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GENETIC DIVERSITY OF OAT (*AVENA SATIVA* L.) GENOTYPES UNDER DIFFERENT CONCENTRATIONS OF POTASSIUM

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SUMMARY

The following study aimed to explore the genetic diversity among 13 oat (*Avena sativa* L.) genotypes (Alguda, Anatolia, Pimula, Genzania, Hamel, ICARDA short, Kangaroo, ICARDA tall, Mitika, Possum, UC-132, Monte Zuma, and Cayuse) with three potassium concentrations (0, 10, and 20 g/L). The experiment, carried out during the winter crop of 2024–2025, transpired in one of the farmers' fields under the Kirkuk Irrigation Project. Foliar application of potassium had the form of potassium sulfate (52% K_2O). The degree of genetic diversity estimates through the genotypic variations in response to potassium used cluster analysis. The oat genotypes revealed significant genetic variability as influenced by potassium concentrations for biochemical traits. The oat genotype Kangaroo emerged with greater genetic potential in reaction to foliar application of potassium (20 g/L), showing the highest percentages of crude protein, soluble carbohydrates, moisture, and ash content (44%, 55.40%, 18.20%, and 3.13%, respectively). Cluster analysis disclosed substantial genetic diversity among the oat genotypes, with the Kangaroo identified as a stable genotype in the main group with potassium levels displaying superiority in biochemical features.

Keywords: Oat (*A. sativa* L.), genotypes, genetic diversity, potassium concentrations, cluster analysis

Key findings: The study showed the highest concentration of potassium (20 g/L) significantly improved the biochemical traits of the oat (*A. sativa* L.) genotypes, particularly in the genotype Kangaroo. Cluster analysis revealed substantial genetic diversity among the genotypes, supporting their potential use in breeding programs.

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INTRODUCTION

Oat (*Avena sativa* L.) is an annual winter cereal crop of the Poaceae family, widely cultivated in regions such as Russia, the United States, Canada, and Australia. Globally, it covers around 9.5 million hectares and produces approximately 23.5 million tons of grain. Cereals, including oats, provide a major portion of human caloric intake, estimated at roughly 60% worldwide (Alatawi *et al.,* 2024). Oats are particularly beneficial for their nutritional content, including proteins, fibers, and essential minerals. Their processing by the food industry takes numerous products, such as breakfast cereals, biscuits, and snacks, often targeted for children due to their digestibility and nutrient richness (USDA, 2023; Al-Mafarji *et al.,* 2024). Additionally, oats contribute to sustainable agriculture through soil improvement and serve as important livestock feed. Their adaptability, health benefits, and economic significance make oats a key crop in global food systems.

Genotype responses to environmental variations can cause instability in their performance, complicating the identification of superior genotypes (Younis *et al.,* 2025b). Therefore, assessing genetic-environment interactions, evaluating stability, and estimating genetic diversity proved crucial for selecting the desired genotypes for cultivation and better production (Al-Jubouri *et al.,* 2024; Abdullah *et al.,* 2025). Plant breeding relies on introducing crossbreeding for developing genetic variations and selecting desirable genotypes with distinct genetic features to ensure novel traits (Hasan and Abdullah, 2021; Younis *et al.,* 2025a).

Cluster analysis is a valuable tool for evaluating genetic diversity and environmental responses, using hierarchical, K-means, and two-step methods based on the dataset size (Abdullah and Hasan, 2020). This study applies cluster analysis to examine potassium concentrations’ effect with foliar application on oat genotypes’ biochemical and physiological traits, as varying potassium doses can alter the genotypic performance and aid further classification in breeding programs (Younis *et al.,* 2022; Jaber *et al.,* 2025).

Different potassium concentrations influence the phenotypic expression of biochemical and physiological traits, generating genetic diversity that cluster analysis can reveal, enabling the identification of promising genotypes for further improvement in crop plants (Hasan *et al.,* 2025; Younis *et al.,* 2025b). The presented study aimed to evaluate the genetic diversity among oat genotypes and assess the impact of potassium concentrations on their traits. It also sought to classify the superior oat genotypes with the highest percentages of crude protein, crude fiber, soluble carbohydrates, moisture, and ash content for future breeding (Hasan *et al.,* 2022; Harbawi *et al.,* 2025).

