

Genetic diversity of the Tornjak shepherd dog

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ABSTRACT

The objective of the study was to assess the genetic diversity of the Tornjak shepherd dog by analyzing 10 microsatellite loci. The dogs were divided into three main groups: Tornjaks from Bosnia and Herzegovina (TBA), Tornjaks from Croatia (THR), and a control group containing four subgroups: German Shepherd (GS), Belgian Shepherd (BS), crossbreeds of Tornjaks and other breeds (MIXT), and various other dog breeds (MIXA). The average number of genotypes (GN) and alleles (AN) was 19.2 and 8.4 (TBA), 8.2 and 5.4 (THR), 7.9 and 5.1 (BS), 4.4 and 3.6 (GS), 7.6 and 5.5 (MIXT), and 8.6 and 6.0 (MIXA), respectively. The average values of observed (HO) and expected heterozygosity (HE) were 0.7261 and 0.7392 (TBA); 0.7625 and 0.7139 (THR); 0.6857 and 0.6837 (BS); 0.4900 and 0.4640 (GS); 0.6786 and 0.6760 (MIXT); and 0.7067 and 0.7160 (MIXA), respectively. In the TBA population, “private” alleles were observed at all ten loci. The average overall inbreeding coefficient (F) value between the Tornjak and the control group was 0.0768. The AMOVA test revealed the highest degree of variation within the TBA group (55.43%), while no significant variations were observed in the control subgroup GS. The smallest differentiation for TBA was found with THR at 1.86% using the pairwise F_{ST} (pF_{ST}). The constructed Neighbor-Joining (NJ) dendrogram shows clear grouping of TBA and THR in comparison to the breeds of the control group. In relation to the data presented, a high level of heterogeneity has been established in the studied Tornjak population (TBA).

Key words: Tornjak; dog; microsatellites; genetic diversity

Introduction

Shepherd (or sheep) dogs guard livestock during grazing and protect them from large predators, including other types of animals. The significant population of wolves in Bosnia and Herzegovina

had an important influence on the development of the Tornjak Bosnian and Herzegovinian – Croatian Shepherd dog as a protector of livestock and property from wolves and unwanted visitors. It is resistant to unpredictable weather conditions, especially

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in the mountains, where all four seasons can change in a single day. The Tornjak is a premier shepherd dog, serving as a guardian of pens (from which its name is derived – *tor* meaning pen) and livestock, with a highly developed olfactory sense that enables it to detect the presence of wolves and bears in a timely manner. The long-standing practice of transhumance, involving the seasonal migration of both livestock and shepherds between permanent summer and winter pastures, has facilitated a continuous genetic flow within and between guardian dog breeds inhabiting overlapping territories ([CEH and DOVC, 2014](#)). The Tornjak, recognized under the name Bosnian and Herzegovinian-Croatian Shepherd Dog, was officially accepted by the FCI on November 7, 2017. It belongs to Group 2 – Pinschers, Schnauzers, Molossers – Swiss Mountain and Herding Dogs, Section 2.2 – Mountain Type ([FCI, 2017](#)).

The importance of breeding and preserving indigenous livestock breeds in Bosnia and Herzegovina, with particular reference to the Tornjak shepherd dog, is a fundamental part of the cultural heritage, passed down from previous generations ([SOFTIĆ et al., 2006](#)). The Tornjak was introduced to the territory of Bosnia and Herzegovina by nomadic herders several centuries ago ([KATICA et al., 2003](#); [KATICA et al., 2004](#)). Even today, numerous specimens of the breed can still be found in their original form in certain areas of central and southwestern Bosnia. Regarding genetic diversity, limited research has been conducted, however, it offers valuable information for the genomic characterization and conservation of Balkan shepherd dog breeds, which, in addition to the Karst Shepherd and Šarplaninac, also includes the Tornjak ([JANEŠ et al., 2021](#)). According to [CEH and DOVC \(2014\)](#), these three breeds share many morphological and behavioral similarities, which are currently genetically well-differentiated. The results of the referenced study indicate that the formal separation of these closely related dog breeds is the principal factor underlying their genetic differentiation. The relationships among these breeds are not solely dictated by their genetic relatedness; in small populations, stochastic effects exert a more pronounced influence on the shaping of this differ-

entiation. The aim of the research was to assess the genetic diversity of the Tornjak shepherd dog. To achieve this goal, allele sizes were determined, allele frequencies at microsatellite loci were estimated, deviations from Hardy-Weinberg equilibrium were evaluated, and genetic parameters, such as genetic differentiation, levels of heterogeneity, genetic distance, and clustering, were analyzed using the Neighbor-Joining dendrogram model.

