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Genetic diversity, heritability, correlation coefficient, and path analysis of forage yield components in Iranian *Phalaris aquatica* L. genotypes

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Abstract: Twenty-six selected genotypes of *Phalaris aquatica* L. from Iranian germplasm were evaluated to evaluate the genetic diversity of some agromorphological characteristics. Each selected genotype was cloned and planted as spaced single plants according to a randomized complete block design (RCBD) with four replications in 2016 and 2017. Large and significant ($p < 0.01$) differences among genotypes were found for all traits. The estimates of broad sense heritability were low to high ($h_b^2 = 0.16 – 0.75$) for studied traits. High heritability estimates for dry matter yield (DMY) indicate a sufficient genetic variability for further improvement. There was the highest heritability rate and genetic advance for plant height and DMY. Selection for traits with high heritability and genetic advance can be successful. The dry matter yield cut 1 (DMY1) correlation with the number of days to flowering, number of days to pollination, plant height, and crown diameter cut 2 was positive and significant. In stepwise multiple linear regression, the plant height, number of stems per plant, and spike length explained more than 84% of the total variation of DMY1. The plant height was the most crucial component of DMY1. The path analysis showed that plant height positively affected DMY1 (0.83). The highest negative indirect effects on DMY1 were observed for plant height via the number of stems per plant (–0.238). Axes 1 and 2 of the principal coordinate analysis explained 40.94% and 18.48% of the variation, respectively, and, although not entirely separated, general groupings can be determined. In factor analysis, component 1 was positively associated with the traits dry matter yield cut 2 (DMY2) (0.855), dry matter yield (0.821), and plant height (0.755). Therefore, the first component can be called the biomass component. Finally, selection would be more effective in improving forage yield based on yield components. In conclusion, the results indicated appropriate genetic variability in the studied genotypes. However, the studied genotypes will deliver a valuable germplasm to employ in breeding programs for forage cultivar production. This progress is crucial in introducing these selected genotypes to develop a core collection of *Phalaris aquatica* germplasm in Iran.

Key words: Genetic advance, factor analysis, principal coordinate analysis, variance components

1. Introduction

Phalaris aquatica L. (Poaceae) is a severe temperate perennial grass native to the Mediterranean and northwest Africa, stretching eastwards to Iraq (Anderson et al., 1999). *Phalaris aquatica* passes summer drought as buds at the base of reproductive tillers attached to the deep root system. Varieties of *Phalaris aquatica* show a range of incomplete endogenous dormancy (Volaire and Norton, 2006). *Phalaris aquatica* is the most widespread perennial grass grown in southeastern Australia's temperate regions, combining high productivity and drought resistance to provide persistent pastures that can maintain high rates, especially for sheep and beef cattle (Archer, 1995).

P. aquatica, 2n = 4x = 28 (Anderson, 1961), is considered an allopolyploid (Ambathsa, 1956) or segmental allotetraploid (Putievsky et al., 1980). Many forage grass species have estimated the heritability of different agronomic traits (De-Araujo and Coulman, 2002). Correlations between traits are essential to distinguish whether selection for one trait will affect another trait. Moreover, selection could be operated on a highly heritable trait related to a more complex trait such as forage yield. Many forage types of grass have estimated correlations among traits (De-Araujo and Coulman, 2002).

The information about heritability values and the correlation estimates among different traits can aid in distinguishing the indirect selection schemes (Hallauer

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and Miranda, 1988). Any germplasm selected for the breeding program must be tested, and germplasm must be examined depending on heritability values. Plant breeders aim to improve dry matter yield and extended seasonal forage yield of perennial pasture plants to improve the productivity and perdurability of pasture in grazing systems (Smith and Fennessy, 2014).

Phenotypic recurrent selection has been effectively applied in grasses to improve quantitative traits (Marshall and Wilkins, 2003). Traits such as yield with low heritability will need more selection cycles than traits with high heritability. The absence of improvement in forage yield may be due to less use of the direct selection method, and direct phenotypic recurrent selection was employed to increase winter dry matter productivity (Dhaliwal, 2009).

