight towards grain yield. PCA study found first four components with eigen value more than one that explained about 86.24% of the total variation. The genotypes, RD 2552, JHSBE 16, JHSBF 28 and JHSBF 21 displayed their position in first quadrant were found superior with respect to PC 1 and PC 2. Consequently, the present findings could be considered while setting the selection criterion for dual purpose barley improvement program.

Key words: Barley, biplot, dual purpose, genetic parameters, PCA

Barley is primarily a cereal grain crop, has the potential to be cultivated under low inputs in marginal environments unsuitable for other cereal crops. Its major uses are livestock or poultry feeding and raw product for malt and starch production (Moustafa *et al.*, 2021). Being a valuable source of beta-glucan and its other substantial health benefits, this crop may be considered as a food crop for human consumption either as its direct use or through blends with other cereals like wheat (Kumar *et al.*, 2014). Because of low input requirements, a good substitute for fodder in lean period, high health benefits for all animal system and crop of commerce and industry; barley is a boon for farmer and farming system in resource deficit areas of the country. In India, barley occupied an area and production of 0.62 million hectare and 1.69 million tonnes grain, respectively during 2022-23 with productivity of 27.33 q/ha (ICAR-IIWBR, 2023).

The availability of green fodder is the major limiting factor of livestock production worldwide during the late winter and early spring and as a result, livestock mainly depends on straw and crop residues which are low in nutritional quality and crude protein (Neelam *et al.*, 2024). Barley straw is an important feed source for cattle and small ruminants during the dry season. In the drier parts of northern plains (Rajasthan, Southern Haryana, South-West Punjab and Western U.P.) as a result of drought and/or limiting moisture, shortage of green fodder may become acute during scarcity period (November to February). Consequently, barley can be utilized as an alternative source of green fodder particularly in the arid and semi-arid region (Yadav *et al.*, 2023).

The genetic variability assessment is quite important for initiation of any crop improvement programme. Grain yield is a complex trait that is highly

reliant on the interrelationships between the various yield components and is also affected by various environmental factors. In order to choose appropriate breeding approach for different environments, it is critical to understand component traits linked to grain yield, as in all of the breeding activities, increasing grain production is a major concern. The study of character association facilitates the breeders in deciding selection criterion for yield enhancement (Hebbache *et al.*, 2023). The average degree of the link between yield and its attributing characters may be determined using correlation analysis, to be utilized to evaluate the relative worth of each contributing character to improve plant yield. Similarly, the effect of component traits on yield can be split into direct and indirect effects using path coefficient analysis (Vasko *et al.*, 2023). This information can be used to incorporate useful traits in optimal combinations for maximizing the yield potential. PCA explains as much of the genetic variability of the original data set as possible by few variables identified out of variables under study that be exploited for key component selection. Furthermore, biplot approach graphically displays the 2-way data and allows visualization of the interrelations among genotypes and variables.

The information on agronomic management of dual purpose barley is cited by many researchers however, studies on genotypic performance of barley for green fodder are scarce. Considering the paucity of research findings on the above, the present work was planned to evaluate the fourteen dual purpose barley genotypes for their performance pertaining to green fodder and grain yield alongwith to magnify the genetic variability intended to breed elite dual purpose barley genotypes for mitigation of fodder scarcity.

MATERIALS AND METHODS

The research work was carried out at the Research Farm of the Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during the crop season 2023-24. The experimental material consisted of fourteen genotypes of barley out of that thirteen represented 6-row and one genotype belonged to 2-row background. The check varieties included RD 2552 and RD 2715 used to compare the performance of genotypes. The experiment was laid in Randomized Block Design (RBD) with four replications. Each genotype was raised in six rows of 5.0 m length spaced at 23 cm apart. The experimental material was sown on 11th November, 2023 under timely sown irrigated

conditions. The recommended package of practices was applied to raise the crop.

