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Analysis of variability, heritability, and genetic advance in seed yield and related traits of orchardgrass (*Dactylis glomerata* L.) populations

Hayati ŞEKER[1,*], Ayşe YAZICI[2], Pınar UYSAL[2]
[1]Küçükçekmece District Food Agriculture and Husbandry Office, Küçükçekmece, İstanbul, Turkey
[2]Eastern Anatolian Agricultural Research Institute, Erzurum, Turkey

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Abstract: Orchardgrass (*Dactylis glomerata* L.) genotypes from different natural sources in the Eastern Anatolian Region of Turkey were clonally evaluated to study genetic variation and the relationships between seed yield and its components using a randomized complete block design. Results showed very significant genotypic variances among genotypes for all traits, including agronomic (seed, dry matter, and biological yields), morphological (plant height; panicle length; crown diameter; numbers of fertile, sterile, and total stems; and stem intensity), physiological (percent fertile stems, harvest and fertility indexes), and phenological (heading and anthesis dates) traits, as well as genotype × year interaction variances. Genotypic components were the main contributor to phenotypic variation of all traits (except physiologic traits, stem intensity, and number of sterile stems), resulting in high broad-sense heritability (>50%). Agromorphological and physiological traits had greater phenotypic (PCV), genotypic (GCV), and environmental coefficients of variation, while these were lower for phenological traits. After the phenological traits, plant height, crown diameter, and panicle length were the least variable traits, while stem intensity and fertility index were highly variable. Heritability estimates increased as GCV values approached PCV values. Expected genetic gain greatly increased as heritability estimates and PCV both increased, rather than heritability values alone. The first 5 principle components accounted for 84.90% of total variance. All agromorphological traits (except number of sterile stems) and fertile stem percentage were primary sources of variation of the PC1 axis, while harvest and fertility indexes were for PC2. Out of the 4 clusters, genotypes in cluster 4 of higher seed yield were faster in aboveground biomass accumulation. They also had the best agromorphological traits coupled with early maturity. Seed yield greatly increased as aerial biomass increased without any change in harvest index, but there was a significant decrease in fertility index. It was concluded that selection for dry matter yield could result in a simultaneous increase in seed yield.

Key words: Biometric parameters, multivariate analysis, orchardgrass, phenotypic traits, seed yield

1. Introduction

Orchardgrass (*Dactylis glomerata* L.) is a highly cross-pollinated perennial forage grass and well adapted to various environmental conditions in temperate zones of the world. It is one of the earliest- and fastest-growing grass species in the spring and exhibits good shade tolerance and regrowth characteristics. Orchardgrass is used in monoculture or binary mixtures with alfalfa (*Medicago sativa* L.) or red clover (*Trifolium pratense* L.) for silage and hay production or in mixtures with white clover (*Trifolium repens* L.) for grazing (Christie and McElroy, 1995).

Seed production is essential to produce a sufficient amount of forage in a vast area of field for effective livestock feeding. However, the seed production of forage grasses is different from that of field crops, such as cereals and edible legumes, due to disjointed areas for both agronomic and seed productions (Christie and McElroy, 1995). Many studies with various forage grass species in different environmental conditions concluded that combining high seed yield with high dry matter production should be possible in grass species by breaking the negative association between hay and seed yields, despite the negative effect of seed yield breeding on forage yield and quality (Bugge, 1987; Marshall and Wilkins, 2003). Moreover, a strong positive correlation between seed yield and dry matter yield was recently reported in many studies for various grass species, including smooth bromegrass, narrow-leaved meadow grass, and orchardgrass (Seker and Serin, 2004; Moradi et al., 2007; Parsa et al., 2012).

Cultivars developed from local genotypes or collections offer more advantages than introduced genotypic materials for breeding studies because of superior adaptation following long-term natural selection. Thus, genetic variability existing in the available domestic populations

* Correspondence: hayatiseker2@gmail.com

or the collections for seed yield and related traits is an important resource in developing new plant cultivars that have desired agronomic and economic traits; in particular, it is very important for the related traits that cause increases in both seed and forage production simultaneously (Singh et al., 1991). Partitioning of total variation into genetic and environmental sources and their interactions is essential to assess genetic or environmental effects on seed yield and its components, as reported in a range of forage species (Rognli, 1987; Jafari and Naseri, 2007).

Forage and seed yields and related characters are quantitatively inherited. Thus, biometrical genetic information on the nature and the extent of genetic variation, genotype × environment interactions, heritability, and prediction of genetic advance by selection is a prerequisite for improvement by direct or indirect selection. Some statistics, such as means, ranges, and variances, are helpful in providing information on the diversity of genotypes. However, they do not enable the simultaneous comparisons of genotypes and plant attributes (Harch et al., 1995). Therefore, the characterization and grouping of genotypes based on multiple traits could be a useful management tool in breeding programs (DeLacy et al., 2000). Multivariate statistical methods and numerical taxonomy, such as principal component (PC) analysis and cluster analysis, have been used extensively in summarizing and describing the variability in a population of accessions or genotypes in a variety of crops (Kandil et al., 2012; Parsa et al., 2012). The reduction of the original variables into a new set of uncorrelated variables (PCs) was achieved by linear transformation. PCs, each of which represented different properties of the original data, were independently orthogonal to each other and so could be interpreted independently (Mohammadi, 2003).