Evaluation of genetic diversity and study of relationships between traits based on morphological and agronomic traits can be helpful for organizing germplasm, selecting parents for hybridization, and producing segregating populations. With the rising interest in applying *P. aquatica* as forage, information on the improvement behavior of potentially valuable germplasm is essential. This research evaluated twenty-six *Phalaris aquatica* genotypes mainly originating from populations native to Iran for two years. The study aimed to estimate the total genetic variance, broad sense heritability, genetic advance, phenotypic correlation for dry matter yield and other measured traits, and path coefficient analysis of DMY1. Principal coordinate analysis (PCoA) was performed to examine clustering of genotypes and factor analysis (FA) to study associations between twelve traits in twenty-six Iranian *Phalaris aquatica* genotypes.

2. Materials and methods

2.1. Plant materials

The twenty-six *Phalaris aquatica* genotypes were selected from a large replicated nursery established in 2015, mainly consisting of natural ecotypes of *Phalaris aquatica* from broad geographical areas of Iran. The selected genotypes (Table 1) were based on data measured during two years, considering forage yield, pollination date, and rust disease resistance. By dividing the plants, every genotype was clonally propagated into four clones in early autumn. Then, genotypes were planted in the field, with 60-cm spacing within and between the rows, according to a randomized complete block design with four replications. The average annual temperature, mean yearly maximum temperature, and average annual temperature were 10 °C, 16 °C, and 2.2 °C, respectively. The average annual rainfall of this region was 271.3 mm.

In the autumn of 2017, after planting, irrigation was done, and the second irrigation was with an interval of two weeks. Fertilization included NPK (20-20-20), which was applied at 50 kg/ha in early spring, and drip irrigation was done in July and August at 15 days intervals. Twelve agromorphological characteristics (Table 2) were measured in 2 years (2016–2017). The experiment was conducted on Research Farm, University of Tabriz, N38.03, E46.39, Tabriz, Iran.

2.2. Data analysis

2.2.1. Analysis of variance

Before performing a combined analysis across years, the homogeneity of error variances was tested using Levene's test (Levene, 1960). A combined analysis of variance was performed to evaluate differences among the years, genotypes, and their interaction and to estimate the genotypic and environmental variance components using MSTAT-C (1991) software. In addition, LSD (least significant difference) test for genotype differences and Pearson's correlation coefficient for the association between variables were used. The variance components, genetic coefficient of variation, and broad sense heritability were computed as Miller et al. (1958) suggested. The genotypic coefficient of variation (CVg) was calculated as follows:

$$CVg = (\sigma_g / \mu) \times 100 ,$$

where σ_g is the standard deviation of the genotypic effect, and μ is the phenotypic mean (Miller et al., 1958).

2.2.2. Broad sense heritability

Broad sense heritabilities (h_b^2) were calculated based on genotype means. Estimates of genetic components from the combined analysis (Table 3) were used to calculate h_b^2 (Daday 1964, 1965; McWilliam and Latter, 1970) as follows:

$$h_b^2 = \sigma_g^2 / (\sigma_g^2 + \sigma_{gy}^2/y + \sigma_e^2/+ ry$$

where σ_G^2 and σ_{GY}^2 are genotypic and genotype × year variance components, respectively, σ_e^2 is residual mean squares in the combined ANOVA.

2.2.3. Genetic advance (GA)

The expected genetic advance for measured characteristics was estimated using the formula suggested by Johnson et al. (1955).

$$GA (\%) = k. h_b^2. \sigma_p$$

where h_b^2 is a broad sense of heritability, σ_p is phenotypic standard deviation and k-constant is the standardize selection differential at 5% selection intensity (K = 2.063).

2.2.4. Principal coordinate analysis (PCoA)

The data for *Phalaris aquatica* genotypes were subject to principal coordinate analysis to examine the ordination of genotypes. Principal coordinate analyses were performed by NTSYS-pc (Rohlf, 1988).

2.2.5. Factor analysis (FA)

Factor analysis (FA) was applied to study associations between traits. Factor analysis was performed based on principal component analysis. The varimax rotation method was used to simplify factor structure, and the

Table 1. Information on twenty-six *Phalaris aquatica* genotypes used in the research.

