

# Historical origin of the chamois in the northern Dinaric Mountains revealed by DNA from old trophy samples

Elena Buzan<sup>1</sup>, Toni Safner<sup>2</sup>, Sandra Potušek<sup>1</sup>, Andrea Rezić<sup>3</sup>, Magda Sindičić<sup>4</sup>, Nikica Šprem<sup>3</sup>

<sup>1</sup>Department of Biodiversity, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska

<sup>2</sup>Department of Plant Breeding Genetics, Biometrics and Experimentation, University of Zagreb, Faculty of Agriculture

<sup>3</sup>Department of Fisheries, Beekeeping, Game Management and Special Zoology, University of Zagreb, Faculty of Agriculture

<sup>4</sup>Department for Game Biology, Pathology and Breeding, Faculty of Veterinary Medicine, University of Zagreb

## Introduction

During the early 1900s, chamois populations in the northern Dinaric region were extirpated due to unsustainable intensive hunting, poaching, livestock grazing, predation, and natural catastrophic events.

The last record of the chamois presence in the Velebit massif date back to 1907, when several animals were observed for the last time.

There were several translocations of chamois in 1970s into the northern Dinaric Mountains from different areas inhabited either by Alpine chamois or Balkan ones.

These events left a clear genetic signature in the new population.

## Aims

To investigate historical origin of chamois in the northern Dinaric Mountains and in order to define subspecies which occupied the area.

## Materials and Methods

We collected four museum male chamois skulls (dated in 1886, 1893, 1895, and 1939).

DNA was successfully extracted from middle layer and outer sheath of horns.

Genetic assignment of genotypes from museum samples to the reference contemporary subspecies, which include chamois from 7 sampled areas in Slovenia, Croatia, and Bosnia and Herzegovina was based on microsatellites loci, and was performed using methods implemented in software STRUCTURE and GeneClass.

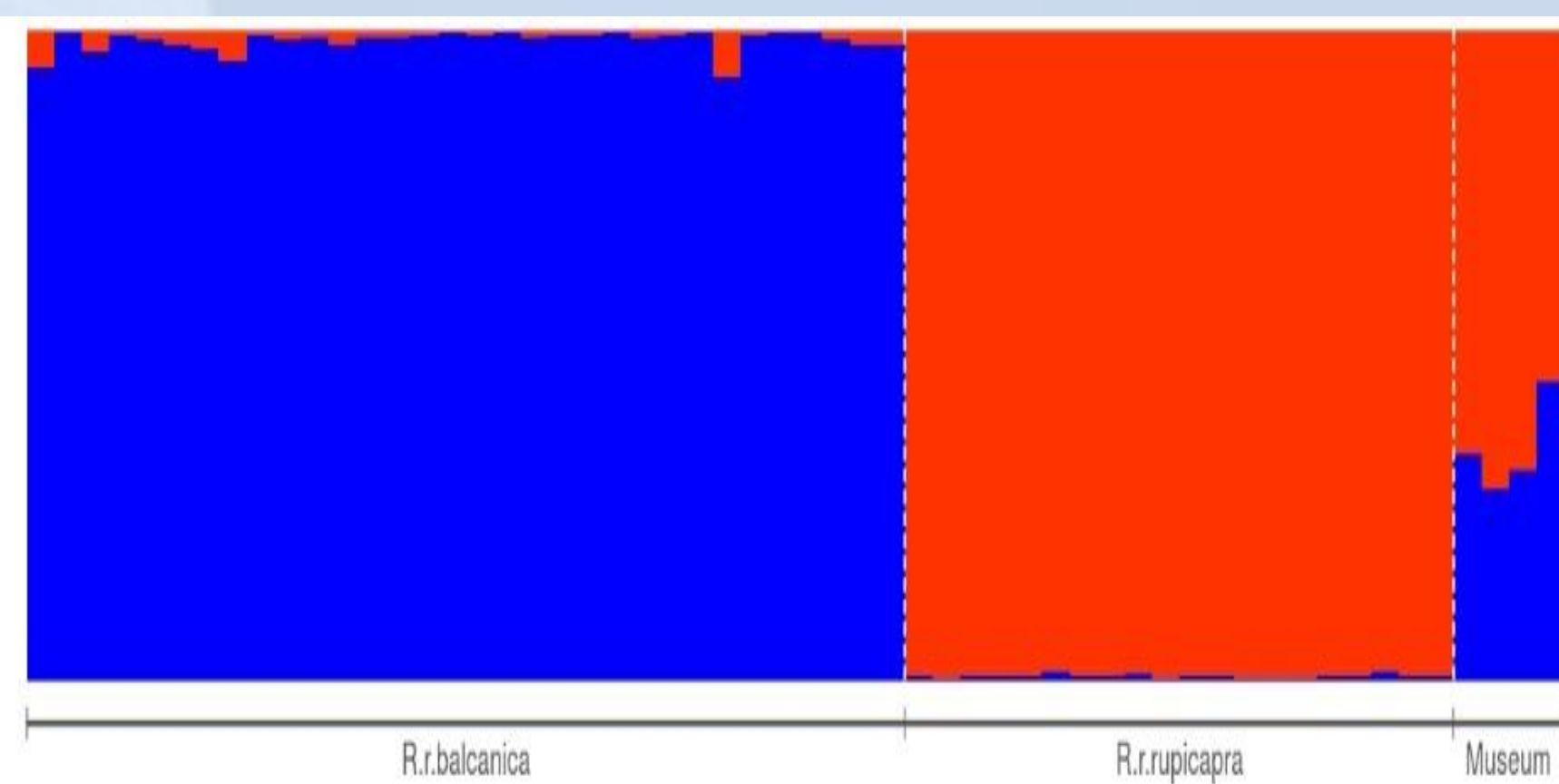
## Study area

All collected museum samples were from Velebit massif in Croatia, which is part of northern Dinaric mountain range (see map below).