Achieving a superior cultivar with satisfactory seed yield along with high hay yield per unit area is an important objective for breeding forage crops, particularly in regions with a short vegetation period and a very long, harsh winter. Thus, the orchardgrass genotypes from natural sources within the Eastern Anatolian Region offer a great opportunity to solve the bottlenecks in the breeding and cultivation of forage crops. The objectives of this field study were to study these genotypes and estimate genetic variability, heritability, and genetic gain from one cycle of selection for seed yield and to identify the traits that differentiate the genotypes into different groups of agricultural traits.

2. Materials and methods

A total of 109 promising orchardgrass (*Dactylis glomerata* L.) genotypes were derived from a nursery garden after 2 years of surveying (1998 and 1999). The nursery garden was established in 1997, using 10 randomly selected seeds from each plant of the ecotypes of various forage species found in the various rangelands and pastures in Erzurum, Ardahan, Kars, and Van provinces of the Eastern Anatolian Region of Turkey. The seeds were separately collected, paper-bagged, labeled, and conditioned in a cool temperature in the summer of 1996. The genotypes in the study are presented in Table 1, along with their origins. The field experiment was conducted in a completely randomized block design with 3 replications at the Pasinler Substation of the Eastern Anatolian Agricultural Research Institute, Erzurum Province, located in the Eastern Anatolian Region of Turkey (46°15′N, 119°45′E) at 1850 m altitude in 2001–2002. The experimental field had fluvaquent silty clay loam. This location is an arid area with a typical continental climate characterized by dry summers and cool temperatures, with an approximately 12.3 °C mean temperature and 204 mm of rainfall from April to August. This rainfall provided 51% of the annual rainfall based on the long-term climatic data between 1929 and 2000. Total rainfall was greater by 10% and 56% in 2001 and 2002, respectively. In 2001, the mean temperature was 2.1 °C greater than the long-term mean of 72 years for the same vegetation period.

The experimental area was prepared by plowing 30 cm deep, disk harrowing, and leveling during the previous autumn. Fertilizers were incorporated in the experimental area 10 days prior to planting at rates of 100 kg ha^{-1} P_2O_5 as triple super phosphate, 60 kg ha^{-1} K_2O as potassium sulfate, and 75 kg ha^{-1} nitrogen as ammonium sulfate. Eight ramets, each of which carried 2 tillers from each mother plant randomly selected from 10 plants of each of the 110 genotypes, including cultivar Modac as a control, for each replication were randomly transplanted, with 40 × 40 cm spacing, with other ramets from the other mother plants into each block. One block consisted of 22 rows, 16.0 m in length with 40 cm interrow spacing. In other words, each block consisted of 880 individual clones; there were 3 blocks, so the whole experiment included 2640 clones

Table 1. Accession numbers and origins of 109 orchardgrass genotypes.

Genotypes	Origins	Altitude (m)
1–6	Sarıkamış, Kars	2300
7–12	Pasinler, Erzurum	1750
13–18	Gevaş, Van	1699
19–69	Center, Erzurum	2000
70–76	Sarıkamış, Kars	2350
77–88	İspir, Erzurum	1225
89–91	Ardahan	1920
92–97	İspir, Erzurum	1275
98–109	Tortum, Erzurum	1385

of 110 genotypes. Nonexperimental spaced plants were planted in 2 borders surrounding each block. All clones were planted on 24 April 2000. In the following years, plots were fertilized with 100 kg ha^{-1} nitrogen as ammonium sulfate in the early spring. They were also kept weed-free by mechanical weeding and, starting at the beginning of June, were irrigated 5 times at 15-day intervals.

Observations and data were gathered from 8 clones of each genotype for each replication during 2 years, 2001 and 2002, for agronomic (seed yield, dry matter yield, and biological yield), morphological (plant height, panicle length, crown diameter, number of fertile stems per plant, number of sterile stems per plant, number of total stems per plant, stem intensity), physiological (percent fertile stem number, harvest index, and fertility index), and phenological (heading date and anthesis date) traits, as described in Table 2.

The means of the ramets obtained for each genotype were subjected to a combined analysis of variance across years using split-plot-in-time design, with years as subplots (Nguyen and Sleper, 1985) using the Proc GLM procedure of SAS (SAS Institute, 2004), because the correlated data from this clonal experiment with perennial orchardgrass over the years did not permit rerandomization for each year of the experiment. Expected mean squares were based on a random effects model for genotypes, years, and replications. Variance components were estimated by computing appropriate linear functions of the mean squares:

$$S^2_P = [(S^2_G) + (\frac{S^2_{GY}}{r} + \frac{S^2_\beta}{y} + \frac{S^2_\epsilon}{yr})]$$

where S^2_P = estimate of phenotypic variance, S^2_G and S^2_{GY} = estimates of variance components due to genotypes and interaction effect of genotype × year, respectively, and S^2_β and S^2_ϵ = estimates of variance components due to genotype × replication (whole plot error) and genotype × year × replication (subplot error), respectively. Variables y and r stand for the numbers of years and replications, respectively. The standard error (SE) for each of the estimated component variances was computed according to Anderson and Bancroft (1952). Genotypic (GCV), phenotypic (PCV), and environmental (ECV) coefficients of variability to compare the variations among the traits (Singh and Chaudhary, 1997) and heritability in a broad

Table 2. Agronomic, physiological, morphological, and phenological traits of orchardgrass genotypes and their measurements and abbreviations.

