POPULATION GENETIC STRUCTURE OF MEDITERRANEAN HORSESHOE BAT RHINOLOPHUS EURYALE IN SERBIA

Ivana Budinski¹*, Blagojević Jelena¹, Jovanović Vladimir¹, Pejić Branka¹, Rajičić Marija¹, Paunović Milan², Vujošević Mladen¹

¹Department of Genetic Research, Institute for Biological Research "Siniša Stanković", University of Belgrade, Bulevar despota Stefana 142, 11060 Belgrade, Serbia ²Natural History Museum, Njegoševa 51, Belgrade, Serbia

*e-mail: ivana.budinski@ibiss.bg.ac.rs

INTRODUCTION

Mediterranean horseshoe bat is considered to be mostly sedentary species, with **seasonal movements usually shorter than 50 km**. Known roosts of *Rhinolophus euryale* in Serbia are distributed in western and eastern parts of the country, overlapping with karst distribution. All but one roosts recorded in last 50 years were caves.

The distance between caves in Western and Eastern Serbia is **greater than 150 km**, and the environment between them is devoid of caves. Furthermore, there were no recent records of this species from Central Serbia.

Bearing in mind the non-migratory nature of this species, our aim was to test for **population structuring** (isolation by distance pattern) among different geographic regions.

MATERIALS AND METHODS

- 241 sampled individuals
- 11 localities (6.4–305 km distance)
- 3 geographic regions: Western Serbia, Eastern Serbia, Montenegro
- 8 nuclear microsatellite loci

- F statistics
- AMOVA
- Mantel test (isolation by distance)



Figure 1. Map of sampling localities

RESULTS

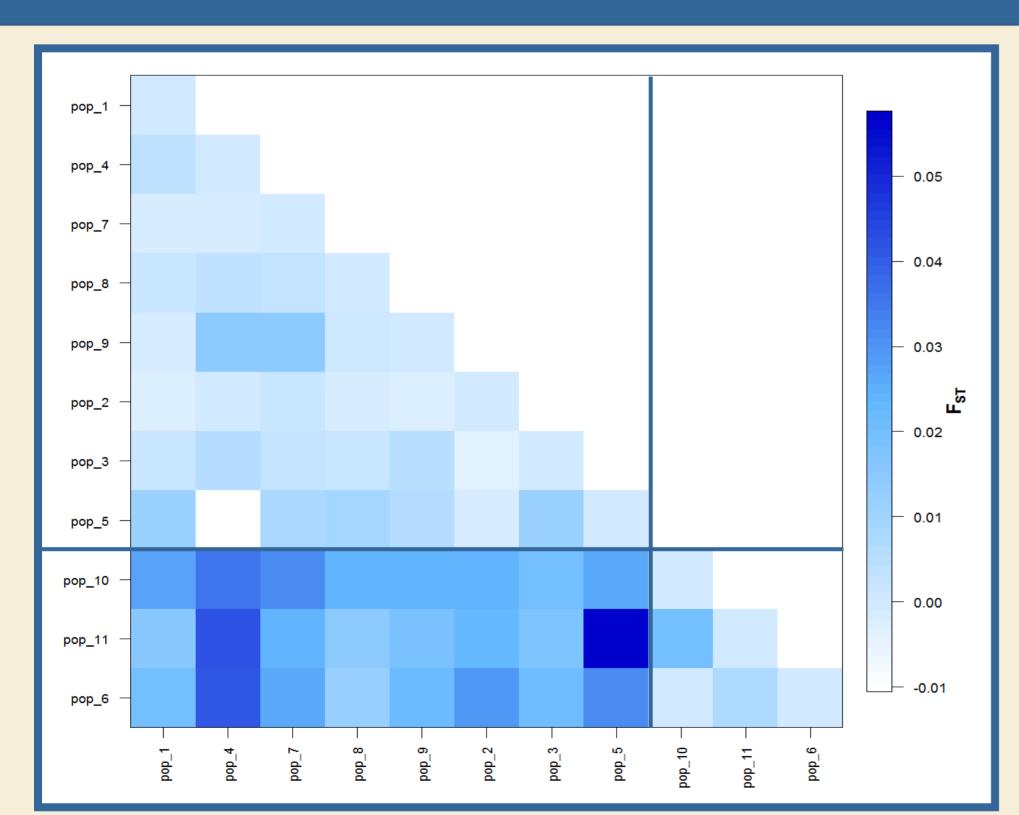


Figure 1. Pairwise F_{ST} matrix

• Pairwise F_{ST} values among colonies ranged from -0.004 (non-significant) to 0.058 (p<0.001)

Alleles Rich. H_{O} H_{E} Locus F_{IS} **RE007** 5.760 0.803 0.782 0.004 **RE017** 4.055 0.736 0.683 -0.082 RM002 13 5.998 0.788 0.784 0.021 RM003 11 6.154 0.628 0.790 0.249 RM010 12 7.327 0.847 0.016 0.849 RM011 4.413 0.472 0.664 0.336 RM015 3.961 0.672 0.655 0.029 6 RM025 0.622 -0.028 8 4.397 0.646

Table 1. Diversity statistics – number of alleles, allelic richness (Rich.)

observed (H_O) and expected (H_F) heterozygosities and fixation index (F_{IS})

- AMOVA: majority of genetic variation was at the individual level (91.46%), and differences among groups explained 1.7 % of genetic variation
- Mantel test: significant correlation between genetic and geographic distances (R²=0.1632, P=0.039)

CONCLUSIONS

- All loci were polymorphic
- Significant differences between populations from Western and Eastern Serbia
- Population from Montenegro is genetically similar to populations from Eastern Serbia
- Significant isolation by distance pattern

Acknowledgements: This study was supported by the Ministry of Education, Science and Technological Development of Serbia (Grant No. 173003) and the Ministry of Agriculture and Environmental protection of Serbia (Project: "Monitoring of bat roosts and populations in Serbia", Grant No. 401-00-200/2016-17)