MATERIALS AND METHODS

The experiment comprised 13 oat (*A. sativa* L.) genotypes (Alguda, Anatolia, Pimula, Genzania, Hamel, ICARDA short, Kangaroo, ICARDA tall, Mitika, Possum, UC-132, Monte Zuma, and Cayuse) with three potassium concentrations (K0: 0, K1: 10, and K2: 20 g/L). Its layout was in a randomized complete block design with three replications during the crop season of 2024–2025. The experiment occurred in one of the farmers' fields under the Kirkuk Irrigation Project. The potassium concentrations with foliar application proceeded in the main plots, with the oat genotypes placed in the subplots. Oat genotype seeds entailed manual sowing, with weeds controlled by hand and irrigation applied as needed. The fertilizer DAP (P_2O_5 46%, N 18%) at the rate of 320 kg/ha had its application during soil preparation, and the use of urea (N 46%) at the rate of 200 kg/ha followed during the crop tillering stage.

Each experimental unit consisted of four rows, each 3 m long and spaced 0.25 m apart, resulting in a 3-m² subplot. A seeding rate of 300 seeds per plot prevailed. Cluster analysis, conducted using the agglomerative method, grouped the oat genotypes according to their response patterns (Shekh and Aziz, 2021; Al-Mafarji and Al-Jubouri, 2023). The evaluated traits included crude protein (%), crude fiber (%), soluble carbohydrates (%), moisture (%), and ash content (%) (Jaber *et*

Table 1. Analysis of variance among the different fertilizers for various traits in oat genotypes.

Sources of variation (S.O.V.)	d.f.	Crude protein (%)	Crude fibers (%)	Soluble carbohydrates (%)	Moisture (%)	Ash (%)
Replications	2	49.25	541.89	1302.01	126.68	10.01
Potassium	2	11.10^{**}	63.19^{**}	160.03^{**}	82.62^{**}	4.14^{**}
Error A	4	1.04	37.42	40.87	0.96	0.39
Genotypes	12	9.47^{**}	70.42^{**}	107.11^{**}	22.77^{**}	1.89^{**}
Potassium x genotypes	24	$0.69^{N.S.}$	16.21^{*}	$18.28^{N.S.}$	4.15^{*}	$0.16^{N.S.}$
Error B	72	0.88	9.57	15.37	2.22	0.19

**,* = Significant at 1% and 5% levels of probability, N.S. = Nonsignificant.

al., 2025). This design enabled the assessment of potassium's influence on biochemical and physiological characteristics across a range of oat genotypes (Hasan *et al.,* 2023).

RESULTS AND DISCUSSION

Genotype by potassium effects

Analysis of variance revealed potassium concentrations and oat (*A. sativa* L.) genotypes individually displayed significant ($P \leq 0.01$) differences for all the biochemical traits (Table 1). The genotype-by-potassium interactions enunciated substantial ($P \leq 0.05$) differences for crude fiber and moisture content, while they were nonsignificant for crude protein, soluble carbohydrates, and ash content. The results indicated potassium could enhance particular physiological and biochemical characteristics; however, its effect was limited for some specific components. The response variability among the traits suggested differential nutrient uptake and metabolic regulation. Potassium application may therefore selectively improve the growth and nutritional quality among the genotypes. The observed results align with previous studies, which also reported notable effects of potassium on some traits in crop plants (Abdullah and Hasan, 2020; Hasan *et al.,* 2024). Understanding these patterns is essential for optimizing fertilization strategies in crop management. Overall, the results demonstrated the importance of targeted nutrient application to achieve desired improvements in plant performance (Hasan *et al.,* 2023).

