

Research Paper

Genetic variation of agronomic traits in a global collection of oats (*Avena sp.*)

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Abstract

This study aimed to evaluate the variation in agronomic traits of 361 cultivated oat genotypes and to identify superior genotypes for oat breeding programs. The experiment was conducted as a simple square lattice design with two replications for two growing seasons (2018-2019 and 2019-2020) in Kermanshah, Iran. There was a significant difference among oat genotypes. The highest grain yield (GY) was obtained in the “OX87:080-2” and “LA Prevision” genotypes. Furthermore, genotypes “Rubida” and “VDO-931-1” were superior regarding the biomass. Several analyses were performed using the best linear unbiased prediction estimates. The correlation coefficients showed a significant positive relationship between GY and biomass, 1000-kernel weight (TKW), and the number of panicles per plot. Biomass was positively and significantly correlated with all studied traits, except TKW. The number of grains per panicle (NGPP) and TKW had the highest positive direct effects on the GY and NPPP imposed the highest positive indirect effect through TKW. While the highest negative indirect effect was exerted by the NGPP through the TKW. The results of pseudo-F for cluster analysis grouped genotypes in five separate groups. The fifth group had the highest values for GY, biomass, TKW, and NPPP. So, these genotypes could be considered as qualified parents to produce superior lines in breeding programs.

Keywords: agronomic traits, BLUPs, genetic diversity, multivariate analyses, oats

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Introduction

A healthy lifestyle depends largely on consuming rich foods free from harmful substances. Oat is an excellent source of soluble fiber, protein, vitamins, carbohydrates,

minerals, polyphenols, and fat. It plays a crucial role in minimizing the effects of micronutrient deficiencies in the body and also has a high potential to provide minerals and essential fatty acids (de Oliveira Maximino et

al. 2021). From another point of view, oats belong to the group of useful grains, that are important in terms of grain yield (GY), dry fodder production, and manufacture of dietetic, and medicinal products (Batalova *et al.* 2019). Oat and barley are considered to be the richest sources of soluble dietary fiber, particularly beta-D-glucan in cereals (Ahmad *et al.* 2010). The beta-glucan content of oats varies between 1.8-7% and is highly dependent on the characteristics of the environment, the plant's food supply, and the growth conditions of the crop (Clemens and van Klinken 2014). The protein content of oats is between 13 and 20% (Paudel *et al.* 2021). In addition, the amount of fat, nitrogen, and starch are 7%, 14%, and 60%, respectively (Holland *et al.* 2001). Because of the health-promoting properties of oats, there is a need to improve grain yield and quality through breeding programs (Musa Özcan *et al.* 2006).

Oats ranked fifth in cultivated areas after wheat, rice, corn, and barley which was 9.7 million hectares in 2020 and its world production was around 25 million tons (FAO 2020). This grain is mainly cultivated in the temperate regions of North America and Europe but has received less attention in Asia, South America, and Africa. Due to this

extensive cultivation area, oats have many ecotypes and a high adaptation capacity (Batalova *et al.* 2019).

Genetic diversity is a main factor in the maintenance of a population in changing environments. Therefore, understanding the diversity of plant materials is critical for the application of appropriate methods in breeding programs (Kumar *et al.* 2009). The decrease in the genetic diversity of cereals, including oats, is one of the major challenges for plant breeders (Frankel and Bennett 1970; Montilla-Bascón *et al.* 2013; Boczkowska and Onysk 2016).

