



13. Hrvatski biološki  
kongres  
Poreč, 19-23. rujna 2018.

# HISTORICAL RECONSTRUCTION OF THE CHAMOIS ORIGIN FROM THE NORTH VELEBIT MOUNTAIN REVEALED BY OLD MUSEUM SAMPLES

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# INTRODUCTION



- NATURA 2000 sites
- Croatia: 37% of the land territory and 15 % of sea shore



## INTRODUCTION

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- ✓ The great abundance of chamois in the north-western Dinaric Mountains
- ✓ Extirpation of chamois populations in the northern Dinaric region in the early 1900s before their taxonomic classification

Conserv Genet (2013) 14:401–412  
DOI 10.1007/s10592-013-0469-8

RESEARCH ARTICLE

### Population genetics of chamois in the contact zone between the Alps and the Dinaric Mountains: uncovering the role of habitat fragmentation and past management

Elena V. Buzan · Josef Bryja · Barbora Zemanová ·  
Boris Kryštufek



# INTRODUCTION

- ✓ The last record of the chamois presence in the Velebit massif – 1907 (Skorup, 2005)
- ✓ Several translocations of chamois between 1964 and 1978

The Journal of Wildlife Management; DOI: 10.1002/jwmg.21081

*Featured Article*

## The Genetic Impact of Chamois Management in the Dinarides

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VACLAV ANDERLE 1898





## INTRODUCTION

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### AIMS:

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





## MATERIALS AND METHODS

### STUDY AREA:

Velebit massif in Croatia, which is part of northern Dinaric mountain range





## MATERIALS AND METHODS

- ✓ Four museum male chamois skulls dated in 1886, 1893, 1895 and 1939
- ✓ DNA extracted from middle layer and outer sheath of horns





## MATERIALS AND METHODS

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### DNA ISOLATION:

- ✓ Special demineralization protocol for better DNA yield
- ✓ 0,3g of bone dust was used per isolation
- ✓ PROBLEM: Fragmented DNA





## MATERIALS AND METHODS

### MICROSATELLITE ANALYSIS:

- ✓ 20 loci, triplicate
- ✓ Fragment analysis - SeqStudio sequencer
- ✓ Results were validated using GeneMapper
- ✓ Statistical analysis: STRUCTURE
- ✓ Reference populations - Šprem & Buzan (2016)





## MATERIALS AND METHODS

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### SEQUENCE ANALYSIS:

- ✓ Specialy designed primers for CR (469bp) and CYTB (348bp)
- ✓ Failed to amplify entire region-PROBLEM with fragmentation
- ✓ SeqStudio sequencer
- ✓ Statistic analysis: MEGA



