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Molecular characterisation of cornelian cherry (*Cornus mas* L.) genotypes

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ABSTRACT

The application of microsatellite simple sequence repeat (SSR) markers has proven to be highly effective in genetically characterising the origins of various fruit species. Bosnia and Herzegovina boast abundant cornelian cherry (*Cornus mas* L.) germplasm within its natural habitats. This study focuses on three geographically distant regions in Bosnia and Herzegovina–Drvar, Mostar and Zenica–comprising a sample of 60 cornelian cherry genotypes. The genetic analysis of cornelian cherry utilised eight microsatellite primers to characterise the genetic makeup of the 60 genotypes. Notably, all observed loci in the three populations demonstrated 100% polymorphism. The total genetic differentiation is 0.042, which is also confirmed by the analysis of molecular variance (AMOVA), which indicates that 3% of the total genetic variation is between groups, 8% between individuals and 89% within individuals. The results of pairwise Fst analysis (pFst) indicate that the greatest differentiation is between the populations of Mostar and Zenica (0.037), between Drvar and Zenica (0.026) and between Drvar and Mostar (0.025). The results of the genetic distance according to Nei confirm these results. Also, the largest difference was observed between the populations of Mostar and Zenica (0.316), then between Drvar and Zenica (0.285), and the smallest between Drvar and Mostar (0.251). This research contributes valuable insights into the genetic diversity and characterisation of cornelian cherry populations in different regions of Bosnia and Herzegovina.

Keywords: *Cornus mas*, genetic diversity, genetic resources, microsatellite, molecular characterisation

INTRODUCTION

The cornelian cherry (*Cornus mas* L.) is one of the most valuable fruits and have been cultivated for 4,000 years in the world (Filipovic et al., 2020). This plant comes from the foothills of the Caucasus and from there spreads over Türkiye, Romania, Bulgaria and Italy into the inland European continents. It is a tall shrub or small tree from 2 m to 8 m high. The trees begin to flower in early spring but bear fruit in the late period. The fruits are light or dark red-coloured, oval-shaped and 10–30 mm long with a weight of 2–5 g (Jacimovic et al., 2015; Skender et al., 2022). Cornelian cherry fruits have regained an increasing interest recently because of their nutraceutical and pharmaceutical potential (Bayram and Ozturkcan, 2020; Guzel, 2021; Szot et al., 2024).

In the Balkan peninsula, fresh cornelian cherry fruits are used for both fresh consumption and processing making cornelian cherry ‘vodka’ and ‘rakia’, which are popular in this region. Wild fruits, local genotypes, ecotypes and local cultivars in the Balkan peninsula are better natural sources of high-quality compounds and

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possess a higher potential as novel functional ingredients compared with introduced cultivars (Celik et al., 2007; Drkenda et al., 2014; Kazimierski et al., 2019; Poljak et al., 2022; Boyaci et al., 2023; Durul and Aktas, 2023; Papagrigoriou et al., 2023; Nincevic Runjic et al., 2024).

Wild berry species and ecotypes, including particular black mulberries and cornelian cherries, are a valuable source of healthy phytonutrients and have been the subject of many studies (Eyduran et al., 2015; Skender et al., 2017; Kazimierski et al., 2019; Szot et al., 2019; Martinovic et al., 2020). Bosnia and Herzegovina are well known by its rich gene pool of cornelian cherry genotypes and large number of natural populations. Cornelian cherry fruits collected in natural populations are a valuable source of natural bioactive compounds and gene stock for breeding programmes (Alibabic et al., 2019; Akagic et al., 2020).

The plant is in general grown wild or semi-wild in natural growing conditions without pesticide treatments. Thus, it is accepted as one of the most important fruit species that could be used in organic fruit production (Akagic et al., 2020). However, it is not a frequently studied fruit species in Bosnia and Herzegovina yet and needs more studies on it.

Morphological, biochemical and molecular characterisation enables the identification of individuals with high economic value in fruit species (Ercisli et al., 2005; Erturk et al., 2012; Lavic et al., 2023). Increasing numbers of studies on the natural population and breeding of cornelian cherry have been started with the increasing demand of these fruits considered as healthy food.