One of the primary methods of studying genetic materials is the assessment of morphological and agronomic traits to investigate the genetic diversity of various plant species. Given that GY is a polygenic trait and it is strongly influenced by the environment, the study of traits that affect the GY is critical to the success of a screening program. The response of oat GY to environmental changes is influenced by the main yield components, namely the number of fertile tillers, the number of grains per spike, the number of spikes, and grain weight (Mahadevan *et al.* 2016). Although the correlation coefficient is used as one of the

methods of determining the relationship between different traits, this criterion alone for determining the relationship of GY with its effective components is not sufficient and other methods such as multiple regression and/or path analysis are needed. Path analysis can provide more accurate and detailed results by analyzing the direct and indirect effects of various characteristics on dependent traits (Hadi *et al.* 2018). To obtain reliable results through indirect selection, traits with high direct effects should be selected and used to develop superior varieties (Wagh *et al.* 2018). In a study, the NGPP had a positive and strong direct effect on GY in spring and winter oat cultivars (McCabe and Burke 2021). The direct and positive effect of the NGPP and grain weight per panicle on GY was reported in a study on GY and its components in oat lines (Dimitrova-Doneva and Savova 2017). The number of panicles per square meter is a significant trait that had a positive effect on GY in normal and water deficit conditions (Zaheri *et al.* 2013). The result of a study on oat genotypes recorded the highest positive direct effects for groats percentage, TKW, dry matter yield/plant, harvest index (HI), and panicle

length (PL), while, the plant height (PH), NGPP, and thousand-groat weight had negative direct effects on GY (Nirmalakumari *et al.* 2013).

Oat, a forgotten crop in Iran, has not been studied extensively. This study focused on the germplasm evaluation of 361 global oat genotypes under Iranian climatic conditions. The main objectives of this research were: 1) assessing the genetic diversity of the oat genotypes from 50 countries for agro-morphological traits affecting GY, and 2) selecting the best genotypes in the two cropping years to be used in subsequent breeding programs to improve the GY and forage yield.

Materials and Methods

Plant materials

In this study, 361 oat genotypes collected from 50 different countries, received from the Australian Grains Genebank (AGG ¹), were investigated (Supplementary 1). Thirty-eight percent of these genotypes belonged to the European continent, and 28%, 19%, 7.5%, and 4.5% to the American, Australian, Asian, and African continents, respectively. However, the

¹Under agreement AGG Reference 2018248

origin of 3% of these genotypes was unknown.

Field trials

A field experiment was carried out as a simple square lattice (19×19) design during two cropping years (2018-2020) under normal irrigation conditions. The experiment was planned at the research field of Razi University in Kermanshah, Iran, which is located in western Iran ($34^{\circ} 21' N$ latitude; $47^{\circ} 90' E$ longitude; 1319 m altitude) with a long-term average annual rainfall of 450-480 mm. The

precipitation regime for two cropping years is shown in Figure 1 and the soil properties are given in Table 1. Seeds of each genotype were sown in two rows of 1 meter long and 0.25 m apart, and 50 seeds per row. Planting was done by hand at the end of November in each year and weeding was carried out by hand during the growing seasons. Depending on the distribution of precipitation in the region, irrigation three to four times per year was carried out depending on the soil moisture.

Table 1. Soil characteristics of the experimental site.

Soil texture	FC (%)	CEC (mg/100g)	EC (ds/m-1)	OC (%)	CaCO ₃ (%)	Ca (mg/kg)	P (mg/kg)	K (mg/kg)	Mg (mg/kg)	PH	Soil particles (%)		
											Sand	Silt	Clay
Loamy	28	18	0.53	1.44	31.41	79.46	14.7	19.83	29.92	7.49	34.6	39	27.6

FC: Field capacity, CEC: Cation exchange capacity, EC: Electrical conductivity, OC: Organic carbon