Trait group	Plant traits (abbreviation)	Measurements
Agronomic	Biological yield (BioY)	Individual plant was harvested and paper-bagged and allowed to air dry; dry weight was expressed in grams per plant
	Seed yield (SdY)	Dried plants were threshed and cleaned; clean seed was weighed and yield was expressed in grams per plant
	Dry matter yield (DMY)	BioY – SdY (grams per plant)
Physiological	Percent fertile stem (%FrSt)	Ratio of fertile stems to total stems
	Harvest index (HvInd)	Ratio of seed yield to biological yield
	Fertility index (FrInd)	Ratio of seed yield to panicle length (grams per cm)
Morphological	Plant height (PH)	Length from soil surface to the tips of the 5 tallest panicles per plant was recorded just before seed harvest and averaged (cm)
	Panicle length (PnLng)	Length of 5 developed panicles was averaged from the peduncles to the tips of panicles at anthesis date (cm)
	Crown diameter (CrD)	Length of crown diameter of individual plant (cm)
	Fertile stems $plant^{-1}$ (FrSN)	Number of panicle-bearing stems per plant
	Sterile stems $plant^{-1}$ (SrSN)	Number of panicleless stems per plant
	Total stems $plant^{-1}$ (TtSN)	FrSN + SrSN
	Stem intensity (StIn)	Ratio of TtSN to crown area
Phenological	Heading date (HdDt)	Measured as the number of days from 1 March to the stage at which the first flowering shoot was visible
	Anthesis date (AnDt)	Measured as the number of days from 1 March to the stage at which the first flowering shoot was pollinating

sense (h^2_b) (Falconer and MacKay, 1996) were estimated. Negative variance components were considered to be 0 in the estimating of heritability. The SE of h^2_b was calculated as described by Dickerson (1969). Expected genetic gain (R) per a cycle of selection with 1.4 standardized selection differential at 20% of selection intensity was calculated (Falconer and MacKay, 1996).

PC and cluster analyses were performed with SAS Software (SAS Institute, 2004) to identify the variability among the genotypes and their groupings (Johnson, 1998). NTSYSpc version 2.1 software was used to generate a dendrogram (Rohlf, 2005). The genotypes in each cluster were then reanalyzed for basic statistics, and the comparison of the clusters was performed for each trait by ANOVA (SAS Institute, 2004).

3. Results and discussion

Descriptive statistics for agronomic (seed, dry matter, and biological yields), morphological (plant height; panicle length; crown diameter; numbers of fertile, sterile, and total stems; and stem intensity), physiological (percent fertile stems, harvest index, and fertility index), and phenological (heading date and anthesis date) traits derived from the analysis of the clonal genotypes of orchardgrass (*Dactylis glomerata* L.) across the years are summarized in Table 3. Analysis of variance showed great ($P < 0.001$) differences among the genotypes for all the traits, indicating the presence of a considerable amount of genetic variability (Table 4). The estimations of components of genotypic (S^2_G), genotype × environment interaction (S^2_{GY}), and environmental (S^2_β and S^2_ε) variances with their corresponding SEs are also presented in Table 4. Examination of the estimates revealed significant components for each effect, except the genotype × block effects of all morphological (excluding crown diameter and plant height), physiological, and phenological traits. This is in contrast to the published data for orchardgrass, which suggest that varying degrees of genotypic variations were present for seed yield, dry matter yield, and various attributes (Jafari and Naseri, 2007; Mut and Ayan, 2008), as well as for a variety of grasses including timothy (Rognli, 1987) and smooth bromegrass (Serin et al., 2001). Rognli (1987) also found significant genotype × year interaction and environmental (genotype × block interaction) effects for seed yield and plant height for timothy, and Jafari and Naseri (2007) for dry matter yield, tiller number, and heading date for orchardgrass. The variance of genotypic components was greater than the total variance of the nonheritable components for only 2 traits (plant height and panicle length), suggesting that their genotypic components should be considered the primary contributors in their phenotypic expression (Table 4). The estimates of genotypic variance for all agromorphological traits (except seed yield, crown diameter, panicle length, and stem intensity) were larger than those for physiological and phenological traits, ranging from 288.78 for plant

Table 3. Summary of descriptive statistics for each trait derived from the 2-year (2001–2002) clonal analysis of 110 orchardgrass genotypes for agronomic, morphological, physiological, and phenological traits.

Trait group	Plant traits	Parameters					
		Mean	Std. error	Minimum	Maximum	Range	Std. deviation
Agronomic	Seed yield per plant (g)	12.9	0.695	1.0	41.8	40.8	7.286
	Dry matter yield per plant (g)	78.6	2.887	7.8	182.2	174.4	30.277
	Biological yield per plant (g)	91.5	3.392	9.8	211.2	201.4	35.580
Physiological	Percent fertile stem	51.6	1.365	23.5	87.6	64.1	14.317
	Harvest index	14.0	0.493	2.9	32.6	29.7	5.173
	Fertility index	1.67	0.075	0.27	5.35	5.08	0.788
Morphological	Plant height (cm)	94.0	1.647	60.5	134.0	73.5	17.271
	Panicle length (cm)	11.3	0.266	6.1	20.2	14.1	2.786
	Crown diameter (cm)	19.5	0.326	10.4	27.6	17.2	3.420
	Fertile stems per plant	73.9	3.650	17.5	221.3	203.8	38.280
	Sterile stems per plant	69.3	2.495	20.0	140.3	120.3	26.165
	Total stems per plant	143.2	3.883	55.7	273.8	218.1	40.723
	Stem intensity	0.56	0.021	0.22	1.54	1.32	0.224
Phenological	Heading date	70.1	0.380	82.3	103.2	20.9	3.988
	Anthesis date	106.5	0.328	103.5	118.8	15.3	3.441

