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Genetic diversity evaluation of *Agropyron desertorum* genotypes by path coefficient analyses for determination effective traits on grain yield in moderate climate condition (Arak Region)

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Abstract

Identifying key yield components can help establish better crop management strategies to increase crop yield. The present research was conducted in moderate conditions of the Arak region to determine the interrelationships among various yield components and their direct and indirect effects of each component on grain yield of 31 genotypes of *Agropyron desertorum* were densely planted in randomized complete block design with four replications. Some of the most important morphological and physiological attributes were measured. The data collected in two years were analysed; principal components analysis and cluster analysis were used to determine genetic distance and genotype classification. In principal components analysis, the specific values obtained from 1 to 5 components were larger than one. Totally, 75 percent of all variances justified the variables. In the first component, attributes of ear emergence time, pollination time, plant height, and forage yield, and in the second component, attributes including number of stems, grain yield, and harvest index had greater specific vector coefficients besides major attributes for genotype classification. Correlation coefficients between grain yield and other attributes including harvest index, number of spike lets in ear, number of stems, and forage yield were positive and significant.

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Introduction

Understanding of interrelationship between component characters helps in determining which character to select when improvement of the related complex character is desired. The correlation coefficient measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for the improvement in associated complex character – yield (Zecevic *et al.*, 2004, Leilah and Al-Khateeb, 2005; Ahmad *et al.*, 2010; Sokoto *et al.*, 2012; Mohammadi *et al.*, 2012). Simple correlation is partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) and environmental (environmental deviation together with non additive genetic variation) components (Singh and Chaudhary, 1985).

Abderrahmane *et al.* (2013) reported that total biomass, number of spikes per plant, number of grains per spike are positively correlated with grain yield. Grain yield per plant was positively correlated with grains per spike, harvest index, spikes per plant, spike length and 1000 grain weight (Majumder *et al.*, 2008). In a study aimed to know relationships between grain yield and yield components in bread wheat under different water availability, Mohammadi *et al.* (2012) reported that grain yield was positively correlated with plant height, spike length, days to physiological maturity, agronomic score and test weight.

Path coefficient analysis, developed originally by Wright (Wright, 1921) and elaborated by Dewey and Lu (1959) and others, has been used to determine the direct and indirect effects of individual yield components on final grain yields in annual pulses such as dry bean (*Phaseolus vulgaris* L.), soybean (*Glycine max* L.) and chickpea (*Cicer arietinum* L.) (Ball *et al.*, 2001; Guler *et al.*, 2001; Gan and Liu, 2005). Path analysis also has been used to determine the interrelationships between grain yields and morphological characteristics in crops such as crested wheatgrass (Dewey *et al.*, 1959), spring wheat (Gebeyehou *et al.*, 1982) and spring barley (*Hordeum vulgare* L.) (Garcia del Moral *et al.*, 1991). Path coefficient analyses usually partition correlation coefficients into direct and indirect effects of various yield components, based on the assumption of mutual relationships among yield components. Statistically, path coefficient is a standardized partial-regression coefficient, obtained from equations, where the yield-related variables are expressed as deviations from the means in units of standard deviation (Steel and Torrie, 1982). *Agropyron desertorum* is one of the valuable fodder Graminaes for creating pastures and for forage production. Plants of *Agropyron* type have good compatibility with dry Mediterranean climatic conditions like that of Iran (Cerpo, 2000; Mehmet, 2014). In order to maximally benefit from dry matter production, the plant is normally cropped after flowering and just before start of pollination. Harvesting later than this stage, despite increase in forage yield, would result in sever worsening of forage grass quality (Jafari *et al.*, 2003).

The plants of this species are outcrossing and tetraploid having 28 chromosomes plus one additional chromosome (Asghari *et al.*, 2007). These plants have originated from central Asian plains; they feature other desirable characteristics such as durable drought persistence (Mellish *et al.*, 2002). Today, along with forage yield enhancement, grain production of forage plants is also particularly significant. Prior to implementation of selective modification plans, it is required to know the relationship between grain yield and its components; because success in modification and production of highly-reproductive cultivars depends upon identification of genetic control of grain yield and its relationship with other yield components and morphological attributes (Jafari and Rezaeifaed, 2010). Although correlation coefficients are widely used for determining and explaining the degree of relationship between two attributes, they might become deceptive since good correlation between two attributes may have resulted from indirect effects of other attributes, and using simple correlation analysis might not generally explain the relationships between attributes (Ali *et al.*, 2003; Gelalcha and Hanchinal, 2013). Therefore, it is necessary to differentiate the direct and indirect effects of attributes affecting the yield. Path analysis enables breeder to distinguish the direct impact of each yield component from indirect effects caused by mutual relationships among them (Emam and Borjan, 2000). For the same purpose, plant modification experts utilize path analysis method as a technique for determining significance of attributes affecting the yield (Jafari *et al.*, 2003). Selection with generation testing is one of the breeding methods of forage plants. Success in selection is dependent on the diversity that creates new genetic combination and heterosis. Heterosis likelihood in anastomosis plants goes up by increasing the genetic distance between genotypes (Humphreys, 1991). The objective of the study was to reveal clear relationships between grain yield and its affecting components to determine true selection criteria for grain yield in *Agropyron desertorum* genotypes. For this reason, it was determined simple correlation coefficients and direct and indirect effects based on path coefficients using field trial data collected from 31 *Agropyron desertorum* genotypes.