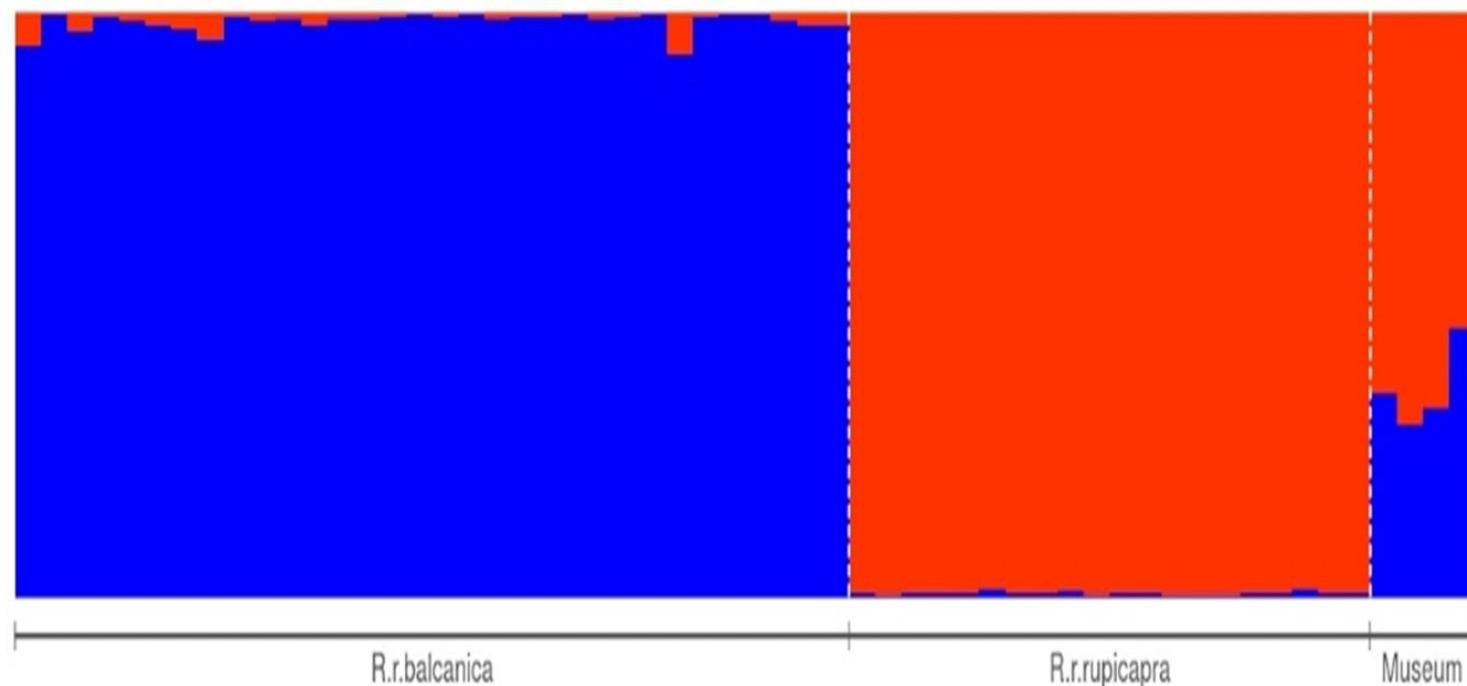


# RESULTS

Microsatellites

STRUCTURE with 20 SSR loci:

- ✓ q values were between 0.6 and 0.7 for alpine subspecies

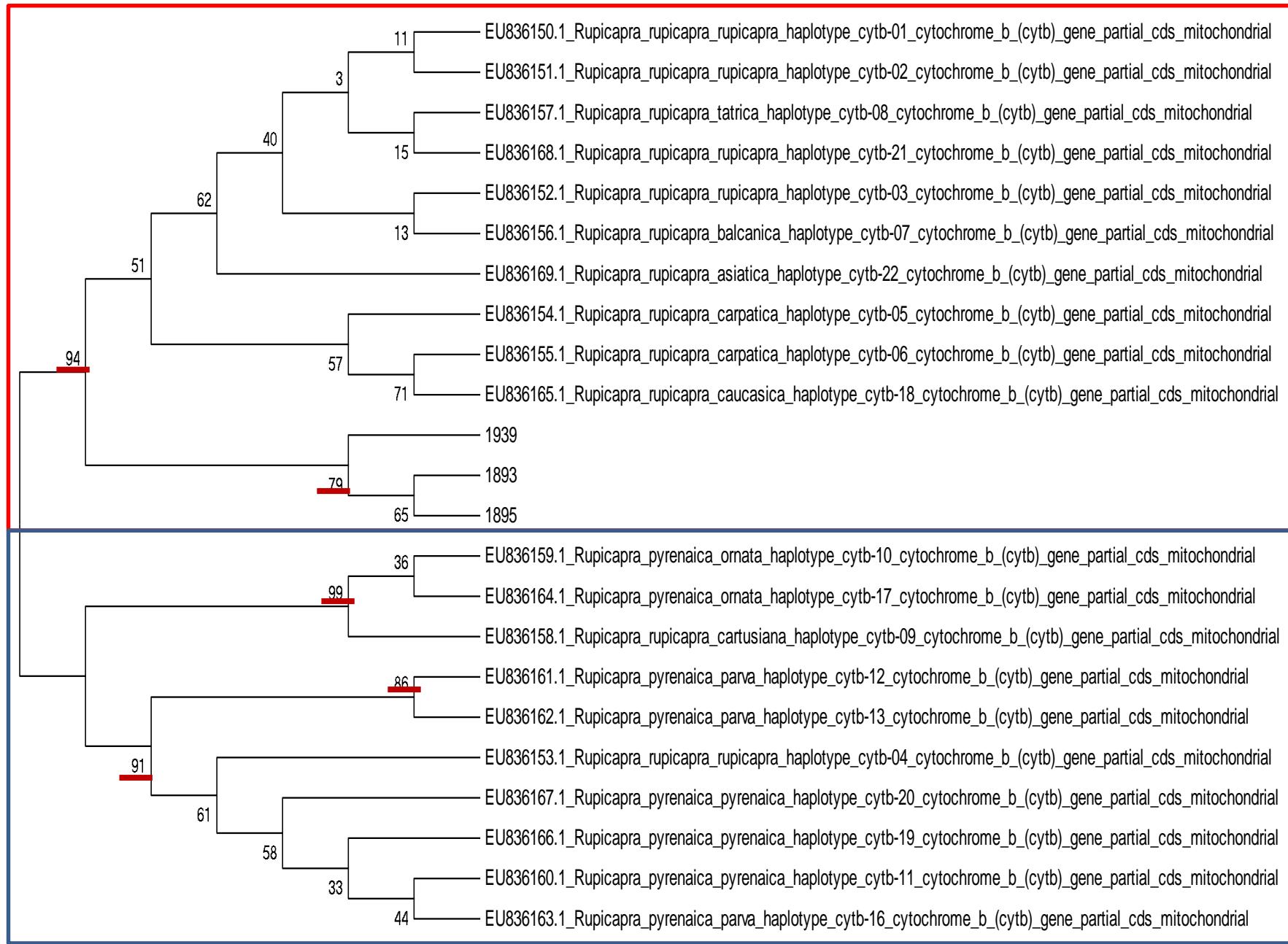




## RESULTS Cytochrome b phylogeography of chamois

EASTERN CLADE

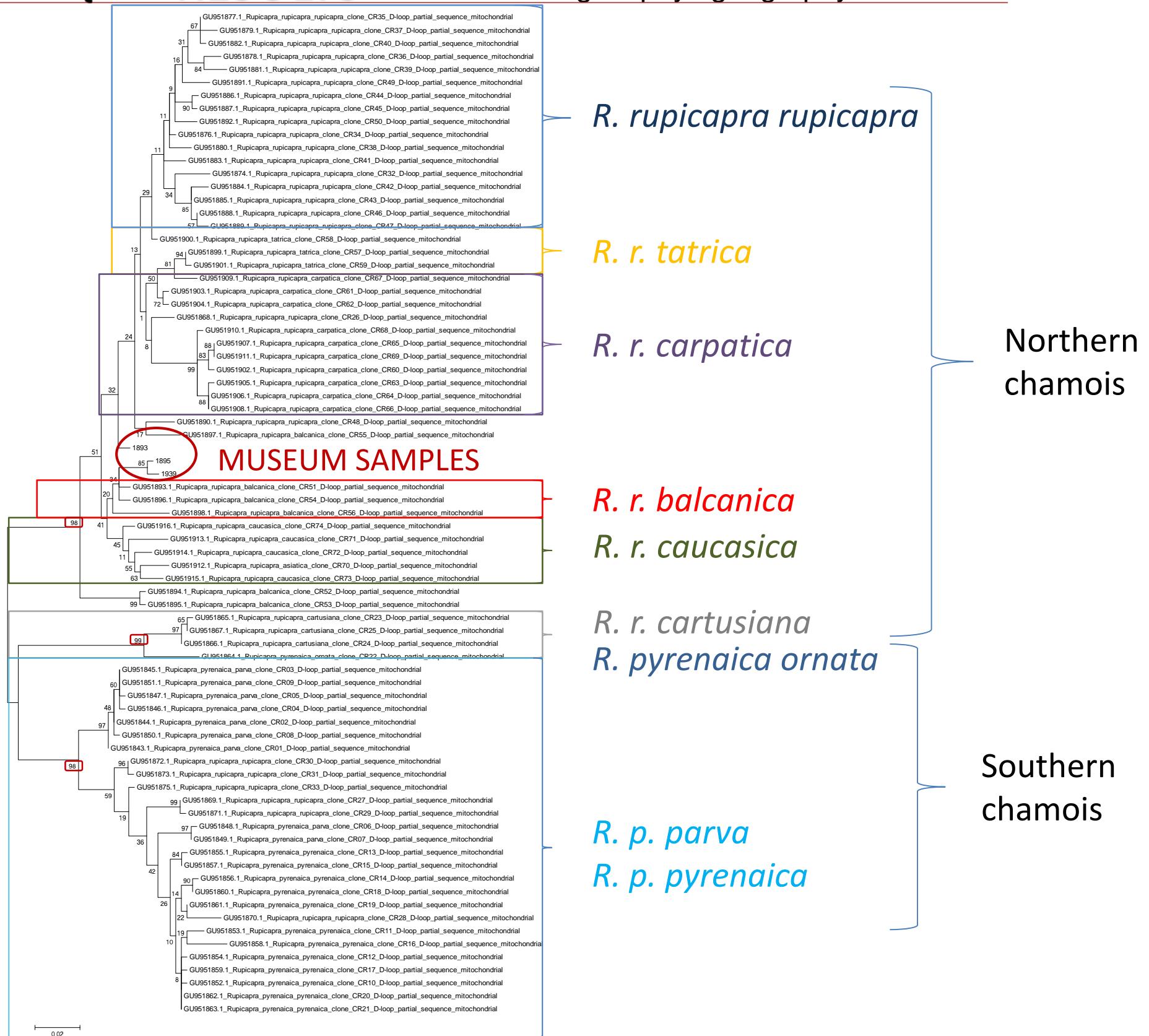
WESTERN CLADE





# RESULTS

## Control region phylogeography of chamois





# CONCLUSIONS

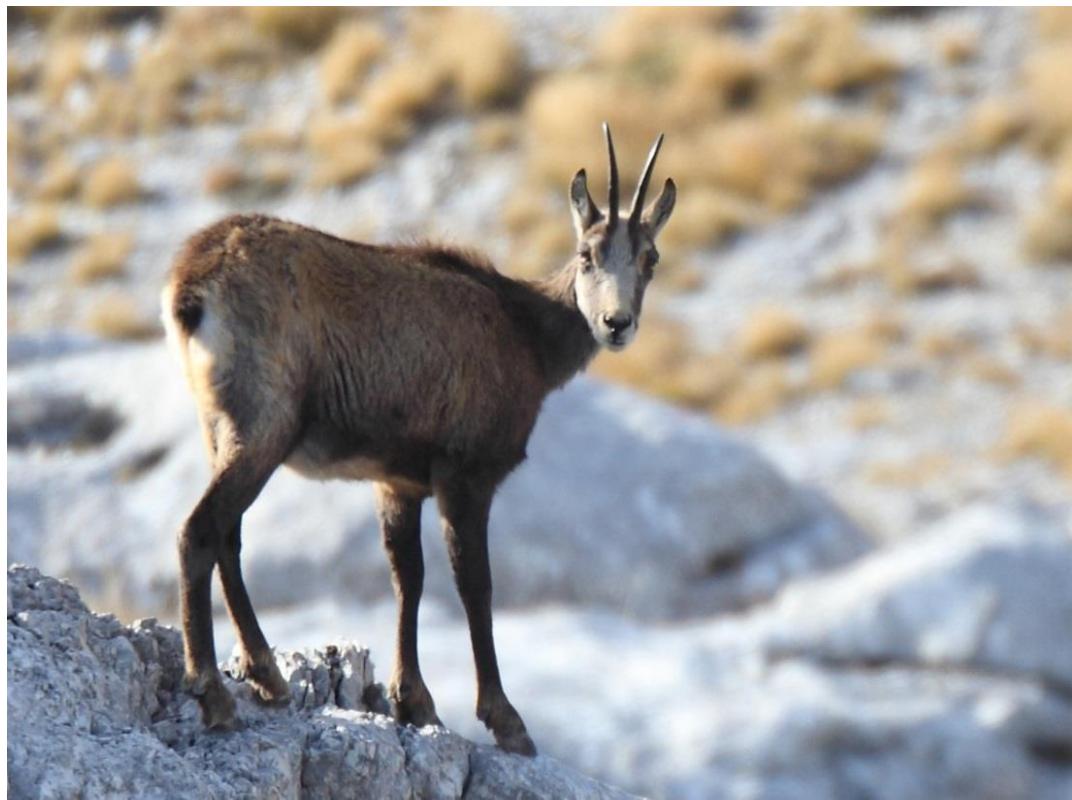
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- ✓ Museum samples could help resolve phylogenetic relationships, but sometimes because of low DNA quality they do not work properly ≈ **Fragmented DNA**
- ✓ Chamois taxonomy is still questionable!!!





# THANK YOU FOR YOUR ATTENTION!



## **ACKNOWLEDGEMENTS**

**DNA as a evidence of distribution  
and vitality of endangered Balkan  
chamois – BalkCham**

**IP-2016-06-5751**