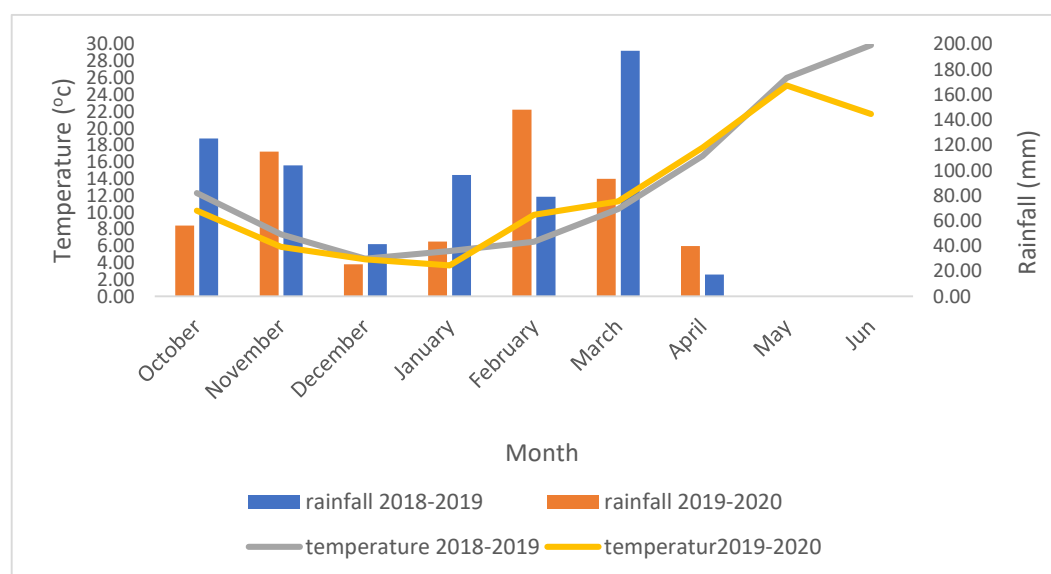


Figure 1. The average monthly temperature and rainfall during the growing seasons in two consecutive crop years (2018-2019 and 2019-2020).

Measuring agronomic traits

The measured traits were GY, NGPP, TKW, PH, PL, HI, number of panicles per plot (NPPP), straw yield (SY), days to heading (DH), days to maturity (DM), and biomass. During the growth phases, phenological traits such as days to 50% of heading and days to 50% of maturity were measured. PH and PL were measured at the physiological maturity stage by randomly selecting five plants from each plot in the field before harvest. Harvesting was carried out from two rows of one meter long (whole plot) to measure GY and biomass. Whole plants in each plot were used to record the number of panicles per plot. five panicles were chosen randomly to measure NPPP.

Data analysis

Combined analysis of variance was accomplished based on best unbiased linear prediction (BLUP) using the META-R software, accounting for year and genotype as random and fixed factors, respectively. Multivariate analyses were conducted on BLUPs (Alvarado *et al.* 2020). Mean comparisons were performed using the LSD method with the 5% probability level.

$$Y_{ijkl} = \mu + \text{Year}_i + \text{Rep}_j (\text{Year}_i) + \text{Block}_k (\text{Year}_i$$

$$\text{Rep}_j) + \text{Gen}_l + \text{Year}_i \times \text{Gen}_l + \varepsilon_{ijkl};$$

μ = Grand average

Year_i = the effects of the i th year

$\text{Rep}_j (\text{Year}_i)$ = the effect of the j th replication in the i th year

$\text{Block}_k (\text{Year}_i \text{ Rep}_j)$ = the effect of k th incomplete block in the i th year in the j th replication

Gen_l = the effect of the l th genotype

ε_{ijkl} = the error associated with the i th year; j th replication, k th incomplete block, l th genotype.

Path analysis, cluster analysis, and the generation of heatmap related to the correlation of traits were carried out by SPSS16 and R-Studio ver. 3.6.3 software, respectively. Cluster analysis was conducted via Ward's method and based on the squared Euclidean distance coefficient to group the 361 oat genotypes based on the measured traits. The SYSTAT 13 software was used to estimate the pseudo-F index (Figure 3) to determine the cutting point of the dendrogram and the number of clusters.

Results

Descriptive statistics and variability

Descriptive statistics and a two-year combined analysis of variance for 361 oat genotypes are

presented in Table 2. Based on these results, a significant genotypic effect was found for all the studied traits. The effect of the year on NGPP, TKW, DH, and DM was significant. The interaction between genotype and year was significant for all the traits, except DM, showing that the difference among genotypes was not consistent in different years.

According to the descriptive statistics (Table 2), the greatest diversity based on the coefficient of variation was recorded for the NGPP (25.55%) and GY (22.45%), respectively. The mean of GY ranged from 164.66 g/plot to 540.98 g/plot with an average of approximately 363.00 g/plot.

