GENETIC DIVERSITY OF ARABIAN HORSES USING MICROSATELLITE MARKERS

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SUMMARY

The horse strains designation system was shaped in the 7th century in the Arabian Peninsula and spread to the neighboring oriental empires and it is still used. The aim of the present study was to investigate genetic diversity among three Arabian horse strains using twelve equine microsatellite markers. The study included 84 Arabian horses representing three major Syrian strains (Hamdani, Kahlawi and Saglawi) from five geographical regions in Syria. To determine genetic population structure within and between the three strains, we applied different methods. The selected panel of microsatellite markers confirmed a general genetic feature of the three main strains of Syrian Arabian horses suggesting low level of population differentiation. To ascertain the results, it will be necessary to collate our findings with the historical pedigree. Furthermore, we need a genome-wide investigation of microsatellites or an analysis of strain/breed specific SNPs across the Syrian Arabian horse populations for better insight into the genetic diversity.

Keywords: Arabian horse strains, Syria, Genetic diversity, Microsatellites

INTRODUCTION

Arabian horses are considered "hot-blooded" horse breed and believed to be the oldest recorded horse breed in the world, traced back to around 2000 years ago. They are thought to be originated either in Mesopotamia or Arab peninsula (Głażewska 2010; Cosgrove *et al.* 2020). Due to its fitness, robustness against shortage of feed and rough environmental circumstances as well as its endurance; Arabian horses are considered as an appreciated breed which is spread all over the world (Khadka 2015). Native populations in the Middle East, such as those in Syria, are suggested as a hot spot for genetic diversity of Arabian horses (Almarzook *et al.* 2017).

Arabian horse breed is thought to have descended from five distinct founder mares which are known as strains; namely Saglawi, Kahlawi, Hamdani, Obeyan and Hadban (Raswan *et al.* 1981; Mayouf *et al.* 2011). The strains designation system was shaped in the 7th century in the Arabian Peninsula and spread to the neighboring oriental empires and it is still being used (Bennett 2008).

In this regard, strains including Saglawi, Kahlawi and Hamdani have been documented in the Syrian national stud-book and the latest estimated number was 6189 horses (AL Shaieb 2016). In historical documents, little information can be found about the characteristics and development of the strains. In addition, knowledge about genetic diversity and relationship among them in Syria is still limited.

Characterization of genetic diversity is important for the maintenance of heterozygosity of the genetic pool, especially under stress situations where the population decline (Toro & Caballero 2005; Tapio *et al.* 2010; Hasler *et al.* 2011). Different genetic markers such as mitochondrial DNA, microsatellites and single nucleotide polymorphisms (SNPs) were used for measuring the genetic diversity and assessing the evolution processes of horse breeds (Cho 2006; Seyedabadi *et al.* 2006; Kakoi *et al.* 2007; Giacomoni *et al.* 2008; Leroy *et al.* 2009; Mackowski *et al.* 2015). At present, only few studies have investigated the genetic diversity and population structure within (Bowling *et al.* 2000; Georgescu *et al.* 2005; Mahrous *et al.* 2011) and among (Khanshour *et al.* 2013a; Almarzook *et al.* 2017) Arabian horse populations in the Middle East and in the world with regard to the strain affiliation.

For genetic diversity, microsatellite markers are widely accepted for such studies within and among populations and breeds. Microsatellites are short repeats of di-nucleotides (e.g. CA), tri-nucleotides (e.g. TCT), tetra-nucleotides (e.g. GATA), penta or hexanucleotides (Ellegren 2004). Microsatellites have the advantage of being highly polymorphic detecting often more than two alleles at one locus. Most microsatellites are neutral in their function. They are evenly distributed across the genome and co-dominantly inherited; in addition, they have a low mutation rate. The first equine microsatellites were reported in 1992 (Ellegren *et al.* 1992). Since then, several studies have been conducted to investigate

origin, genetic structure, and relationships among different horse breeds (Cho 2006; Seyedabadi *et al.* 2006; Kakoi *et al.* 2007; Giacomoni *et al.* 2008; Leroy *et al.* 2009; Ling *et al.* 2011; Xu *et al.* 2012; Mackowski *et al.* 2015). However, only a few studies have been carried out using microsatellites to investigate genetic diversity and population structure within (Georgescu *et al.* 2005; Mahrous *et al.* 2011; Mostafa *et al.* 2011; Sargious *et al.* 2014) and between (Khanshour *et al.* 2013a) Arabian horse populations world-wide.

