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GENETIC DIVERSITY AND POPULATION STRUCTURE AMONG ARABIAN HORSE IN IRAQ

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ABSTRACT

This study was conducted at the Department of Animal Genetic Resources Protection, Directorate of Animal Resources, Ministry of Agriculture, Baghdad, Iraq. Data for Arabian horse pedigree verification were obtained from the Iraqi Arabian Horse Organization for the period 2020–2024. The objective of this study was to provide a comprehensive genetic assessment and investigate the current status of genetic diversity, inbreeding, and genetic relationships among six extant Arabian horse lineages in Iraq (Kuhailan, Managi, Ubaiyah, Saglawia, Dahman, and Julfan) using 17 microsatellite markers.

A total of 205 hair samples were analyzed following standardized protocols. All markers exhibited polymorphism, with HTG7 showing the highest allelic diversity (9 alleles) and HMS2 the lowest (4 alleles). Among the populations, the Saglawia lineage exhibited the highest genetic diversity ($H_e = 0.72$); ($I = 1.49$), whereas the Julfan lineage showed the lowest ($H_e = 0.65$); ($I = 1.32$). Within-population inbreeding coefficients (FIS) varied from 0.082 (Dahman) to 0.112 (Julfan), with an overall (FIS) of 0.089 ($P < 0.01$). To mitigate the high inbreeding observed in the Julfan lineage, breeding programs should modify current mating systems and avoid the excessive use of specific sires. Across the six Arabian horse populations, nine loci exhibited 13 private alleles.

Nei's genetic distance analysis revealed two primary branches: one consisting of the Julfan lineage as an outgroup, and another dividing the remaining populations into subgroups that aligned with the STRUCTURE clusters. (FST) values demonstrated statistically significant differentiation between all population pairs ($P < 0.001$) after 10,000 permutations). The highest genetic similarity was found between Ubaiyah and Saglawia (FST = 0.025), while the greatest divergence was observed between Kuhailan and Julfan (FST = 0.079). Corresponding gene flow estimates (Nm) ranged from 2.9 (Kuhailan–Julfan) to 9.8 (Ubaiyah–Saglawia). In conclusion, these findings suggest that Arabian horses in Iraq possess unique genetic features. This data could serve as a valuable foundation for developing conservation strategies, enhancing breeding programs, and managing native horse populations.

Keywords: Arabian horse, Genetic diversity, Microsatellites, Population horse.

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INTRODUCTION

The Arabian horse is considered profoundly regarded breed eminent, for its exceptional intelligence, unwavering drive, and unparalleled perseverance. Historically, horses originated in the Middle East and were later distributed globally through warfare and commerce. Their superior traits, such as speed, elegance, stamina, and strong bone structure, made them invaluable for enhancing other horse breeds [14]. A sculpted artifact from the archaeological site of Nippur, dating back to around 4500 BCE, serves as historical evidence for the early presence of the Arabian horse in Mesopotamia [6, 8]. The modern Arabian horse possesses a unique conformational phenotype that includes a dish-shaped facial profile, wide-set eyes, arched neck, and high tail carriage [33]. However, Arabian horses in photographs made in the late 1800s and early 1900s often show less pronounced facial dishing and lower tail carriage [23], suggesting that these traits may be under strong selection by modern Arabian breeders, particularly for lines of horses used primarily for non-ridden show competitions [13].

Considering their high polymorphism and repeatability, microsatellite markers continue to be the most reliable method for assessing horse genetic variation [36]. A panel of 17 microsatellites has been approved by the International Society for Animal Genetics (ISAG) for use in population research and parentage testing, allowing for crossbreed comparisons [26]. Significant genetic difference amongst population of Arabian horses, including the Egyptian, Polish, and Desert-bred populations, has been found in earlier research [29]. However, there is still a lack of information on Iraqi subpopulations, such as the Kuhailan, Saglawia, manage, Ubaiyah, Dahman and Julfan.

