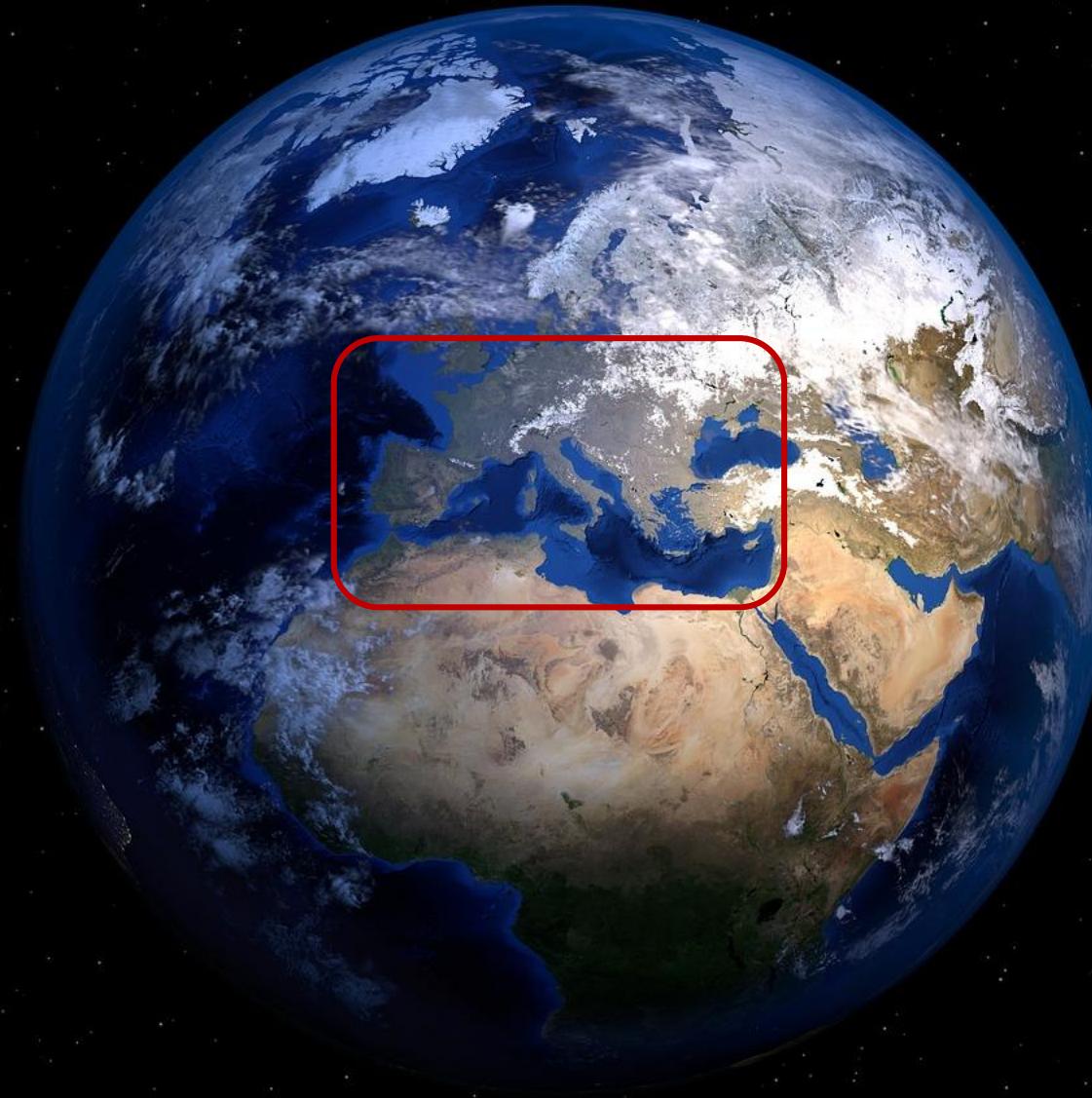


A photograph of two chamois standing on a rocky, mountainous terrain. One chamois is in the foreground, facing right, and the other is slightly behind it, also facing right. The background shows more rugged mountains under a clear sky.

L. Iacolina, A. Rezić, T. Safner,
U. Gerić, T. Tesija, N. Bašić,
H. Ambarli, F. Bego, A. Farkas,
D. Gačić, V. Maletić, G. Markov,
D. Milošević, H. Papaioannou,
E. Bužan, N. Šprem