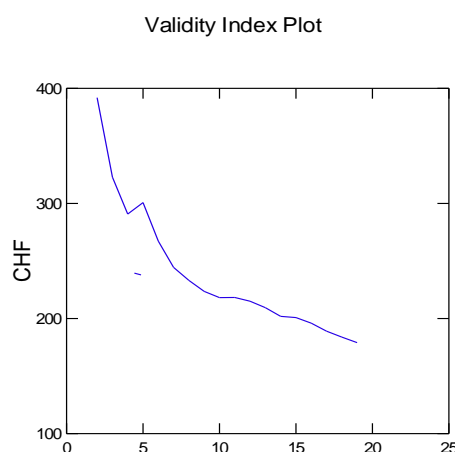


Figure 3. The amount of pseudo-F for determination of the number of groups in the hierarchical cluster analysis.

Table 2. Summary of combined analysis of variance and descriptive statistics related to the studied traits in oat genotypes in two years.

Statistics	GY (g/plot)	NPPP	NGPP	TKW (g)	Bio (g/plot)	SY (g/plot)	PH (cm)	PL (cm)	HI (%)	DH (day)	DM (day)
Mean	363.00	221.84	86.75	26.49	1188.46	825.42	92.26	22.18	0.31	180.55	212.75
Min	164.66	115.15	37.65	13.28	686.68	450.87	53.40	14.56	0.11	163.59	206.41
Max	540.98	412.50	164.29	41.91	1642.29	1330.58	120.78	30.70	0.51	194.33	226.4
F test for Year (Y)	ns	ns	*	*	ns	ns	ns	ns	ns	*	*
F test for Genotype (G)	**	**	**	**	**	**	**	**	**	**	**
F test for G*Y	**	**	**	**	**	**	**	**	**	**	ns
CV (%)	22.45	20.63	25.55	6.25	18.78	20.10	6.89	10.72	15.11	2.30	1.54

ns: Nonsignificant; *, **: Significant at 0.05 and 0.01 levels, respectively; PH: Plant height, PL: Panicle length, NPPP: Number of panicles per plot, NGPP: Number of grains per panicle, TKW: 1000-kernel weight, Bio: Biomass, GY: Grain yield, SY: Straw yield, HI: Harvest index, DH: Day to 50% heading, DM: Days to 50% maturity.

According to the BLUPs (Supplementary 2), the genotypes 336 (OX87:080-2), 203 (LA PREVISION), and 161 (NILE) were high-yielding over the two years. The NPPP fluctuated in the range of 115.15-412.50 and its average was 221.84, for which, genotypes 305 (VIR5226.5), 316 (E/S6409- 3), and 286 (NMO787) had the maximum NPPP. The NGPP ranged from 37.65 to 164.29, with an average of 86.75, and the genotypes 32 (Kalott) and 332 (Munin) had the highest values. The genotypes 250 (Yarran), 56 (AK5), and 20 (Swan) had the highest TKW. The average of this trait over two years was 26.49 grams, and its value for different genotypes ranged from 13.28 to 41.91 grams. The highest two-year average for biomass was obtained for the genotypes 221 (Rubida), 298 (VDO-931.1), and 242 (Yulaf). On the other hand, genotypes 280 (WDO-9326), 300 (SDO-186), and 279 (Forward) produced high SY. The PH ranged from 53.04 to 120.78 cm. which was related to the genotypes 42 (Numbat) and 166 (Alber), respectively. Genotypes 279 (Forward) and 109 (Gordon) had the longest PL. Genotype 26 (Potoroo) had a better HI (51%), and genotypes 1 (Carrolup) and 12 (Echinda) came second with an HI of 45%. Genotypes 111 (Great

Mogul), 124 (Manu), and 267 (Karhu), with an average of 194 days in two years, had the highest DH. Genotypes 21 (Kingfisher), and 109 (Gordon), with an average of 226 days DM, and genotype 135 (Omihi), with an average of 223 DM, were the late-maturing and early-maturing genotypes, respectively. Genotype 17 (GA-Mitchel) with an average of 206 DM, genotypes 67 (P. Lotek), and 151 (South African Skinless) with an average of 207 DM in two years were the early-maturing genotypes.