In Iraq, Arabian horses are culturally revered, yet their genetic diversity is poorly documented [1]. While neutrality tests (Tajima's D) may identify demographic bottlenecks, metrics such as observed heterozygosity, inbreeding coefficients, and pairwise analysis can quantify these potential risks of wrong inbreeding programmes [43].

The aim of this study is to determine the genetic diversity and assess population structure across six population of Iraqi Arabian horses by using 17 ISAG microsatellites. Additionally, check for changes in the population using AMOVA analysis. In addition to international initiatives to conserve equine genetic resources, this study fills these gaps and lays the groundwork for breeding programmes to reduce genetic erosion in Iraqi Arabian horses.

MATERIALS AND METHODS

This study was conducted by the Department of Animal Genetic Resources Protection/ Directorate of Animal Resources/ Ministry of Agriculture, Baghdad, Iraq. Data for Arabian horse pedigree verification were provided by the Iraqi Arabian Horse Organization as part of its routine operations for the period 2020–2024. According to standard protocols, the organization sends 20 hair follicles per horse to an internationally accredited laboratory (Dr. van Heeringen, a VHL Genetics company). This laboratory compares the horses' genetic markers with the previous dam and sire reference files to issue pedigree certificates. Based on these collected data, an analytical study was performed on 205 horse hair samples from six populations: (86 Kuhailan horse, 12 manage horse, 14 Ubaiyah horse, 75 Saglawia horse, 11 Dahman horse and 7 Julfan horse).

The laboratory tested seventeen microsatellite markers: AHT4, AHT5, ASB2, ASB17, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG4, HTG6, HTG7, HTG10, LEX3, VHL20 distributed on chromosomes of the horse genome. All markers are included in the panel recommended by the International Society for Animal

Genetics (ISAG). Information about the loci location, primer sequences can be found in table 1.

Table 1: The primer sequences of the microsatellite loci used in this study

Name of marker	Localization in the genome, No of chromosome	Primer sequence (5'→3')	Reference
AHT4	24q14	AACCGCCTGAGCAAGGAAGT, GCTCCCAGAGAGTTTACCCT	Binns <i>et al.</i> (1995).
AHT5	8	ACGGACACATCCCTGCCTGC, GCAGGCTAAGGGGGCTCAGC	Binns <i>et al.</i> (1995).
ASB2	15	CCACTAAGTGTCTGTTTCAGAAGG, CACAAGTGAAGTTCTCTGATAGG	Breen <i>et al.</i> (1997).
ASB17	2q14p15	GAGGGCGGTACCTTTGTACC, ACCAGTCAGGATCTCCACCG	Breen <i>et al.</i> (1997).
ASB23	3q22.1-q22	GCAAGGATGAAGAGGGCAGC, CTGGTGGGTTAGATGAGAAGTC	Irvin <i>et al.</i> (1998).
CA425	28q18	AGCTGCCTCGTTAATTCA, CTCATGTCCGCTTGTCTC	Eggleston-Stott <i>et al.</i> (1997).
HMS1	1	CATCACTCTTCATGTCTGCTTGG, TTGACATAAATGCTTATCCTATGGC	Guerin <i>et al.</i> (1994).
HMS2	10	CTTGCAAGTCGAATGTGTATTAAAT, ACGGTGGCAACTGCCAAGGAAG	Guerin <i>et al.</i> (1994).
HMS3	9	CCAAGTCTTTGTACATAACAAGA, CCATCCTCACTTTTCACTTTGTT	Guerin <i>et al.</i> (1994).
HMS6	4	GAAGCTGCCAGTATTCAACCATG, CTCCATCTTGTGAAGTGTAAGTCA	Guerin <i>et al.</i> (1994).
HMS7	1q25	CAGGAACTCATGTTGATACCATC, TGTTGTTGAAACATACCTTGACTGT	Guerin <i>et al.</i> (1994).
HTG4	9	CTATCTCAGTCTTGATTGCAGGAC, CTCCCTCCCTCCCTCTGTTCTC	Ellegren <i>et al.</i> (1992).
HTG6	15q26-q27	GAAGCTGCCAGTATTCAACCATG, CTCCATCTTGTGAAGTGTAAGTCA	Ellegren <i>et al.</i> (1992).
HTG7	4	CCTGAAGCAGAACATCCCTCCTTG, ATAAAGTGTCTGGGCAGAGCTGCT	Marklund <i>et al.</i> (1994).
HTG10	21	CAATTCCTCCGCCCCACCCCGGCA, TTTTTATTCTGATCTGTCACATTT	Marklund <i>et al.</i> (1994).
LEX3	4	ACACTCTAACCAGTGCTGAGACT, GAAGGAAAAAAGGAGGAAGAC	Coogler <i>et al.</i> (1996).
VHL20	30	CAAGTCCTCTTACTTGAAGACTAG, AACTCAGGGAGAATCTTCCTCAG	Van Haeringen <i>et al.</i> (1994).