The Balkan chamois across space and time

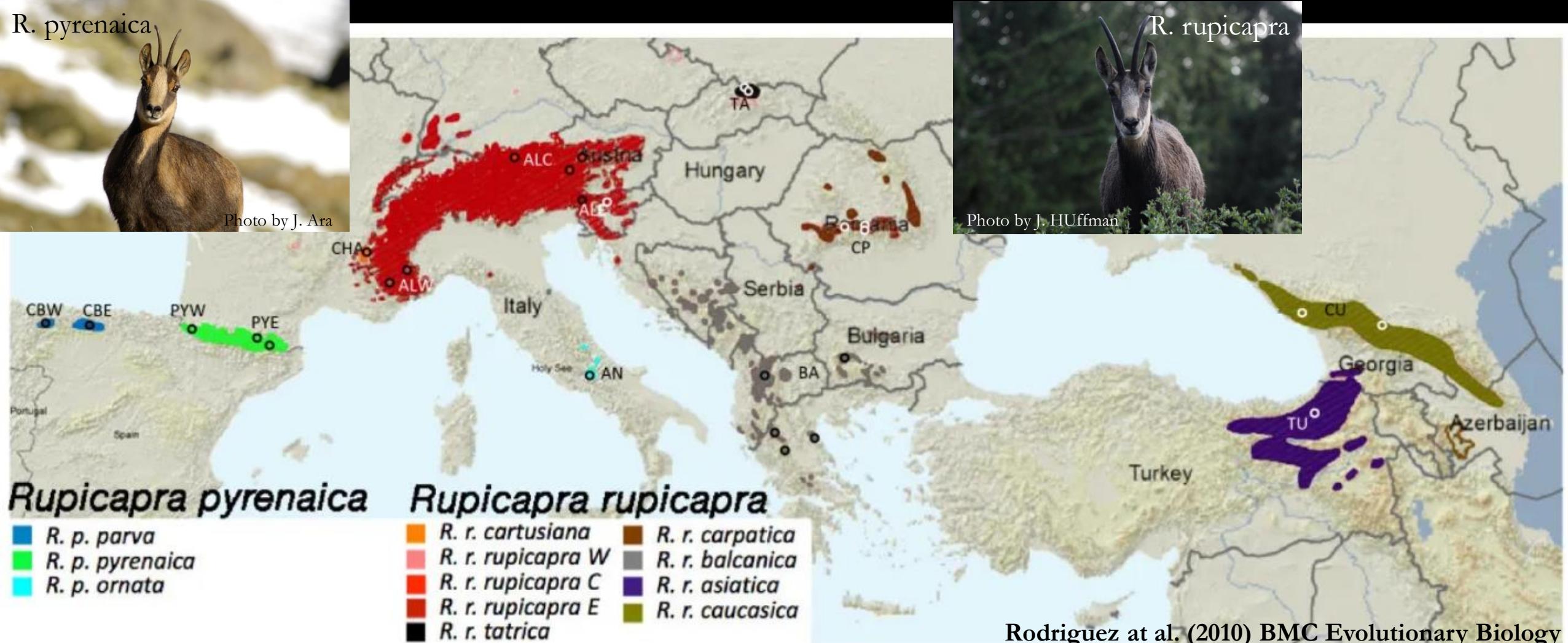




Genus Rupicapra



Photo by J. Ara



Rupicapra rupicapra balcanica

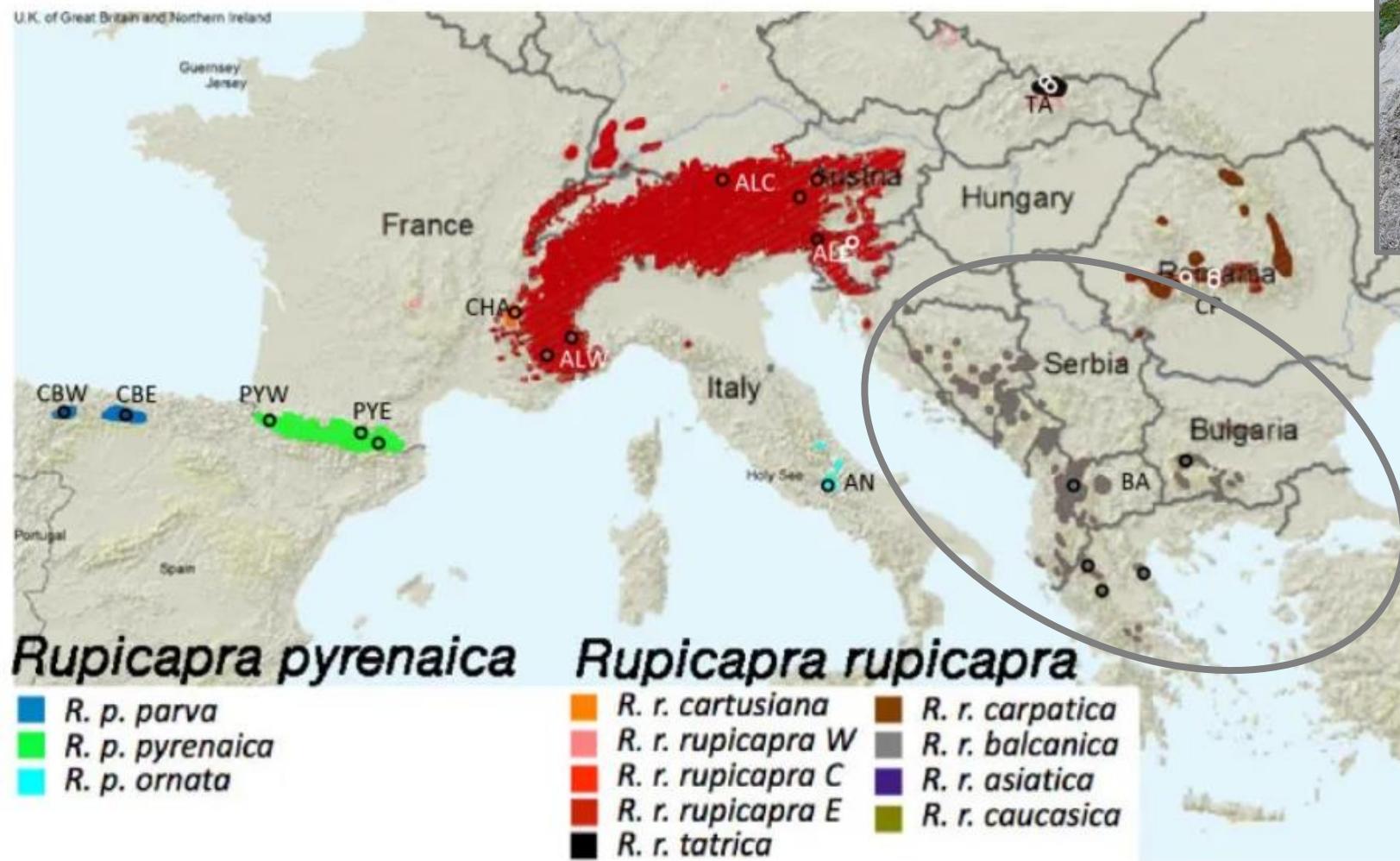
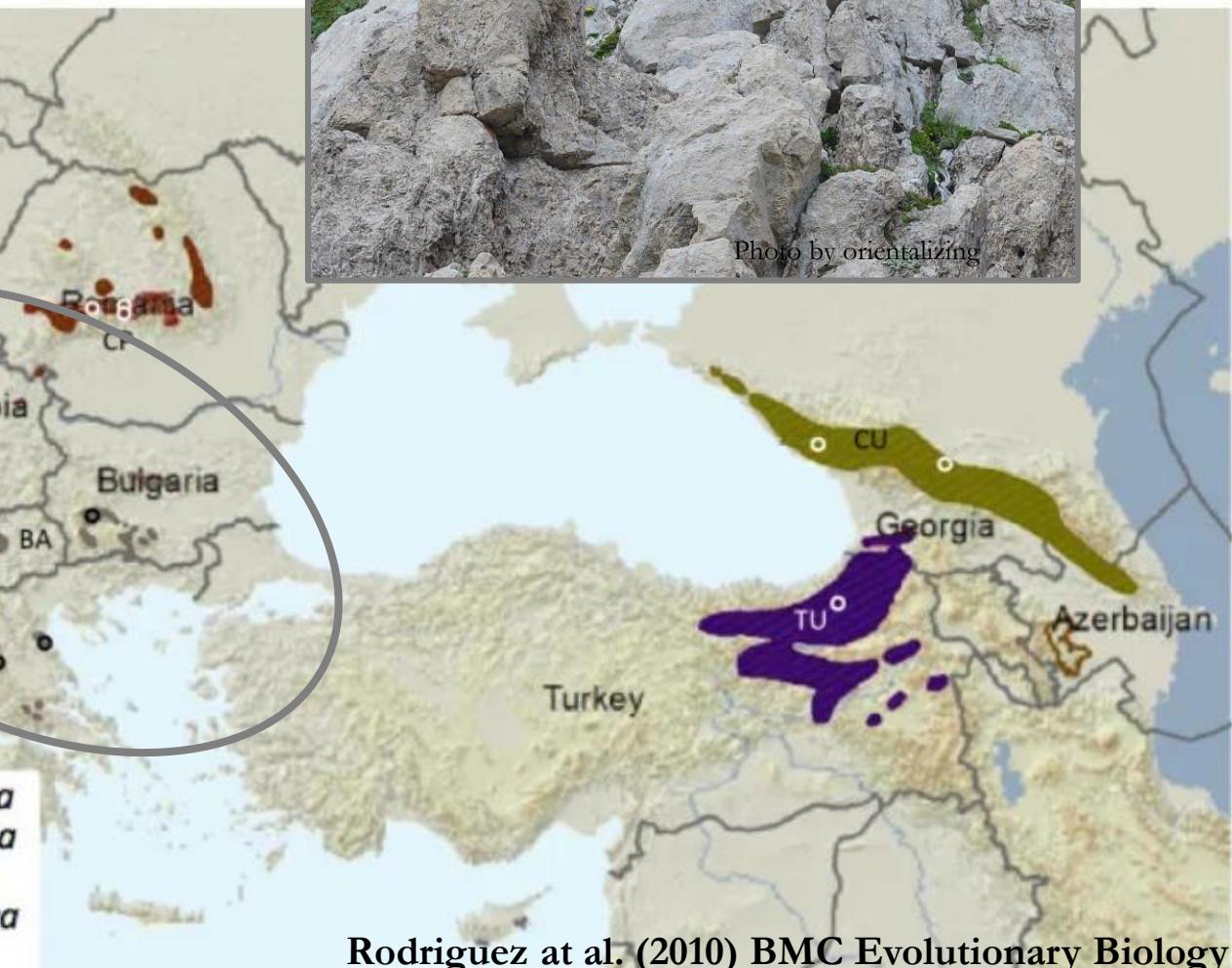