Genotype code	Population code	Origin
Ph. aq-01	19000/36	Isfahan-Fozveh Seed Bank
Ph. aq-02	16000/83	Isfahan-Fozveh Seed Bank
Ph. aq-03	16000/128	Kashan-Yazd Abad
Ph. aq-04	16000/F1-3	Isfahan-Fozveh Seed Bank
Ph. aq-05	19000/86	Isfahan-Fozveh Seed Bank
Ph. aq-06	16000/24	Isfahan-Fozveh seed Bank
Ph. aq-07	16000/F1-6	Isfahan-Fozveh Seed Bank
Ph. aq-08	16000/F1-5	Isfahan-Fozveh seed Bank
Ph. aq-09	16000/24	Isfahan-Fozveh Seed Bank
Ph. aq-10	16000/60	Kashan-Yazd Abad
Ph. aq-11	16000/147	Isfahan-Fozveh Seed Bank
Ph. aq-12	19000/22	Chaharmahal and Bakhtiari-Natural Resources Station
Ph. aq-13	16000/F1-7	Isfahan-Fozveh Seed Bank
Ph. aq-14	16000/60	Kashan-Yazd Abad
Ph. aq-15	19000/36	Isfahan-Fozveh Seed Bank
Ph. aq-16	16000/F1-8	Isfahan-Fozveh Seed Bank
Ph. aq-17	16000/F1-1	Isfahan-Fozveh Seed Bank
Ph. aq-18	16000/59	Kashan-Yazd Abad
Ph. aq-19	16000/24	Isfahan-Fozveh Seed Bank
Ph. aq-20	16000/59	Kashan-Yazd Abad
Ph. aq-21	16000/F1-2	Isfahan-Fozveh Seed Bank
Ph. aq-22	19000/22	Chaharmahal and Bakhtiari-Natural Resources Station
Ph. aq-23	19000/36	Isfahan-Fozveh Seed Bank
Ph. aq-24	19000/36	Isfahan-Fozveh Seed Bank
Ph. aq-25	19000/22	Chaharmahal and Bakhtiari-Natural Resources Station
Ph. aq-26	19000/86-2	Isfahan-Fozveh Seed Bank

percentage variability explained by each factor was determined (Johnson and Wichern, 2007). Factor analyses were conducted by Minitab Statistical Software version 17.

2.2.6. Multiple linear regression and path coefficient analysis

Stepwise multiple linear regression defined the variables explaining most DMY1 variability. Path coefficient analysis was carried out based on phenotypic correlation coefficients counting DMY1 as the effect and the traits added to multiple linear regression models as the cause (Montgomery, 2006). Appropriate statistical analysis was performed using SAS (SAS Institute, 2002) and SPSS (SPSS Incorporation, 2001) packages.

3. Results and discussion

3.1. Genetic variation

Large and significant ($p < 0.01$) differences among genotypes were found for all traits. For all traits except PH and FFY1, the effects of the year were highly significant ($p < 0.01$). The year × genotype interaction effect was highly significant only for NDF, NDP, and SL (Table 4). In general, most traits had high phenotypic and genetic diversity. This diversity promises high efficiency of breeding methods in improving these traits and their related traits. In other words, the high genetic diversity between selected genotypes, especially for essential traits, indicates a considerable genetic distance between genotypes. This

Table 2. Abbreviations and measurement units for the twelve traits in 2016 and 2017.

Trait 1st 2nd	Abbreviation	Unit of measurement
Number of days to flowering	NDF	day
Number of days to pollination	NDP	day
Plant height	PH	cm
Spike length	SL	cm
Number of stems	NS	-
Fresh forage yield (1st year)	FFY1	g
Dry matter yield (1st cut)	DMY1	g
Crown diameter (1st cut)	CD1	cm
Fresh forage yield (1st cut)	FFY2	g
Dry matter yield (2nd cut)	DMY2	g
Crown diameter (2nd cut)	CD2	cm
Dry matter yield (1st + 2nd cut)	DMY	G

Table 3. Combined analysis of variance on *Phalaris aquatica* genotypes.