Correlation among traits

Based on Pearson's correlation coefficients, GY was significantly and positively correlated with biomass, NPPP, TKW, SY, and HI. Conversely, a negative correlation was observed between GY and PL, DH, and DM (Figure 2). The highest positive correlation was observed between GY and biomass. The correlation between biomass and NPPP, NGPP, PH, PL, SY, DH, and DM was positive and significant, while the correlation between biomass and HI was negative and significant. TKW had a positive and significant correlation with biomass, NPPP, and HI, whereas it had a negative and significant correlation with NGPP,

PH, PL, DH, and DM.

Path analysis

The results of path analysis are shown in Table 3. The effects of the NPPP, NGPP, TKW, and SY on GY were investigated according to the logical relationships between these traits. These traits explained 66% of the total

variation for GY. The direct effect of these traits on GY was positive and significant. TKW, NGPP, and NPPP had the largest direct effect on GY, while NPPP exerted the most positive indirect impact on GY via TKW. The NPPP had the highest negative indirect influence on GY via the NGPP. Straw yield had the lowest positive direct effect on GY.

Table 3. Direct and indirect effects of traits on grain yield resulting from the path analysis.

Dependent variable	Indirect effect					Direct effect	Correlation	R ²
	NPPP	NGPP	TKW	SY				
GY	NPPP	-	-0.42	0.25	0.01	0.51**	0.470**	0.66**
	NGPP	-0.37	-	-0.36	0.03	0.57**	-0.011	
	TKW	0.23	-0.38	-	-0.01	0.60**	0.510**	
	SY	0.07	0.14	-0.06	-	0.31**	0.287**	

ns: Nonsignificant; *, **: Significant at 0.05 and 0.01 levels, respectively; NPPP: Number of panicles per plot, NGPP: Number of grains per panicle, TKW: 1000-kernel weight, SY: Starw yield.

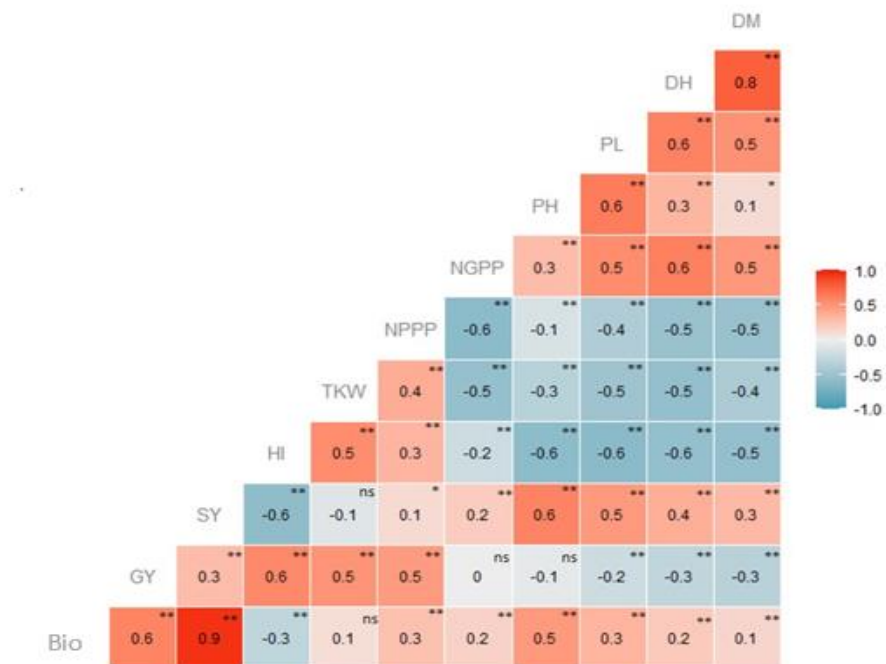


Figure 2. Heatmap plot rendered from the Pearson's correlation coefficients (n=361).

ns: Nonsignificant; *, **: Significant at 0.05 and 0.01 levels, respectively; PH: Plant height, PL: Panicle length, NPPP: Number of panicles per plot, NGPP: Number of grains per panicle, TKW: 1000-kernel weight, Bio: Biomass, GY: Grain yield, SY: Straw yield, HI: Harvest index, DH: Day to 50% heading, DM: Days to 50% maturity.