Genetic Diversity Analysis

Allele frequencies, observed and effective allele numbers (N_a and N_e), observed heterozygosity (H_o), expected heterozygosity (H_e), and Shannon's information index (I) were calculated for each locus and population using GenAlEx v6.5 [35]. Private alleles and population-specific allelic richness were also recorded. Deviations from Hardy-Weinberg equilibrium (HWE) were estimated using exact tests implemented in popgene v4.7 [37], with significance levels adjusted using the Bonferroni correction.

Population Differentiation and Structure

The hierarchical partitioning of genetic variation was evaluated using Analysis of Molecular Variance (AMOVA) and fixation indices (F_{IS} , F_{IT} , and F_{ST}), as implemented in Arlequin v3.5 [21]. Significance was tested using 10,000 permutations. Pairwise F_{ST} values were calculated between all breed pairs and estimates of gene flow

(Nm) were derived using the formula $Nm = (1 - F_{ST})/4F_{ST}$ [39]. Population clustering was further explored using Bayesian model-based inference in STRUCTURE v2.3.4 [36], testing $K = 1$ to $K = 6$ under an admixture model with correlated allele frequencies. The most likely number of clusters (K) was determined using the ΔK method of Evanno *et al.* [20], via Structure Harvester [17].

Genetic Relationships and Phylogenetic Analysis

Genetic distances among populations were calculated using Nei's standard genetic distance [32] implemented in Populations v1.2.32. An unweighted pair group method with arithmetic mean (UPGMA) dendrogram was constructed and visualized using MEGA v11 [41]. Bootstrapping (1,000 replicates) was performed to assess the reliability of tree topology. The cophenetic correlation coefficient was calculated to evaluate congruence between the genetic distance matrix and dendrogram structure.

Neutrality Tests and Demographic Inferences

To detect signatures of demographic expansion or selection, neutrality tests were conducted using Tajima's D [40] and Fu's F_s [24], implemented in DnaSP v6.12 [38]. The raggedness index of mismatch distributions was also evaluated to test for population expansion versus bottleneck scenarios. Statistical significance was assessed with 10,000 simulations.

Allele frequency homogeneity across populations was tested using contingency chi-square tests implemented in GenAlEx. Loci exhibiting significant inter-population differences ($p < .001$) were further examined for their potential functional roles and relevance to environmental adaptation or population-specific traits.

RESULTS AND DISCUSSION

Genetic Diversity Analysis

Microsatellite analysis of 205 individuals across six Arabian horse population revealed substantial genetic variation. All 17 microsatellite markers were found to be polymorphic across the analyzed horse populations. The highest level of polymorphism was observed at the HTG7 locus (9 alleles), while the lowest was recorded at HMS2 (4 alleles). Descriptive statistics demonstrated substantial genetic variation, with a mean of 6.4 ± 1.4 alleles per locus (range: 4-9) and an effective allele number of 3.9 ± 0.8 (range: 2.5-5.3), while Shannon's Information Index (I) values ranged from 1.12 to 1.68 (mean: 1.45 ± 0.19) (Table 2).