Source	*df*	Expected mean squares E(MS)
Year (Y)	*y-1*	$\sigma_e^2 + g\sigma_{r/y}^2 + rg\sigma_y^2$
Replication/year	*y(r-1)*	$\sigma_e^2 + g\sigma_{r/y}^2$
Genotype (G)	*g-1*	$\sigma_e^2 + r\sigma_{gy}^2 + ryV_g$
G × Y	*(g-1) (y-1)*	$\sigma_e^2 + r\sigma_{gy}^2$
Error	*y(r-1) (g-1)*	σ_e^2

r, *g*, and *y* are the number of replicates, genotypes, and years, respectively.

Table 4. Analysis of variance for agromorphological traits in twenty-six genotypes of *Phalaris aquatic.*

Trait	MS		
	Year	Genotype	Year × genotype
NDF	4007.5**	80.4**	32.2**
NDP	3069.2**	63.3**	9.5**
PH	335.1ns	3144.3**	170.5ns
SL	468.0**	15.7**	4.5**
NS	295884.7**	9701.1**	2787.5ns
FFY1	147076.7ns	1097993.9**	125306.5ns
DMY1	1640278.1**	241117.2**	23071.2ns
CD1	6117.2**	86.9**	21.3ns
FFY2	6573550.6**	2008966.2**	101989.7ns
DMY2	350058.1**	259409.1**	12701.4ns
CD2	8749.1**	77.7**	23.1ns
DMY	3505846.2**	822902.5**	42370.1ns

*, ** significant at $p < 0.05$, $p < 0.01$; ns nonsignificant.

genetic distance increases the possibility of high heterosis in later generations and promises high-yielding varieties. The results showed significant genetic diversity between the studied genotypes, and some genotypes with high production capacity or other desirable traits can be used in breeding programs such as resistance to biotic and abiotic stresses (Oram et al., 2002). However, the studied genotypes will deliver valuable germplasm to employ in *Phalaris aquatica* breeding programs for forage cultivar production (Ludemann and Smith, 2015). This progress is essential in introducing these selected genotypes to develop a core collection of *Phalaris aquatica* germplasm in Iran.

The number of days to pollination ranged from 53.38 days for genotype 16 to 64.25 days for genotype Ph.aq-20. The highest PH was observed for genotype Ph.aq-20, while the lowest belonged to genotype Ph.aq-16. The highest and lowest yielding genotypes were genotypes Ph.aq-15 and Ph.aq-16, and Ph.aq-3, respectively (Table 5). Low yield in *Phalaris aquatica* genotypes results from partial winter dormancy induced by short day length (Arnold et al., 1967) and correlates with late flowering (Oram and Freebairn, 1984).

3.2. Correlations

The relationship of DMY1 with NDF, NDP, PH, and CD2 was positive and significant. There were no significant associations between SL and NS with DMY (Table 6).

Table 5. The means of measured traits in twenty-six *Phalaris aquatica* genotypes for two years.