Materials and methods

Sample collection and genotyping. The dogs were divided into three main groups: Tornjaks from Bosnia and Herzegovina (TBA), Tornjaks from Croatia (THR), and a control group containing four subgroups: German Shepherds (GS), Belgian Shepherds (BS), crossbreeds of Tornjak and other breeds (MIXT), and various other dog breeds (MIXA). Of the total 161 genotyped samples, 92 were from the TBA group, 16 from the THR group, 10 from the GS group, 14 from the BS group, 14 from the MIXT group, and 15 from the MIXA group. Genomic DNA was extracted using the original blood extraction protocol described by [MILLER et al. \(1988\)](#). The quality and quantity of the extracted DNA were assessed using gel electrophoresis and spectrophotometry. For nuclear DNA analysis, 10 specific microsatellite loci were amplified using the *StockMarks® for Canine Genotyping Kit* (Applied Biosystems, Foster City, CA, USA). Markers were amplified in a 10 µl multiplex PCR reaction following the chemical and thermal protocols recommended by the manufacturer (ABI, Foster City, CA, USA). PCR products were analyzed on an *ABI Prism™ 310 Genetic Analyzer*, and allele variants were scored using *GeneMapper ID v3.2 software*.

Data analysis. Basic measures of genetic diversity were estimated by calculating allele and genotype frequencies, as well as observed (H_o) and expected (H_e) heterozygosity ([NEL, 1987](#)). The number of different alleles (A_n) and different genotypes (G_n), as well as their number per locus were obtained by direct counting. Deviations from the Hardy-Weinberg equilibrium were assessed using the exact p-value test ($P < 0.05$) ([GUO and THOMP-](#)

[SON, 1992](#)), while the polymorphism information content (PIC) test proposed by [BOTSTEIN et al. \(1980\)](#) was applied for analysis of polymorphism in the observed microsatellite markers. Genetic differentiation analysis between populations of each breed pair (pF_{ST}) was described by [WEIR and COCKERHAM \(1984\)](#). These calculations were performed using POWERMARKER ver. 3.32 software ([LIU and MUSE, 2005](#)). For determining genetic distances between the studied (TBA, THR) and control breeds (GS, BS, MIXT, MIXA), the genetic distance method by [REYNOLDS et al. \(1983\)](#) was used. Construction of the Neighbor-Joining dendrogram was carried out using MEGA4 software ([TAMURA et al., 2007](#)). The proportion of genetic variation was tested using the AMOVA test ([EXCOFFIER et al., 1992](#)).

Results

In this study, all ten specific microsatellite loci included in the *StockMarks® for Canine Genotyping Kit* (Applied Biosystems) were successfully amplified in individuals of the breeds listed and mixed breed animals. The values for genotype number (G_N), allele variants (A_N), private alleles (N_{PA}), expected (H_E) and observed heterozygosity (H_O) at the analyzed loci, polymorphic information content (PIC), and deviations from the Hardy-Weinberg equilibrium (HWE) are presented in Tables 1 and 2. In the TBA group, the average numbers of genotypes and alleles were 19.2 and 8.4, respectively. The average observed heterozygosity in this dog population was 0.7261, while the expected heterozygosity was 0.7392. Statistically significant deviations from the Hardy-Weinberg equilibrium ($P < 0.05$) were observed for the loci PEZ1, PEZ12, PEZ3, and PEZ6. The average polymorphic information content (PIC) value was 0.7002. Considering the allele variants in the THR group and control groups of other breeds, 'private' alleles were identified at all ten loci in the TBA population (three alleles at the PEZ1 locus, one allele at the FHC2054 locus, two alleles at the FHC2010 locus, one allele at the PEZ5 locus, three alleles at the PEZ20 locus, two alleles at the PEZ12 locus, three alleles at the PEZ3 locus, one allele at the PEZ6 locus, one allele at the PEZ8 locus, three