The observations were recorded for eleven agro-morphological traits *viz.*, days to heading, days to maturity, number of effective tillers per meter row, plant height (cm), spike length (cm), number of grains per spike, 1000-grain weight (g), biological yield per plot (kg), grain yield per plot (kg), harvest index (%) and green fodder yield per plot (kg). The green fodder yield was taken at 55 days after sowing the experiment and crop was allowed to regenerate after fertigation.

Genotypic and phenotypic coefficients of variation were calculated by the formula given by Burton (1952). Heritability in broad sense was calculated as per formula suggested by Hanson *et al.* (1956). Estimates of appropriate variance components were substituted for the parameters to predict expected genetic gain suggested by Lush (1949) and Johanson *et al.* (1955). The genotypic and phenotypic coefficients of variation as well as genetic advance were classified as low (<10%), moderate (10-20%) and high (>20%) while, heritability was categorized as low (<40%), moderate (40-60%) and high (>60%). The estimates of phenotypic correlation coefficients were calculated as suggested by Al-Jibouri *et al.* (1958). These estimates were used to work out path coefficient analysis as elaborated by Dewey and Lu, 1959). The recorded observations were subjected to statistical analysis including Principal Component Analysis (PCA) using R software version 4.4.1.

RESULTS AND DISCUSSION

The analysis of variance and estimates of various genetic parameters, pertaining to various agro-morphological traits are presented in Table 1. The results indicated highly significant differences among the genotypes unveiling their further investigation for genetic analysis. The estimates of genetic parameters also showed a wide range for all the traits that offered score for selection of desirable types. An appropriate breeding program can be employment to improve the trait depending on its genetic make-up and the degree of environmental effect on its expression.

The genotypic coefficient of variation (GCV) was found to be lower than the corresponding phenotypic coefficient of variation (PCV) for all the characters studied, indicating the impact of environment on the expression of these traits. The estimates of GCV and PCV varied from 1.58 to 25.97 % and 2.16 to 27.85 %, respectively. The perusal of data revealed high estimates of GCV and PCV for

TABLE 1
Analysis of variance and genetic parameters of different variables in barley

Variables	Treatment MSS	Significance level	Mean \pm SE (m)	Range		σ^2g	σ^2p	GCV	PCV	h ² (bs) (%)	GA (% mean)
				Min.	Max.						
DH	47.95	**	100.39 \pm 0.78	92	110	11.38	13.82	3.36	3.70	82	6.28
DM	24.34	**	141.38 \pm 1.04	135	147	5.00	9.33	1.58	2.16	54	2.39
TM	1935.18	**	86.84 \pm 3.76	50	133	469.69	526.12	24.96	26.41	89	48.58
PH	389.12	**	93.20 \pm 2.71	75	122	89.96	119.23	10.18	11.72	75	18.21
SL	4.89	**	8.26 \pm 0.19	5.8	10.5	1.19	1.33	13.18	13.94	89	25.66
GS	808.15	**	66 \pm 1.61	28	90	199.45	209.81	21.40	21.95	95	42.98
TGW	93.49	**	31.7 \pm 0.94	23.5	44.5	22.49	26.03	14.96	16.09	86	28.64
BY	7.42	**	6.46 \pm 0.32	2.39	9.73	1.75	2.16	20.51	22.75	81	38.10
GY	1.06	**	1.95 \pm 0.10	0.73	3.03	0.26	0.29	25.97	27.85	87	49.89
HI	40.18	**	30.10 \pm 1.48	22.67	39.60	7.87	16.57	9.32	13.53	47	13.23
GFY	10.45	**	8.54 \pm 0.54	5.1	13.0	2.32	3.48	17.85	21.86	67	30.02