Therefore, the aim of the current study was to gain a better insight into the genetic diversity within and between the three major Arabian horse strains in Syria (Hamdani, Kahlawi and Saglawi) and possibilities of being related to each other using twelve equine microsatellites on different chromosomes.

MATERIALS AND METHODS

Animals:

DNA was isolated from hair roots and/or whole blood samples of 84 Arabian horses. Samples were randomly collected from diverse regions in Syria: South (Daraa, n = 2), Middle-West (Hims, n = 2 and Hama, n = 2) and North-East (Al-Hasakeh, n = 10), as well as from the National Centre of the Arab Horse in Damascus (n = 68). The sampled horses are registered in the national stud-books representing the Syrian strains: Hamdani (n = 26), Kahlawi (n = 30) and Saglawi (n= 28). Sampling had the permission of local owners and official authorities in the Syrian Ministry of Agriculture and Agrarian Reform and was preformed according to the national law for animal welfare and protection.

Extraction of the DNA from hair roots was done by incubating the roots in 180 µl T1 buffer followed by the salting out procedure with some modifications (Miller *et al.* 1988). This method involves salting out of the cellular proteins by dehydration and precipitation with a saturated NaCl solution. While for DNA extraction from whole blood, we used the Puregene Core Kit (Qiagen, Hilden, Germany). We used two tubes for each blood sample filled with 500 µl fresh EDTA as an anticoagulant.

Microsatellites markers:

All horses were genotyped for the twelve equine microsatellite markers: AHT4, ASB17, ASB23, HMS1, HMS2, HMS3, HMS6, HMS7, HTG4, HTG7, LEX3 and VHL20 (Table S1). Microsatellites used in the current study were chosen from the recommended standard panel of the International Society of Animal Genetics (ISAG 2014). Polymerase chain reaction (PCR) conditions were provided by the ISAG-FAO advisory group protocol (FAO 2011). The detection of the microsatellite allele length was performed with a LI-COR gel electrophoresis system using fluorescence-labelled M13-tailed primers. Reference samples were used for correct allele length detection.

Statistical analyses:

Standard genetic diversity analyses were carried out using GenAlEx 6.5 (Peakall & Smouse 2012) including number of alleles for individual markers (Na), number of private alleles (NPa), observed heterozygosity (Ho), expected heterozygosity (He), and allele frequencies. The genetic variation existing within and among the three strains was assessed through the Analysis of Molecular Variance (AMOVA); while, Wright`s F statistics (FIS, FIT and FST) were used to quantify the genetic variances. The polymorphism information content (PIC) was calculated to investigate the polymorphic status of each locus per each strain. Furthermore, we created and used the first three principal component analysis (PCA) for the twelve microsatellites of the three Arabian horse strains based on genetic distance matrix. We used POPTREE2 (Takezaki *et al.* 2010) to construct the phylogenetic tree from the genetic distance matrix of allele frequencies data by using the neighbor-joining (NJ) method (Saitou & Nei 1987) with 5000 bootstrap tests.

RESULTS AND DISCUSSION

Diversity within strains:

In the current study, we used a set of twelve recommended equine microsatellites to investigate the genetic structure of 84 Arabian horses descended from the three main Arabian horse strains in Syria (Hamdani, n = 26; Kahlawi, n = 30; and Saglawi, n = 28).