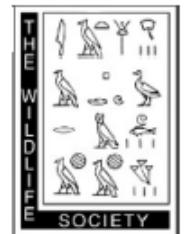
Photo by orientalizing



Rupicapra rupicapra balcanica



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



Featured Article

The Genetic Impact of Chamois Management in the Dinarides

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

RESEARCH ARTICLE

NIKICA ŠPREM,¹ Faculty of Agriculture, Department of Svetosimunska cesta 25, Zagreb 10000, Croatia

ELENA BUZAN, Science and Research Centre, Institute for

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

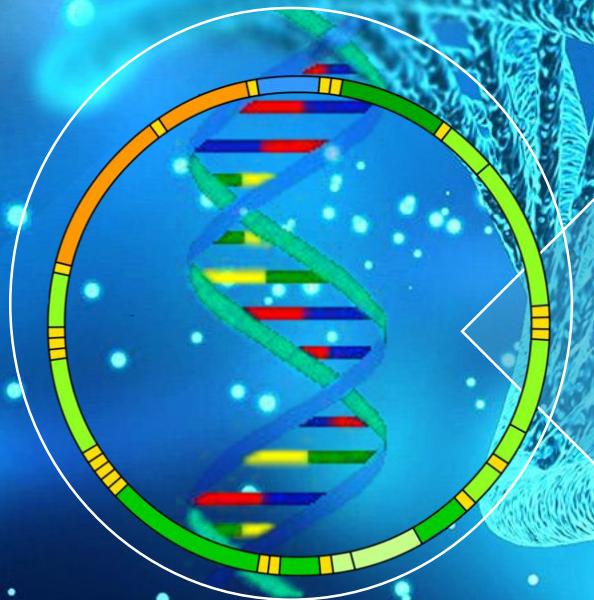
Elena V. Buzan · Josef Bryja · Barbora Zemanová · Boris Kryštufek

Genetic variability and population structure of chamois in Greece (*Rupicapra rupicapra balcanica*)

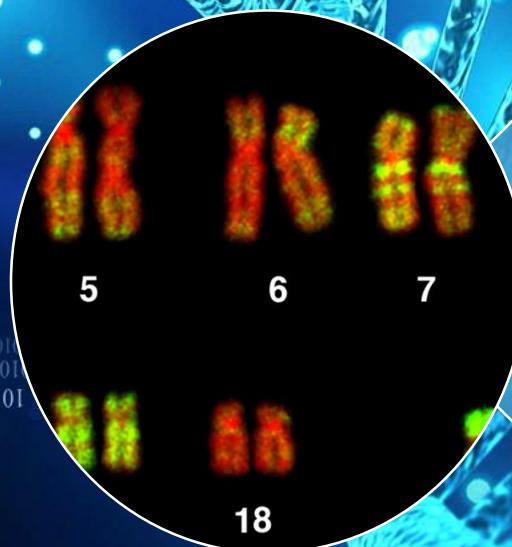
Haritakis Papaioannou² · Margarita Fernández¹ · Trinidad Pérez¹ · Ana Domínguez¹