Table 4. Estimates of components of genotypic variance (S^2_G), genotype × year interaction variance (S^2_{GY}), environmental variance (S^2_β and S^2_ε), broad-sense heritability (h^2_b), genotypic (GCV), phenotypic (PCV), and environmental (ECV) coefficients of variability, and expected genetic gain (R) for all the traits of orchardgrass genotypes for 2 years (2001–2002).[Ŧ]

Plant traits	Parameters[‡]								
	$S^2_G \pm$ SE	$S^2_{GY} \pm$ SE	$S^2_\beta \pm$ SE	S^2_ε	$h^2_b \pm$ SE	PCV	GCV	ECV	R (%)
SdY	47.83 ± 7.3**	51.98 ± 7.7**	11.81 ± 4.1**	21.08	0.64 ± 0.10	66.94	53.61	35.60	60.11
DMY	703.56 ± 30.4**	607.30 ± 29.9**	470.99 ± 25.8**	861.99	0.55 ± 0.02	45.61	33.75	37.35	34.96
BioY	1011.80 ± 16.3**	773.81 ± 17.9**	632.78 ± 22.0**	965.05	0.58 ± 0.01	45.68	34.76	33.95	37.04
% FrSt	178.95 ± 14.5**	456.72 ± 22.6**	19.51 ± 9.5 ns	159.82	0.49 ± 0.04	37.16	25.92	24.50	25.32
HvInd	31.50 ± 2.5**	87.33 ± 3.7**	−1.50 ± 4.5 ns	40.03	0.47 ± 0.04	58.59	40.09	45.19	38.41
FrInd	1.07 ± 0.7**	2.64 ± 1.0**	−0.11 ± 1.2 ns	2.74	0.44 ± 0.28	92.86	61.88	99.19	57.73
PH	288.78 ± 17.4**	31.73 ± 7.4**	21.22 ± 6.8*	70.46	0.90 ± 0.05	19.08	18.08	8.93	23.98
PnLng	7.20 ± 2.8**	2.47 ± 1.9**	0.27 ± 1.3 ns	3.16	0.83 ± 0.32	26.08	23.75	15.74	30.28
CrD	9.47 ± 1.6**	6.46 ± 1.4**	8.83 ± 1.7**	6.02	0.56 ± 0.09	21.17	15.78	12.58	16.47
FrSN	1372.00 ± 38.3**	1032.29 ± 35.1**	−8.54 ± 17.1 ns	592.89	0.76 ± 0.02	57.65	50.12	32.95	61.01
SrSN	583.83 ± 26.8**	1533.30 ± 42.7**	−47.92 ± 20.3 ns	868.90	0.47 ± 0.02	50.81	34.87	42.54	33.50
TtSN	1471.26 ± 41.0**	1148.81 ± 39.8**	−66.36 ± 24.9 ns	1308.44	0.71 ± 0.02	31.79	26.79	25.26	31.60
StIn	0.03 ± 0.2**	0.07 ± 0.3**	0.00 ± 0.3 ns	0.21	0.34 ± 2.09	53.46	31.23	81.87	25.54
HdDt	13.67 ± 4.0**	8.59 ± 3.5**	1.58 ± 2.4 ns	10.12	0.72 ± 0.21	6.21	5.27	4.53	6.25
AnDt	11.05 ± 0.9**	7.75 ± 1.3**	0.03 ± 1.5 ns	4.77	0.77 ± 0.24	3.57	3.12	2.05	3.82

[Ŧ]: *, **, and ns, Mean squares associated with variance component were significant at the $P < 0.05$, 0.001 levels and nonsignificant, respectively.
[‡]: S^2_β and S^2_ε are the interactions of genotype × block (whole plot error) and genotype × year × block (subplot error), respectively; SE is standard error.

height to 1471.26 for number of total stems, resulting in those traits' greater contributions to observed variability among the genotypes. The genotypic variances (S^2_G) were larger than the interaction variances (S^2_{GY}), suggesting that all traits might be relatively stable across environments, except physiological traits, seed yield, number of sterile stems, and stem intensity (Table 4). On the other hand, the estimates of components of the environmental variances (S^2_β and/or S^2_ε) for dry matter yield and its components (numbers of fertile, sterile, and total stems) and biological yield were greater than those for the other traits. The variance of the environmental effect (S^2_ε) was the largest of all the effects for dry matter yield. The SEs estimated for all the components were smaller, reflecting higher precision, than those of similar investigations by Nguyen and Sleper (1983, 1985) of tall fescue and by Rognli (1987) of timothy, probably due the single plant basis and lower number of clones per replication in their studies, respectively.

