

# POPULATION GENETIC STUDIES OF GREY WOLVES (*CANIS LUPUS* L. 1758) FROM BOSNIA AND HERZEGOVINA



Dragana Šnjegota<sup>1</sup>, Milomir Stefanović<sup>2</sup>, Nevena Veličković<sup>2</sup>, Duško Čirović<sup>3</sup>, Mihajla Djan<sup>2</sup>

<sup>1</sup>University of Banja Luka, Faculty of Sciences, Mladena Stojanovića 2, Banja Luka, Republika Srpska, Bosnia and Herzegovina. <sup>2</sup>University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Trg Dositeja Obradovica 2, 21000 Novi Sad, Serbia. <sup>3</sup>University of Belgrade, Faculty of Biology, Studentski trg 3, 11000 Belgrade, Serbia

## Introduction & Aims

The grey wolves of Bosnia and Herzegovina form a subpopulation of the Dinaric-Balkan wolf population and represent one of Europe's least studied wolf populations. Since the Dinaric-Balkan population is a valuable source of genetic diversity for neighboring populations, comprehensive assessments are warranted. First genetic researches encompassed analyses of mtDNA control region, but recently, analyses of autosomal microsatellite loci have been included.

A field monitoring (by using photo trapping) has also been implemented for the population of grey wolf at several localities across Bosnia and Herzegovina with the aim to detect wolves presence at each locality and to make conclusions about their behavior and abundance.



The main aims of wolf population genetic studies in Bosnia and Herzegovina are: i) determination of the genetic variability ii) estimation of population structure of the grey wolf population from Bosnia and Herzegovina iii) estimation of levels of gene flow and inbreeding iv) evaluation of genetic signals of a bottleneck v) detection of mtDNA haplotypes and vi) detection of wolf presence at the specific locality.

## Study area

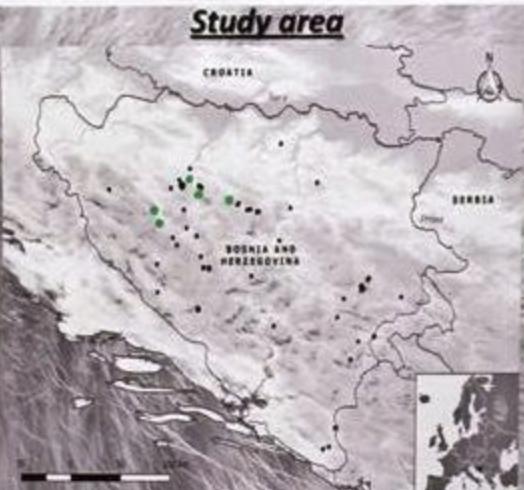


Fig. 1. Map showing the sampling localities of grey wolves from Bosnia and Herzegovina.

- Genetic analyses
- Photo trapping

## Materials & methods

### Genetic analyses

- N=69 (muscle tissue samples)
- 18 microsatellite autosomal loci – The Canine Genotypes™ Panel 1.1 kit (Finnzymes, Thermo Fisher Scientific, Finland)
- Control region of mtDNA – CR1, CR2R primers (Palomares et al., 2002)



Fig. 2. Software which have been used for genetic analyses.

### Field activities

- Photo trapping – 5 photo traps; 5 localities (feeding places, nature, wolf transects)
- Non-invasive sampling – throughout monitored localities (hair, faeces)

## Results & Discussion

### Analyses of microsatellite loci

Moderately high heterozygosity was detected ( $H_o=0.73$ ,  $H_e=0.76$ ) for the total sample and absence of signs of genetic bottleneck and inbreeding. A weak signal of population structure was detected by using different software (sPCA in R, TESS, DAPC in R) ( $K=2$ ), where some individuals from the south and south-east part of the country formed separate cluster (Figure 3a, b, c) (Šnjegota et al., 2017).

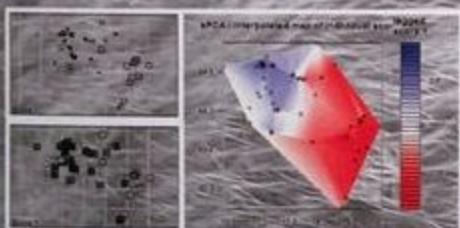


Fig. 3a. Results of grey wolf population structure from Bosnia and Herzegovina by applying sPCA analysis in R. slight signs of wolf's population at the western and eastern parts of Bosnia and Herzegovina in comparison to the wolves from the other parts of the country. Left: individual-based clusters (red and blue). Right: interpolated map of individual scores.