DH: Days to heading; DM: Days to maturity; TM: Number of effective tillers per meter row; PH: Plant height; SL: Spike length; GS: Number of grains per spike; TGW: 1000- grain weight; BY: Biological yield per plot; HI: Harvest index; GY: Grain yield per plot; GFY: Green Fodder Yield; ** Significant at 0.01 level

number of tillers per meter row, number of grains per spike, biological yield and grain yield, whereas, plant height, spike length and 1000-grain weight exhibited medium estimates of GCV and PCV. Days to heading and maturity were recorded with lower estimates of GCV and PCV. These findings are in congruence with earlier reports by Matin *et al.* (2019) for number of tillers per meter and number of grains per spike; Shiferaw *et al.* (2020) for biological yield and grain yield; Kumar and Shekhawat (2013a) for green fodder yield; Kumar and Sehrawat (2021) for plant height and spike length; Shiferaw *et al.* (2020) for 1000-grain weight and harvest index (PCV); Kumar *et al.* (2018) for days to heading and maturity; and Kumar and Sehrawat (2021) for harvest index (GCV). The heritability is quite important for plant breeder to predict the response to selection and to assess the usefulness and precision of results from cultivar testing and screening trials. Heritability in broad sense ranged from 47 to 95 % and was found medium for days to maturity and harvest index, however all other traits possessed high heritability. Similar results have also been delineated by Kumar *et al.* (2018) and Shiferaw *et al.* (2020) for days to heading, number of effective tillers per meter, plant height, number of grains per spike, 1000-grain weight, grain yield, biological yield and spike length; Kumar and Shekhawat (2013a) for green fodder yield; and Tahar *et al.* (2015) for days to maturity and harvest index.

The highest and lowest estimates of genetic advance as percent of mean were 49.89 and 2.39 %, respectively. These estimates were found low for days

to heading and maturity, medium for plant height and harvest index; and recorded high for rest of the traits. High heritability coupled with genetic advance was observed for grain yield, number of tillers per meter row, number of grains per spike, biological yield, green fodder yield, 1000-grain weight and spike length. These findings were further validated by the results of Shiferaw *et al.* (2020) for spike length, number of grains per spike, 1000-grain weight, biological yield and grain yield; and Kumar *et al.* (2018) for number of effective tillers.

The mean performance of all the genotypes for 11 characters is depicted in Table 2. The genotype DWRB 2314 was recorded with minimum number of days to heading and was also exhibited early maturity compared to other studied genotypes. The genotype JHSBD 22 followed by JHSBF 28 was found with maximum number of effective tillers per meter row along with highest grain yield. In addition, the genotype JHSBF 28 also showed superiority over others for 1000-grain weight and biological yield. The genotype namely DWRB 2316 was characterized by longest spike along with by highest number of grains per spike. The check variety *i.e.* RD 2715 followed by DWRB 2318, JHSBB 19 and JHSBD 22 were found promising for plant height, these genotypes could be incorporated in breeding barley for lodging resistance. The green fodder yield recorded with a cut at 55 days after sowing was observed highest for JHSBD 22 and this genotype was also found elite for harvest index. The genotypes *viz.*, JHSBD 22, JHSBF 28, JHSBE 16 and JHSBF 21 were identified promising over the best performing

TABLE 2
Relative performance of barley genotypes for different traits

Genotypes	RT	DH	DM	TM	PH	SL	GS	TGW	BY	GY	HI	GFY
DWRB 2314	6	95	137	68	87	8.2	74	24.3	5.43	1.53	28.48	6.73
JHSBB 19	6	99	142	76	86	7.0	69	24.9	7.57	1.97	26.01	10.55
RD 2552 (c)	6	104	143	104	94	7.2	58	32.7	6.22	2.07	33.43	9.65
JHSBE 16	6	100	139	104	99	8.8	74	34.2	7.57	2.31	30.57	9.05
JHSBD 22	6	98	140	126	86	6.2	51	32.8	8.05	2.90	36.01	11.15
DWRB 2316	6	101	144	84	91	10.0	88	31.4	6.17	1.58	25.67	5.95
JHSBD 11	6	101	139	56	92	8.8	63	32.0	5.52	1.68	30.40	8.85
RD 2715 (c)	6	97	141	58	80	9.8	73	30.7	3.07	0.93	30.38	8.90
DWRB 2317	2	100	143	66	94	8.2	30	36.8	5.75	1.65	28.77	5.98
DWRB 2318	6	98	138	96	85	8.0	69	35.5	6.72	2.23	33.21	10.20
DWRB 2313	6	100	143	68	87	9.2	74	27.1	6.09	1.71	28.26	7.65
JHSBF 28	6	99	142	112	110	7.2	62	41.9	8.16	2.79	34.38	8.80
JHSBF 21	6	105	144	94	114	9.0	81	33.0	7.85	2.09	26.81	8.63
DWRB 2315	6	108	145	106	102	8.2	61	26.7	6.26	1.80	28.97	7.45