alleles at the FHC2079 locus). Within the THR population, the average number of genotypes was 8.2 and the average number of alleles was 5.4. The Polymorphic Information Content (PIC) value was (0.6692). The average observed heterozygosity in this dog population (THR) was 0.7625, while the expected heterozygosity was 0.7139. Statistically significant deviations from the Hardy-Weinberg equilibrium ($P < 0.05$) were observed at the loci PEZ5 and PEZ20 in the studied population (Table 1). In the control group (Table 2), deviations from the Hardy-Weinberg equilibrium ($P < 0.05$) were detected at the loci PEZ1, FHC2054, PEZ5, PEZ12, PEZ3, and PEZ6. In the Belgian Shepherd (BS) population, the average number of genotypes was 7.9 and the average number of alleles was 5.1, with the Polymorphic Information Content (PIC) test indicating the highest polymorphism at the PEZ8 locus (0.8101). The average observed heterozygosity in this dog population was 0.6857, while the expected heterozygosity was 0.6837. In the German Shepherd (GS) population, the average number of genotypes was 4.4 and the average number of alleles was 3.6, with the Polymorphic Information Content (PIC) test indicating the highest polymorphism at the PEZ6 locus (0.6896). The average observed heterozygosity in this population was 0.4900, while the expected heterozygosity was 0.4640. In the mixed-breed population (MIXT), the average number of genotypes was 7.6 and the average number of alleles was 5.5, with the PIC test indicating the highest polymorphism at the PEZ1 locus (0.7687). The average observed heterozygosity in this dog population was 0.6786, while the expected heterozygosity was 0.6760. In the population of other breeds (MIXA) from the control group (Table 2), the average number of genotypes was 8.6 and the average number of alleles was 6.0. The average observed heterozygosity in this population was 0.7067, while the expected heterozygosity was 0.7160. The Polymorphic Information Content (PIC) test indicated the highest polymorphism at the PEZ8 locus (0.7950).

The highest degree of genetic differentiation (θ) was observed at the PEZ5 locus (0.0780), while the lowest was recorded at the FHC2010 locus,

Table 1. Number of genotypes (G_N), number of alleles (A_N), number of private alleles (N_{PA}), expected heterozygosity (H_E), observed heterozygosity (H_O), polymorphic information content (PIC) and p-value of exact test of deviation from the Hardy-Weinberg equilibrium (HWE)

TBA (SOFTIĆ et al., 2016)								THR					
Locus	(G_N)	(A_N)	(N_{PA})	(H_E)	(H_O)	PIC	(HWE)	(G_N)	(A_N)	(H_E)	(H_O)	PIC	(HWE)
PEZ1	20.0000	9.0000	3	0.8134	0.7283	0.7860	0.0192	9.0000	5.0000	0.7188	0.6250	0.6793	0.2390
FHC2054	20.0000	8.0000	1	0.6985	0.7065	0.6601	0.2352	9.0000	6.0000	0.7148	0.8750	0.6831	0.5950
FHC2010	18.0000	7.0000	2	0.7498	0.7717	0.7084	0.3716	6.0000	4.0000	0.6523	0.7500	0.5883	0.9380
PEZ5	10.0000	5.0000	1	0.6803	0.7174	0.6202	0.5171	5.0000	3.0000	0.6387	0.4375	0.5666	0.0140
PEZ20	12.0000	7.0000	3	0.6108	0.5870	0.5346	0.2917	6.0000	5.0000	0.6973	0.8750	0.6490	0.0160
PEZ12	28.0000	13.0000	2	0.7770	0.7065	0.7479	0.0155	11.0000	7.0000	0.7773	0.7500	0.7462	0.6500
PEZ3	14.0000	9.0000	3	0.6776	0.8370	0.6457	0.0001	6.0000	5.0000	0.6699	0.9375	0.6264	0.4310
PEZ6	27.0000	8.0000	1	0.8442	0.7717	0.8245	0.0033	7.0000	5.0000	0.7266	0.8750	0.6777	0.4310
PEZ8	19.0000	8.0000	1	0.7737	0.7826	0.7405	0.4144	11.0000	7.0000	0.7500	0.7500	0.7116	0.7390
FHC2079	24.0000	10.0000	3	0.7668	0.6522	0.7339	0.1641	12.0000	7.0000	0.7930	0.7500	0.7635	0.6160
Average	19.2000	8.4000	-	0.7392	0.7261	0.7002	-	8.2000	5.4000	0.7139	0.7625	0.6692	-