Conservation Genetics
<https://doi.org/10.1007/s10592-019-01177-1>

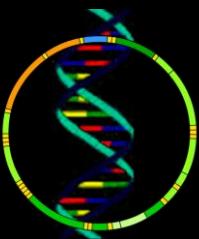
SHORT COMMUNICATION



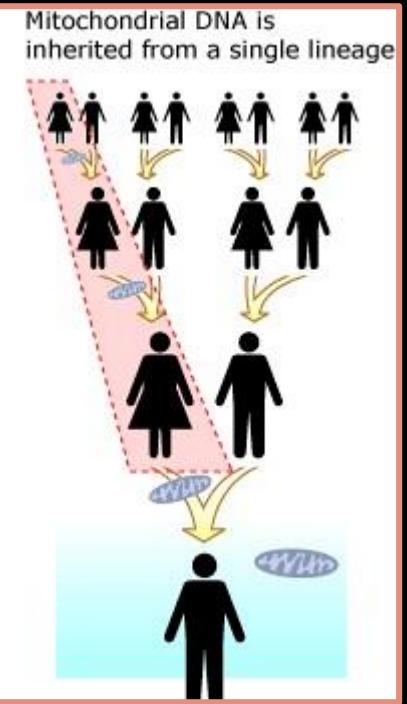
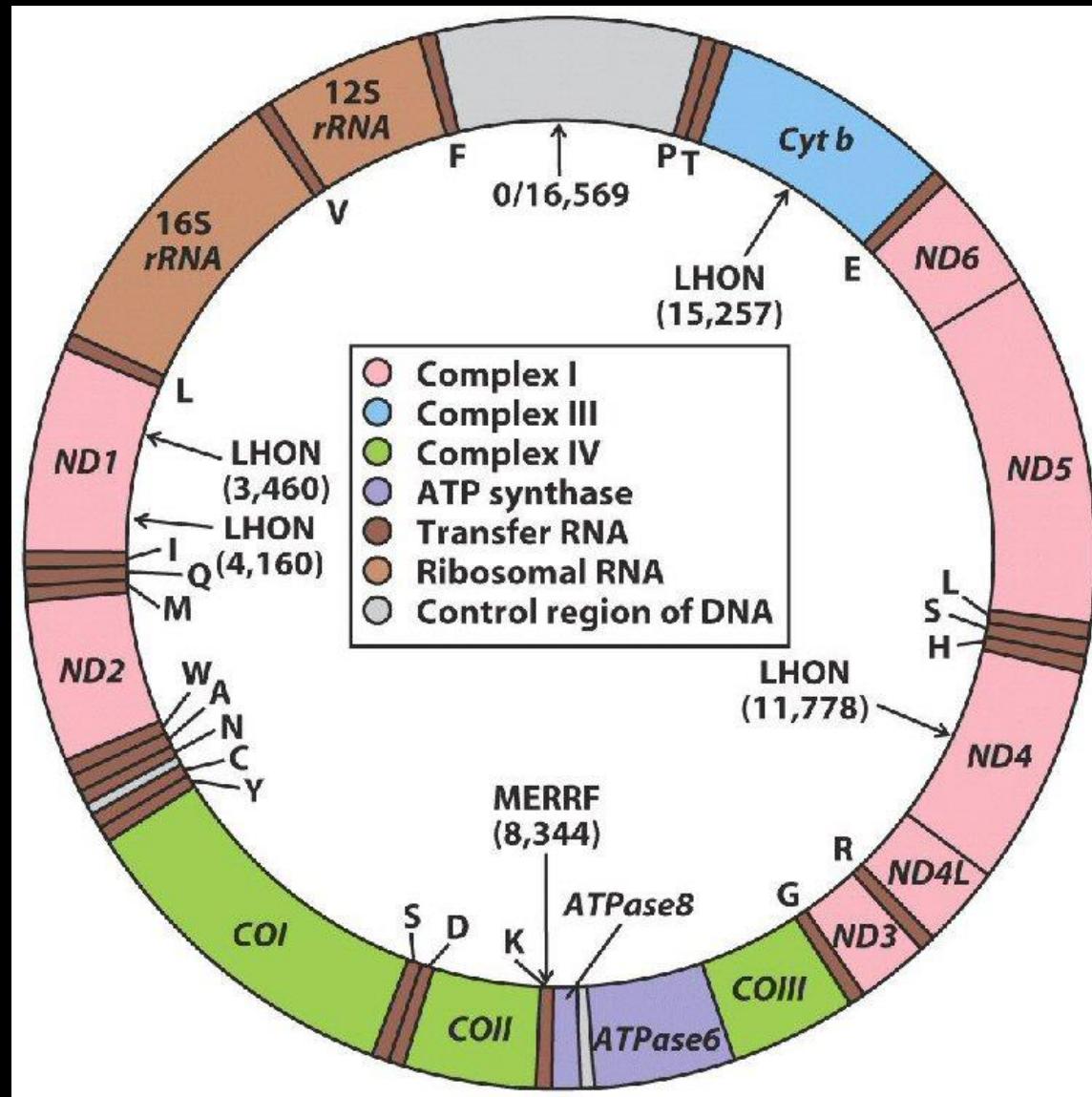
1. whole mtDNA