Nowadays, molecular markers are often used to manage plant genetic resources. They are very effective for identifying cultivated and wild plants. Microsatellite markers have great advantages over other molecular markers: high polymorphism, informative content, availability, codominance and easy interlaboratory comparisons (Benjak et al., 2005; Akin et al., 2016; Skender et al., 2022). Also, molecular markers are used to study genetic diversity and identification of cornelian cherry. An increasing number of researchers in Bosnia and Herzegovina are investigating autochthonous fruit varieties, natural populations and wild fruit relatives using simple sequence repeat (SSR) markers (Gasi et al., 2013a, b; Skender et al., 2017). This means that there is a huge wealth of genes that have not been sufficiently researched. Such genetic resources can be used in plant breeding.

The aim of this paper is to present the results of genetic characterisation using SSR markers of cornelian cherry genotypes from the natural populations from three areas in Bosnia and Herzegovina. One of the aims was to determine the correlation between the genetic distances of the analysed genotypes based on molecular data, using adequate statistical methods and analyses. Identification of the natural populations of cornelian cherry and explanation of the phylogenetic relationships among the genotypes of these areas are of great interest for continuous breeding programmes to improve germplasm cornelian cherry.

MATERIALS AND METHODS

Plant material and experimental site

Cornelian cherry wild genotypes were used in Bosnia and Herzegovina from three geographically separated regions (Drvar, Mostar and Zenica). Drvar region has average annual air temperatures of 11.0°C and annual precipitation of 1250–1500 mm. Mostar region has average annual air temperatures of 14.6°C and annual precipitation of 1515 mm. Zenica region has average annual air temperatures of 10.1°C and annual precipitation of 782.5 mm. The sample included 20 genotypes of cornelian cherry in Drvar, 20 genotypes in Mostar and 20 genotypes in Zenica. Plant material (leaves) for the DNA extraction was collected from selected plants on each analysed site. Leaves were harvested during spring and summer from each marked tree in 2021. Cold drying of leaf tissue by lyophilisation was performed under vacuum, using lyophiliser (Christ, Model Alpha 1–2 Ldplus). Dried samples were vacuumed in PVC bags and stored at −80°C until DNA isolation. Isolation and genetic characterisation were performed at the Institute of Genetic Engineering and Biotechnology, University of Sarajevo.

SSR analyses

DNA was isolated from approximately 50 mg of leaf powder. A modified CTAB protocol was used for DNA isolation (Gasi et al., 2013a, b). After successful DNA isolation from cornelian cherry samples, the PCR protocol was performed. Eight SSR markers were chosen based on their polymorphism reported in previous studies: CM007, CM008, CM010, CM026, CM031, CM037, CM039 and CM043 (Table 1). These markers were originally developed for *Cornus mas* by Wadl et al. (2014).

Amplification of microsatellite sequences was performed in a PCR device ABI GeneAmp® PCR System 9700 (Applied Biosystems, Foster City, CA, USA). Fluorescently labelled primers were used for amplification in order to be able to multiplex and analyse the PCR product on a DNA genetic analyser. Amplification of selected loci was performed in two separate PCR reactions (mix 1 and mix 2) with four microsatellite loci each (Table 2). All PCR reactions were conducted in a total volume of 15 µL, containing 2.5 mM of $MgCl_2$, 1 × PCR buffer, 0.2 mM dNTPs, 0.2 U · μL^{-1} of TrueStart Taq polymerase (Thermo Scientific) and 10–50 ng of template DNA. The temperature conditions for the amplification reaction were the same for both PCR reactions (Table 3). Before amplification, DNA was tested for quality by horizontal electrophoresis on agarose gel.

Allele sizes were determined by analysis of PCR products on an ABI 3500 genetic analyser Applied Biosystems), by vertical capillary electrophoresis. Aliquots of amplified DNA (1 µL), mixed with

Table 1. SSR markers and characteristics.

SSR markers	Primer sequence (5′ → 3′)	A repetitive pattern
CM007	R:tccagggaatgttcggtagattag L:gtttaggtgtgagtgcagatgg	(GT)24
CM008	L:tcgttaatgtgaaattggaacg R:caccgtacacgcaaagtcc	(GT)11
CM010	L:gctagcagaagcacagttagcc R:tccaacatgtaaaacctagatgc	(CA)12
CM026	L:gaattcatgtaatgttgttgtctgc R:cctgcatataattcaggtaaagagc	(CA)14
CM031	L:taccctctcttgctctttgtcc R:aaacaatcaaacccaaacaacc	(AG)26(TG)13
CM037	L:aacacagagaaacacgtgcaa R:tggagatctttgaagaacagga	(TG)20
CM039	L:gggtattgtaatcaatgtaaaaccaa R:tcacaccaccagcaatcact	(GT)18
CM043	L:gtccacacctgttgttcagc R:ggttgcaatgctttcttgg	(TG)16(TA)5

SSR, simple sequence repeat.