A total of 251 alleles were detected across all horses for the twelve microsatellites. Total numbers of alleles per each strain were 84, 76 and 91 in Kahlawi, Hamdani and Saglawi, respectively (Table 1 and supplementary Table S2). All loci were polymorphic and the number of alleles (Na) per locus ranged from three (HTG4 and HTG7) to eleven (ASB17 and LEX3).

The average number of alleles per locus was ranged between 6.333 and 7.583, and the average number of alleles was varied only slightly between the strains with an average of 6.972±0.364 across the strains. The effective number of alleles (Ne) was the lowest in Hamdani (3.797±0.357) while Saglawi showed the highest value (7.583 ±0.621).

The average number of alleles (Na), and polymorphic information content (PIC) estimates per locus in each strain showed that all microsatellites were polymorphic. The average number of alleles per locus were ranged between 6.333 and 7.583; close to those previously detected in the Middle-Eastern Arabian horses (5.130 to 8.470) (Khanshour *et al.* 2013a), African Arab-Barb horses (7.86) (Berber *et al.* 2014), and differed slightly from those reported in Arabian horses from Iran and Chaharmahal va

Bakhtiari province (3 to 9) (Moshkelani *et al.* 2011; Mostafa *et al.* 2011). Our PIC values (0.383 to 0.890) were close to those reported in Iranian Arabian horses (0.402 to 0.764) (Moshkelani *et al.* 2011; Khanshour *et al.* 2013b). The slight differences may be due to the differences of population structure, number of horses, and/or chosen microsatellites panel.

Our studied loci were more polymorphic in Saglawi (Na=7.583, PIC=0.743) meaning that Saglawi have the highest genetic variation than Kahlawi and Hamdani strains. Additionally, Saglawi possessed the highest number of private alleles (Npa=12) which was notably different from the observed numbers in Kahlawi (Npa= 9) and Hamdani (Npa=5) strains. This shows that Saglawi contributed more than the other two strains to the total polymorphic information content.

The average effective number of alleles (Ne) in the three strains per locus falls in the range reported by Khanshour *et al.* (2013a) for Middle-Eastern and Western Arabian horses (3.51 to 4.23), but it was higher than the values reported by Rukavina *et al.* (2015) for Arabian horses raised in Bosnia and Herzegovina (2.04, 4.08).

Microsatellites over all the three strains showed high heterozygosity. In the three strains, the mean observed heterozygosity (Ho) and the mean expected heterozygosity (He) were similar but slightly higher in Saglawi. Detailed heterozygosity values per locus and strain are shown in the supplementary Table S3.

Inbreeding coefficients (FIS) in each strain for the twelve loci are also shown in Table 1. Low FIS values were present in Hamdani and Kahlawi (0.010 and 0.027, respectively), while Saglawi showed a higher value (0.123). The polymorphic information content (PIC) of every microsatellite within the strains fluctuated from 0.363 (HTG7 in Kahlawi) to 0.890 (ASB17 in Saglawi).

All PIC values in terms of means and standard errors per strain/locus are shown in the supplementary Table S3. For the three strains, no significant variation was detected.

Wright`s F-statistics (FIS, FST, FIT) estimated over all individuals per locus are listed in Table 2. The average FIS value per locus over all horses was 0.054, and over all strains was 0.019 ranging from 0.007 (HTG07) to 0.037 (LEX3). Additionally, the mean of global deficit of heterozygotes across strains (FIT) was 0.072.

Table 1. Statistics for genetic diversity in the main Syrian horse strains using twelve microsatellite markers

Strain	TNa	Npa	Na	Ne	Ho	He	FIS
Kahlawi	84	9	7.000± 0.663	4.044± 0.414	0.697± 0.050	0.717± 0.037	0.027± 0.047
Hamdani	76	5	6.333± 0.607	3.797± 0.357	0.696± 0.031	0.707± 0.031	0.010± 0.032
Saglawi	91	12	7.583± 0.621	4.582± 0.537	0.646± 0.046	0.743± 0.037	0.123± 0.054
Overall mean± SE	251	26	6.972± 0.364	4.141± 0.254	0.680± 0.025	0.722± 0.020	0.053± 0.027

TNa: total number of alleles, NPa: number of private or rare alleles with a frequency less than 0.1, Na: average number of alleles per locus, Ne: average number of effective alleles, Ho: observed heterozygosity, He: expected heterozygosity, FIS: inbreeding coefficient, and SE: standard error.