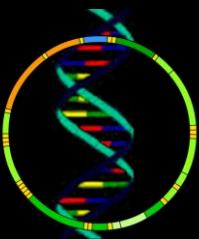
2. Microsatellites



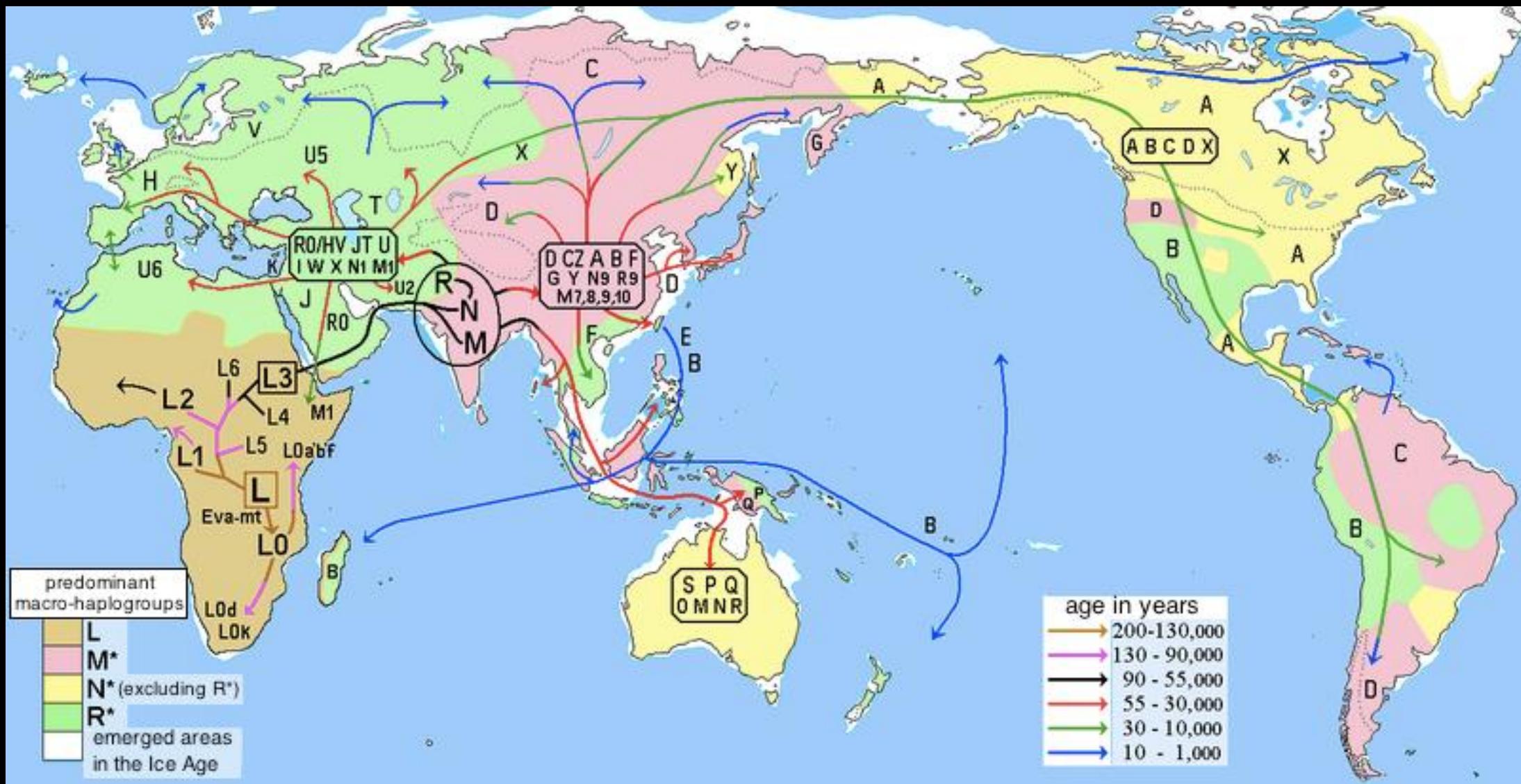
mtDNA

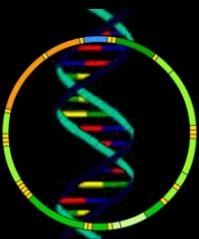


UCMP and the National Center for Science Education



mtDNA





mtDNA

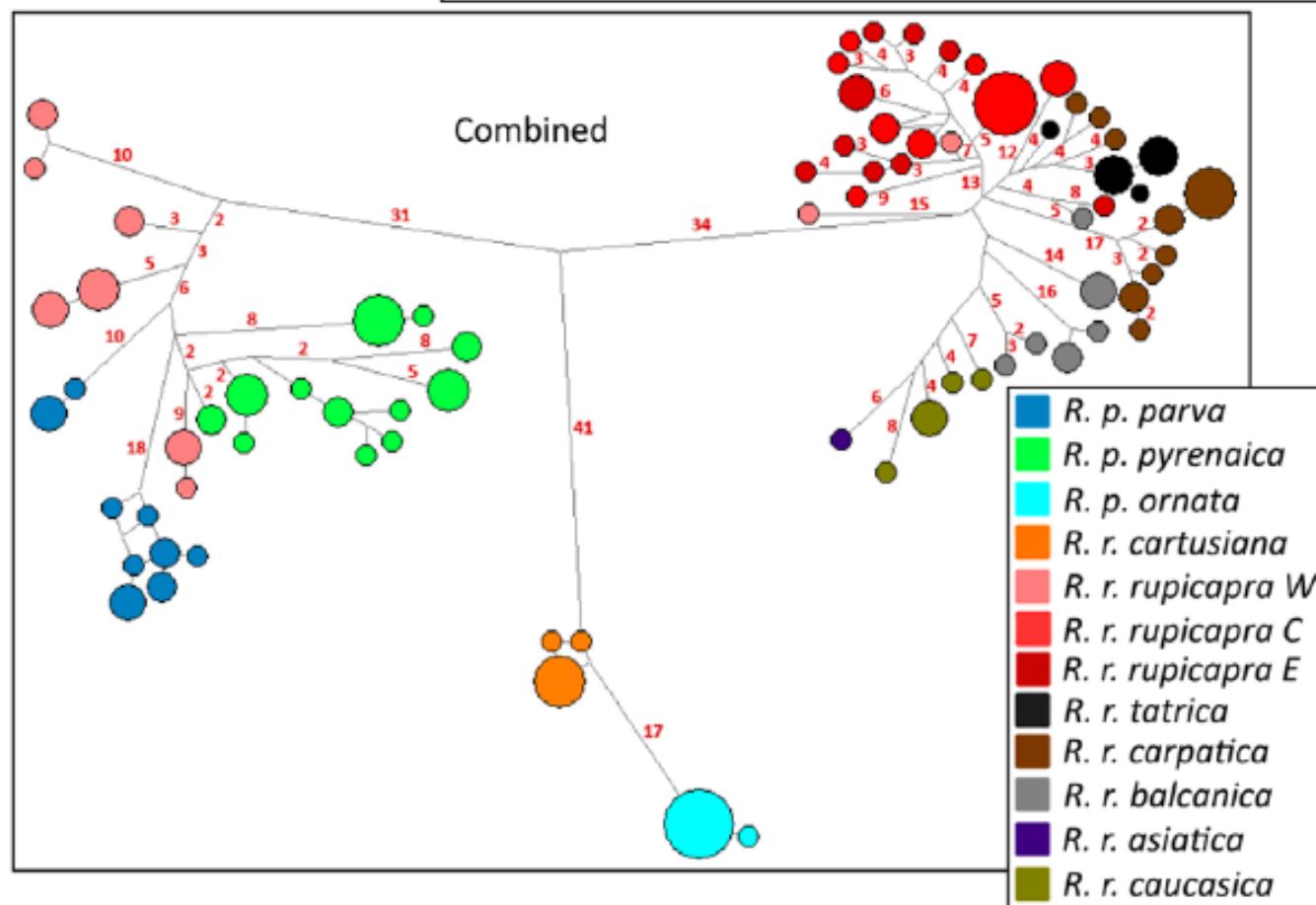
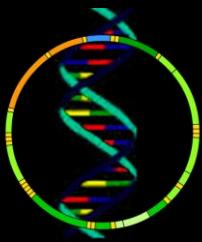