Table 2. Proportion of components used in PCR reaction mix 1 and mix 2.

Mix 1		Mix 2	
Components	Reaction concentration	Components	Reaction concentration
CM007	0.1 µM	CM031	0.2 µM
CM008	0.2 µM	CM037	0.2 µM
CM010	0.1 µM	CM039	0.2 µM
CM026	0.1 µM	CM043	0.2 µM
dNTP	0.2 mM	dNTP	0.2 mM
PCR buffer	1×	PCR buffer	1×
$MgCl_2$	2.5 mM	$MgCl_2$	2.5 mM
Taq pol.	0.2 U · μL^{-1}	Taq pol.	0.2 U · μL^{-1}
DNA	10 ng	DNA	10 ng
ddH_2O	to 15 µL	ddH_2O	to 15 µL

Table 3. PCR protocol temperature regime for two separate PCR reactions (mix 1 and mix 2).

Protocol			
	Temperature (°C)	Duration (min:s)	Number of cycles
Enzyme activation	95	5:00	
Denaturation	94	0:40	
Annealing	52	0:40	35
Elongation	72	0:30	
Final elongation	72	4:00	

formamide and GeneScan-350 ROX Size Standard (Applied Biosystems) were run on an ABI 3500 genetic analyser. LIZ 500 (Applied Biosystem) was used as an internal standard. SSR profiles were scored using the GeneMapper ID 5 Software (Applied Biosystems).

Biostatistical analyses of molecular data

Allele frequencies, private alleles, detected and effective number of alleles, observed and expected heterozygosity, as well as within-group inbreeding (Gasi et al., 2013b; Wadl et al., 2014) and deviation from Hardy–Weinberg (HW) equilibrium were calculated in GenAlex v6.503 (Doyle and Doyle, 1987). The ratio of the effective and detected number of alleles as well as its statistical significance were calculated using the ALRATIO script (Wadl et al., 2014). Fst genetic differentiation analysis (Cullings, 1992) and analysis of molecular variance (AMOVA) between observed groups was performed in GenAlex v6.503 software (Nei, 1987). Genetic distance analysis according to the Nei (1973) and principal coordinate analysis (PCoA) analysis, based on the results of individual and population genetic distance, were performed in the same software. Based on the results of the interindividual genetic distance, a neighbour-joining (NJ) dendrogram was constructed in the MEGA X software (Peakall and Smouse, 2012).

RESULTS AND DISCUSSION

Genetic analysis of cornelian cherry

Genetic analysis of cornelian cherry involved the use of eight microsatellite markers for genetic characterisation of 60 examined genotypes and are given in Table 4. The markers, which successfully amplified PCR product, were found to be highly polymorphic (Table 4). A total of 25 private alleles were detected in these three populations. There are 7 private alleles in the Drvar population, 14 in the Mostar population and 4 private alleles in the Zenica population. Private alleles are alleles that are found only in a single population among a broader collection of populations. These alleles have proven to be informative for diverse types of population-genetic studies. Different processes can lead to the appearance of private alleles (isolation, inbreeding and self-fertilisation in wild populations, or targeted selection during cultivar breeding). A large number of private alleles in these three populations show that the genetic material of cornelian cherry from Bosnia and Herzegovina is unused for breeding purposes. The Mostar population stands out in particular (14 private alleles). The number of alleles in Drvar group was 8.6 per locus, in the Mostar group 9.8, in the Zenica group 7.6 and for all groups 8.7. The total average number of detected alleles in all groups was 8.70 (Table 4).

Parameters of heterozygosity are given in Table 4. The number of detected alleles (Na) within the Drvar population shows that it is the highest for the CM031 locus, and the lowest for the CM043 locus. For the Mostar population, the largest number of alleles was observed at the CM010 locus, and the smallest at the CM031 and CM043 loci.

When it comes to the Zenica population, the lowest number of alleles was recorded at the CM043 locus, and the highest at the CM031 locus. The average number of detected alleles in the Drvar group was at eight SSR loci.