Material and methods

Field and Treatment Information's

31 genotypes of *Agropyron desertorum* were collected from natural resource genetic bank of Iran's Forests and Forages Research Organization. The experiment plot was located in the research field of Islamic Azad University of Arak City (with longitude: 50°57`, latitude: 34°33' and altitude 1760 m from free sea level). It was disked in autumn 2003 following composting with 200 kg phosphate and 100 kg nitrogen fertilizers per hectare. The test was implemented at the density of 10 kg of grain per hectare and in randomized complete blocks design with four replications. The experimental plots had 1*2 meters dimensions consisting of four 2-meter lines, 25 cm apart from each other.

Traits measure

In this research, attribute measurements were conducted for two years as follows:

1) Ear emergence time: based on number of days from 21 March until emergence of one third of ears in each plot

2) Pollination time: based on number of days from 21 March until emergence of anthers in one third of each plot

3) Plant height: 10 plants were randomly selected in each plot and the longest stem was chosen in each plant; the height was measured in centimeters and the average was recorded as the plant height

4) Number of stems: 10 plants were randomly selected in each plot and the average number of reproductive tillers was identified

5) Forage yield: after cutting forage of each plot from height of 6cm, the samples were dried in oven at 75° C for 12 hours and then weighed and expressed in tones per hectare

6) Ear length: 10 plants were randomly selected from each plot and the average length of ears was measured with a ruler in centimeters

7) Number of grains in ear: 10 plants were randomly selected from each plot and number of grains was counted and averaged

8) Grain weight in ear: after cleaning and winnowing ten ears in each plot, the average grain weight was computed in each ear

9) Number of spikelets in ear: 10 plants were randomly selected from each plot and number of spikelets was counted and averaged

10) Weight of 100 grains: was evaluated by counting and weighing 1000 grains by grain-counter machine

11) Flag leaf surface area: 10 plants were randomly selected from each plot and average of multiplication of width by length of the flag leaf was computed in square centimeters

12) Peduncle length: Average distance between ear and flag leaf and in each plant was measured in centimeters for 10 selected plants in each plot

13) Grain yield: after cutting and drying all plants of each plot, and threshing and separating the chaffs and straws, the grain weights were measured in kg.hectare^{-1}

14) Harvest index: was obtained by dividing grain weight of each plot to the weight of aerial biomass

Simple phenotypic correlation coefficients between fourteen attributes and stepwise regression coefficients for identifying significant attributes affecting grain yield were computed (Table 1).

Table 1. Correlation analysis between traits.

Traits	Spike Appearance date	Pollination date	Plant height	Tiller number	DM yield	Spike length	Leaf size	Grain weight per spike	Grain yield	Grain no. per spike	Spikelet no. per spike	Thousand grain weight	Harvest index
Pollination date (day)	**0.91****												
Plant height (cm)	**-0.51****	**-0.44****											
Tiller number (No/m^2)	-0.03	-0.10	0.17										
DM yield (t/ha)	-0.25	**-0.40***	**0.60****	**0.46****									
Spike length (cm)	-0.12	-0.10	-0.03	0.03	0.21								
Leaf size (cm^2)	0.18	0.28	-0.01	0.21	-0.20	-0.09							
Grain weight per spike (g)	-0.24	-0.29	0.26	-0.19	**0.36***	0.18	**-0.45****						
Grain yield (kg/ha)	0.00	-0.05	0.02	**0.79****	**0.44****	0.28	0.01	0.16					
Grain number per spike	-0.12	-0.23	0.17	-0.09	**0.34***	0.26	**-0.39***	**0.71****	0.07				
Spikelet number per spike	-0.16	-0.22	-0.10	0.08	-0.04	0.26	-0.14	0.14	**0.31***	0.05			
Thousand grain weight	-0.08	-0.01	0.15	-0.04	0.06	-0.04	-0.12	0.29	0.18	**-0.34***	0.06		
Harvest index (%)	0.28	0.13	-0.23	**0.52****	**-0.36***	-0.06	0.01	-0.12	**0.66****	-0.12	0.26	0.05	
Length of peduncle (cm)	-0.04	0.07	0.08	-0.06	0.05	0.20	0.17	0.13	-0.06	-0.14	-0.14	0.25	-0.29

*significant at the 0.05 probability level, ** significant at the 0.01 probability level.