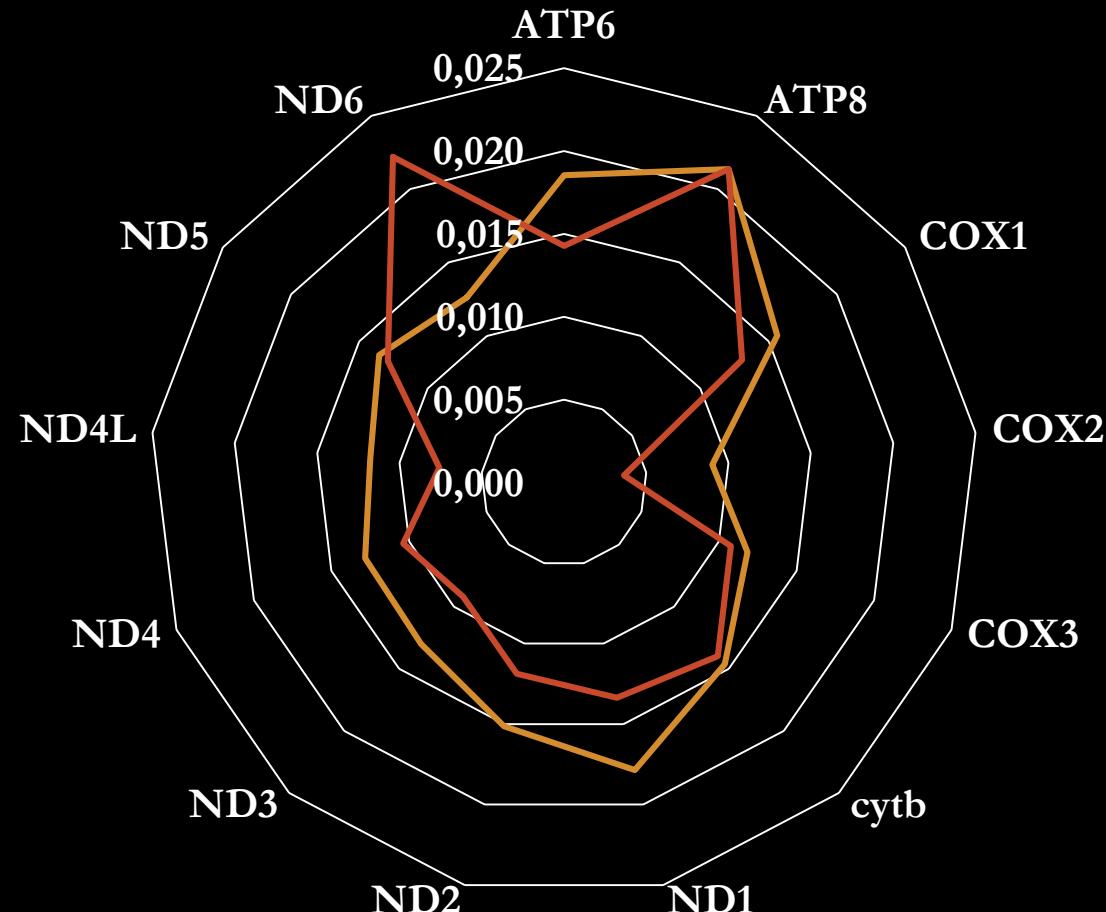
Figure 3 Networks of mitochondrial haplotypes. Median-joining networks for the mtDNA fragments of ND1, 12S, tRNA-pro, the Control Region and for the combined sequence (which in addition includes *cytb*). The size of pie areas corresponds to haplotypic frequencies and the proportion accounted for by the different subspecies is represented in different colours as in Figure 1. Branch lengths greater than 1 between haplotypes are indicated as a red number on the branches. Branch lengths are not scaled.