On the contrary, the effective number of alleles (Ne) within the Drvar population was recorded at the CM007 locus, and the smallest at the CM026 locus. For the Mostar population, the highest effective number of alleles is observed at the CM010 locus, and the lowest at the CM026 locus. The number of effective alleles within the Zenica population shows that it is the highest at the CM007 locus, and the lowest at the CM043 locus. The total average effective number of alleles in all groups was 5.48 per locus.

In a study conducted on cornelian cherry by Wadl et al. (2014), the number of alleles per locus ranged

Table 4. Parameters of heterozygosity.

Populations	Locus	Na	Ne	R	P (R)	*Ho*	*He*	F
Drvar	CM007	10.000	7.339	0.735	0.1979	0.950	0.864	−0.100
	CM008	9.000	5.517	0.614	0.1311	0.550	0.819	0.328
	CM010	9.000	6.723	0.746	0.2046	0.550	0.851	0.354
	CM026	7.000	3.846	0.549	0.1	0.650	0.740	0.122
	CM031	11.000	4.938	0.45	0.059	0.600	0.798	0.248
	CM037	9.000	4.348	0.483	0.0717	0.800	0.770	−0.039
	CM039	8.000	5.298	0.661	0.1556	0.850	0.811	−0.048
	CM043	6.000	4.145	0.692	0.1727	0.700	0.759	0.077
Mostar	CM007	13.000	7.339	0.566	0.1078	0.950	0.864	−0.100
	CM008	11.000	8.000	0.727	0.1931	0.750	0.875	0.143
	CM010	14.000	9.877	0.707	0.1813	0.850	0.899	0.054
	CM026	7.000	4.571	0.652	0.1508	0.750	0.781	0.040
	CM031	8.000	5.063	0.634	0.1413	0.800	0.803	0.003
	CM037	11.000	5.594	0.508	0.082	0.850	0.821	−0.035
	CM039	8.000	5.298	0.661	0.1556	0.700	0.811	0.137
	CM043	7.000	4.651	0.664	0.1572	0.650	0.785	0.172
Zenica	CM007	10.000	8.602	0.862	0.2857	1.000	0.884	−0.132
	CM008	8.000	3.687	0.461	0.0631	0.750	0.729	−0.029
	CM010	10.000	7.843	0.787	0.2309	0.800	0.873	0.083
	CM026	5.000	4.188	0.837	0.2663	0.550	0.761	0.278
	CM031	11.000	4.790	0.435	0.0535	0.850	0.791	−0.074
	CM037	7.000	4.469	0.638	0.1434	0.900	0.776	−0.159
	CM039	6.000	3.448	0.575	0.112	0.850	0.710	−0.197
	CM043	4.000	2.067	0.516	0.0854	0.400	0.516	0.225
Average (Drvar)		8.625	5.269	0.584	0.1163	0.706	0.801	0.118
Average (Mostar)		9.875	6.299	0.595	0.1217	0.788	0.830	0.052
Average (Zenica)		7.625	4.887	0.535	0.0937	0.763	0.755	−0.001
Average (Total)		8.708	5.485	0.561	0.1055	0.752	0.795	0.056

F, intragroup inbreeding; He, expected heterozygosity; Ho, observed heterozygosity; Na, number of detected alleles; No, effective number of alleles; P (R), *p*-value of the ratio of the detected and effective number of alleles; R, ratio of detected and effective number of alleles.

from 1 to 11 and averaged 6.73, whereas the effective number of alleles per locus ranged from 1.00 to 5.53 with an average of 3.29. Another study on 447 wild grown cornelian cherry genotypes represented in Austria, using seven microsatellite markers, came to the following results: the average number of alleles per locus was 10.57 and the effective numbers of alleles was 3.86 (Borroto Fernandez et al., 2023).

From Table 4, it can be concluded that the highest observed heterozygosity (*Ho*) in the Drvar population was recorded for locus CM007, and the lowest was for CM008 and CM010. Also, the highest expected heterozygosity (*He*) in the mentioned population was observed for locus CM007, and the lowest for CM026. Within the Mostar population, the highest observed heterozygosity was recorded for the CM007 locus, and the lowest for the CM043 locus. On the contrary, the highest expected heterozygosity was observed at the CM010 locus, and the lowest at the CM026 locus. In the Zenica population, the highest observed heterozygosity was recorded at the CM007 locus, and the lowest at the CM043 locus. For the expected heterozygosity parameter within the mentioned population, the highest value was observed at the CM007 locus, and the lowest at the CM043 locus. In all three populations, the mentioned loci are 100% polymorphic.