RT: Row Type.

check variety RD 2552 for grain and biological yield, however, JHSBD 22, JHSBB 19 and DWRB 2318 exhibited superiority for green fodder yield (Fig. 1).

The estimates of correlation coefficients for the variables are depicted in Table 3. Both positive and negative trends were observed for correlation between the variables studied. The grain yield exhibited significant positive association with number of tillers per meter row, plant height, 1000-grain weight, biological yield, harvest index and green fodder yield. Similar observations were also substantiated for grain yield with number of tillers per meter row, plant height, 1000-grain weight (Patial *et al.*, 2023); biological yield, harvest index (Aklilu *et al.*, 2020); and green fodder yield (Sarkar *et al.*, 2014). The significant negative association of grain yield with spike length was also observed, can be compared and interpreted in context to the study of Devi *et al.* (2019). The positive and significant correlation were also found for days to heading with days to maturity; number of tillers per meter row with days to heading, plant height, 1000-

grain weight, biological yield, harvest index and green fodder yield; plant height with days to heading, maturity, 1000-grain weight and biological yield; spike length with number of grains per spike; 1000-grain weight with biological yield and harvest index; biological yield with green fodder yield; and harvest index with green fodder yield. Some findings were in consonance with these results *i.e.* significant positive association of days to heading with days to maturity and number of effective tillers per meter (Kumar *et al.*, 2013); days to heading and maturity with plant height (Ahmadi *et al.*, 2016); number of effective tillers per meter row with plant height, 1000-grain weight, biological yield (Hailu *et al.*, 2016), harvest index (Kumar and Sehrawat, 2021) and green fodder yield (Kumar and Shekhawat, 2013b); plant height with 1000-grain weight, biological yield (Aklilu *et al.*, 2020), green fodder yield (Sarkar *et al.*, 2014); spike length with number of grains per spike (Patial *et al.*, 2023); and 1000-grain weight with biological yield, harvest index (Hailu *et al.*, 2016).

Similarly, significant negative correlation was found for days to maturity with harvest index; number of tillers per meter row with spike length; spike length with biological yield, harvest index and green fodder yield; number of grains per spike with 1000-grain weight and harvest index. These results were also corroborated for days to maturity with harvest index (Shiferaw *et al.*, 2020); spike length with number of tillers per meter row, harvest index (Devi *et al.*, 2019; Kumar and Sehrawat, 2021); and number of grains per spike with 1000-grain weight, harvest index (Kumar *et al.*, 2013).

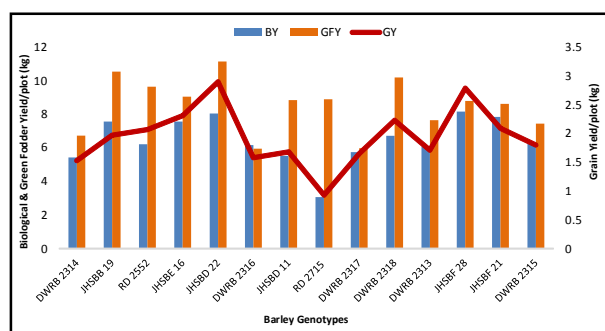


Fig. 1. Relative performance of barley genotypes for biological yield, green fodder and grain yield.

