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GENETIC PARAMETERS OF DIFFERENT OAT GENOTYPES USING CLUSTER ANALYSIS

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SUMMARY

The timely study aimed to assess the oat (*Avena sativa* L.) genotypes through cluster analysis, genetic and phenotypic variations, and the heritability (broad sense) during the winter crop season of 2022–2023, held at the University of Basrah, Basrah, Iraq. Three oat cultivars (Genzania, Shifaa, and Carrolup) were in a randomized complete block design (RCBD) sampling, with factorial arrangement and three replications. The results revealed for total grain yield, the genetic, environmental, and phenotypic variations, the values recorded were 1.143, 0.1746, and 1.3176, respectively, and the heritability (broad sense) was 86.74% for the said trait. The hierarchical cluster analysis showed the genetic convergence of the genetic structures between the cultivars Genzania and Carrolup amounted to 53.257, and the genetic distance of 12528.264 between the cultivars Genzania and Shifaa. However, the genetic distance between the cultivars Shifaa and Carrolup amounted to 11430.981. Therefore, based on the results, the cluster analysis helps draw the mutual relationship between oat varieties, making a comparison between them is easier.

Keywords: Oat (*Avena sativa* L.) cultivars, genetic, environmental, and phenotypic variations, heritability, cluster analysis, genetic distance

Key findings: Cluster analysis proved efficient in analyzing the interrelationship and genetic kinship among the studied oat (*Avena sativa* L.) cultivars and facilitating the selection process for cultivars with high genetic distancing while preserving the genetic origins.

INTRODUCTION

Oat (*Avena sativa* L.) crop is one of the winter annual cereal crops belonging to the family of Poaceae and ranks seventh for importance and

production in cereal crops, after wheat, rice, barley, maize, sorghum, and millet. In various countries, oat growing has a dual purpose, as a

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grain and fodder crop. Russia and Canada lead as the producing countries, with 74% of oats used in animal nutrition. Oats are also characteristic of an intensity of vegetative growth and the abundance of leaves, which gives it a high nutritional value of fodder and a widespread cultivation in cold and humid areas (Al-Dulami and Al-Khalifawi, 2016).

Oat grains are also favorable in the human diet and enter the manufacture of bread and pasta. Its grains contain a high percentage of antioxidants, which have beneficial effect on cardiovascular and diabetic diseases compared with other grains (Duda *et al.*, 2021 and AlRubaiee, *et al.*, 2019). In Iraq, the oat cultivation is still less, with its production rate very low compared with global production. The cultivated area was about 9.94 million hectares, producing 24.94 million tons during 2022 worldwide (USDA, 2022). However, in Iraq during 2018, the cultivation of oats covered only 25 hectares, yielding 10 tons, with an average yield of 0.400 t ha⁻¹ (CSO, 2019).

The selection and use of appropriate oat cultivars with high productivity under existing environmental conditions is one critical factor for its successful production (Alrubaiee, 2021). Genetic variation among the cultivars also play an influential role in determining the growth and productivity of grain crops, including oats; therefore, it is necessary to select genotypes with high production efficiency (Alshadiwi and Alrubaiee, 2022). Cultivars' adaptation to prevailing environmental conditions expands the crop area and raises its productivity, while giving attention to other production factors (Al-Hamdawi, 2017).

Cluster analysis is highly valuable in plant sciences, as it serves to classify plant species based on the degree of genetic similarity, morphological, or environmental characteristics. It helps to understand the biological diversity of plants and identify factors affecting them, such as, environment, terrain, and genetic factors (Chawla *et al.*, 2023). Understanding the performance of crop genotypes will enable scientists to discover their genetic potential, as reflected in increasing productivity, helping them choose

the appropriate cultivar. Given the lack of studies on cluster analysis (genetic tree drawing) in the Southern region of Iraq on the oat crop and to know the best cultivar suitable for best growth and grain yield was the concern of the presented study. This research aimed to determine the genetic and phenotypic variations, broad sense heritability, and cluster analysis for the degree of genetic kinship.