Genotype	NDF (day)	NDP (day)	PH (cm)	SL (cm)	NS	FFY1 (g)	DMY1 (g)	CD1 (cm)	FFY2 (g)	DMY2 (g)	CD2 (cm)	DMY (g)
1	49.38	61.00	172.50	9.500	248.50	1355.38	585.38	35.75	589.88	194.00	37.63	779.38
2	49.75	61.25	189.88	8.188	166.50	1046.50	478.50	29.88	415.25	162.50	33.13	641.00
3	49.38	61.50	176.63	9.313	142.63	632.38	**329.13**	24.38	453.13	145.00	29.88	474.13
4	46.38	57.50	182.00	11.813	180.88	1139.63	545.00	28.75	823.50	243.63	36.38	788.63
5	45.63	57.38	216.63	12.313	114.88	1394.63	665.75	28.63	1890.25	626.00	37.25	1291.75
6	48.13	59.38	224.13	10.188	162.75	1470.38	671.38	31.50	2114.13	757.00	37.50	1428.38
7	42.13	54.88	213.00	7.688	115.50	836.00	423.13	25.00	829.75	298.25	29.88	721.38
8	41.88	57.63	209.25	8.750	119.00	937.38	478.13	25.63	874.13	272.38	29.38	750.50
9	45.50	57.38	211.63	9.188	137.38	1244.75	555.63	28.75	827.75	241.38	34.88	797.00
10	49.00	62.00	176.13	9.375	191.50	1233.00	551.00	31.75	921.13	285.63	34.75	836.63
11	46.38	57.50	215.63	10.500	143.00	1489.00	677.38	31.63	1270.50	370.38	37.88	1047.75
12	47.38	63.00	200.50	8.875	126.00	1154.75	471.38	28.75	1182.38	345.00	35.63	816.38
13	45.13	57.50	210.88	12.375	135.00	1361.88	617.13	32.63	1164.00	386.25	35.50	1003.38
14	48.13	59.63	185.75	10.250	138.13	893.00	428.63	27.00	469.13	163.63	29.88	592.25
15	49.38	62.50	223.25	12.688	168.25	1756.88	859.63	31.88	2026.13	636.63	37.88	1496.25
16	39.75	53.38	203.75	8.813	232.50	1994.13	954.63	29.88	1576.63	622.25	37.63	1576.88
17	47.50	59.25	218.13	10.063	112.13	1320.88	716.75	28.75	860.13	240.63	37.63	957.38
18	51.50	63.25	167.00	10.000	163.88	1020.25	437.88	34.63	742.75	240.75	36.13	678.63
19	45.13	56.88	244.00	11.375	168.00	2028.50	922.63	34.75	1101.25	362.63	38.13	1285.25
20	53.50	64.25	176.25	7.688	169.00	1029.75	420.13	33.50	723.00	178.13	38.38	598.25
21	47.38	58.88	207.50	9.250	156.75	1524.63	613.88	31.63	1745.50	601.00	35.00	1214.88
22	51.13	63.25	197.38	8.438	208.13	1429.38	677.75	26.88	1026.38	323.50	32.13	1001.25
23	49.25	60.75	223.13	8.563	143.13	1689.75	724.25	28.38	1446.25	451.00	37.38	1175.25
24	48.75	60.75	209.38	9.063	145.63	1426.88	607.75	26.63	1122.13	328.38	32.63	936.13
25	44.13	56.13	228.13	8.750	159.75	1528.50	755.88	32.63	1970.25	678.38	39.88	1434.25
26	43.88	57.13	209.38	10.125	196.88	2121.25	**982.25**	36.25	1327.13	464.63	39.13	1446.88
LSD (1%)	4.52	2.27	12.61	1.50	53.55	429.26	190.85	6.96	363.19	134.24	5.97	295.27

Table 7 shows the phenotypic coefficient of variation, genetic coefficient of variation, and broad sense heritability of studied traits. DMY2 had the highest genetic coefficient of variation, while NDP had the lowest values.

Phenotypic diversity coefficients for traits NDP, PH, FFY2, DMY2, and DMY were greater than genetic diversity coefficients (Table 7). The small phenotypic variation coefficient for these traits indicates that the genetic effects are more significant than the environmental effects. On the other hand, the low difference between the phenotypic and genotypic coefficients of variations for mentioned traits shows that these traits are controlled mainly by genetic factors. The selection of parents based on these traits is appropriate for hybridization for breeding purposes.

The high heritability of traits PH and DMY compared to other traits indicates the low effect of the environment on these traits. The impact of the environment on traits with high heritability is negligible, and phenotype-based selection is effective in these traits. Also, high heritability values for traits indicate the prominent role of genetic effects in controlling these traits. Since these traits are also considered components of forage yield, indirect selection can increase the efficiency of selection to improve forage yield.

Although high heritability indicates the effectiveness of selection based on phenotypic performance, it does not imply any indicator of the amount of genetic advance for selecting the best plants. It is possible through genetic advances (Table 7). Traits NDF, NDP, SL, CD1, and CD2

Table 6. The correlation coefficient between traits in *Phalaris aquatica* genotypes.