Cluster analysis

The genotypes were placed in five separate groups (Figure is not shown). Based on the results of the cluster analysis, 30 genotypes were assigned to the first group, 99 genotypes to the second group, 104 genotypes to the third group, 102 genotypes to the fourth group, and 26 genotypes to the fifth group. For better evaluation of genotypes in different clusters, an analysis of variance was performed between groups (Table 4). Except for DM, this analysis revealed significant differences between the groups for all other characteristics. The first group, which comprised 8.3% of the examined

genotypes, had the lowest average for all examined characteristics, except for NPPP. The genotypes in the second group, which included 27.42% of all genotypes, had moderate values for NPPP, TKW, PL, and PH. In the third group, which included 28.81% of genotypes, individuals had average GY, NPPP, and biomass with the highest TKW. There was no significant difference between the fourth and fifth groups for most of the characteristics, except for biomass, GY, and NPPP. The genotypes in the fifth group had the highest average in terms of all traits.

Table 4. The average of evaluated characteristics in the clusters.

Cluster-No	Number of genotypes	GY (g/plot)	NPPP	NGPP	TKW (g)	Bio (g/plot)	PH (cm)	PL (cm)	DH	DM
1	30	280.45e	211.58c	69.11b	25.44b	891.42e	78.99d	19.28c	175.72b	211.74b
2	99	334.82d	200.73c	87.03a	25.68ab	1057.26d	86.63c	21.99b	180.84a	212.66ab
3	104	361.66c	227.62cb	88.27a	26.80ab	1179.24c	94.39b	21.21b	180.77a	212.56ab
4	102	395.01b	231.03b	90.22a	26.69ab	1328.35b	97.22ab	22.73ab	181.18a	213.14ab
5	26	445.28a	268.41a	86.31a	27.65a	1518.79a	101.03a	24.03a	181.62a	213.54a
F test	-	**	**	**	*	**	**	**	**	ns

ns: Nonsignificant; *, **: Significant at 0.05 and 0.01 levels, respectively; PH: Plant height, PL: Panicle length, NPPP: Number of panicles per plot, NGPP: Number of grains per panicle, TKW: 1000-kernel weight, Bio: Biomass, GY: Grain yield, SY: Straw yield, HI: Harvest index, DH: Day to 50% heading, DM: Days to 50% maturity.

Discussion

This study showed significant differences among the genotypes for all traits, indicating the existence of a high degree of variability among genotypes that may depend on the spread of geographic origin, lineages, and the

diverse nature of these genotypes. This diversity promises the proper selection efficiency for improving the current oat genotypes. Similarly, previous reports have also shown an extensive and significant variation in their oat germplasm (Chauhan and

Singh 2019; Ihsan *et al.* 2021).

In our study, the effect of year on NGPP, TKW, DH, and DM was significant, similar to previous studies (Peterson *et al.* 2005). The genotype \times year interaction effect was significant for all the traits except days to maturity, demonstrating the influence of year on these traits and the need to study these genotypes across locations and years to assess their performance.

Observing the high diversity of genotypes in terms of GY under the same environmental conditions depends on the genetic potential and adaptability of genotypes (Tessema and Getinet 2020). Some genotypes are highly adaptable to different environmental conditions and behave similarly in most environments, while many others are heavily influenced by environmental factors such as temperature, precipitation, and soil. Selected genotypes with a better performance in one environment cannot be transferred to other environments with different conditions because the yield will be different in the new environment (Kebede *et al.* 2021).