TBA – group of the Tornjak Bosnian-Herzegovinian-Croatian Shepherd Dog from the region of the Bosnia and Herzegovina; THR – group of the Tornjak Bosnian-Herzegovinian-Croatian Shepherd Dog from the region of the Republic of Croatia

Table 2. Number of genotypes (G_N), number of alleles (A_N), expected heterozygosity (H_E), observed heterozygosity (H_O), polymorphic information content (PIC) and p-value of exact test of deviation from the Hardy-Weinberg equilibrium (HWE)

CONTROL GROUP											
Locus											
	PEZ1	FHC2054	FHC2010	PEZ5	PEZ20	PEZ12	PEZ3	PEZ6	PEZ8	FHC2079	Average
(HWE)	0.0064	0.0061	0.4980	0.0185	0.5513	0.0080	0.0032	0.0272	0.5790	0.0834	-
(G_N)	8.0000	10.0000	11.0000	5.0000	6.0000	9.0000	3.0000	10.0000	11.0000	6.0000	7.9000
(H_E)	0.6735	0.7883	0.7679	0.4566	0.6352	0.7883	0.4490	0.7704	0.8316	0.6760	0.6837
PIC	0.6315	0.7547	0.7322	0.4222	0.5871	0.7560	0.4065	0.7374	0.8101	0.6165	0.6454
	PEZ1	FHC2054	FHC2010	PEZ5	PEZ20	PEZ12	PEZ3	PEZ6	PEZ8	FHC2079	Average
(A_N)	2.0000	5.0000	4.0000	3.0000	3.0000	4.0000	4.0000	5.0000	3.0000	3.0000	3.6000
(H_O)	0.1000	0.8000	0.4000	0.3000	0.4000	0.4000	1.0000	0.7000	0.6000	0.2000	0.4900
MIXT											
(G_N)	9.0000	11.0000	8.0000	7.0000	8.0000	7.0000	4.0000	9.0000	10.0000	3.0000	7.6000
(H_E)	0.7985	0.7577	0.7321	0.4974	0.6607	0.6658	0.6556	0.7908	0.7551	0.4464	0.6760
PIC	0.7687	0.7222	0.6889	0.4577	0.6124	0.6372	0.5946	0.7622	0.7299	0.4014	0.6375
Locus	PEZ1	FHC2054	FHC2010	PEZ5	PEZ20	PEZ12	PEZ3	PEZ6	PEZ8	FHC2079	Average
(A_N)	6.0000	9.0000	5.0000	4.0000	5.0000	6.0000	6.0000	6.0000	8.0000	5.0000	6.0000
(H_O)	0.8000	0.6000	0.7333	0.5333	0.9333	0.8000	0.8667	0.6667	0.8000	0.3333	0.7067
PIC	0.7015	0.7639	0.6147	0.6170	0.6861	0.7415	0.6027	0.6572	0.7950	0.5813	0.6761

BS – subgroup of the Belgian Shepherd as a control group; GS – subgroup of the German Shepherd as a control group; MIXT – subgroup of Tornjak crossbreeds with other breeds as a control group; MIXA – subgroup of various other dog breeds as a control group

with an overall θ value of 0.0451. The range of subpopulation inbreeding coefficients varied from -0.2809 (indicative of outbreeding) at the PEZ3 locus to 0.1413 at the FHC2079 locus (indicative of more pronounced inbreeding). The average inbreeding coefficient between subpopulations was 0.0331. The overall inbreeding coefficients ranged from -0.2658 at the PEZ3 locus to 0.1816 at the PEZ1 locus. The average overall inbreeding coefficient was 0.0768 (Table 3). The AMOVA test indicates that, of the total genetic variation, 16.01% was attributed to variation between the observed populations, while 84.00% was attributed to variation within populations. The highest degree of variation was found within the TBA group, accounting

for 55.43%. No significant variation was detected in the GS subgroup of the control group (Table 4).