TABLE 3
Estimates of correlation coefficients among 11 variables in barley

Variables	DH	DM	T M	PH	SL	GS	TGW	BY	HI	GFY
DH	1									
DM	0.623**	1								
T M	0.264*	0.067	1							
PH	0.512**	0.328 *	0.357**	1						
SL	0.069	0.173	-0.545**	-0.059	1					
GS	-0.029	0.019	-0.093	0.028	0.531**	1				
TGW	0.009	-0.012	0.336*	0.412**	-0.132	-0.315*	1			
BY	0.217	0.090	0.664**	0.471**	-0.528**	-0.010	0.291*	1		
HI	-0.179	-0.322 *	0.436**	-0.054	-0.447**	-0.327*	0.344**	0.048	1	
GFY	-0.073	-0.227	0.371**	-0.156	-0.479**	-0.058	0.108	0.271*	0.442**	1
GY	0.071	-0.100	0.785**	0.352 **	-0.671**	-0.194	0.435**	0.853**	0.555**	0.449**

*, ** Significant at 0.05 and 0.01 level, respectively.

In the present study, phenotypic correlation coefficients were used for path coefficient analysis. Path analysis was done for all agro-morphological characters; the results have been depicted in Table 4. The estimates of direct effects ranged from -0.002 to 0.817 and the magnitude of residual effect recorded was 0.0059. A perusal of path coefficient analysis revealed highest positive direct effect of biological yield per plot on grain yield, followed by harvest index, number of tillers per meter row, spike length and 1000-grain weight, while the traits *viz.*, days to heading, maturity, plant height, number of grains per spike and green fodder yield exerted negative direct effect on grain yield per plot.

Days to heading and maturity showed negative direct effect to grain yield but these traits also contributed to grain yield *via* biological yield. Number of tillers per meter row and 1000-grain weight though illustrated positive direct effect as well as contributed

to grain through biological yield and harvest index. Similarly, green fodder yield contributed towards grain yield *via* biological yield and harvest index; however, it had negative direct effect on grain yield. Spike length exhibited significant negative association with grain yield, still directly added to grain yield as a consequence of direct positive effect. The positive direct effect of number of tillers per meter, spike length, 1000-grain weight, biological yield and harvest index on grain yield (Devi *et al.*, 2019; Ashok *et al.*, 2024) was also validated in barley. Similarly, the negative direct effect of days to heading and maturity, plant height and number of grains per spike (Hailu *et al.*, 2016; Kumar and Sehrawat, 2021); and green fodder yield (Kumar and Shekhawat, 2013b) towards grain yield were also confirmed in previous studies.

Principal Component Analysis represents the association between all variables at once, is better criterion over correlation coefficient for assorting

TABLE 4
Direct (diagonal) and indirect effects of different variables on grain yield in barley

Variables	DH	DM	T M	PH	SL	GS	TGW	BY	HI	GFY	rp with GY
DH	-0.026	-0.002	0.012	-0.007	0.001	0.001	0.000	0.177	-0.086	0.000	0.071
DM	-0.016	-0.004	0.003	-0.004	0.003	-0.001	0.000	0.073	-0.156	0.001	-0.100
T M	-0.007	0.000	0.047	-0.005	-0.010	0.003	0.005	0.543	0.210	-0.001	0.785**
PH	-0.013	-0.001	0.017	-0.013	-0.001	-0.001	0.006	0.385	-0.026	0.000	0.352 **
SL	-0.002	-0.001	-0.025	0.001	0.018	-0.015	-0.002	-0.431	-0.216	0.001	-0.671**
GS	0.001	0.000	-0.004	0.000	0.010	-0.029	-0.005	-0.008	-0.158	0.000	-0.194
TGW	0.000	0.000	0.016	-0.006	-0.002	0.009	0.015	0.238	0.166	0.000	0.435**
BY	-0.006	0.000	0.031	-0.006	-0.010	0.000	0.004	0.817	0.023	-0.001	0.853**
HI	0.005	0.001	0.020	0.001	-0.008	0.009	0.005	0.039	0.483	-0.001	0.555**
GFY	0.002	0.001	0.017	0.002	-0.009	0.002	0.002	0.221	0.214	-0.002	0.449**

Residual effect=0.0059.