The relative contributions of the different variance components to the phenotypical variance of each trait are depicted in Figure 1. The contribution of genotypic variance to the phenotypical variance was larger than the total contribution of nonheritable components for all the traits (except stem intensity, number of sterile stems, fertility index, harvest index, and fertile stem percentage). The only trait in which phenotypical variation was primarily influenced by the environmental component was stem intensity, indicating the great masking effect of environment on the genotypical effect. After the genotypical component for the traits under consideration, the genotype × year interaction component was the main contributor for the phenotypic variations in most of the traits, except plant height and panicle length. Environmental effects were the main contributors only for crown diameter, dry matter yield, and biological yield, as shown in Figure 1. The genotype × year interaction component in particular contributed to the total phenotypical variation for 3 physiologic traits with number of sterile stems nearly as much as genotypic component did.

One of the best tools for comparing various plant traits of different scales is the coefficient of variation, or the relative amount of variability to the corresponding phenotypical mean of a trait as a percentage (Rognli, 1987). The results (Table 4) revealed that all the agromorphological and physiological traits had greater coefficients of variation; these were lower for the phenological traits of earliness as an indicator of less scope for improvement. The phenological traits of the genotypes were the least

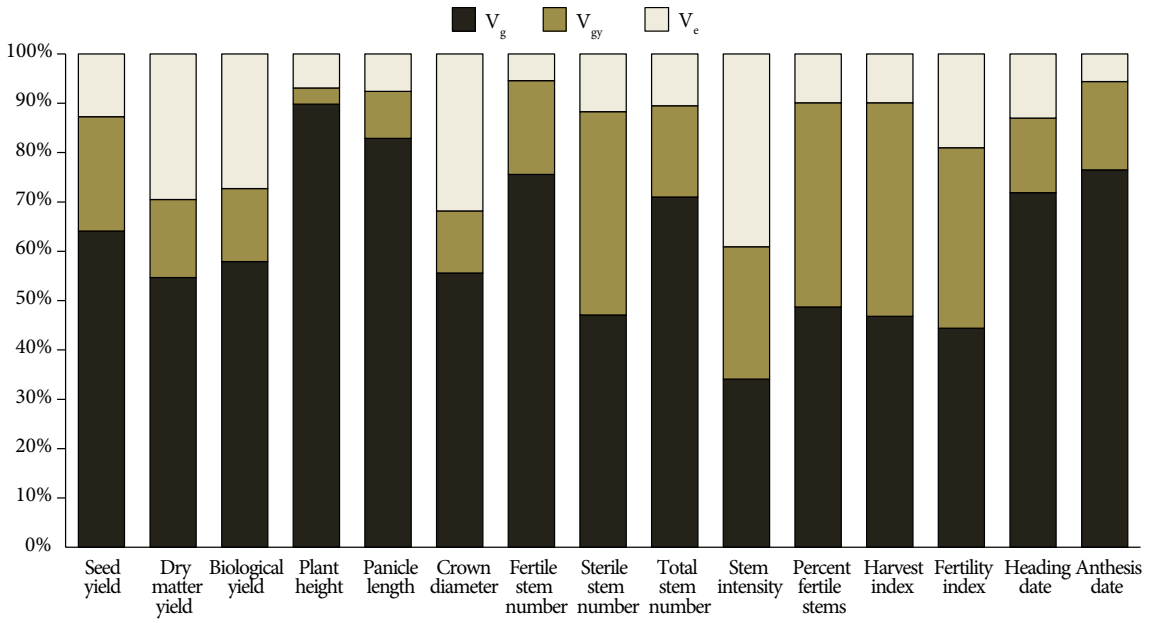

Figure 1. Relative contributions of different variance components to the phenotypical variation for the various traits of the genotypes; V_g, V_{gy}, and V_e = genotypic, genotype × year interaction, and environmental variances, respectively; $V_e = S^2_\beta + S^2_\varepsilon$.

variable, as reported previously for various forage crop plants (Rognli, 1987; Jafari and Naseri, 2007). The results indicated that fertility index had the highest phenotypic coefficient of variability (92.86%), followed by seed yield, harvest index, number of fertile stems, stem intensity, and number of sterile stems in descending order, ranging from 66.94% to 50.81%. High PCV is an indicator of a considerable amount of variability for the improvement of the traits by selection. Fertility index exhibited the greatest genotypic coefficient of variation (61.88%), despite a low corresponding genetic variance. Fertility index was followed by seed yield (53.61%) and number of fertile stems (50.12%) as a measure of exploitable genetic variability. However, the magnitude of the differences between GCV and PCV values could be a measure of the extent of the environmental influence on these traits; larger differences reflect greater environmental influence on the expression of traits. This can also be seen from the increasing environmental variation as the differences between GCV and PCV values increased. Fertility index had the largest ECV (99.19%) and was followed by stem intensity (81.87%), reflecting the largest environmental influence on their expressions. After phenological traits, ECV was the lowest for plant height, crown diameter, and panicle length.