	NDF	NDP	PH	SL	NS	FFY1	DMY1	CD1	FFY2	DMY2	CD2	DMY
NDF	1											
NDP	0.922**	1										
PH	–0.487*	–0.511**	1									
SL	–0.083	–0.150	0.248	1								
NS	0.122	0.089	–0.350	–0.084	1							
FFY1	–0.295	–0.330	.592**	0.299	0.418*	1						
DMY1	–0.389*	–0.418*	0.638**	0.346	0.370	0.968**	1					
CD1	0.139	0.059	0.001	0.280	0.506**	0.540**	0.451*	1				
FFY2	–0.272	–0.277	0.656**	0.327	–0.007	0.636**	0.630**	0.226	1			
DMY2	–0.351	–0.364	0.628**	0.285	0.066	0.642**	0.645**	0.230	0.981**	1		
CD2	0.017	–0.093	0.304	0.324	0.327	0.690**	0.652**	0.765**	0.541**	0.502**	1	
DMY	–0.408*	–0.431*	0.698**	0.348	0.237	0.884**	0.903**	0.373	0.892**	0.910**	0.635**	1

Table 7. Genetic coefficient of variation and broad sense heritability of traits in *Phalaris aquatica* genotypes.

Trait	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Broad sense heritability	Genetic advance (%)
NDF	8.28	5.21	0.18	2.94
NDP	3.30	4.37	0.28	3.23
PH	5.34	9.54	0.75	36.96
SL	13.22	12.19	0.23	1.46
NS	28.96	19.17	0.29	24.07
FFY1	27.45	25.72	0.47	432.99
DMY1	26.50	26.36	0.50	217.97
CD1	19.87	8.51	0.16	1.37
FFY2	27.61	43.07	0.70	886.47
DMY2	31.29	47.41	0.69	314.85
CD2	14.54	7.17	0.19	1.51
DMY	25.69	31.12	0.60	491.36

had low genetic advance. The traits' insufficient genetic advance indicates epistasis effects in the loci controlling these traits. There was the highest rate of heritability and genetic advance for traits DMY.

Selection for traits with high heritability and genetic advance can be successful. The genetic advance due to selection for high heritability traits will be good in breeding programs.

3.3. Principal coordinate analysis (PCoA)

The data for *Phalaris aquatica* genotypes were subject to principal coordinate analysis to examine the clustering of genotypes. In PCoA, the genetic distance between the studied *Phalaris aquatica* genotypes was shown as a three-dimensional plot. The distance on the plot indicates the degree of dissimilarity of genotypes (Mohammadi and Prasanna, 2003). In this analysis, the first four components explained 83.90% of the phenotypic variation (Table 8). When the first three components explain more than 25% of the variation between genotypes, grouping using a plot will be an effective method (Mohammadi and Prasanna, 2003). According to the three-dimensional plot of PCoA based on the first three components (Figure 1), it is a pretty evident that studied *Phalaris aquatica* genotypes were classified into two clusters.

3.4. Factor analysis

To determine the most variable characters, factor analysis based on PCA was performed. The first three components

Table 8. Principal coordinates and their eigenvalues in *Phalaris aquatica* genotypes for measured traits.

Principal coordinate	Initial eigenvalue		
	Total	% of variance	Cumulative %
1	10.54	40.94	40.94
2	4.76	18.48	59.43
3	3.45	13.41	72.84
4	2.84	11.06	83.90

(FAC1, FAC1, and FAC1) explained 80.49% of the total phenotypic variation (36.29%, 23.31%, and 20.89%, respectively). The first component FAC1 was positively associated with the traits FFY2 (0.914), DMY2 (0.855), DMY (0.821), and PH (0.755). For the second component FAC1, traits NS (0.883) and CD1 (0.8) had significant positive coefficients (Table 9).

To determine the genotypes with high forage yield, the factor scores of the first component were used (Table 10). As can be seen, genotypes Ph.aq-15 and Ph.aq-3 had the highest and lowest scores, respectively, consistent with the results obtained from genotypes mean comparison in a combined analysis.

3.5. Multiple linear regression and path coefficient analysis

The stepwise multiple linear regression was used to define the variables accounting for most DMY1 variability. The plant height, number of stems per plant, and spike length explained more than 84% of the total variation of DMY1. The other variables were not included in the analysis owing to their low relative portions. The plant height was the most crucial component of DMY1 (partial R^2 = 0.41%).

Path analysis partitioned the correlation coefficients into direct and indirect effects (Table 11, Figure 2). Results showed that plant height had a high positive direct impact on DMY1 (0.83). The highest adverse indirect effects on DMY1 were observed for plant height via the number of stems per plant (–0.238).

Although correlation coefficients estimate the type and amount of relationship of DMY with other traits, the effect of yield components on DMY is not yet explained by this statistic. Correlation path analysis has been used to characterize yield variables' direct and indirect associations. No related information was found in *Phalaris aquatica*.