Table 2: Summary Statistics across Loci

Measure	Overall Mean $\pm$ SD	Range
Allele Number	6.4 ± 1.4	4-9
Effective Alleles	3.9 ± 0.8	2.5-5.3
Gene Diversity	0.69 ± 0.07	0.58-0.79
Shannon Index	1.45 ± 0.19	1.12-1.68

Among populations, Saglawia exhibited the highest genetic diversity ($H_e = 0.72$; $I = 1.49$), whereas Julfan showed the lowest diversity ($H_e = 0.65$; $I = 1.32$) (table.3).

Table 3: Genetic diversity parameters across six Arabian horse Measures by Population

Population	N	Na	Ne	He (SD)	I (SD)
Kuhailan	86	5.8	3.7	0.67 (.03)	1.38 (.12)
Managi	12	5.9	3.8	0.69 (.04)	1.42 (.14)
Ubaiyah	14	6.1	4.0	0.71 (.03)	1.47 (.11)
Saglawia	74	6.3	4.1	0.72 (.02)	1.49 (.10)
Dahman	11	6.0	4.2	0.73 (.04)	1.51 (.13)
Julfan	8	5.4	3.4	0.65 (.05)	1.32 (.15)

Hardy-Weinberg Equilibrium

Significant deviations from Hardy-Weinberg equilibrium were observed across populations (global $\chi^2 = 243.7$, $df = 85$, $p < .001$). Population-specific analyses revealed deviation frequencies ranging from 35% (Dahman) to 76% (Julfan) of loci. The ASB23 locus showed particularly strong deviation in Kuhailan ($p < .0001$ after Bonferroni correction), while LEX3 demonstrated significant deviation in Saglawia ($p < .0001$). Within-population inbreeding coefficients (FIS) varied from 0.082 (Dahman) to 0.112 (Julfan), with an overall FIS of 0.089 ($p < .01$) (table: 4).

Table 4: HWE Deviations by Breed

Population	% Loci Deviating	Most Deviated Locus (p-value)
Kuhailan	71%	ASB23 ($p=0.0001$)
Managi	53%	HTG10 ($p=0.0003$)
Ubaiyah	47%	HMS6 ($p=0.0008$)
Saglawia	65%	LEX3 ($p=0.0001$)
Dahman	35%	CA425 ($p=0.002$)
Julfan	76%	ASB17 ($p=0.0001$)

Global HWE test: $\chi^2=243.7$, $p<0.0001$

Population Structure

Analysis of molecular variance (AMOVA) revealed significant genetic differentiation among populations, F-statistics indicated moderate differentiation among populations ($F_{ST} = 0.068$, $p < .001$) with 6.8% of total variation, and the majority of variation occurring within populations (93.2%). Bayesian clustering analysis identified $K=3$ as the optimal number of genetic clusters ($\Delta K = 412.7$): Cluster 1 comprised Kuhailan and Managi; Cluster 2 contained Ubaiyah, Saglawia, and Dahman; and Cluster 3 consisted exclusively of Julfan individuals. Pairwise F_{ST} values ranged from 0.025 (Ubaiyah-Saglawia) to 0.079 (Kuhailan-Julfan), all significant after Bonferroni correction (adjusted $\alpha = .003$).

Table 5: AMOVA Results and F-Statistics

Source	% Variation	Fixation Index
Among Pops	6.8%	$F_{ST} = 0.068^{**}$
Within Pops	93.2%	$F_{IS} = 0.089^{**}$
Total Inbreeding	-	$F_{IT} = 0.151$

Genetic Distances and Relationships

Nei's genetic distance analysis produced a UPGMA dendrogram with two primary branches: one containing Julfan as an out group, and the other dividing remaining populations into subgroups matching the STRUCTURE clusters. The cophenetic correlation coefficient ($r = 0.91$) indicated strong congruence between the distance matrix and dendrogram topology.

The matrix of pairwise F_{ST} values (Table 6) demonstrated statistically significant differentiation between all population pairs ($p < 0.001$ after 10,000 permutations). The most genetically similar populations were Ubaiyah and Saglawia ($F_{ST} = 0.025$), while the most divergent were Kuhailan and Julfan ($F_{ST} = 0.079$). Corresponding gene flow estimates (N_m) ranged from 2.9 (Kuhailan-Julfan) to 9.8 (Ubaiyah-Saglawia).