Genotype evaluation

As mentioned before, the oat genotypes revealed significant differences for all the biochemical features examined (Tables 2, 3, and 4). Among them, the oat genotype Kangaroo with potassium (K2: 20 g/L) foliar application recorded the highest crude protein content (7.44%), while the genotypes Anatolia and Pimula exhibited the lowest values for the said trait. Crude fiber content was apparent with the greatest percentage in the genotype ICARDA Short with potassium treatments (K0: 0 and K2: 20 g/L), with values of 47.4% and 52.06%, respectively. The lowest was in genotype Kangaroo at K0 (33.36%) and Pimula at K1 (34.8%). Soluble carbohydrates were the highest in genotype Kangaroo (47.93%) with the increased concentration of potassium (K2), whereas oat genotypes Anatolia and Alguda showed the lowest percentages. Moisture and ash contents were also optimal in the genotype Kangaroo with K2 (15.96% and 3.13%, respectively), while the lowest percentages resulted in the genotypes Anatolia and Pimula with K0 and K1 (Alatawi *et al*., 2024).

The results indicated the oat genotype Kangaroo was consistently distinct with higher protein, carbohydrates, moisture, and ash and lower fiber content. This combination reflects superior nutritional quality compared with the other genotypes under the potassium treatments. The findings suggested genotypic variation considerably influenced the response to potassium concentrations (Abdullah *et al.,* 2025). However, such variations appeared important for selecting desirable genotypes with better nutritional values. Potassium application remarkably improved the key

Table 2. Effect of foliar application of potassium (K0 level) on oat genotypes for the various traits.

Features Oat genotypes	Crude protein (%)	Crude fibers (%)	Soluble carbohydrates (%)	Moisture (%)	Ash (%)
Alguda	3.78	40.50	38.06	10.80	1.33
Anatolia	1.66	42.70	34.43	8.96	0.56
Pimula	2.97	37.93	43.00	12.03	1.70
Genzania	3.28	42.80	41.80	10.36	1.53
Hamel	3.03	43.56	41.13	11.33	1.36
ICARDA short	3.83	47.40	42.96	9.63	1.40
Kangaroo	6.45	33.36	47.93	15.96	2.66
ICARDA tall	4.00	42.46	37.13	12.26	1.53
Mitika	4.08	41.66	41.90	11.96	1.60
Possum	2.84	42.30	42.56	12.20	1.86
UC-132	3.10	43.26	41.40	9.86	0.96
Monte Zuma	2.88	42.90	42.36	11.83	1.63
Cayuse	3.25	42.63	41.63	10.56	0.66
$LSD_{0.05}$	1.297	5.298	5.799	2.593	0.531

Table 3. Effect of foliar application of potassium (K1 level) on oat genotypes for the various traits.

Features Oat genotypes	Crude protein (%)	Crude fibers (%)	Soluble carbohydrates (%)	Moisture (%)	Ash (%)
Alguda	4.05	42.50	35.83	10.86	1.40
Anatolia	3.43	44.03	44.03	12.03	0.93
Pimula	1.62	34.80	41.23	8.50	1.66
Genzania	4.05	43.80	43.80	12.20	1.60
Hamel	3.56	47.56	44.23	13.50	1.90
ICARDA short	3.44	42.06	46.06	12.20	1.50
Kangaroo	6.87	38.56	51.46	16.83	2.63
ICARDA tall	4.34	43.80	45.46	12.76	1.70
Mitika	4.13	42.66	44.00	11.63	1.53
Possum	3.89	42.63	43.63	11.70	1.73
UC-132	3.93	44.60	44.60	13.16	1.43
Monte Zuma	4.25	44.23	45.23	13.10	1.63
Cayuse	4.13	43.96	36.63	12.80	1.53
$LSD_{0.05}$	1.839	4.748	7.703	1.649	0.775

Table 4. Effect of foliar application of potassium (K2 level) on oat genotypes for the various traits.

Features Oat genotypes	Crude protein (%)	Crude fibers (%)	Soluble carbohydrates (%)	Moisture (%)	Ash (%)
Alguda	4.67	42.16	35.83	12.83	2.23
Anatolia	2.83	45.36	45.36	13.10	0.93
Pimula	3.72	41.26	39.70	9.43	2.30
Genzania	4.37	46.80	46.80	13.73	2.60
Hamel	3.69	43.56	45.23	14.73	1.66
ICARDA short	4.77	52.06	44.60	15.53	2.06
Kangaroo	7.44	39.70	55.40	18.20	3.13
ICARDA tall	4.68	37.80	45.46	14.26	1.60
Mitika	4.72	45.33	47.33	15.00	2.33
Possum	4.59	45.96	45.96	13.66	2.53
UC-132	5.26	47.93	47.26	14.60	1.90
Monte Zuma	4.56	42.56	48.23	15.06	2.20
Cayuse	3.71	45.63	41.63	15.00	1.56
$LSD_{0.05}$	1.573	5.567	6.163	3.077	0.902