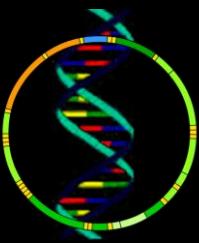


mtDNA

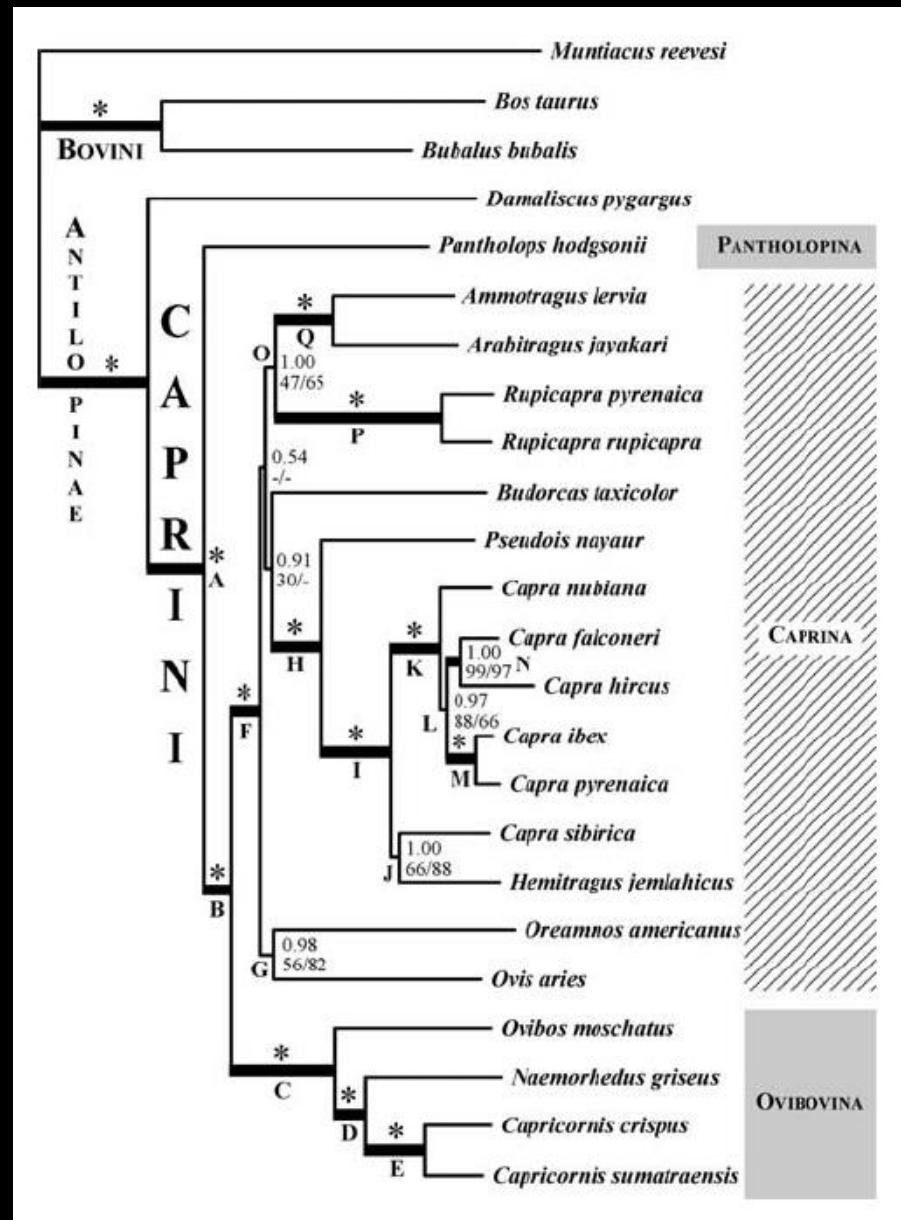
Nucleotide polymorphisms

— Rupicapra pyrenaica — Rupicapra rupicapra

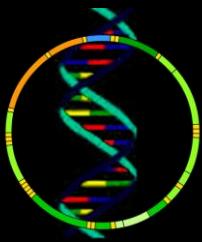




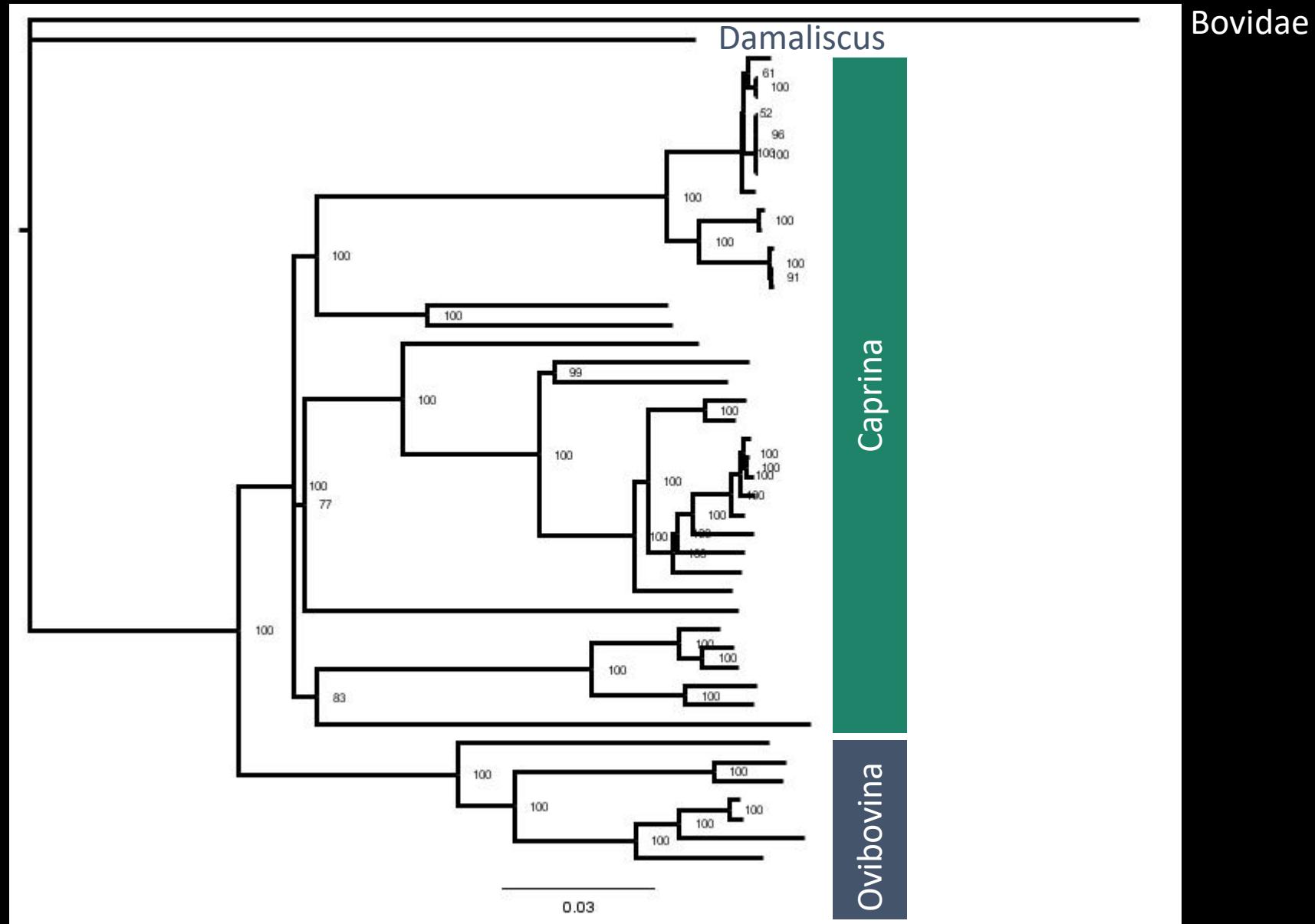
mtDNA

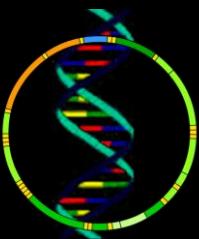


Hassanin et al. (2009) J. Mol. Evol.