MATERIALS AND METHODS

The latest study on the oat (*Avena sativa* L.) genotypes materialized during the winter crop season of 2022–2023 at the University of Basrah, Basrah, Iraq (longitude of 47.80° W and latitude of 30.57° N). The three oat cultivars (Genzania, Shifaa, and Carrolup) were samples in a randomized complete block design (RCBD) with factorial arrangement and three replications in alluvial mixture soil. For soil analysis, the samples' random collection from the experimental site had the depth of 0–30 cm and reached mixing, before drying pneumatically, then bore grinding, gracing, and passing through a sieve with a diameter of 2 mm holes. The soil sample underwent an analysis of the chemical and physical properties of the field soil before planting, with the analysis of samples carried out in the central laboratory of the College of Agriculture, University of Basrah, Basrah, Iraq (Table 1).

Field practices

Determining the land required for the said experiment, its preparation comprised plowing with the plow dump, smoothing the soil by disc combs, and then leveling with the settlement bale. Afterward, dividing the land into experimental units employed the RCBD. The experimental soil had divisions of three sectors, and each sector contains 12 experimental units, and thus, a total of 36 experimental units. The area of each experimental unit had the dimensions of 2 m × 2 m = 4 m². The panels' separation comprised a distance of one meter to prevent interference between the treatments.

Table 1. Chemical and physical properties of the experimental field soil before planting.

Traits	Values	Units
Degree of soil reaction (PH)	7.47	-
Electrical conductivity (E.C)	7.18	DC-Siemens M ⁻¹
Organic matter	1.8	g kg ⁻¹
Elements available	Nitrogen	49.8
	Phosphorus	3.09
	Potassium	122.3
Soil components	Sand	260.47
	Silt	420.77
	Clay	318.78
Tissue	Alluvial blend	

Oat planting began in rows, with each experimental unit consisting of 10 lines with a 20 cm spacing and a seeding rate of 120 kg h⁻¹ (Al-Husnawy and Al-Rifai, 2016). Phosphate fertilizer was applied in the form of DAP (P₂O₅ 46%) at a rate of 100 kg h⁻¹, all at once before planting. Potassium sulfate fertilizer (k 41.5%) was used during planting (Al-Abody, 2011), while nitrogen fertilizer was applied at 240 N kg h⁻¹ in the form of urea fertilizer (N 46%). The nitrogen fertilizer was administered in two equal batches, the first immediately after seedling emergence and the second at branching. The experimental soil received immediate irrigation upon planting on November 25, 2022. Irrigation and weeding activities continued throughout the crop season, depending on the crop's needs. Crop harvesting began after the plants achieved physiological maturity on May 13, 2023.

Hierarchical cluster analysis

According to Hamdalla (2011), the conduct of cluster analysis used the Agglomerative method to simplify the data by grouping the oat genotypes into trait groups (Sneath and Sokai, 1973; Williams, 1976). Cluster analysis comprised several steps. It starts with the formation of a matrix for the degree of similarity between the studied genetic structures called matrix proximities, and then forming a dendrogram. Following the Unweighted Pair Group Method Analysis

(UPGMA) (Sneath and Sokai, 1973), which is a simple cluster hierarchical grouping method, calculated the Euclidean distances. These calculated values express the degree of similarity between the rates of the sums from the matrix proximities, formed in the first stage using the SPSS version-22 program based on the following equation (Punitha *et al.*, 2010).

$$\text{Distance (x, y)} = (\sum_i [x_i - y_i]^2)^{1/2}$$

The collection of similar genetic structures in homogeneous groups using cluster analysis and estimating the degree of genetic divergence among the genes of the studied genetic structures used the Hierarchical Clustering technology to analyze the data of genetic structures. For the studied genetic traits, forming a matrix to estimate the degree of similarity and distances of Euclidean among the groups formed continued. The said technique helped approximate the degree of genetic spacing between the genes of the genetic structures for seed yield and its components. It aided the classification of the studied genetic structures into groups for use in subsequent breeding programs.

Genetic variables

Genotypic and phenotypic variations' estimation followed these equations by Walter (1975).

$$\sigma_G^2 = \frac{Msv - Mse}{r \times a}$$

$$\sigma^2 E = Mse$$

$$\sigma^2 P = \sigma^2 G + \sigma^2 E$$

Where, $\sigma^2 G$ = Genetic variance, $\sigma^2 E$ = Environmental variance, $\sigma^2 P$ = Phenotypic variance, Msv = Average squares of the oat cultivars, Mse = Average test error squares, r = number of replications, and a = Factor levels a .