Previously, Peakall and Smouse (2012), Wei and Becher (1984) and Kumar et al. (2018) reported the observed heterozygosity from 0.00 to 0.71, while the expected heterozygosity spanned from 0.00 to 0.82.

The examination of the relationship between the effective and detected number of alleles (R) revealed no statistically significant reduction in the effective number of alleles compared with the detected number ($p(Ra) > 0.05$). This finding is highly significant as it indicates that the majority of detected alleles at the observed locus contribute significantly to the genetic diversity within the observed groups (Table 4).

Analysing the inbreeding coefficient (F) for the Drvar population showed the highest value at locus CM010 and the lowest at locus CM007, indicating signs of outbreeding. In the Mostar population, the highest F was observed at locus CM043, while the smallest was at locus CM007, once again suggesting outbreeding. Concerning the Zenica population, the highest F was recorded at the CM026 locus, and the lowest at the CM039 locus, where a negative value implies outbreeding. The total inbreeding across all three observed populations was calculated as 0.056 (Table 4).

The results of the test for deviations from HW equilibrium using the χ^2 test are given in Table 5. Within the population of Drvar, four loci deviate statistically

Table 5. Deviation of eight examined SSR loci from HW equilibrium in the total set samples.

Population	Locus	SS	χ^2	*p*-value	Significance
Drvar	CM007	45	63.942	0.033	*
Drvar	CM008	36	71.652	0.000	***
Drvar	CM010	36	76.893	0.000	***
Drvar	CM026	21	14.129	0.864	ns
Drvar	CM031	55	61.856	0.245	ns
Drvar	CM037	36	27.500	0.845	ns
Drvar	CM039	28	58.890	0.001	***
Drvar	CM043	15	14.860	0.462	ns
Mostar	CM007	78	90.510	0.157	ns
Mostar	CM008	55	75.422	0.035	*
Mostar	CM010	91	104.822	0.153	ns
Mostar	CM026	21	22.016	0.399	ns
Mostar	CM031	28	28.657	0.430	ns
Mostar	CM037	55	56.788	0.408	ns
Mostar	CM039	28	69.540	0.000	***
Mostar	CM043	21	18.345	0.627	ns
Zenica	CM007	45	48.200	0.345	ns
Zenica	CM008	28	10.674	0.999	ns
Zenica	CM010	45	55.142	0.143	ns
Zenica	CM026	10	15.985	0.100	ns
Zenica	CM031	55	41.147	0.917	ns
Zenica	CM037	21	15.396	0.803	ns
Zenica	CM039	15	78.395	0.000	***
Zenica	CM043	6	5.235	0.514	ns

HW, Hardy–Weinberg; ns, there is no statistically significant deviation from HWE; SS: sum of squares; SSR, simple sequence repeat.
*$p < 0.05$.
**$p < 0.01$.
***$p < 0.001$.

significantly from HW equilibrium, two in the population of Mostar, and one locus in the population of Zenica. From all of the above, it can be concluded that the observed cornelian cherry groups show a moderate level of heterozygosity without significant inbreeding, with a good basis when it comes to allelic diversity.

However, certain loci (CM008, CM010, CM031), especially within the Drvar population, show a tendency towards a more intense level of inbreeding, which may indicate an upcoming trend of heterozygosity reduction. Therefore, it is necessary to analyse possible changes in genetic heterozygosity in certain annual examinations, all with the aim of preventing its rapid reduction, which would ultimately lead to inbreeding depression.

The results of the PCoA analysis are shown in Figure 1. There is a tendency of differentiation of the samples from the three mentioned populations, but a clear differentiation of the samples was not observed. This is consistent with the results of genetic differentiation (Fst, pFst and AMOVA).

The total genetic differentiation is also confirmed by the AMOVA, which indicates that 3% of the total genetic variation is between groups, 8% between individuals and 89% within individuals (Table 6).

The highest genetic differentiation (Fst) between the observed groups was recorded for the CM043 locus, while the smallest was for the CM007 locus (Table 7). The total genetic differentiation is 0.042, which is also confirmed by the AMOVA, which indicates that 3% of the total genetic variation is variation between groups, 8% between individuals and 89% within individuals (Table 6). In a study of Fst was between 0.05 and 0.15.