Table 6. Pairwise F_{ST} (below diagonal) and N_m (above diagonal)

	Kuhailan	Managi	Ubaiyah	Saglawia	Dahman	Julfan
Kuhailan	-	8.1	5.2	4.8	4.3	2.9
Managi	0.030	-	6.7	6.0	5.4	3.5
Ubaiyah	0.046	0.036	-	9.8	8.2	4.1
Saglawia	0.049	0.040	0.025	-	9.1	4.3
Dahman	0.055	0.044	0.030	0.027	-	4.0
Julfan	0.079	0.067	0.057	0.055	0.059	-

Phylogenetic Relationships

The UPGMA dendrogram based on Nei's genetic distances (Figure 2) showed strong bootstrap support ($>85\%$ for all major nodes) and revealed two primary clades:

1. A monophyletic Julfan clade (bootstrap = 89%).
2. A clade containing all other populations, with Dahman, Saglawia and Ubaiyah forming a well-supported subclade (bootstrap = 92%).

The cophenetic correlation coefficient ($r = 0.91$) indicated excellent congruence between the genetic distance matrix and the dendrogram topology.

Genetic Analysis

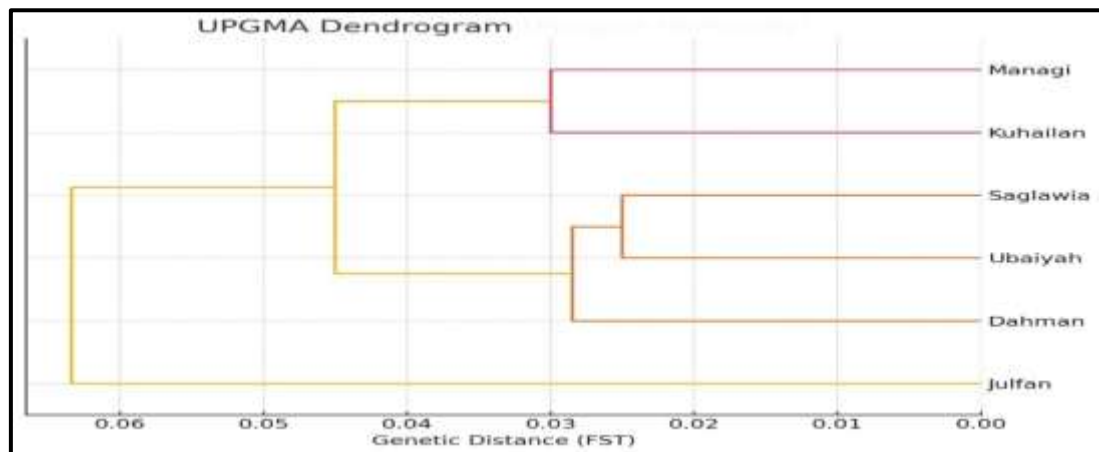


Figure 1. UPGMA dendrogram based on Nei's genetic distance. Bootstrap values ($>50\%$) from 1000 replicates are shown at nodes. Scale bar indicates genetic distance (FST units).

Gene Flow and Evolutionary History

Migration rate estimates revealed asymmetric gene flow, with the highest N_m value between Ubaiyah and Saglawia ($N_m = 9.8$) and the lowest between Kuhailan and Julfan ($N_m = 2.9$). Neutrality tests produced negative values for both Tajima's D (overall $D = -0.85$) and Fu's F_s (overall $F_s = -1.23$), with Tajima's D reaching significance in Julfan ($D = -0.62$, $p < .05$), suggesting potential population expansion table (7).

These results are consistent with either population expansion or purifying selection acting on the studied markers. The raggedness index ($H_{ri} = 0.032$, $p > 0.05$) did not support sudden population decline.