quality parameters in most oat genotypes, though the magnitude of response varied (Al-Jubouri *et al.,* 2024). Overall, the genotype Kangaroo demonstrated the most balanced and desirable profile across all studied traits. These results can further help and guide fertilization practices and breeding programs aimed at improving the oat quality. The results highlighted the importance of considering both genotypes and nutrient management to optimize the crop performance (Younis *et al.,* 2025a).

Nitrogen is an essential component for protein synthesis in oat (*A. sativa* L.) seeds, and its metabolism gained influences from potassium fertilization, which, in turn, affected the crude protein and fiber content. The genotype Kangaroo consistently exhibited the highest protein and nitrogen concentration, while crude fiber generally rose with the potassium with a higher concentration (Alatawi *et al*., 2024). Soluble carbohydrates also increased across all the oat genotypes, indicating potassium's considerable role in photosynthesis and enzymatic activity. Ash content was also maximum in genotype Kangaroo under a higher concentration of potassium, likely due to its genetic potential, enhanced nutrient uptake, and larger leaf area. Environmental factors may have further contributed to these elevated values (Hasan and Abdullah, 2020).

Cluster analysis

The clustering and PCA results of the oat genotypes under different potassium concentrations appear in Figures 1–6. Without potassium application (K0), the oat genotypes grouped into two main clusters. The genotype Kangaroo formed a single superior cluster with the highest performance and adaptability, while the second cluster comprised the genotypes with varying responses, such as Possum and Pimula, found closely related. Anatolia was distinct, and the oat genotypes Genzania, Hamel, UC-132, and Monte Zuma emerged with similar biochemical traits. Under a low potassium concentration (K1), the genotypes again broke down into two main groups with subclusters reflecting metabolic and physiological similarities (Al-Jubouri *et al.,* 2024).

The genotype Kangaroo remained distinct, while other Kangaroo genotypes (Genzania, ICARDA Short, Monte Zuma, Hamel, Cayuse, UC-132, Pimula, Possum, Mitika, Anatolia, and Alguda) clustered based on the same biochemical responses and potential genetic relatedness (Humada *et al.,* 2025). Cluster and PCA analyses highlighted the variations in potassium utilization, enzyme activation, osmotic regulation, and stress adaptation. The oat genotype Kangaroo showed a unique metabolic efficiency and potential regulatory genes for potassium use, antioxidant defense, and osmotic adjustment (Al-Jubouri *et al.,* 2024; Agha *et al*., 2024).

Cluster and principal component analyses consistently grouped the oat genotypes based on their biochemical characteristics. Genotypes within the same cluster shared the same phenotypic traits, which can guide the selection of compatible parents in breeding programs (Younis *et al.,* 2025b). These genotypes' groupings help identify promising parental genotypes for hybridization and the traits' further improvement. Potassium application positively influenced the expression of genes related to biochemical features, such as protein, carbohydrate, and mineral accumulation, supporting stable performance across varying environments. The genotype Kangaroo repeatedly outperformed other genotypes in multiple traits, showing the highest overall nutritional quality (Al-Jubouri *et al.,* 2024).

Potassium foliar application with the highest concentration (K2) produced the most considerable improvement in protein, soluble carbohydrates, moisture, and ash content. The variation observed among the oat genotypes underscores substantial genetic diversity, which is advantageous for breeding programs (Hasan and Abdullah, 2021). This genotypic diversity allows the breeders to select the genotypes with complementary traits for hybrids' development. Genotypes' genetic potential in integration with potassium fertilization can optimize both yield and