The results of pairwise Fst analysis (pFst) indicate that the greatest differentiation is between the populations of Mostar and Zenica (0.037), between Drvar and Zenica (0.025) and between Drvar and Mostar; the smallest is 0.025 (Table 7). The results of the genetic distance according to Nei confirm the mentioned results and point to the fact that the biggest difference was observed between the populations of Mostar and Zenica (0.316), then between Drvar and Zenica (0.285) and the smallest between Drvar and Mostar (0.251).

The present research revealed significant differences between individuals and within population groups. For a given SSR, high genetic variation in a sample of population might be due to an increase in gene flow or the mutation of a number of repeats of a given genotype.

Table 6. AMOVA.

Source	df	SS	MS	Estimated Var.	%
Among Pops	2	16.650	8.325	0.120	3
Among Indiv.	57	201.300	3.532	0.262	8
Within Indiv.	60	180.500	3.008	3.008	89
Total	119	398.450	3.390	100	

AMOVA, analysis of molecular variance; df, degree of freedom; MS: mean squares; SS: sum of squares; Var: estimated variance component.
%: percentage of genetic variation.

Table 7. Results of F statistical analysis.

Locus	F_{IS}	F_{IT}	F_{ST}
CM007	−0.111	−0.086	0.022
CM008	0.154	0.201	0.056
CM010	0.161	0.191	0.036
CM026	0.146	0.189	0.051
CM031	0.059	0.083	0.025
CM037	−0.077	−0.052	0.023
CM039	−0.029	0.012	0.040
CM043	0.150	0.224	0.086
Average	0.057	0.095	0.042

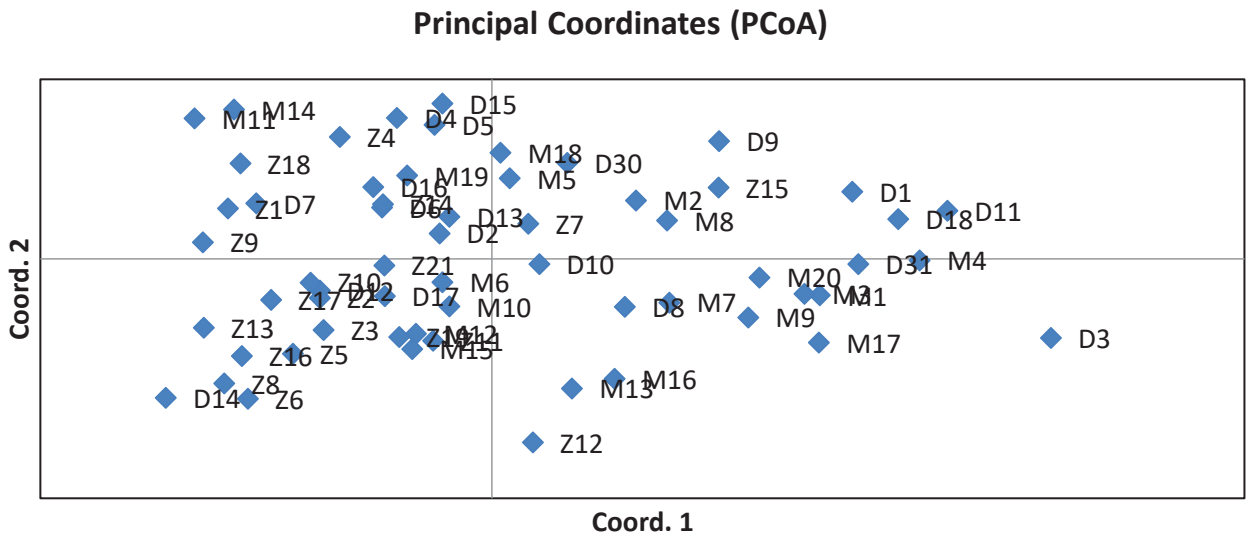


Figure 1. Results of PCoA analysis of individual cornelian cherry genotypes. PCoA, Principal coordinate analysis.