Table 2. F-statistics of the twelve microsatellites analyzed in 84 Syrian Arabian horses

Locus	FIS	FIT	FST
AHT04	-0.195	-0.180	0.013
ASB17	0.025	0.046	0.021
ASB23	0.221	0.242	0.027
HMS01	-0.083	-0.053	0.028
HMS02	0.064	0.073	0.010
HMS03	0.107	0.125	0.020
HMS06	0.008	0.028	0.020
HMS07	0.115	0.126	0.012
HTG 4	0.031	0.043	0.013
HTG 7	-0.037	-0.030	0.007
LEX3	0.248	0.275	0.037
VHL20	0.150	0.167	0.021
Overall mean± SE	0.053± 0.036	0.072± 0.037	0.019± 0.003

FIS: inbreeding coefficients of individuals relative to each strain. FIT: inbreeding coefficients of individuals relative to the total population. FST: fixation index (measure of population differentiation due to genetic structure).

The overall expected (0.722) and observed (0.680) heterozygosity in the studied population did not significantly differ from those previously reported in Barb horses (Ho= 0.75 and He= 0.75), Arab-Barb horses (Ho= 0.73 and He= 0.77), English thoroughbred (Ho =0.71 and He = 0.71), AkhalTeke (Ho =0.72 and He = 0.65), Iranian Arabian (Ho =0.70 and He = 0.71), and Polish Arabian horses (Ho =0.69 and He = 0.68) (Cho 2006; Khanshour *et al.* 2013a; Berber *et al.* 2014).

Results showed that Ho estimates were less than the He, which is rather expected because the traditional breeders avoid strictly outcrossing with foreign or unknown horses. This suggests that our studied Arabian horses have received less external gene flow (Crawford 2007), but fortunately, still have high heterozygosity. Both, polymorphic alleles and high heterozygosity are essential for maintaining the diversity of the Arabian horse populations and eventually for future breeding programs (Hill & Rasbash 1986).

The inbreeding coefficient values (FIS) were around zero. The highest value was found in Saglawi (0.123) implying some relatedness among its ancestors. Overall, FIS reported in this study (0.053) is a bit higher than that reported in Syrian Arabian horses (-0.007), and Iranian Arabian horses (0.017), but close to that reported in Egyptian Arabian horses in the USA (0.047) (Khanshour *et al.* 2013a).

Diversity among strains:

The analysis of molecular variance (AMOVA) of the twelve microsatellites (where the input was the allelic distance matrix for the F-statistics analysis) revealed an estimated variation of 0.045 among the three strains and 0.343 among individuals within the strains (Table 3).

Genetic differentiation values (FST) between pairs of strains are shown in Table 4. The FST estimations were ranged between 0.013 (Saglawi vs. Kahlawi) and 0.015 (Hamdani vs. Saglawi and Kahlawi). In general, values showed low differentiation among the three tested strains.

Moreover, the principal component analysis (Figure 1; A, B and C) displayed no partition among the three Arabian strains.

In the Nei's phylogenetic tree, Hamdani strain (POP2) showed a slight separation from Kahlawi and Saglawi (POP1 and POP 3) (Figure 2).

AMOVA results revealed that only 0.045 of the genetic variation was attributed to strain differences, as evidenced by the low pairwise FST values across the three strains. FST values were close to each other and to the overall value (0.019) showing a low level of population stratification of the three strains.