In the crosspollinating forage grass crops, information about genetic variation for the different traits and their genetic relationship is represented in statistical parameters for broad sense heritability, genetic correlations, and

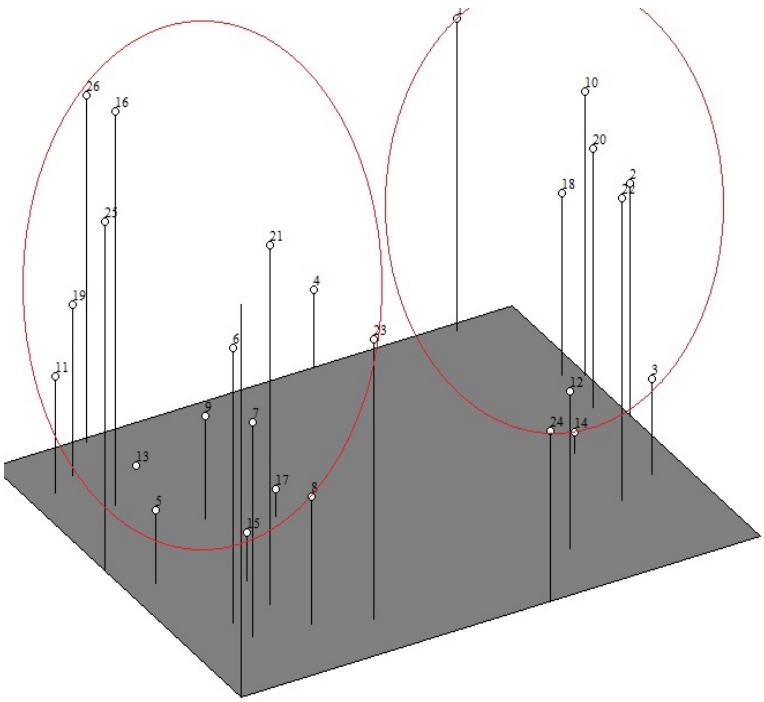

Figure 1. Principal coordinate analysis of *Phalaris aquatica* genotypes based on measured traits. Circles show the grouping of *Phalaris aquatica* genotypes.

Table 9. The coefficients of the studied traits in the components obtained from the factor analysis.

Rotated component matrix			
Traits	Component		
	FAC1	FAC2	FAC3
NDF	–0.136	0.071	0.949
NDP	–0.169	0.009	0.927
PH	**0.755**	–0.155	–0.455
SL	0.531	0.054	0.086
NS	–0.208	**0.883**	–0.002
FFY1	**0.624**	0.634	–0.315
DMY1	0.630	0.570	–0.406
CD1	0.246	**0.800**	0.198
FFY2	**0.914**	0.105	–0.157
DMY2	**0.855**	0.150	–0.256
CD2	0.572	0.655	0.087
DMY	**0.821**	0.393	–0.364

genotype × environment interactions (Aastiveit and Aastiveit, 1990). In the present research, considerable and significant variation was obtained among *Phalaris aquatica* genotypes for all measured traits.

Effective genetic variation was found for all traits evaluated, and genotype × environment interaction was not observed for most traits. The differences between genotypes were adequate to permit promising breeding materials to be distinguished. Genotypes superior in dry matter yield, which generally had values close to the overall mean of the genotypes evaluated, were characterized.

The heritability of traits and the correlations between traits are essential for evaluating genetic advances in DM yield, which could be used in a plant breeding program (Ludemann and Smith, 2015). In the present study, the correlation between DMY and SL, NS, and CD1 was not significant but was positively correlated with other characteristics. With the positive and meaningful relationship of DMY with NDF, NDP, PH, and CD2, indirect selection would be helpful in improving forage yield. Cogliatti et al. (2011) in *Phalaris canariensis* and Oram (1984) in *Phalaris aquatica* reported a positive correlation between plant height with dry matter yield and seedling yield with second-year winter yield, respectively.