Heritability (broad sense)

Estimating the heritability (broad sense) followed the explanation by Hanson *et al.* (1956) below.

$$h^2_{b.s} = \frac{\delta^2 G}{\delta^2 p} \times 100$$

Where, $h^2_{b.s.}$ = Represents the inheritance in broad sense, $\delta^2 G$ = Genetic variation of the trait, and $\delta^2 P$ = Phenotypic variation of the trait.

RESULTS AND DISCUSSION

Hierarchical clustering analysis

The quantitative characteristics of the oat cultivars were the basis of the cluster analysis to determine the genotype groups based on their genetic spacing, depending on the similarity of their response to environmental conditions. It mostly depends on verifying different distances that express the distribution of cultivars in groups, established on their performance and genetic origins. The values of genetic convergence among the cultivars and their observed genetic relationship link them as groups. According to cluster analysis, the genetic distance and kinship among the oat cultivars appear in Figure 1 and Table 2.

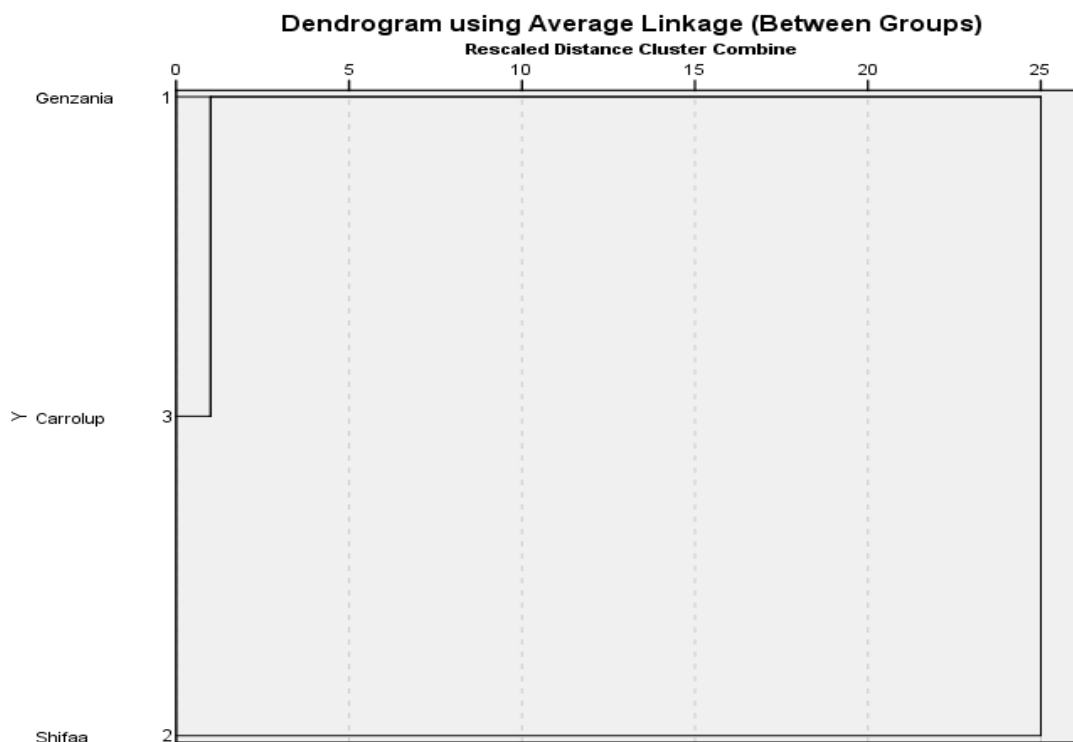


Figure 1. Genetic tree of the three oat cultivars using cluster analysis of similarity values.

Table 2. Genetic distance and kinship between the oat cultivars based on the cluster analysis.