The results of genetic differentiation between pairs of the observed populations ($pFST$) indicate low to moderate, and in some cases pronounced differentiation (Table 5). The greatest differentiation (ranging from 5.25% to 21.26%) was observed globally between the German Shepherd and other breeds, while the smallest differentiation for the TBA group was found with the THR group, at 1.86%.

The Neighbor-Joining dendrogram, based on genetic distance analysis, shows a clear clustering of the TBA and THR groups. The German Shepherd is the breed most likely contributing to the gene pool of mixed-breed individuals (Fig. 1).

Table 3. Results of genetic differentiation (Θ), overall inbreeding coefficient (F), and inbreeding coefficient (f) between TBA, THR and the control group (BS, GS, MIXT, MIXA)

Between TBA, THR and CONTROL GROUP			
Locus	θ	F	f
PEZ1	0.0729	0.1816	0.1173
FHC2054	0.0529	0.1094	0.0596
FHC2010	0.0093	0.0102	0.0009
PEZ5	0.0780	0.1424	0.0698
PEZ20	0.0469	0.0382	-0.0091
PEZ12	0.0334	0.1317	0.1017
PEZ3	0.0118	-0.2658	-0.2809
PEZ6	0.0324	0.1158	0.0862
PEZ8	0.0652	0.0671	0.0020
FHC2079	0.0448	0.1798	0.1413
Average	0.0451	0.0768	0.0331

Table 4. Results of the Analysis of Molecular Variance (AMOVA) test

Source	Sum of Square	Percentage (%)
Among population	127.1023	0.1601
Within population (TBA)	440.1522	0.5543
Within population (THR)	68.4375	0.0862
Within population (BS)	51.4286	0.0648
Within population (MIXA)	64.8000	0.0816
Within population (MIXT)	49.2857	0.0621
Within population (GS)	-7.2000	-0.0091
Total	794.0062	1.0000

Table 5. Genetic Differentiation Matrix between breed pairs (pFST)

	TBA	BS	MIXA	THR	MIXT	GS
TBA	0.0000	0.0485	0.0306	0.0186	0.0466	0.1413
BS	0.0485	0.0000	0.0234	0.0844	0.0367	0.1335
MIXA	0.0306	0.0234	0.0000	0.0524	0.0087	0.0992
THR	0.0186	0.0844	0.0524	0.0000	0.0865	0.2126
MIXT	0.0466	0.0367	0.0087	0.0865	0.0000	0.0525
GS	0.1413	0.1335	0.0992	0.2126	0.0525	0.0000

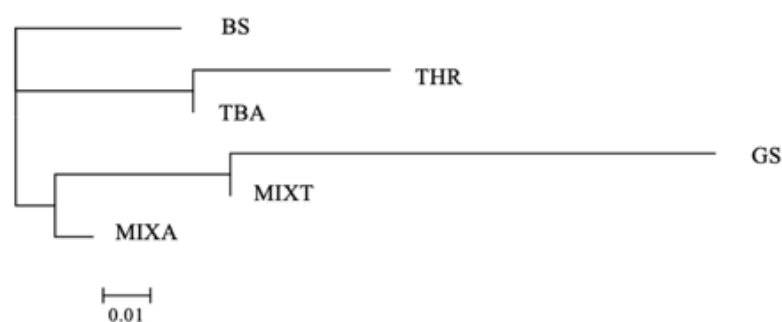


Fig. 1. Neighbor-Joining (NJ) tree based on the results of genetic distance analysis

Discussion

The heterogeneity of parameters may differ across studies, as is evident in our research, where the results contrast with those reported in the literature ([LEMO, 2005](#)). It is important to note that the author in the referenced study utilized different microsatellites (LE107, LE108, LE122, LE132, Ren02K, Ren010, Ren44K, and Ren49F), in contrast to the microsatellites employed in our study (PEZ1, FHC2054, FHC2010, PEZ5, PEZ20, PEZ12, PEZ3, PEZ6, PEZ8, FHC2079), which are part of the Canine Genotyping Kit (Applied Biosystems).