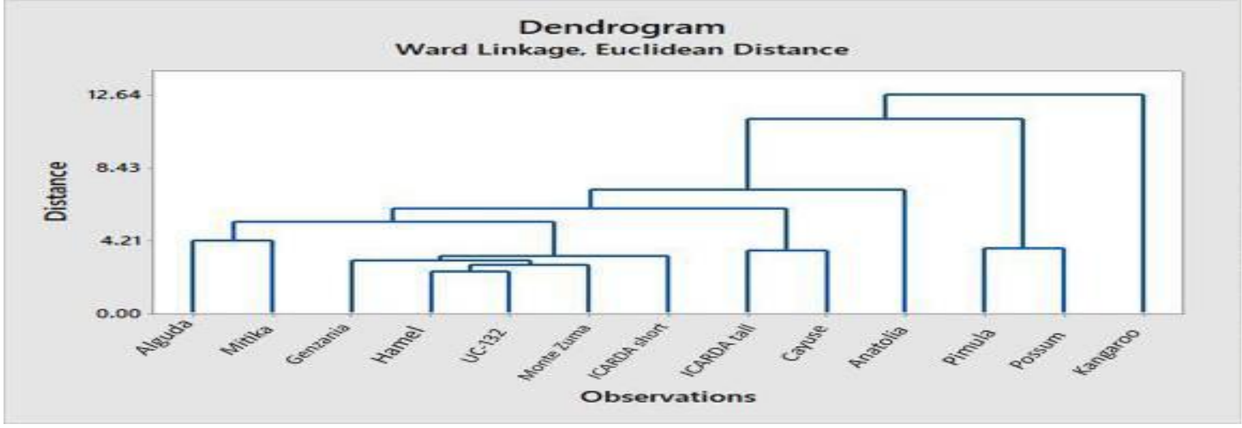

Figure 1. Cluster analysis of the ICARDA oat genotypes with potassium concentration K0 (0 g/L).

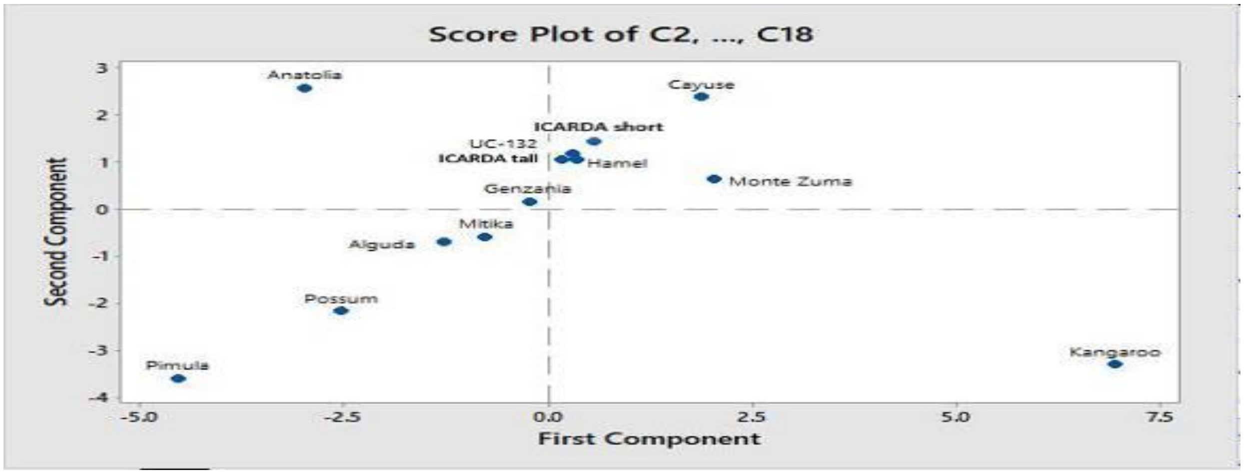

Figure 2. Analysis of the ICARDA oat genotypes with potassium concentration K0 (0 g/L).