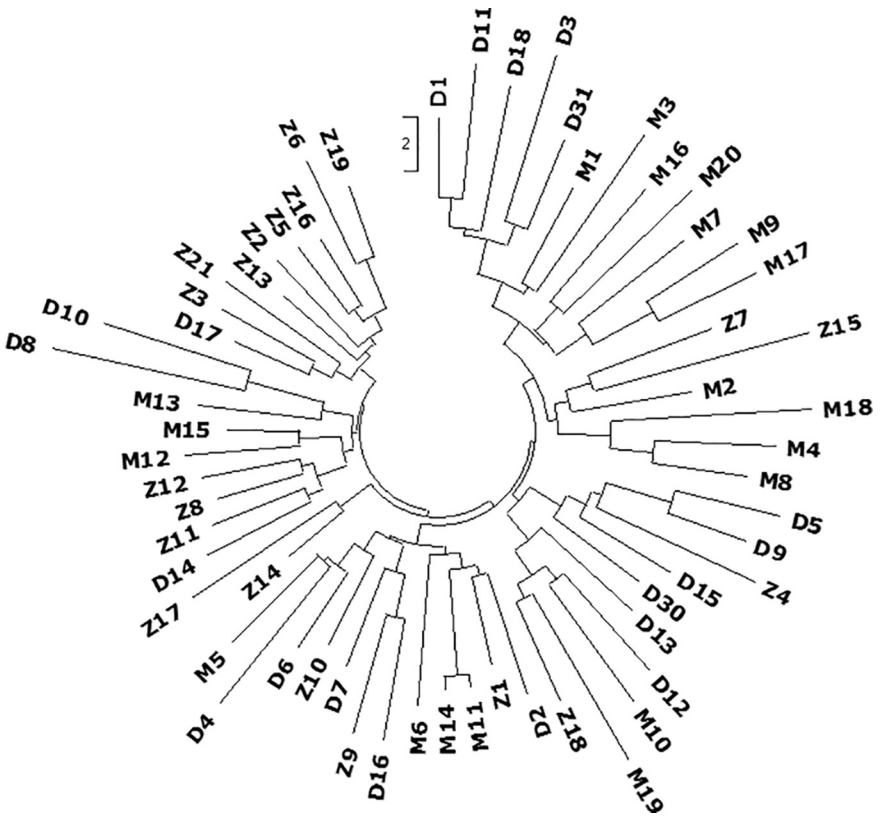


Figure 2. NJ dendrogram of the cornelian cherry genotypes based on the results of the interindividual genetic distance analysis. The codes of the genotypes are: D1,2,3,…(Drvar1,2,3,…); M1,2,3,…(Mostar1,2,3,…); Z1,2,3,…(Zenica1,2,3,…). NJ, Neighbour-Joining.

Additionally, this high genetic variation could be due to the natural selection process within the studied genotypes of cornelian cherry. The lower genetic variation between these populations may be related to the possibility of sharing a common ancestry, despite growing in different regions.

The constructed NJ dendrogram based on the results of the interindividual genetic distance analysis is shown in Figure 2. The NJ dendrogram indicates similar results of the PCoA analysis where there is a certain grouping of samples, but no pronounced grouping of complete populations can be observed, which would indicate a more pronounced genetic differentiation.

CONCLUSIONS

This is the first study of cornelian cherry using microsatellite markers in Bosnia and Herzegovina. By the genetic characterisation of cornelian cherry populations using eight microsatellite markers, they showed a high degree of genetic variability. Certain loci, especially within the Drvar population, show a tendency towards a more intense level of inbreeding, which may indicate an upcoming trend of heterogeneity reduction. Therefore, it is necessary to analyse the possible changes in genetic heterogeneity in certain annual examinations, all with the aim of preventing its rapid reduction, which would ultimately lead to inbreeding depression. Based on the NJ dendrogram and PCA analysis, it can be concluded that there is a certain grouping of samples, but no pronounced grouping of complete populations can be observed, which would indicate a more pronounced genetic differentiation. Identification of the natural populations of cornelian cherry and explanation of the phylogenetic relationships among the genotypes of these areas are of great interest for continuous breeding programmes to improve cornelian cherry germplasm. The results of this study will be used to supplement the dataset of reference genetic profiles of fruit crops with SSR profiles of cornelian cherry genotypes that are present in Bosnia and Herzegovina. The results of this study will significantly contribute towards establishing a regional conservation and utilisation strategy, in regard to cornelian cherry in the western Balkans. Finally, the results encourage further multidisciplinary studies to unravel the genetic factors responsible for the adaptation to specific environments and potential quality traits of our natural populations of cornelian cherry genotypes.

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AUTHOR CONTRIBUTIONS

AS and GD conceived and designed the experiments. AS and GD performed the experiments. RL, AA, SE and GI analysed data and prepared the graph. AS, GD, RU and AB prepared the first draft of the manuscript. AS, GD, AA and SE revised and finalised the manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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