[JANEŠ et al. \(2021\)](#), investigating three Balkan shepherd dog breeds (Tornjak, Šarplaninac, and Kraški Ovčar) by analyzing high-throughput genomic data, found greater heterogeneity and lower relatedness for Šarplaninac and Tornjak as shepherd and livestock guardian dogs. In contrast, our results present the TBA group as highly heterogeneous. Compared to, for example, the German

Shepherd, a breed that has been carefully selected, heterogeneity is reduced, indicating a decrease in diversity. This observation aligns with the findings of the same author, who reported lower genetic diversity and higher inbreeding in the Kraški Ovčar, a slightly genetically divergent population influenced by the German Shepherd. When comparing the results with those of [DIMITRIJEVIĆ et al. \(2020a\)](#), who used the same set of microsatellite loci in 51 individuals of the Kangal breed, only minor differences were observed in the average number of alleles (N_A) for TBA (8.4), THR (5.4), BS (5.1), GS (3.6) versus the Kangal breed (6.9), and in the PIC values (TBA, 0.7002; THR, 0.6692; BS, 0.6454; GS, 0.4229; Kangal breed, 0.717), respectively. According to [RADKO and PODBIELSKA \(2021\)](#), the PIC value for the German Shepherd was 0.4941, which is slightly higher compared to our result of 0.4229. The observed high genetic heterogeneity of the TBA breed aligns with the findings of [NIKITVIĆ \(2020\)](#) and [NIKITVIĆ et al.](#)

(2023). The author also examined other dog breeds in the context of a comparative analysis of Barak. Genetic diversity is also considered one of the measures of genetic variation. In this regard, the results of our study, which indicate a high level of genetic diversity in the examined TBA population ($H_E = 0.7392$), THR ($H_E = 0.7139$), and MIXA ($H_E = 0.7160$), are consistent with the findings of [DIMITRIJEVIĆ et al. \(2020b\)](#) ($H_E = 0.728 \pm 0.027$). These authors investigated the Yugoslav Shepherd Dog – Šarplaninac (YSD). The results of the average observed heterozygosity estimation for the tested microsatellite loci suggest moderate to slightly increased heterozygosity (TBA, 72.61%; THR, 76.25%). In contrast, the study by [LEMO \(2005\)](#) found a lower percentage of heterozygosity among Tornjaks registered in Croatia (64.93%) and those from Bosnia and Herzegovina (58.34%), compared to our results. However, this remains one of the potential hypotheses that cannot be confirmed without further genetic analyses, including the use of additional genetic markers. In the aforementioned study ([LEMO, 2005](#)), the polymorphism information content (PIC) of the observed loci was generally similar to our results, except for the Ren010 locus. However, it should be noted that the number of observed allele variants, as a general measure of genetic variability, is highly dependent on sample size. Therefore, when comparing populations of unequal sizes on the basis of this parameter, conclusions should be drawn with caution. In this context, the slightly smaller number of individuals analyzed in the aforementioned study compared to our research may explain the discrepancy observed. It is also noteworthy that ‘private’ alleles, only present in the given population, were detected at all ten loci in our study, whereas [LEMO \(2005\)](#) reported that no allele specific to the Tornjak breed was found at any of the eight microsatellite loci used in their study. Given the pronounced interpopulation variability, which is also reflected in the small to moderate interpopulation F_{ST} values, the observed small to moderate genetic distance between the studied breeds is logical. In the study by [NIKITOVIĆ \(2020\)](#), in relation to the phylogenetic relationships of the Bosnian broken-haired hound