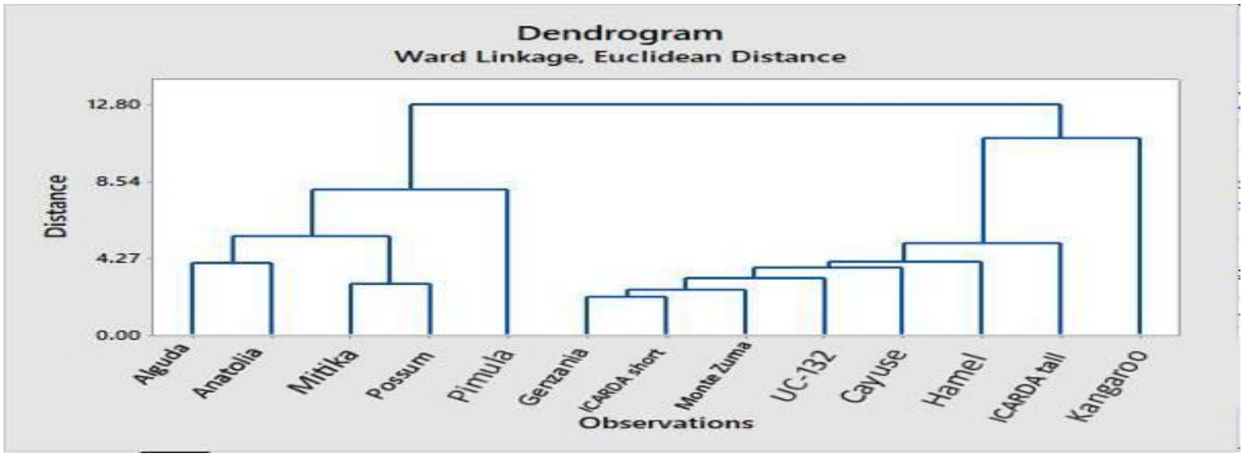

Figure 3. Cluster analysis of the ICARDA oat genotypes with potassium concentration K1 (10 g/L).

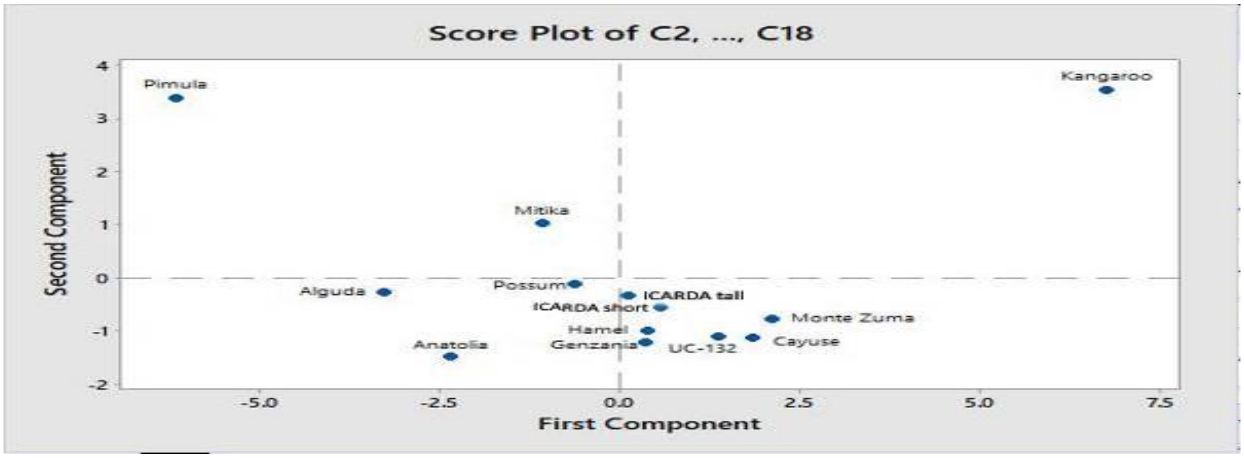

Figure 4. Analysis of the ICARDA oat genotypes with potassium concentration K1 (10 g/L).