TABLE 5
Principal component analysis in barley genotypes

Components	PC 1	PC 2	PC 3	PC 4
Eigen value	4.489	2.668	1.285	1.045
Proportion of total variation (%)	40.806	24.255	11.680	9.496
Cumulative percentage of variance	40.806	65.061	76.741	86.237
DH	0.155	0.854	-0.039	-0.283
DM	-0.070	0.859	-0.096	-0.328
TM	0.863	0.214	0.179	0.015
PH	0.420	0.756	-0.123	0.302
SL	-0.790	0.268	-0.025	0.462
GS	-0.372	0.192	0.742	0.468
TGW	0.563	0.045	-0.561	0.533
BY	0.799	0.301	0.333	0.078
GY	0.963	0.026	0.146	0.103
HI	0.724	-0.469	-0.255	0.080
GFY	0.607	-0.402	0.406	-0.162

promising genotypes with reduced number of variables that accounted for maximum variability of the original data set. PCA based on variables under study as depicted in Table 5 revealed first four components with eigen value more than one explained about 86.24 % of the total variation. The remaining PCs with an eigen value of less than one were ignored as a consequences of their lesser contribution towards total variability. The first PC accounted for 40.81 % of the total variance. The second, third and fourth PCs explained 24.26, 11.68, 9.50 % of the total variability, respectively. Number of tillers per meter row, spike

length, 1000-grain weight, biological yield, harvest index, green fodder and grain yield showed strong association with PC 1, hence could be considered as yield component. Days to heading, maturity and plant height exhibited high loading and showed strong correlation with PC 2. Likewise, number of grains per spike was highly associated with PC 3. In agreement with this study, Angassa and Mohammed (2021) reported 67.68% of the total variations cumulatively accounted by first two principal components while studying 138 barley accessions using nine quantitative traits. The relative contribution of various traits to the total variability has also been validated by Kaur *et al.* (2018) in barley.

The biplot was constructed in order to compare the relationship between genotypes and variables employing first two principal components that explained 65.06 % of the total variation (*Fig. 2*). The biplot demonstrated positive association of grain yield with days to heading, plant height, biological yield, harvest index, 1000-grain weight, number of tillers per meter row and green fodder yield as indicated by the acute angles between their vectors. Likewise, obtuse angles of number of grains per spike, days to maturity and spike length with grain yield showed negative correlation of these variables with grain yield. Hence, the results of correlation analysis are hereby confirmed by biplot analysis. The distribution of the genotypes over the quadrants delineated the presence of significant genetic diversity among the studied barley genotypes. The distinctiveness of a genotype