(Barak) with 15 selected breeds, one of which is indigenous to Bosnia and Herzegovina, the Tornjak, they established the smallest genetic distance at the same microsatellite loci (0.0444) between the Barak and the Tornjak, while the largest was determined with the West Highland White Terrier breed. The smallest genetic distance in our study was observed between the TBA and THR groups (0.0369). For both mutation models tested, the constructed dendrogram shows the clear and expected grouping of the TBA and THR. There is a distinct separation of the GS breed from the BS and MIXT. The distinction from other observed groups is also visible from the dendrogram. In comparison with the results of [NIKITOVIĆ \(2020\)](#) and [NIKITOVIĆ et al. \(2023\)](#), the analysis revealed a clear genetic position based on allele structure and their frequencies among the indigenous breeds of Tornjak and Barak in Bosnia and Herzegovina, where the Barak-Tornjak cluster is clearly separated from the other studied breeds. The AMOVA test indicates the highest degree of variation within the observed TBA group (55.43%), while no significant variation was found in the GS subgroup of the control group. The average overall inbreeding coefficient was ($F = 0.0768$), with a negative value for the PEZ3 locus (-0.2658). In comparison with the results of [DIMITRIJEVIĆ et al. \(2020b\)](#) in the YSD population, the fixation index was low, positive, and significant ($F = 0.041$), and negative for the FHC2054 locus (-0.016).

Conclusions

On the basis of the data presented, a high level heterogeneity of has been established in the studied Tornjak population (TBA). The TBA group exhibited the greatest variability within the breeds, which may indicate that its gene pool contains genetic contributions from other similar shepherd-type breeds. The clear position of the Tornjak (TBA and THR) relative to the breeds in the control group is evident. From this, it follows that the Tornjak breed is genetically distinct from other shepherd breeds and the other breeds of the control group. Therefore, it can be concluded that the Tornjak is a genetically distinct breed.

Ethics approval

This study was in accordance with the Rules of Procedure of the Ethical Committee of the Veterinary Faculty, University of Sarajevo, and was approved by the Committee (01-02-18-7/20).

Declaration of competing interest

No potential conflicting interest was reported by the authors.

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SOFTIĆ, A., M. VARATANOVIĆ, A. KAVAZOVIĆ, A. HRKOVIĆ-POROBIJA, T. GOLETIĆ: **Genska raznolikost pastirskog psa tornjaka.** *Vet. arhiv* 96, 31-40, 2026.

SAŽETAK

Cilj istraživanja bio je analizom 10 mikrosatelitskih lokusa procijeniti gensku raznolikost pastirskog psa tornjaka. Psi su podijeljeni u tri glavne skupine: tornjake iz Bosne i Hercegovine (TBA), tornjake iz Hrvatske (THR) te kontrolnu skupinu koja se sastojala od četiriju podskupina: njemački ovčar (GS), belgijski ovčar (BS), križanci tornjaka i drugih pasmina (MIXT) te različite druge pasmine pasa (MIXA). Prosječan broj genotipova (GN) i alela (AN) bio je 19,2 i 8,4 (TBA), 8,2 i 5,4 (THR), 7,9 i 5,1 (BS), 4,4 i 3,6 (GS), 7,6 i 5,5 (MIXT) te 8,6 i 6,0 (MIXA). Prosječne vrijednosti opažene (HO) i očekivane heterozigotnosti (HE) bile su 0,7261 i 0,7392 (TBA); 0,7625 i 0,7139 (THR); 0,6857 i 0,6837 (BS); 0,4900 i 0,4640 (GS); 0,6786 i 0,6760 (MIXT) te 0,7067 i 0,7160 (MIXA). U populaciji TBA „privatni” aleli uočeni su na svih deset lokusa. Prosječna (F) vrijednost između tornjaka i kontrolne skupine iznosila je 0,0768. AMOVA test pokazao je najveći stupanj varijacije unutar skupine TBA (55,43 %), dok znakovite varijacije u kontrolnoj podskupini GS nisu uočene. Najmanja diferencijacija za TBA pronađena je u skupini THR, od 1,86%, upotrebom pFST-a. Konstruirani dendrogram Neighbor-Joining (NJ) pokazuje jasno grupiranje TBA i THR u usporedbi s pasminama iz kontrolne skupine. Na osnovi prikazanih podataka u istraživanju je populaciji tornjaka (TBA) utvrđen visok stupanj heterogenosti.

Ključne riječi: tornjak; pas; mikrosateliti; genska raznolikost