Cultivars	Squared Euclidean Distance		
	1: Genzania	2: Shifaa	3: Carrolup
1: Genzania	0.000	12528.264	53.257
2: Shifaa	12528.264	0.000	11430.981
3: Carrolup	53.257	11430.981	0.000
Stage	Cluster Combined		Coefficients
	Cluster 2	Cluster 1	
1	1	3	53.257
2	1	2	11979.623

Oat cultivars Genzania and Carrolup exhibited with the genetic distance of 53.257 due to their sharing of genetic material. Similarly, an observation revealed the cultivars from different sources were not necessarily genetically distant. The phenotypic variation existing between the members of each non-isolated clan was due to the environmental variation because their members carry similar genetic patterns. The phenotypic variation existing between the members of each isolated clan refer to genetic and environmental variation because these genotypes carry different genetic patterns, assuming no interaction exist between the genetic pattern and the environment. The values of the phenotypic variance of the second generation population were greater than the phenotypic variance values of the regressive generation of the first father and the second father. Therefore, one can conclude low values appear for environmental effects, however, were highly significant for all studied traits and for all the genetic structures under study (Khan *et al.*, 2000; Youssef and Al-Hayali, 2006).

The reason for the convergence of the two oat cultivars (Genzania and Carrolup) was these genotypes have the most similar genes, reflecting positively in their performance with the main favorite genes, benefitting from them in subsequent breeding programs. Therefore, it was possible to replace one of the two genetically close cultivars with other genotypes in the loss of one cultivar and to avoid taxation between them. Through this analysis, the genetic distance between the two oat cultivars (Genzania and Shifaa) reached 12528.264, as a result of possessing different genetic make-up and genes. The reason for the widening of

the genetic distance between the two oat cultivars (Shifaa and Carrolup amounting to 11430.981) may also be due to the differences in their genetic basis. These genotypes provided with the high genetic distance and therefore, can be useful in future breeding programs, especially through hybridization, followed by selection to find an excellent cultivar under the existing environmental conditions.

The said biometrical technology can serve as a successful alternative to molecular technologies. The cluster analysis proved efficient in analyzing the genetic kinship by presenting the interrelationship between the studied cultivars and facilitating comparison through drawing the relationship between the crop cultivars. Likewise, it facilitated the selection process for cultivars with high genetic kinship and genetic distances and preserved the genetic assets (Hamdalla, 2011). Past studies also reported the efficiency of this technology in identifying genetic similarity among the crop cultivars (Azzam and Al-Obaidi, 2018; Al-Sadoon *et al.*, 2022).

Genetic parameters

The results revealed the genetic variations for the oat growth traits, i.e., days to 50% flowering, days from 50% flowering to full maturity, plant height, flag leaf area, and seedlings m^{-2} , amounted to 5.250, 5.405, 12.743, 8.779 and 1030.551, respectively (Table 3). This could be due to some alleles contained by the oat cultivars stimulated the flowering, and the alleles associated with photoperiod sensitivity and stimulation insensitivity must be evident in the Leggett

Table 3. Estimation of genetic, environmental, and phenotypic variations, and heritability (broad sense) of the studied traits in oat genotypes.

Studied qualities	δ^2G	δ^2E	δ^2P	$h^2_{b.s}$ (%)
Days to 50% flowering	5.250	0.0280	5.278	99.47
Days from 50% flowering to maturity	5.405	0.0124	5.417	99.78
Plant height (cm)	12.743	1.843	14.586	87.36
Flag leaf area (cm ²)	8.779	0.560	9.339	94.00
Tillers m ⁻²	1030.551	25.49	1056.041	97.59
Panicles m ⁻²	1330.96	14.25	1345.21	98.94
Grains panicle ⁻¹	2.221	1.448	3.669	60.53
1000-grain weight (g)	0.228	0.771	0.999	22.82
Total grain yield (t ha ⁻¹)	1.143	0.1746	1.3176	86.74
Biological yield (t ha ⁻¹)	1.121	0.2440	1.365	82.12
Harvest index (%)	1.243	0.558	1.801	69.02
Grain protein (%)	0.847	0.5154	1.362	62.18

δ^2G : Genetic variation, δ^2E : Environmental variation, δ^2P : Phenotypic contrast, $h^2_{(bs)}$: Heritability (broad sense).

genome. Past studies enunciated the *Ppd-H1* gene plays a key role in regulating sensitivity to photoperiod in the crop plants (Pearce *et al.*, 2017). In these species, *Ppd-H1* accelerates the long-day flowering through positive regulation of the *Vrn3* gene, which is a flowering time enhancer, and integrates responses to photoperiod, temperature, and vernalization (Turner *et al.*, 2005).