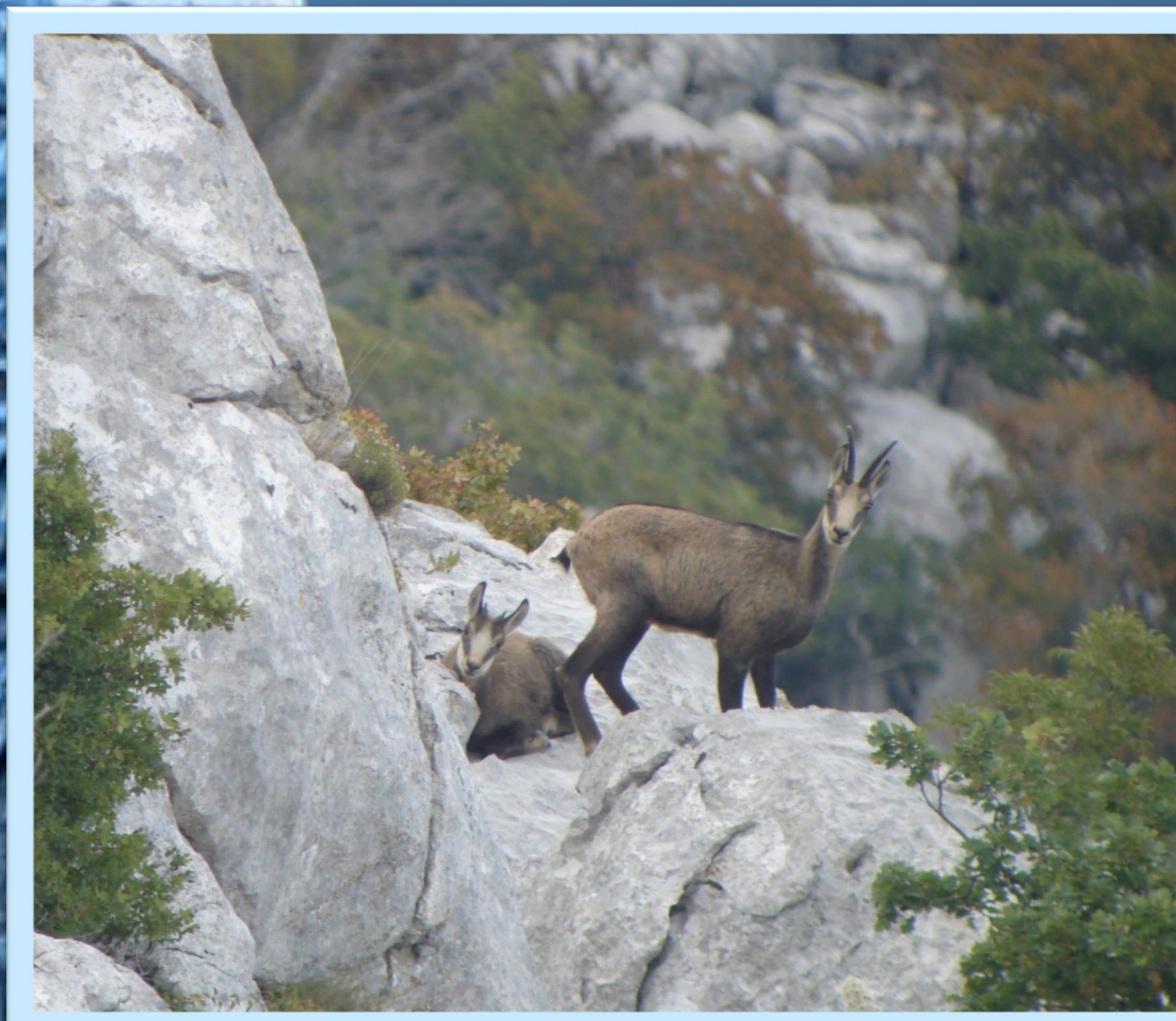
## Results

All four samples were assigned to the Alpine chamois according to the STRUCTURE program q values were between 0.6 and 0.7, and GeneClass with all scores above 95%, respectively.

Weak resolution of the STRUCTURE results probably showed consequence of reintroduction from donor populations that were unrelated to the native populations in this massif.



Genetic structure of chamois within 7 sampled areas in Slovenia, Croatia, and Bosnia and Herzegovina from samples collected in 2010 and 2012 assigned with museum specie. Shaded segments corresponding to its membership in a specific cluster.



## Literature

Buzan E V., Bryja J, Zemanová B, Kryštufek B (2013) Population genetics of chamois in the contact zone between the Alps and the Dinaric Mountains: uncovering the role of habitat fragmentation and past management. *Con Gen* 14: 401–412.

Šprem N, Buzan E (2016) The genetic impact of chamois management in the Dinarides. *J Wildlife Management* 80: 783–793.

## Conclusion

Further analysis on mitochondrial DNA is need to confirm existence of Alpine chamois in northern Dinaric Mts.

MtDNA as uniparental markers is very applicable for systematic identification and reconstruction of evolutionary history of populations.

Acknowledgement: This study was supported by the Croatian Science Foundation, IP 2016-06-5751, „DNA as evidence of distribution and vitality of endangered Balkan chamois“.