Heritability estimates in a broad sense (h^2_b) with SEs for the traits under consideration are presented in Table 4 and also depicted visually as the columns of genotypic variances (S^2_G) in Figure 1. As the value of GCV approached that of PCV, the heritability estimate increased, as happened in plant height and panicle length, indicating that those traits were mostly governed by genetic factors with minimal environmental influence on their phenotypical expression. Contrary to this, the heritability estimates decreased as the difference between the PCV and GCV increased alongside increasing ECV, as observed in stem intensity and fertility index. This caused a reduction in the response to phenotype-based selection. Thus, the heritability estimates in a broad sense for the various traits of the study were greatly different (h^2_b = 34%–90%). In the present study, heritability estimates based on combined analyses taking into account the components of genotypic × environment interactions were at least 2.6 times greater than their SEs, except stem intensity and fertility index (less than twice that of the corresponding SE; Table 4). The traits (plant height, panicle length, anthesis date, number of fertile stems, heading date, and number of total stems) showed very high heritability (0.90%, 0.83%, 0.77%, 0.76%, 0.72%, and 0.71%, respectively), which suggested that selection for these traits would be effective in future breeding programs as they are likely to be controlled by additive genes. Regarding plant height in particular, a large proportion of genetic variance is additive (Berdahl and Barker, 1997). This is true for other traits, including maturity score, number of fertile stems, panicle length, and seed yield (Nguyen and Sleper, 1983; Jafari and Naseri, 2007), while both additive and nonadditive gene effects for dry matter yield were reported (Jafari and

Table 5. Principle component (PC) analysis associated with 110 orchardgrass genotypes showing eigenvalues, eigenvectors, and total and cumulative total variances of 15 plant traits in the first 5 PC axes.

Parameters	PC Axes					Communality
	1	2	3	4	5	
Eigenvalue	5.856	2.203	1.828	1.660	1.188	
Cumulative eigenvalue	5.856	8.059	9.887	11.547	12.735	12.735
Total variance (%)	39.04	14.69	12.19	11.07	7.92	
Cum. total variance (%)	39.04	53.73	65.92	76.99	84.91	0.849
	Eigenvectors					
Plant Traits	1	2	3	4	5	Communality
Seed yield	0.771	0.523	0.195	0.232	–0.059	0.963
Dry matter yield	0.857	0.069	0.083	–0.232	0.034	0.801
Biological yield	0.887	0.166	0.111	–0.150	0.017	0.850
Plant height	0.767	–0.226	–0.068	0.055	–0.034	0.648
Panicle length	0.847	–0.208	–0.076	0.111	–0.047	0.780
Crown diameter	0.698	–0.333	0.181	0.020	–0.468	0.851
Total stems per plant	0.698	0.138	0.461	–0.340	0.092	0.844
Fertile stems per plant	0.881	0.114	–0.061	–0.045	0.201	0.836
Sterile stems per plant	–0.202	0.047	0.808	–0.464	–0.151	0.933
Stem Intensity	–0.157	0.530	0.142	–0.170	0.755	0.924
Percent fertile stems	0.696	0.011	–0.504	0.281	0.217	0.863
Harvest index	0.133	0.665	0.100	0.606	–0.159	0.862
Fertility index	–0.335	0.640	0.278	0.396	–0.299	0.846
Heading date	–0.028	–0.563	0.484	0.520	0.253	0.887
Anthesis date	0.062	–0.456	0.513	0.528	0.305	0.847

Naseri, 2007). Phenotypical selection would be more suitable for these traits. Heritability estimates for crown diameter and agronomic traits, which are complex traits, were tolerably lower (ranging from 55% to 64%) than the former traits. Heritability was moderate for all remaining traits, including all 3 physiologic traits, ranging from 0.34% to 0.49%, due to the greater contribution of nonheritable variance components. Most of the results are in accordance with findings by Nguyen and Sleper (1985) in tall fescue, Rognli (1987) in timothy, and Jafari and Naseri (2007) in orchardgrass for plant height, heading date, number of fertile stems, panicle length, seed yield, and dry matter yield. The high heritability determined for heading and anthesis dates in the present study due to low nonheritable components is in accordance with the findings in many grasses reported by Nguyen and Sleper (1985), Rognli (1987), and Jafari and Naseri (2007). Therefore, it can be inferred that the heritability estimates of these traits increased as the difference between PCV and GCV decreased, regardless of their magnitudes. Thus, heritability was not always accompanied by high GCV, which is in accordance with the findings of Kandil et al. (2012) in flax.

Expected genetic gains estimated as a percentage of the means (Table 4) were the greatest with number of fertile stems (61%) and seed yield (60%) due to both