The environmental variations of the above oat growth traits were 0.0280, 0.0124, 1.843, 0.560, and 25.49, respectively, while the phenotypic variation values of the same traits were 5.278, 5.417, 14.586, 9.339, and 1056.041, respectively. The heritability (broad sense) of the specified oat growth traits has reached 99.47%, 99.78%, 87.36%, 94.00%, and 97.58%, sequentially. This indicates the stability of the genetic factors, which led to an enhancement in the phenotypic variation values, resulting from the interaction of genetic and environmental variations. Some of this difference can be traced back to things in the surroundings. However, the segregation patterns made it clear that there were allelic differences between the maternal genes of each group. These differences played a big role in the formation of different phenotypic groups among the types of oat that were studied. These differences also give us a great chance to choose the oat strains that do best in the widest range of growth conditions. On the other hand, estimates of heritability show that the reaction to selection for starting date in

oats may happen more slowly in the first generations that reproduce themselves (Maral *et al.*, 2013). Use of mixed selection methods based on phenotype and genotype through molecular marker-assisted selection (MAS) can lead to more noticeable genetic improvements. In the future, it will be very important to do more advanced molecular genetic studies, such as finding, mapping, and controlling the genes that control the key processes that determine when oats bud. The goals of these studies were to learn more about the genetic root of these useful qualities and to make oat cultivars that are more productive (Helsel and Skrdla, 1983; Mazurkiewicz *et al.*, 2019).

The outcomes further indicated the genetic variations of the oat yield traits and its components (number of panicles m⁻², number of grains per panicle, 1000-grain weight, total grain yield, biological yield, and harvest index) and protein percentage, at 1330.96, 2.221, 0.228, 1.143, 1.121, 1.243, and 0.847, respectively (Table 3). The environmental variations for all variables mentioned amounted to 14.25, 1.448, 0.771, 0.1746, 0.2440, 0.558, and 0.5154, respectively, while the phenotypic variation values were 1345.21, 3.642, 0.999, 1.3176, 1.365, 1.606, and 1.362, sequentially (Table 3). The broad sense heritability for the oat traits (number of panicles m⁻², number of grains per panicle, 1000-grain weight, total grain yield, biological yield, and harvest index) and protein content

amounted to 98.94%, 60.53%, 22.82%, 86.74%, 82.12%, 69.02%, and 62.18%, respectively.

The results depicted the number of days to 50% flowering and the number of days from 50% flowering to full maturity in oat owned the highest genetic variation. This caused a rise in the values of phenotypic variation, positively affecting the increase in the broad sense heritability (99.47% and 99.78%, respectively). This could be due to the low values of environmental variation, despite their significance, and the high values of the additive-dominant genetic variation influencing and controlling these traits. Heritability in the narrow sense is more accurate than inheritance in the broad sense because it also expresses the proportion of additive genetic variations that can be fixed and transmitted across the generations (Saleem *et al.*, 2016; Hasan *et al.*, 2023).

The oat traits, i.e., plant height, flag leaf area, and number of seedlings m⁻², displayed the maximum genetic variation, playing a primary role in confirming the higher values of phenotypic variation. This was the reason for giving the highest percentage of the heritability (broad sense) for the above traits, reaching 87.36%, 94.00%, and 97.58%, respectively. For the total grain yield, the topmost genetic and phenotypic variations also positively affected the high value of heritability (86.75%). This indicates these traits have a wider genetic variation, usually incurring fewer effects from environmental factors, and thus, can undergo improvement through selection. The genetic components alone provide no indication of the genetic advancement that would lead to selection of the promising individuals. In crop plants, the index of selection mainly depends on more than one trait, especially if selection for a grain crop is inactive due to yield consideration of a quantitative trait controlled by many genes. These results were consistent with past findings in wheat (Almajidy *et al.*, 2017; Ayooob, 2019).

CONCLUSIONS

Cluster analysis demonstrated the interrelationship among the oat cultivars, making the comparison easier by sketching the relationship between them. It also helps in selecting the oat cultivars with high genetic distance and preserving their genetic origins.

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