The Neighbor-joining dendrogram showed Kahlawi (POP1) clustering with Saglawi (POP3), while Hamdani (POP2) branched off slightly away from Kahlawi and Saglawi strains. Interestingly, in the former study of maternal lineages diversity of the same strains (Almarzook *et al.* 2017), the results showed that the lowest pairwise FST value was between Saglawi and Kahlawi (0.098), while a comparison of Hamdani with Saglawi and Kahlawi showed higher pairwise FST values (0.205 and 0.138, respectively), which suggested that individuals of Kahlawi and Saglawi strains share closely maternal related ancestors. However, the genetic distances suggested that the three studied strains are closely related.

The distribution of individuals in the PCA indicates high similarities between the three strains. The greatest amount of variation captured on axis 1 was 8%, but no clear pattern of subdivision was observed. This result is in agreement with the pairwise FST estimates. Furthermore, the samples were collected from different geographical regions in Syria, but the PCA presents a possible blood accessibility outwards and inwards strains due to mating horses from different strains.

Table 3. Analysis of molecular variance (AMOVA) for twelve microsatellite loci in the three strains of Syrian Arabian horses

Source of variation	df	Sum of squares	Mean squares	Estimated variation	Percentage variation (%)
Among strains	2	14.512	7.256	0.045	1%
Among individuals within strains	81	385.833	4.763	0.343	8%

Table 4. Pairwise population differentiations (FST) among the three Syrian Arabian horse strains

	Kahlawi	Hamdani	Saglawi
Kahlawi	0.000		
Hamdani	0.015	0.000	
Saglawi	0.013	0.015	0.000