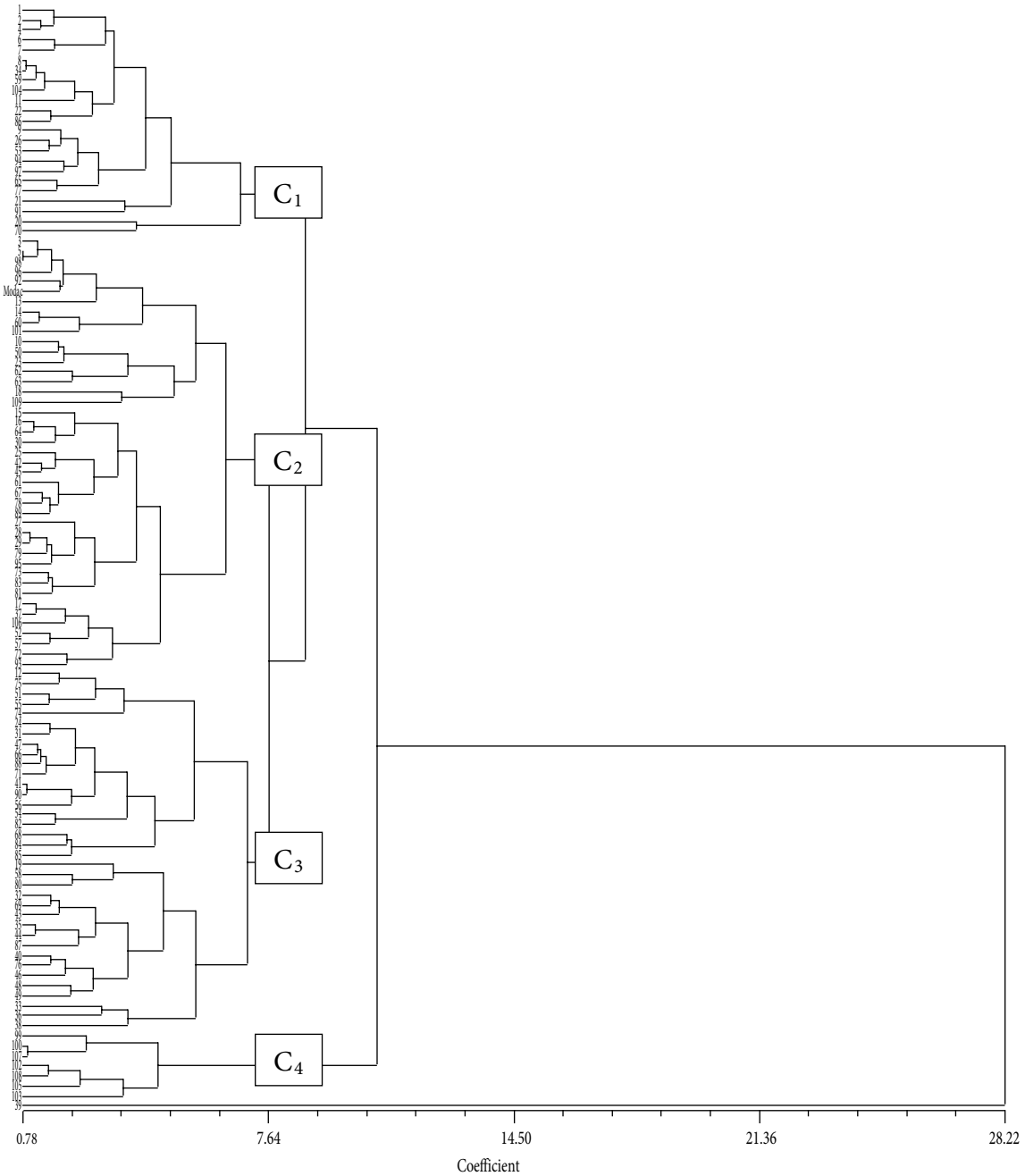

Figure 2. Dendrogram of 110 genotypes of orchardgrass (*Dactylis glomerata* L.) using UPGMA, including cultivar Modac as the control. C_1, C_2, C_3, and C_4 are clusters 1–4, respectively.

high heritability and PCV. They were followed by fertility index (58%), which had the highest PCV but lower heritability. The lowest rates for the phenological traits of high heritability (>70%) were due to significantly lower GCV and PCV. It was moderate (16% to 38%) for the other agromorphological and physiological traits. Despite high heritability (>70%), plant height, panicle length, and number of total stems exhibited significantly low genetic gains, due in particular to their low PCVs, which were lower or equal to those of all the agrophysiological traits and number of sterile stems for the moderate heritability estimates. Thus, as speculated by Kandil et al. (2012), a selection based on phenotypical variations of the traits based on heritability estimates and strong GCV values would be better at predicting the resulting effects of selection than with heritability values alone. Based on

Table 6. Mean, range (min– max), and standard deviation (SD) of traits used in classification of 4 clusters.†

Cluster	Parameter	SdY	DMY	BioY	%FrSt	HvInd	FrInd	HdDt	AnDt
C4 (n = 7)	Min–max	20.3–41.8	103.5–182.2	124.0–211.2	63.5–87.6	13.7–24.2	0.6–1.39	85.0–93.0	103.5–112.2
	Mean*	27.7 A	134.0 A	161.8 A	77.9 A	17.1 a	1.00 B	88.9 B	106.3 B
	SD	7.85	27.28	31.48	9.93	3.48	0.32	3.26	2.92
C3 (n = 36)	Min–max	1.0–16.8	7.8–132.2	9.8–145.3	23.5–66.5	7.4–26.2	0.68–3.31	83.0–100.5	104.0–117.5
	Mean	9.6 C	60.6 B	70.2 B	46.0 C	14.6 a	2.06 A	89.9 A	106.1 B
	SD	4.19	29.23	31.91	10.91	5.24	0.72	3.64	2.97
C2‡ (n = 43)	Min– max	2.0–25.8	32.0–125.5	38.5–138.6	26.7–87.1	2.9–21.3	0.27–3.10	82.3–99.0	103.7–116.0
	Mean	9.9 C	76.5 B	86.4 B	58.6 B	11.3 b	1.28 AB	89.8 AB	106.0 B
	SD	4.94	21.38	24.40	14.35	4.17	0.54	3.64	3.06
C1 (n = 23)	Min–max	10.3–31.5	52.3–124.1	74.3–144.8	32.6–69.7	11.3–32.6	1.25–5.35	83.3–103.2	104.0–118.8
	Mean	18.8 B	92.8 B	111.6 B	52.8 BC	17.0 a	2.03 A	91.4 A	107.7 A
	SD	5.44	19.35	21.24	8.93	4.96	0.90	5.21	4.78
Cluster	Parameter	PH	PnLng	CrD	FrSN	SrSN	TtSN	StIn	
C4 (n = 7)	Min–max	101.8–120.2	15.3–20.2	23.0–27.6	136.8–221.3	2.5–97.7	165.3–273.8	0.41–0.56	
	Mean*	110.8 A	17.0 A	24.8 A	168.8 A	53.5 B	222.3 A	0.48 B	
	SD	6.01	1.64	1.70	33.93	28.44	37.87	0.056	
C3 (n = 36)	Min–max	60.5–104.2	6.1–11.9	10.4–21.1	17.5–98.9	34.8–140.3	76.3–196.5	0.23–1.54	
	Mean	80.2 C	9.1 C	16.9 C	52.5 C	76.2 AB	128.7 C	0.69 A	
	SD	11.02	1.53	2.64	19.56	26.40	30.37	0.28	
C2* (n = 43)	Min–max	68.3–134.0	7.5–15.3	13.9–24.5	21.7–150.8	20.0–117.0	55.7–202.5	0.22–1.30	
	Mean	98.31 B	11.6 B	20.0 B	71.3 C	56.7 B	128.0 C	0.46 B	
	SD	17.36	2.29	2.77	32.00	21.84	31.89	0.17	
C1 (n = 23)	Min–max	69.0–123.3	7.7–15.5	13.7–27.0	44.6–165.2	52.5–123.7	129.9–264.8	0.27–0.90	
	Mean	101.8 B	12.4 B	20.9 B	81.4 B	86.1 A	167.5 B	0.57 AB	
	SD	14.15	2.00	3.06	25.96	20.39	32.84	0.15	