The amount of GY varied between 164.66-540.98 g/plot in the current experiment. Observing a high diversity for this trait among the evaluated genotypes indicates the proper potential of these genotypes for further studies.

One of the main goals of this research was to separate fodder and grain varieties from each other. The genotypes with high biomass

such as 280 (WDO-9326), 279 (Forward), 300 (SDO-186), 320 (NO.124), 277 (Stormont Iris), 329 (USSR 11100), 199 (Jarli), 197 (Honami), 249 (DE_Santa_Luzia), and 179 (Caesar) could be used in the future programs to produce better fodder varieties, as they would be easily identifiable based on their straw. Similar discrepancies have been noted by other researchers (Ayub *et al.* 2011). Also, the results showed that traits such as biomass and PH had an extensive range, which was in accordance with the results obtained from previous studies on oats (Bibi *et al.* 2012). The results of the research could help to divide the genotypes into fodder and grain types for future studies. In other words, depending on the goal of the breeding program, the breeders can select the appropriate genotypes to improve the quality of genotypes for food, feed, or hay.

Correlation analysis can help researchers to identify the relationships among different traits and be a practical guide for selecting yield-related traits (Sarker 2020). The correlation between GY and PL, DH, and DM was negative and significant in the current experiment. Selection based on early heading has an important role in escaping from terminal drought stress (Celestina *et al.* 2023). Early heading can be considered as a specific plant strategy to improve adaptation to different climatic conditions (Gharib *et al.* 2021).

The results showed a positive and

significant correlation between biomass and PH. It means that selection based on the PH can be effective in increasing the biomass in oats. Furthermore, the results demonstrated a significant positive correlation between GY and biomass, NPPP, TKW, SY, and HI. A positive and significant relationship between GY with HI and TKW was observed in studies on 236 oat genotypes (Ihsan *et al.* 2021). Also, a positive correlation was found between NPPP and GY in wheat by Aghaei *et al.* (2023).

Breeders need to pay more attention to the relationships among various traits because grain yield is a quantitative and polygenic trait that is influenced by many independent traits. Therefore, the selection based only on grain yield may not be more efficient and the direct and indirect effects of each trait on grain yield need to be investigated. Path analysis, as a suitable method, allows breeders to break down the simple correlations into direct and indirect effects on GY. This method effectively selects functional traits to improve GY (Dewey and Lu 1959; Milligan 1990). TKW and NGPP had the highest direct impact on GY, similar to the study by Lorencetti *et al.* (2006) who found a strong positive correlation between NPPP and GY as well as a considerable direct effect of NGPP on GY in oat plants.

TKW and NGPP played an important role in explaining the variation in GY in the current study. Therefore, these important traits can be useful in improving the grain yield in the

breeding programs. Previous studies, performed on a wide range of oat germplasm, showed relatively similar results (Vaisi and Golparvar 2013).

The results of the cluster analysis divided the oat genotypes into five groups. Given the great diversity of genotypes examined and considering the lack of improved oat cultivars in Iran, by choosing the appropriate breeding method, there is a possibility of breeding new improved varieties.

Clusters were not compatible with the geographic distribution of the genotypes. In other words, genotypes from different geographical backgrounds were assigned to the same cluster. For example, the first group included 50% of the genotypes from the American continent, 25% to the Australian continent, 14% from the European continent, and 7% from the African continent.

The genotypes of the first group demonstrated the greatest difference from the genotypes of the other groups. The first group had the lowest mean for all the studied traits in this research. Therefore, individuals in this group could be used in breeding programs to produce early-flowering varieties in crosses with optimal-yielding genotypes. Genotypes in the fifth group had the highest mean for GY, biomass, TKW, and NPPP. Crosses between individuals with the greatest distance can result in the offspring with the highest grain and forage yields (Rahim *et al.* 2010).