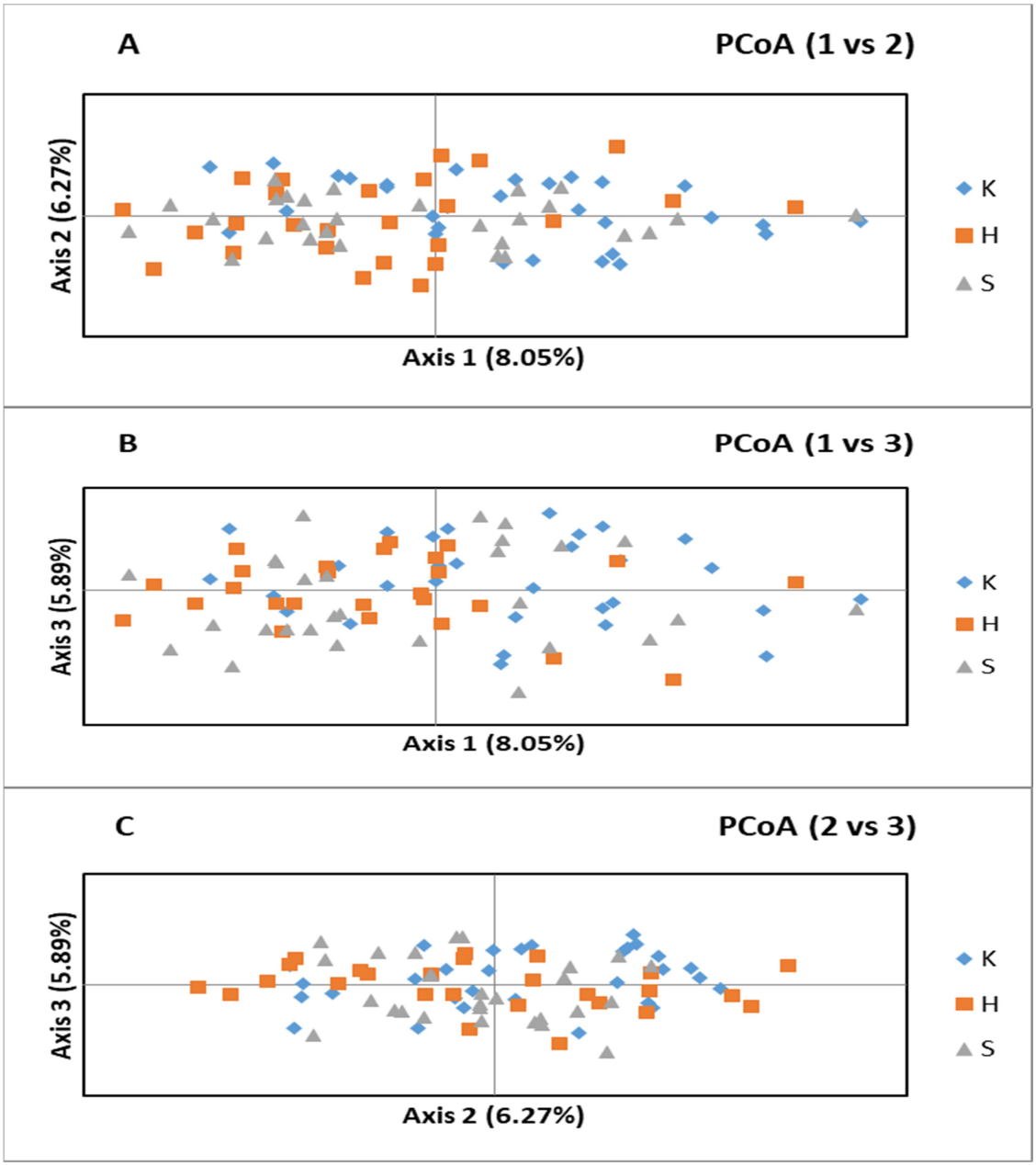

Figure1. First three principal component analysis (PCoA) of the Syrian Arabian horses descended from three strains; K: Kahlawi, H: Hamdani and S: Saglawi.

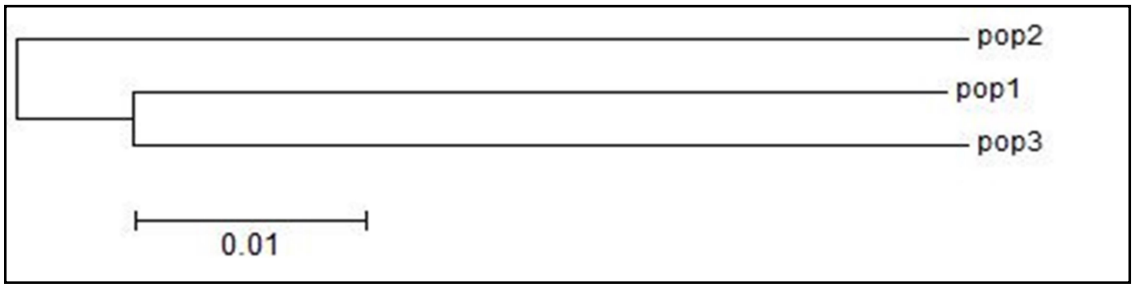

Figure 2. Neighbor-joining dendrogram based on Nei's genetic distance of the three Syrian strains (POP1: Kahlawi, POP2: Hamdani, POP3: Saglawi) using POPTREE2.

Our study with limited markers did not support the legend assumed. Increasing the number of markers (Koskinen *et al.* 2004) or using other methods (e.g. SNP chip) that covering the whole genome would be more beneficial for a better population characterization.

Supplementary Tables:

Table S1. Primer sequence of the twelve equine specific microsatellites

Loci	ECA	Primer Sequence (5'-3')	Expected and size range (bp)	Repeat motif	Reference
AHT4	24	AACCGCCTGAGCAAGGAAGT GCTCCCAGAGAGTTTACCCT	142 - 164	(AC)nAT(AC)n	(Binns *et al.* 1995)
ASB17	2	ACCAGTCAGGATCTCCACCG GAGGGCGGTACCTTTGTACC	81 - 125	(AC)n	(Breen *et al.* 1997)
ASB23	3	ACATCCTGGTCAAATCACAGTCC GAGGGCAGCAGGTTGGGAAGG	181 - 209	(TG)n and (TG)nTT(TG)4	(Breen *et al.* 1997)
HMS1	15	CATCACTCTTCATGTCTGCTTGG TTGACATAAATGCTTATCCTATGGC	170 - 186	(TG)n	(Guérin *et al.* 1994)
HMS2	10	CTTGCAGTCGAATGTGTATTAAATG ACGGTGGCAACTGCCAAGGAAG	216 - 244	(CA)n(TC)2	(Guérin *et al.* 1994)
HMS3	9	CCAACTCTTTGTCACATAACAAGA GCCATCCTCACTTTTTCACTTTGTT	152 - 180	(TG)2(CA)2TC(CA)n and (TG)2(CA)2TC (CA)n GA(CA)5	(Guérin *et al.* 1994)
HMS6	4	CTCCATCTTGTGAAGTGTAACTCA GAAGCTGCCAGTATTCAACCATTG	155 - 169	(GT)n	(Guérin *et al.* 1994)
HMS7	1	CAGGAAACTCTCATGTTGATACCATC GTGTTGTTGAAACATACCTTGACTGT	171 - 189	(AC)2(CA)n	(Guérin *et al.* 1994)
HTG 4	9	CTATCTCAGTCTTGATTGCAGGAC GCTCCCTCCCTCCCTCTGTTCTC	126 - 142	(TG)nAT(AG)5AAG (GA)5, ACAG(AGGG)3	(Ellegren *et al.* 1992)
HTG 7	4	CCTGAAGCAGAACATCCCTCCTTG ATAAAGTGTCTGGGCAGAGCTGCT	118 - 128	(GT)n	(Marklund *et al.* 1994)
LEX3	X	ACACTCTAACCAGTGCTGAGACT GAAGGAAAAAAAGGAGGAAGAC	142 - 164	(TG)n	(Coogle *et al.* 1996)
VHL20	30	CAAGTCCTCTTACTTGAAGACTAG AACTCAGGGAGAATCTTCCTCA	85 - 109	(TG)n	(Haeringen *et al.* 1994)

Equus caballus autosomes (ECA)

Table S2. Number of polymorphic alleles (Na), effective alleles (Ne), private or rare alleles with frequency less than 0.1 (NPa) and allelic range size (bp) per locus per strain

Strains	Kahlawi			Hamdani			Saglawi			Allelic range (bp)
Loci	Na	Ne	Npa	Na	Ne	Npa	Na	Ne	Npa	
AHT4	8	4.478	1	5	3.725	-	7	3.689	-	148 - 162
ASB17	11	7.171	1	11	6.531	1	11	9.064	-	91 - 135
ASB23	7	3.020	-	6	3.549	-	7	4.455	1	148 - 170
HMS1	5	3.358	-	7	3.066	2	6	3.350	1	171 - 189
HMS2	11	5.294	4	8	4.333	-	7	4.653	-	218 - 240
HMS3	7	4.905	-	5	3.684	-	10	5.851	3	148 - 170
HMS6	6	3.888	1	6	4.097	1	6	3.548	1	131 - 171
HMS7	6	4.891	-	6	4.212	-	7	4.766	-	169 - 181
HTG 4	6	3.659	1	3	2.499	-	5	3.213	-	127 - 137
HTG 7	3	1.569	-	4	1.767	1	5	1.620	2	118 - 179
LEX3	8	3.462	1	8	5.121	-	11	6.078	2	190 - 214
VHL20	6	2.839	-	7	2.978	-	9	4.695	2	87 - 105
Total	84	-	9	76	-	5	91	-	12	-
Mean ±S.E.	7.000 ±0.663	4.044 ±0.414		6.333 ±0.607	3.797 ±0.357		7.583 ±0.621	4.582 ±0.537		

Table S3. Observed (Ho) and expected (He) heterozygosity and polymorphic information content (PIC) for loci in twelve microsatellites set in three Syrian Arabian horse strains