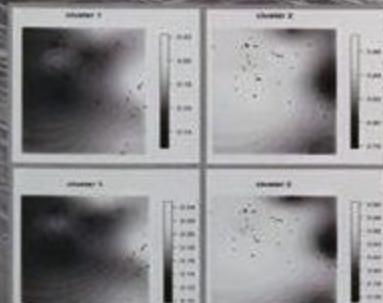


Fig. 3b. Results of grey wolf population structure from Bosnia and Herzegovina by applying DAPC analysis (DAPC model vs CAV model, metric interpretation: M = posterior proportion for individuals belong to the same detected cluster). The first two axes (PC1 and PC2) explain the highest probability for the individuals to belong to the detected clusters. At it can be seen, cluster 1 is predominantly supported with very young wolves, whereas the cluster 2



Fig. 3c. Results of grey wolf population structure from Bosnia and Herzegovina by applying DAPC analysis in R. Bar plot showing the number of detected clusters (K=2). Each color corresponds to the cluster. The higher level of bar plot corresponds to individuals from the western and central parts of Bosnia and Herzegovina.

### Analyses of CR mtDNA

Tab. 1. Results of the basic genetic parameters of CR mtDNA analyses for grey wolf from Bosnia and Herzegovina.

n	h	Hd	π	k
69	10	0.752±0.00085	0,0183	K=4,835

(n = number of individuals; h = number of haplotypes; Hd = Haplotype diversity; π = nucleotide diversity; K = the number of clusters)

### Photo trapping

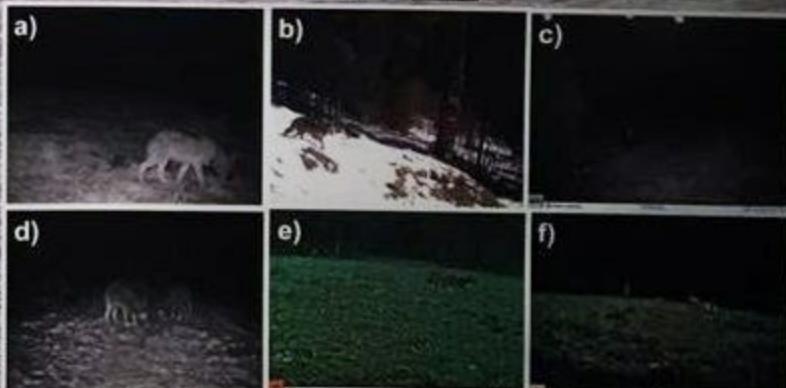


Fig. 4. Captured grey wolf (adults) in the monitored localities within Bosnia and Herzegovina.  
(a) Trebišnjica - adult  
(b) Trebišnjica - adult  
(c) Trebišnjica - female (Trebišnjica)  
(d) pup - pup  
(e) pup in a tree  
(f) Trebišnjica - female

### Rufford Foundation projects

2018 Let's make better future for grey wolves in Bosnia and Herzegovina: coordination of community wolf education

2016 The Grey Wolf Conservation in Bosnia and Herzegovina: the next step

2015 Monitoring of grey wolf population from Bosnia and Herzegovina with the aim to estimate its abundance

## Management implication

Continued genetic monitoring based on the results of our study may provide further insights into the genetic diversity and structure of the Dinaric-Balkan wolf population, and in monitoring of individuals, and provide estimates of the contribution of Dinaric-Balkan wolves to newly-formed wolf populations in Western Europe.

### References

- Palomares, F., Godoy, J.A., Pitra, A., O'Brien, S.J., Johnson, W.E., 2002. Fecal genetic analysis to determine the presence and distribution of elusive carnivores: design and feasibility for the Iberian lynx. *Mar. Ecol. Prog. S.* 217: 217-228.

- Šnjegota, D., Stefanović, M., Veličković, N., Čirović, D., Djan, M., 2017. Genetic characterization of grey wolves (*Canis lupus* L. 1758) from Bosnia and Herzegovina. *Int. J. Biol. Sci.* 13(10): 1042-1049.