In this study, twelve measured traits have a mean heritability among genotypes of 0.42, with coefficients of variation in the range 4.37%–47.41%. In *Phalaris tuberosa,* eight traits had a mean heritability of 0.256, with coefficients of variation in the range 8%–38% (Latter, 1971). The estimated heritability for the tillering rate on an individual seedling basis was 0.23 (Latter, 1971). The estimate of broad sense heritability (h_b^2) for DMY (0.60) in the present research was commonly in disagreement with formerly reports for *Bromus riparius* (Jensen et al., 2006) and *Pahalaris arundinacea* (Casler, 1982). Estimated heritabilities and genetic correlations, the limit to which these may be used to predict involved parameters in the breeding, and the limitation to which they agree with estimates formerly published for other species. Overall, the high heritability estimates for dry matter yield were observed, indicating sufficient genetic variability for further improvement.

Factor analysis provided marks of genotypes combining valuable traits, and distinguished three components that explained approximately 80.499 % of the phenotypic variation.

Table 10. Factor scores for 26 *Phalaris aquatica* genotypes in factor analysis.

Genotype	FAC1	FAC2	FAC3
1	–1.4631	2.2110	0.5095
2	–1.2392	0.0235	0.4254
3	**–1.2941**	–1.3234	0.5778
4	–0.6592	0.2091	–0.1687
5	1.7108	–1.0465	0.0301
6	1.7141	–0.1660	0.4412
7	–1.0170	–1.6680	–1.7769
8	–0.7891	–1.5435	–1.3073
9	–0.4925	–0.4847	–0.6559
10	–0.7491	0.6899	0.6818
11	0.4556	0.0318	–0.2169
12	0.1414	–0.7956	0.7776
13	0.5062	–0.2979	–0.1580
14	–1.0404	–1.0129	0.1322
15	**2.1625**	0.1938	1.1826
16	–0.1977	1.7339	–2.6162
17	0.3193	–0.5789	0.0775
18	–0.6359	0.5188	1.6792
19	0.7444	0.9560	–0.8210
20	–0.8300	0.6556	1.8845
21	0.7492	–0.0605	0.0530
22	–0.4384	0.3430	0.6032
23	0.8477	–0.2063	0.3411
24	0.0447	–0.6732	0.1794
25	1.1328	0.3286	–0.8380
26	0.3170	1.9627	–1.0173

Table 11. Direct and indirect effects of DMY1 components in evaluated *Phalaris aquatica* genotypes.

Character	Direct effect	Indirect effect via			Total correlation with DMY1
		Plant height	Number of stems	Spike length	
Plant height	0.83	-	–0.238	0.05	0.638
Number of stems	0.68	–0.290	-	–0.016	0.370
Spike length	0.20	0.207	–0.054	-	0.346
Residual = 0.85					

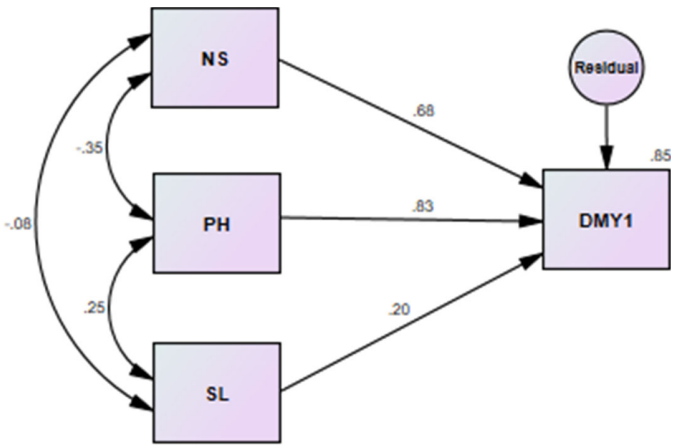

Figure 2. Diagram of path coefficient analysis of DMY with yield components.

4. Conclusion

In conclusion, results indicated appropriate genetic variability in the studied *Phalaris aquatica* genotypes. The path analysis, broad sense heritability, genetic advance, and correlation analysis revealed that the plant height and number of stems per plant were the most important yield components. Therefore, the results suggest that the plant height and number of stems per plant are significant yields contributing traits, and selection based on these traits would be most effective. Finally, remarkable genetic variation and low to high broad sense heritability estimates show that selection for rising forage yield and its components could be effective.

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