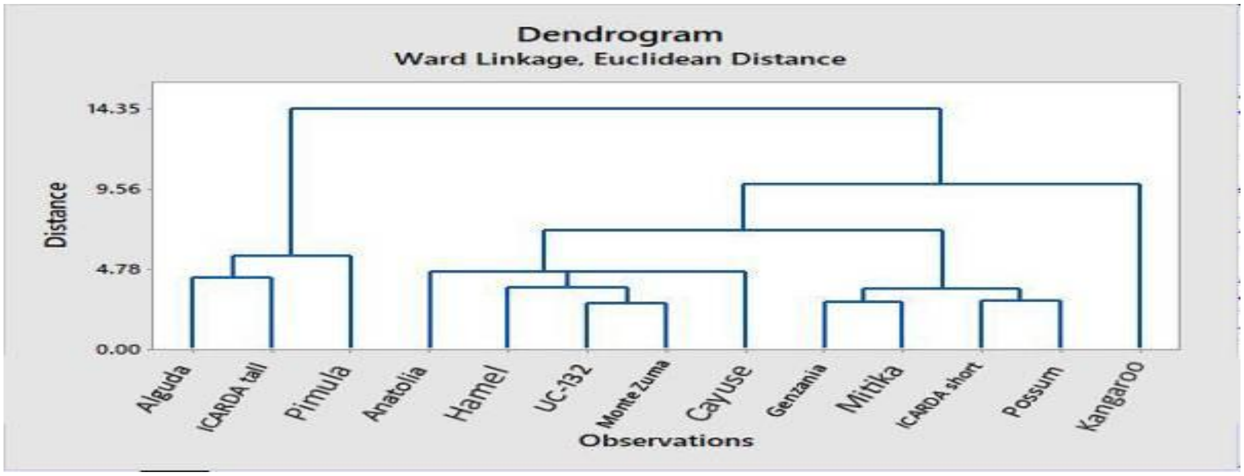

Figure 5. Cluster analysis of the ICARDA oat genotypes with potassium concentration K2 (20 g/L).

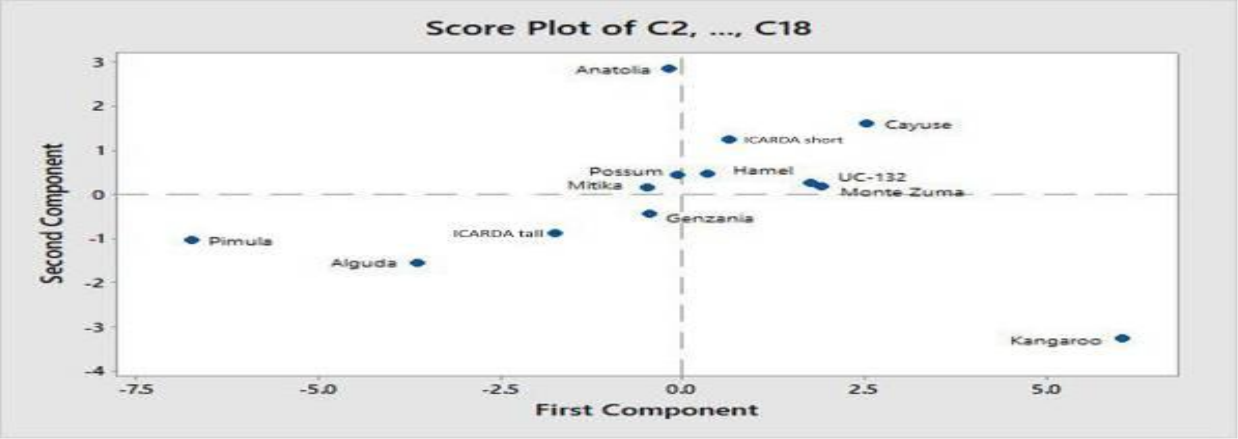

Figure 6. Analysis of the ICARDA oat genotypes with potassium concentration K2 (20 g/L).

nutritional quality traits (Hasan *et al*., 2025). Overall, the results highlighted the importance of integrating selected genotypes with nutrient management to achieve superior performance in oat growth and productivity. These findings provide practical guidance for cultivar improvement and fertilizer application strategies (Younis *et al.,* 2025a).

CONCLUSIONS

The existing study explained the ability of the utilized rRNA sequences to detect the investigated *Veronica* species and discriminate them from each other. These ribosomal amplicons can efficiently help identify the biological diversity of a wider spectrum of *Veronica* DNA sequences. These promising amplicons can also serve to determine the further details within these identified *Veronica* sequences in various biological and geographical sources.

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