Statistical analysis

Path analysis was subsequently performed to identify the direct and indirect effects of significant attributes imposed to regression model (Table 2). The software SAS.8. and Path.2 were used to statistically analyze the data.

Table 2. Path coefficients of direct and indirect effects of the measured traits.

Traits	Direct effect	Indirect effect				Total effect correlation
		Tiller number	Harvest index	DM yield	Spike length	
Tiller number	0.310		**0.332**	0.184	-0.030	0.79
Harvest index	**0.631**	0.163		-0.132	-0.002	0.66
DM yield	**0.518**	**0.202**	-0.062		-0.041	0.42
Spike length	-0.06	0.191	0.015	0.112		0.26

Residual Error = 0.35.

Results and discussion

Correlation between attributes

Explaining the relationship between grain yield and morphological attributes is highly important in implementation of selection plans. For this reason, correlation coefficients between grain yield and other attributes were computed. The correlation between grain yield and number of stems per plant was positive and significant at 1% probability level. In other words, a higher capability to produce reproductive stems would bring about higher grain yield in a genotype. Results of binary phenotypic correlation analysis between averages of attributes are shown in Table (1). Similar positive correlation between grain yield and number of stems per plant was reported in *Setaria sphacelata* by Hacker and Cauny (1997), in *Dactylis glomerata* by Jafari and Naseri (2007), and in *Bromus catharitcus* by Abbott *et al.* (2007). Also, correlation coefficients between grain yield and other attributes including harvest index, number of spikelets in ear, number of stems, and forage yield were positive and significant. Such correlation is expected taking into account that harvest index is obtained from the ratio of grain yield to biomass yield. Also, the positive and significant relationship between forage yield and plant height, number of reproductive stems, number and weight of grains in ear, and grain yield indicate the significance of these attributes in forage yield improvement. Negative correlation of forage yield with pollination time is indicative of the fact that the sooner a genotype starts its pollination, the higher is forage yield. Similar results were reported by Jafari *et al.* (2006) in tall fescue and by Jafari and Naseri (2007) in *Dactylis glomerata*.

Regression analysis

In stepwise regression analysis, grain yield was treated as the dependent variable of function (Y) and the attributes: number of stems (X_1), harvest index (X_2), forage yield (X_3) and ear length (X_4) were regarded as independent variables; the following equation was obtained:

Formula 1. $Y= -383.25+0.38X_1+19.10X_2+93.9X_3+21X_4$

The significant determination coefficient ($R^2= 0.90$) observed in the above regression equation indicates effectiveness of these attributes in grain yield improvement. As observed, all attributes X_1-X_4 affected grain production with positive coefficient. Comparison of regression and correlation coefficients is suggestive of agreement between regression and correlation analyses reconfirming the significance of aforementioned attributes in enhancement of grain and forage yields in *Agropyron desertorum*. Similar to these results, Jafari and Naseri (2007) reported a positive and significant correlation between grain and forage yields of *Dactylis glomerata* in which grain yield was function variable and other attributes were supposed as independent variables.

Path analysis

In path (causality) analysis, grain yield was similarly supposed as the function variable and the rest four attributes in the stepwise regression model (number of stems, harvest index, forage yield and ear length) were introduced as independent variables (Table 2). As the path analysis results suggest, harvest index showed the greatest direct effect on grain yield; its total effect was 0.66. After harvest index, forage yield and number of reproductive stems assumed the largest direct effects on grain yield improvement. Number of reproductive stems exhibited the largest indirect effect (through improvement of harvest index) on grain yield.

Furthermore, forage yield, in additions to its direct effect, indirectly influenced grain yield enhancement (through an increasing number of stems).

Conclusion

Its recommended to use cultivars with high grain and forage yields for producing synthetic cultivars and to create heterosis via anastomosis between genotypes featuring desirable attributes, which possess the largest portion in principal components analysis and greatest genetic distance in cluster analysis.

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