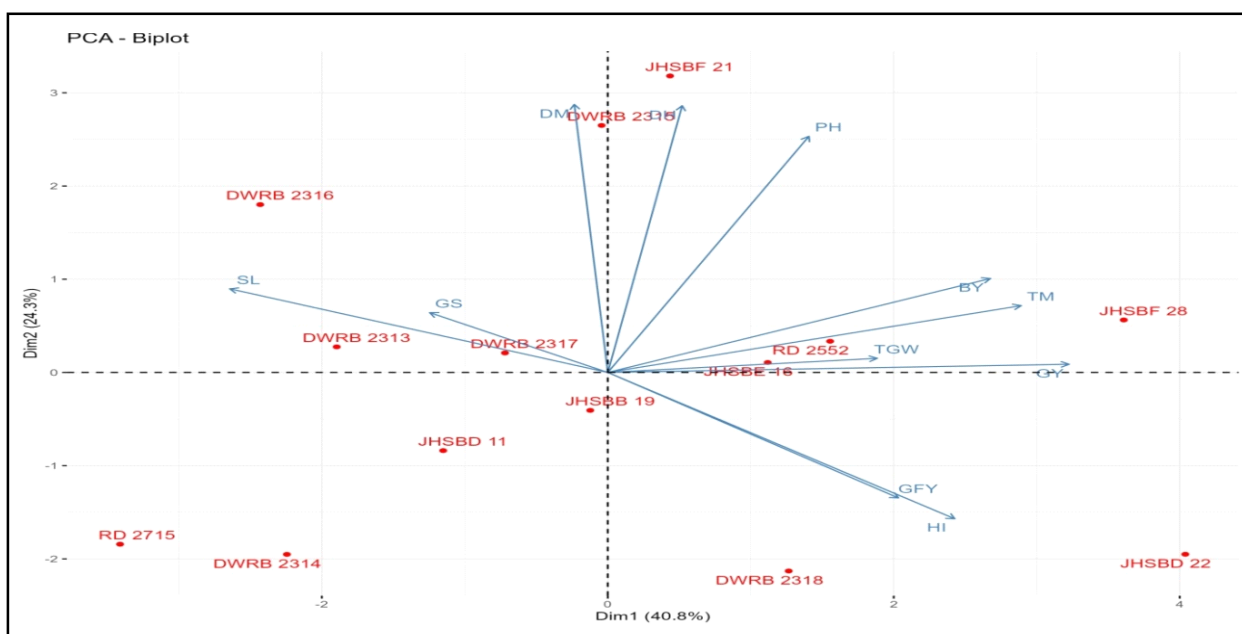


Fig. 2. Biplot analysis of genotypes vis-a-vis variables.

from other genotypes is measured by the vector length from their origin to the position of genotypes. The genotypes with long vector length may possess higher or extreme values for one or more variable and consequently their utilization in breeding program may respond heterotically. The genotypes, RD 2552, JHSBE 16, JHSBF 28 and JHSBF 21 occupied their position in first quadrant were positively correlated with PC 1 & PC 2; and possessed superiority for traits associated positively with these components. Four genotypes namely, DWRB 2316, DWRB 2317, DWRB 2313 and DWRB 2315 belongs to second quadrant were found promising for PC 2, while genotypes of fourth quadrant *i.e.* JHSBD 22 and DWRB 2318 performed better only for PC 1. However, genotypes JHSBB 19, JHSBD 11, DWRB 2314 and RD 2715 placed in third quadrant do not performed well with respect to PC 1 & 2. Similar kind of biplot approach has also been applied by Abdullah *et al.* (2018) in barley for visualizing the association between variables. In addition, the variability explained by different variables can also be seen by the length of vectors pertaining to a particular variable. Long vectors denote the higher magnitude of variability and vice-versa. Similarly, the genotypes occupying position nearer to the origin of biplot performed stable performance compared to other ones for the studied variables.

CONCLUSION

The current study indicated existence of enough genetic variability among the barley genotypes evaluated to be exploited for development of potential dual purpose genotypes. The association study reflected significant positive correlation of grain yield with number of tillers per meter row, plant height, 1000-grain weight, biological yield, harvest index and green fodder yield considered as component traits for yield determination. In addition, perusal of path analysis revealed positive direct and high indirect effects of biological yield per plot, and harvest index on grain yield. First four components identified by Principal Component Analysis cumulatively explained 86.24% of the total variation. Among all genotypes, RD 2552, JHSBE 16, JHSBF 28 and JHSBF 21 displayed superiority with respect to PC 1 & PC 2. Multivariate with biplot analysis proved to be appropriate for diversity analysis intended to select the promising diverse genotypes for genetic improvement irrespective of crops. Therefore, these findings may be considered while breeding dual purpose barley for obtaining green fodder coupled with high grain yield.

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