Table 7: Neutrality Tests

Population	Tajima's D	Fu's Fs
Overall	-0.85	-1.23
Kuhailan	-0.78	-1.15
Julfan	-0.62*	-0.98

$p < 0.05$

Homogeneity Testing

The χ^2 test for allele frequency homogeneity across populations was highly significant ($\chi^2 = 201.6$, $df = 102$, $p < 0.0001$), confirming substantial heterogeneity in genetic composition among breeds. This was particularly evident at loci HTG7 ($\chi^2 = 38.2$, $p < 0.0001$), ASB17 ($\chi^2 = 42.7$, $p < 0.0001$) LEX3 ($\chi^2 = 35.9$, $p < 0.0001$). Private alleles were detected in all populations, with Julfan showing the highest number of population-specific alleles ($n = 7$).

The present study provides a comprehensive assessment of genetic diversity and population structure across six Arabian horse population using 17 polymorphic microsatellite markers. The study findings reveal important patterns of genetic variation that have significant implications for the conservation and management of these populations.

Despite being somewhat lower than values reported for other horse breeds (Pritchard et al., 2021), the observed genetic diversity metrics (mean $H_e = 0.69 \pm 0.07$) are consistent with other studies on Arabian horse populations [4, 29]. The particularly low diversity in the Julfan population ($H_e = 0.65$) is concerning and consistent with reports of declining genetic variability in isolated equine populations (Bowling et al., 2020). This reduced diversity may reflect both historical population bottlenecks and recent breeding practices, as suggested by the significant negative Tajima's D values ($D = -0.62$, $p < 0.05$).

The moderate but significant population differentiation ($F_{ST} = 0.068$, $p < 0.001$) supports the traditional classification of these breeds as distinct genetic entities. This level of differentiation is comparable to that observed among other geographically proximate horse breeds (Cosgrove et al., 2020). The Bayesian clustering analysis revealed three distinct genetic clusters, with Julfan forming a separate group from the other populations. This finding corroborates historical records suggesting long-term reproductive isolation of Julfan horses [2].

The significant deviations from Hardy-Weinberg equilibrium observed in all populations, particularly at loci ASB23 and LEX3, may indicate several evolutionary processes at work. While some deviations could result from technical artifacts like null alleles [15], the consistent patterns across multiple loci suggest biological factors such as population substructure (Wahlund effect) or selection pressures [3]. The significant deviation from HWE, indicate that there was non-random mating likely due to a selection program favouring some morphological characters [32]. The high FIS values in Julfan (0.112) are particularly noteworthy and may reflect both intentional inbreeding and small population size [32].

The Saglawia population is a significant genetic reservoir because of its pivotal position in the population network, low inbreeding ($F_{IS} = 0.082$), and high diversity ($H_e = 0.72$). The high variation in the Saglawia could be explained by the reconstruction of the breeding stock population after 2003, and the enrichment of its gene pool to

improve their performance by using outcrossing with foreign Arabian [31]. The highest genetic diversity may be associated with introgression from the other lineages [27].

The gene flow patterns revealed by migration estimates ($N_m = 2.9-9.8$) provide important insights into historical breed management practices. The exceptionally high gene flow between Ubaiyah and Saglawia ($N_m = 9.8$) suggests these populations have been managed as a metapopulation, possibly reflecting traditional breeding practices in the region [10]. In contrast, the limited gene flow involving Julfan horses supports their historical isolation.

The neutrality tests showing significantly negative Tajima's D and Fu's F_s values across populations suggest possible demographic expansion following historical bottlenecks. This pattern has been observed in other desert-adapted livestock breeds (Ciani et al., 2020) and may reflect adaptation to harsh environmental conditions. However, considering previous correlations between certain markers and the qualities that are being selected for in horses, it is impossible to completely rule out the effect of selection at the loci under study [5].