Strains	Kahlawi			Hamdani			Saglawi		
Loci	**Ho**	**He**	**PIC**	**Ho**	**He**	**PIC**	**Ho**	**He**	**PIC**
AHT4	0.933	0.790	0.777	0.846	0.746	0.732	0.893	0.742	0.729
ASB17	0.900	0.875	0.861	0.846	0.863	0.847	0.786	0.906	0.890
ASB23	0.567	0.680	0.669	0.654	0.732	0.718	0.464	0.790	0.776
HMS1	0.767	0.714	0.702	0.769	0.687	0.674	0.714	0.714	0.702
HMS2	0.800	0.825	0.811	0.808	0.784	0.769	0.607	0.799	0.785
HMS3	0.700	0.810	0.796	0.615	0.743	0.729	0.786	0.844	0.829
HMS6	0.867	0.755	0.743	0.654	0.771	0.756	0.679	0.731	0.718
HMS7	0.600	0.809	0.796	0.692	0.778	0.763	0.786	0.805	0.790
HTG 4	0.733	0.739	0.727	0.577	0.612	0.600	0.643	0.701	0.689
HTG 7	0.367	0.369	0.363	0.500	0.443	0.434	0.357	0.390	0.383
LEX3	0.467	0.723	0.711	0.731	0.821	0.805	0.571	0.851	0.835
VHL20	0.667	0.659	0.648	0.654	0.677	0.664	0.464	0.801	0.787
Mean	0.697	0.729	0.717	0.696	0.721	0.707	0.646	0.756	0.743
±S.E.	±0.050	±0.037	±0.037	±0.031	±0.032	±0.031	±0.046	±0.038	±0.037

CONCLUSIONS

The selected panel of microsatellites markers confirmed a general genetic feature of the three Syrian main strains suggesting a low level of population differentiation.

We think that this method did not validate the variation between the legendary founder mares, since the three strains appear to be genetically related. To ascertain the results, a genome-wide investigation of markers across the whole genome of Syrian Arabian horses is highly required to gain a better insight into the genetic diversity of the maternal lines (strains) of the entire population.

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التنوع الوراثي للخيول العربية باستخدام واسمات المايكروستلايت

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ظهر نظام الأرسان في الخيول العربية منذ مطلع القرن السابع الميلادي وانتشر استخدامه في شبه الجزيرة العربية والإمبراطوريات الشرقية المجاورة، ولا يزال قيد الاستخدام عند غالبية المربين والهيئات التي تعنى بالحصان العربي الأصيل. الهدف من هذه الدراسة هو التحقق من التنوع الوراثي لثلاثة من أهم أرسان من الخيول العربية في سوريا وذلك باستخدام اثني عشر واسماً وراثياً من نوع المايكروستلايت. ثم أخذ العينات من أربعة وثمانين من الخيول العربية المسجلة في كتب الأنساب السورية والتي تتحدر من الأرسان الرئيسية الثلاث: الحمداني والكحلاوي والصقلاوي. تعود الخيول المدروسة إلى خمس مناطق جغرافية في سوريا. لتحديد التنوع الوراثي وتحليل العلاقات داخل الأرسان من جهة وبين الأرسان الثلاثة من جهة أخرى، عمدنا إلى استخدام طرق تحليلية متنوعة. أكدت نتائج تحليل واسمات المايكروساتالايت وجود سمة وراثية عامة تجمع الأرسان المدروسة من الخيول العربية السورية مما يشير إلى مستوى منخفض من التمايز بين الأرسان الثلاث. للتأكد من النتائج، كان من الضروري مقارنة النتائج التي توصلنا إليها مع الدراسات السابقة على الخيول العربية وغيرها من السلالات التي تتبع منهجاً مماثلاً في التربية التقليدية. للحصول على رؤية أعمق ونتائج أكثر دقة عن التنوع الوراثي للأرسان المدروسة، نحن بحاجة دون شك إلى تغطية أعلى مستوى تشمل مناطق أوسع من جينوم الخيول العربية.