Conclusion

In this global oat germplasm, significant genetic variation was found for most of the analyzed traits. The Genotypes 336 (OX87; 080-2), 203 (LA Prevision), 161 (Nile), 192 (Duns), 342 (Slavuj), 360 (Dunnart), 194 (Hiuga), 354 (SV95057-35), 299 (NMO-714), and 296 (NMO-712) were characterized by the highest GY, therefore they could be used as parents in crosses to produce new grain varieties. According to the results of the path analysis, TKW and NGPP had the highest positive direct effects on the GY. Moreover, the NPPP had the highest positive indirect effect on Gy via TKW, which shows that these traits can be used as selection criteria in oat breeding programs.

Cluster analysis did not concord with the geographical distribution of the oat genotypes. Based on cluster analysis, the best genotypes were in the fifth group regarding GY, biomass, TKW, and NPPP. Hence, the superior genotypes in yield and some yield components were located in this group.

This experiment allowed us to separate forage genotypes from grain ones. Genotypes 221 (Rubida), 298 (VDO-931.1), 242 (Yulaf),

342 (Slavuj), 280 (WDO-9326, NMO-712, 279 (Forward), 201 (Kent), 361 (Houdan), and 300 SDO-186 had the highest biomass. According to this research, separating the forage and grain genotypes would be feasible.

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Conflict of interest

The authors declare that they have no conflict of interest with any people or organization concerning the subject matter discussed in the manuscript.

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تنوع ژنتیکی صفات زراعی در مجموعه جهانی ژنوتیپ‌های یولاف (*Avena sp.*)بفرین مولایی^۱، صحبت بهرامی نژاد^{۲*} و لیلا زارعی^{۲،۱}

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چکیده

هدف از این مطالعه ارزیابی تنوع ژنتیکی ۳۶۱ ژنوتیپ یولاف بر اساس صفات زراعی به منظور شناسایی ژنوتیپ‌های برتر برای برنامه‌های آتی اصلاحی بود. آزمایش در قالب طرح لاتیس مربع ساده با دو تکرار و در دو سال زراعی ۱۳۹۷-۱۳۹۸ و ۱۳۹۸-۱۳۹۹ در کرمانشاه اجرا شد. بر اساس نتایج به دست آمده، ژنوتیپ‌های "OX87: 080-2" و "LA Prevision" به ترتیب بیشترین عملکرد دانه را داشتند. ژنوتیپ‌های "Rubida" و "VDO-931.1" برترین ژنوتیپ‌ها از نظر زیست توده بودند. در این تحقیق تعدادی تجزیه روی داده‌های BLUP برآورد شده، انجام شد. با توجه به ضرایب همبستگی حاصل، عملکرد دانه با صفات زیست توده، وزن هزار دانه و تعداد پانیکول در کرت آزمایشی همبستگی مثبت و معنی دار نشان داد. زیست توده نیز با تمام صفات مورد بررسی به جز وزن هزار دانه همبستگی مثبت و معنی داری داشت. صفات وزن هزار دانه و تعداد دانه در پانیکول بیشترین اثر مستقیم و مثبت را روی عملکرد دانه داشتند و بیشترین اثر غیر مستقیم مثبت را صفت تعداد پانیکول در کرت آزمایشی از طریق وزن هزار دانه بر عملکرد دانه اعمال کرد. در حالی که بیشترین اثر غیرمستقیم منفی روی عملکرد دانه را صفت تعداد دانه در پانیکول از طریق وزن هزار دانه اعمال کرد. بر اساس مقدار F کاذب، ژنوتیپ‌ها پس از انجام تجزیه خوشه‌ای در پنج گروه مجزا قرار گرفتند. گروه پنجم برای عملکرد دانه، بیوماس، وزن هزار دانه و تعداد پانیکول در کرت آزمایشی بالاترین مقادیر را به خود اختصاص داد. از این رو، می‌توان ژنوتیپ‌های این گروه را به عنوان والدین برای تولید لاین‌های برتر در برنامه‌های آتی اصلاحی پیشنهاد کرد.

واژه‌های کلیدی: تجزیه‌های چند متغیره، تنوع ژنتیکی، صفات زراعی، یولاف، BLUPs