†: Except genotype 39. *: Different letters in uppercase indicate significance at $P < 0.001$.‡: Including cultivar Modac and n = number of genotypes.

the present findings, clonal evaluation appeared to be adequate for selecting parent plants of high seed yield for highly heritable and stable agromorphological traits with great phenotypic variation, such as plant height, panicle length, number of fertile stems, number of total stems, and seed yield per plant.

The most important variables for seed yield traits were identified by PC analysis. In the analysis with 15 variables, the first 5 components with an eigenvalue greater than 1 were extracted. They contributed 84.90% of total variability among the genotypes (Table 5). PC1 to PC5 explained 39.04%, 14.69%, 12.19%, 11.07%, and 7.92% of the total variance, showing maximum eigenvalues of 5.856, 2.203, 1.828, 1.660, and 1.188, respectively. The first PC in particular was related to all agromorphological traits of the aboveground biomass. All traits with high coefficients (biological yield, number of fertile stems, dry matter yield, panicle length, seed yield, plant height, crown diameter, number of total stems, and fertile stem percentage) were the primary sources of variation in the PC1 score for the genotypes and contributed positively to PC1. Hence, the higher the PC1 score for genotypes, the higher their values for aboveground traits would be, as concluded by Kandil et al. (2012) with flax for seed yield attributes. The PC1 axis was essentially a component dealing with seed yield and agromorphological yield components, which directly or indirectly affect seed yield, as determined in a great variety of grasses (Rognli, 1987; Seker and Serin, 2004; Moradi et al., 2007), as well as on dry matter yield. The plant traits with the greatest positive weight on PC2 were harvest index and fertility index. This axis dealt with assimilate partitioning of plant physiology. The other PC axes dealt with numbers of sterile stems (PC3) and 2 phenological traits of earliness (PC4) and stem intensity (PC5). After studying these patterns, the findings suggested that the genotypes with larger aboveground biomass and greater hay yield components and attributes tended to have greater seed yield without any change in harvest index, despite the great reduction in fertility index as aboveground plant size increased.

The genotypes were grouped into 4 clusters based on average linkage, with genotype 39 discarded. A distance coefficient of 7.64 was chosen to separate the genotypes into 4 cluster groups in a dendrogram (Figure 2; Table 6). The genotypes from a defined geographic area (Tortum District, Erzurum) tended to assemble in cluster 4(C4) of the 7 genotypes; other genotypes from various locations of the region were spread across the other 3 cluster groups. A similar result was reported by Parsa et al. (2012) for orchardgrass accessions. Mean values along with standard deviations (SDs) for each cluster (Table 6) revealed that the genotypes in C4 had greater agromorphological traits, which are important characters for both seed yield and dry matter yield, but shorter periods to reach certain phenological dates than in other clusters. Thus, they were significantly faster in aboveground biomass accumulation, resulting in greater biological yield. This result is in accordance with the findings of Martiniello (1998), who suggested that selection for early flowering accessions of tall fescue would increase both seed yield and dry matter yield.

Consequently, considerable amounts of genetic variability were determined among the orchardgrass genotypes for all the traits under consideration. The relative contribution of genetic variance to phenotypical variance was larger than the total contribution of nonheritable components for all the traits (except stem intensity, number of sterile stems, and 3 physiological traits, all which were very variable traits with <50% broad-sense heritability). Agromorphological traits were the principal sources of variation. The results obtained from this study should be useful for grass breeders and seed producers concerned about simultaneous high seed and hay yield. Strict selection for the many-culmed genotypes of large aerial biomass with longer panicle lengths could result in greater seed yields, despite its adverse effect on fertility due to low seed set.

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