Conclusion

This study provides the most comprehensive genetic characterization of these Arabian horse populations to date in Iraq. The results from microsatellite analysis demonstrated high genetic diversity in the Saglawin lineage ($H_e = 0.72$; $I = 1.49$), whereas the Julfan lineage showed the lowest diversity ($H_e = 0.65$; $I = 1.32$). The low diversity indices and significant genetic distinctiveness of the Julfan population are concerning, as they suggest high levels of inbreeding and diversity loss. The observed patterns of genetic variation (e.g., the distinct clusters identified by STRUCTURE analysis) reflect both natural evolutionary processes and human-mediated breeding practices. These findings establish a crucial genetic baseline that can inform conservation strategies and help maintain the health and cultural heritage of these important horse populations. Our results will also enhance efforts to implement appropriate and strategic breeding programs by pinpointing which lineages require immediate conservation attention (Julfan) and which maintain high genetic health (Saglawin). The use of molecular studies to analyze population structure and genetic diversity is imperative for effective management. Finally, future studies should prioritize whole-genome sequencing to provide a higher resolution, as it is more sensitive in detecting introgression or subtle genetic admixtures that may not be apparent with microsatellite markers alone.

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التنوع الوراثي وتركيبية العشائر لسلالة الخيل العربية الاصيلية في العراق

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الملخص

اجريت هذه الدراسة من قبل قسم حماية المصادر الوراثية الحيوانية / دائرة الثروة الحيوانية / وزارة الزراعة، بغداد، العراق. وقد وُقِّرت المنظمة العراقية للخيول العربية بيانات التحقق من نسب الخيول العربية كجزء من عملياتها الروتينية للفترة 2020-2024. تهدف هذه الدراسة إلى توفير تقييم وراثي شامل، والتحقيق في الوضع الحالي للتنوع الوراثي، والتزاوج الداخلي، والعلاقات بين ستة عشائر من سلالة الخيل العربية الموجودة في العراق (كحيلان، معنكية، عبية، صقلاوي، دهماء، وجلفة) باستخدام 17 علامة ميكروستلايت، خلّلت 205 عينات شعر وفقاً لبروتوكولات موحدة.

أظهرت جميع العلامات تعدد أشكال، حيث أظهر HTG7 أعلى تنوع أليلي (9 أليلات) بينما أظهر HMS2 أدنى تنوع (4 أليلات). بين المجموعات، أظهرت مجموعة الصقلاوي أعلى تنوع وراثي ($I = 1.49$; $He = 0.72$)، بينما أظهرت مجموعة الجلفة أدنى تنوع ($I = 1.32$; $He = 0.65$). تراوحت معاملات التزاوج الداخلي داخل المجموعات (FIS) من 0.082 (دهماء) إلى 0.112 (جلفة)، مع FIS إجمالي قدره 0.089 ($p < 0.01$) أظهرت مجموعة الجلفة تزاوجاً داخلياً مرتفعاً يجب تصحيحه عن طريق تعديل نظام التزاوج من خلال تجنب الاستخدام المفرط لبعض الآباء في برنامج التربية. من بين ستة مجموعات من الخيول العربية، أظهرت تسعة مواضع 13 أليلاً خاصاً.

أشار تحليل المسافة الوراثية Nei إلى فرعين رئيسيين: أحدهما يحتوي على مجموعة الجلفة كمجموعة خارجية، والآخر يقسم المجموعات المتبقية إلى مجموعات فرعية. أظهرت قيم FST تمايزاً إحصائياً مهماً بين جميع أزواج المجموعات ($P < 0.001$) بعد 10000 تبديل). كانت أكثر المجموعات تشابهاً وراثياً هي صقلاوي وعبية ($FST = 0.025$)، بينما كانت الأكثر تباعدًا هي كحيلان وجلفة ($FST = 0.079$). تراوحت تقديرات التدفق الجيني المقابلة (Nm) بين 2.9 (كحيلان-جلفان) و 9.8 (عبية-صقلاوية). تشير النتائج الحالية إلى أن الخيول العربية الاصيلية في العراق تتمتع بخصائص فريدة ويمكن استخدام هذه الخصائص في وضع استراتيجيات للحفاظ عليها وتحسين برامج التربية وإدارة الخيول العربية الاصيلية في العراق.

الكلمات الدالة: الخيل العربية الاصيلية، التنوع الوراثي، الميكروساتلايت، عشائر الخيل.

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