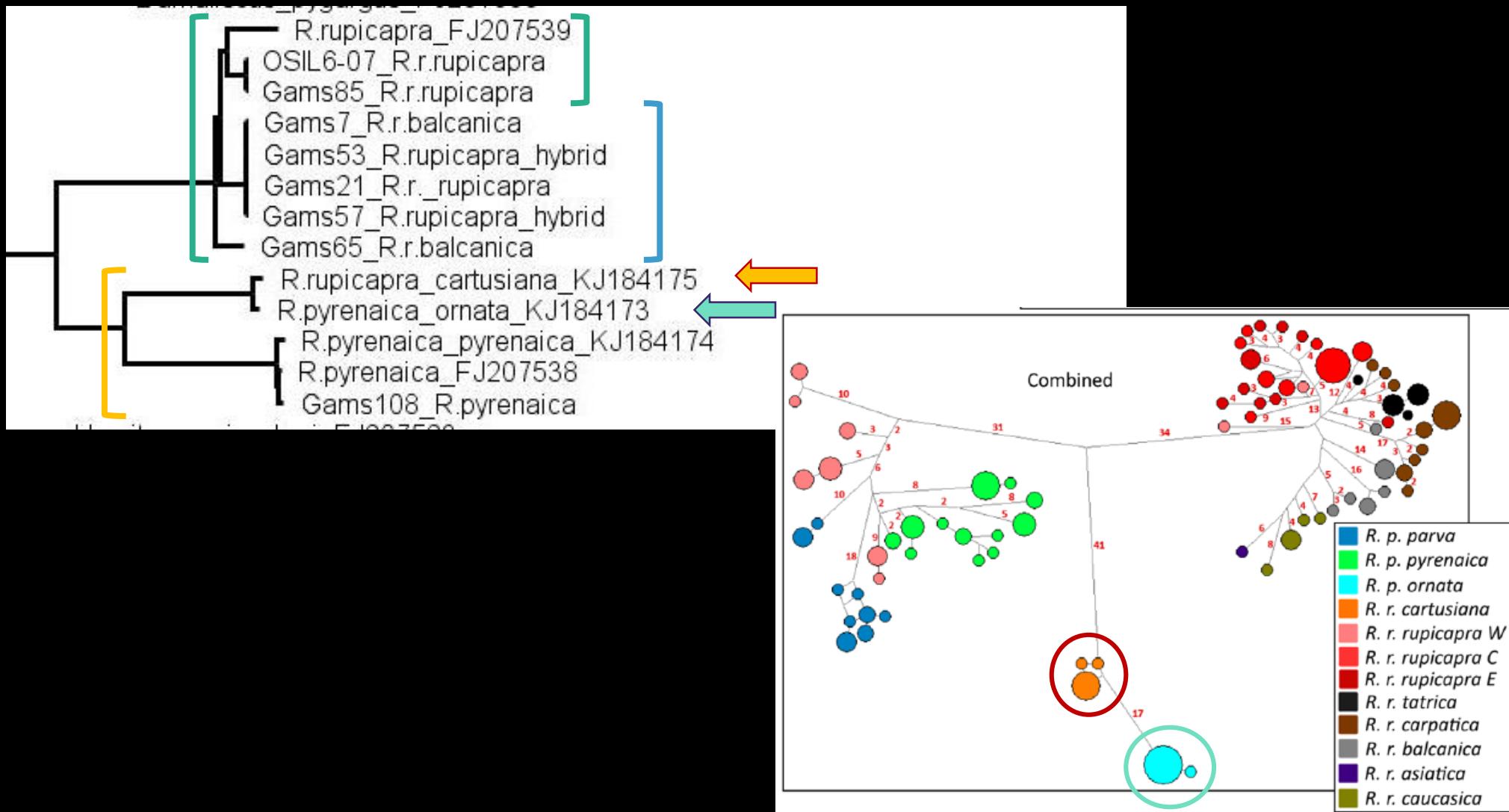


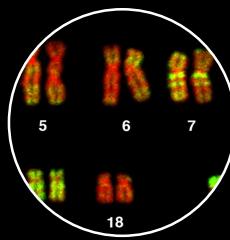
mtDNA





mtDNA





Microsatellite analysis

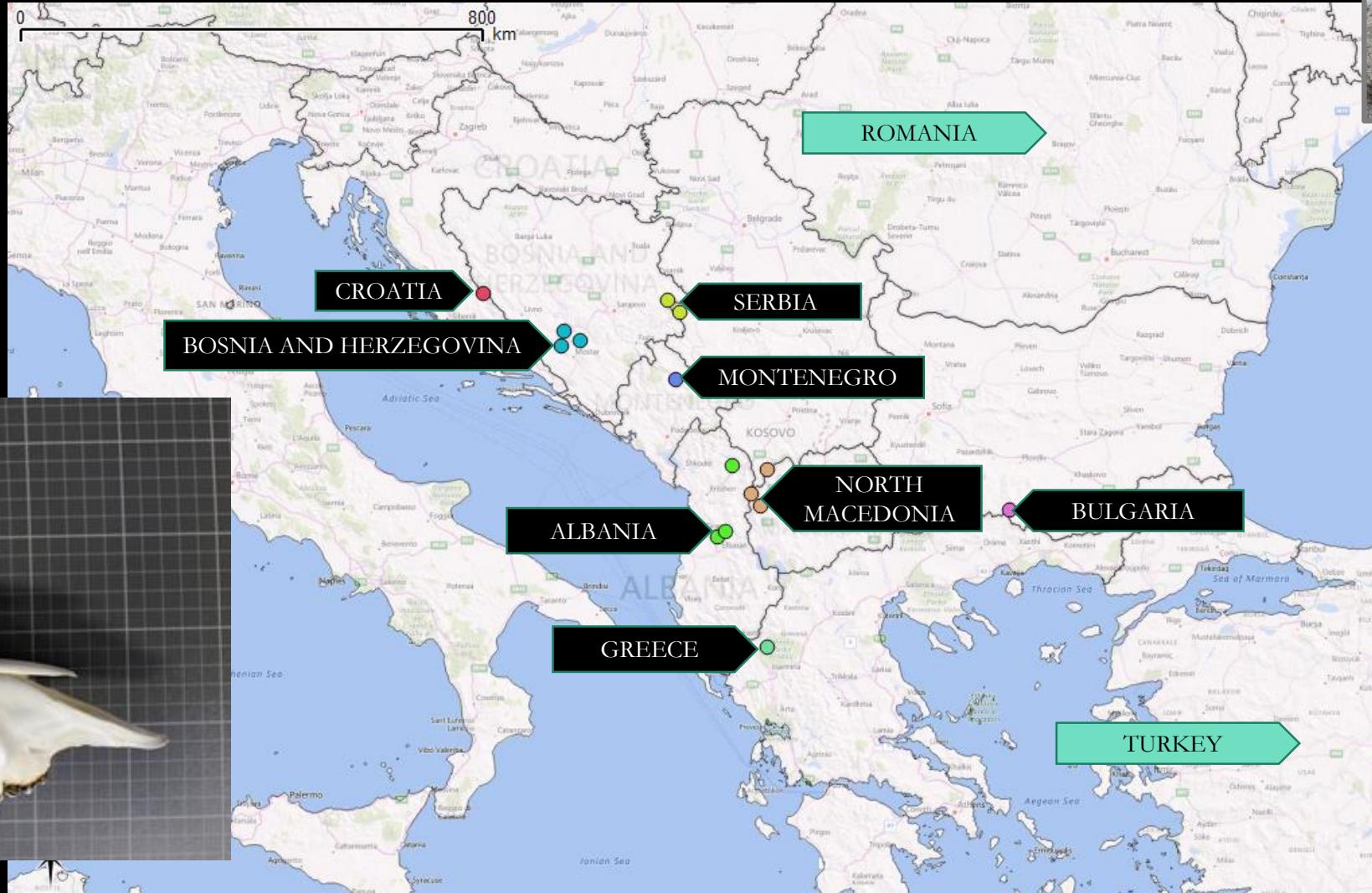
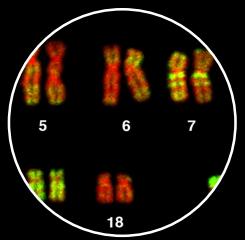
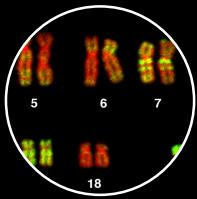


Photo by orientalizing

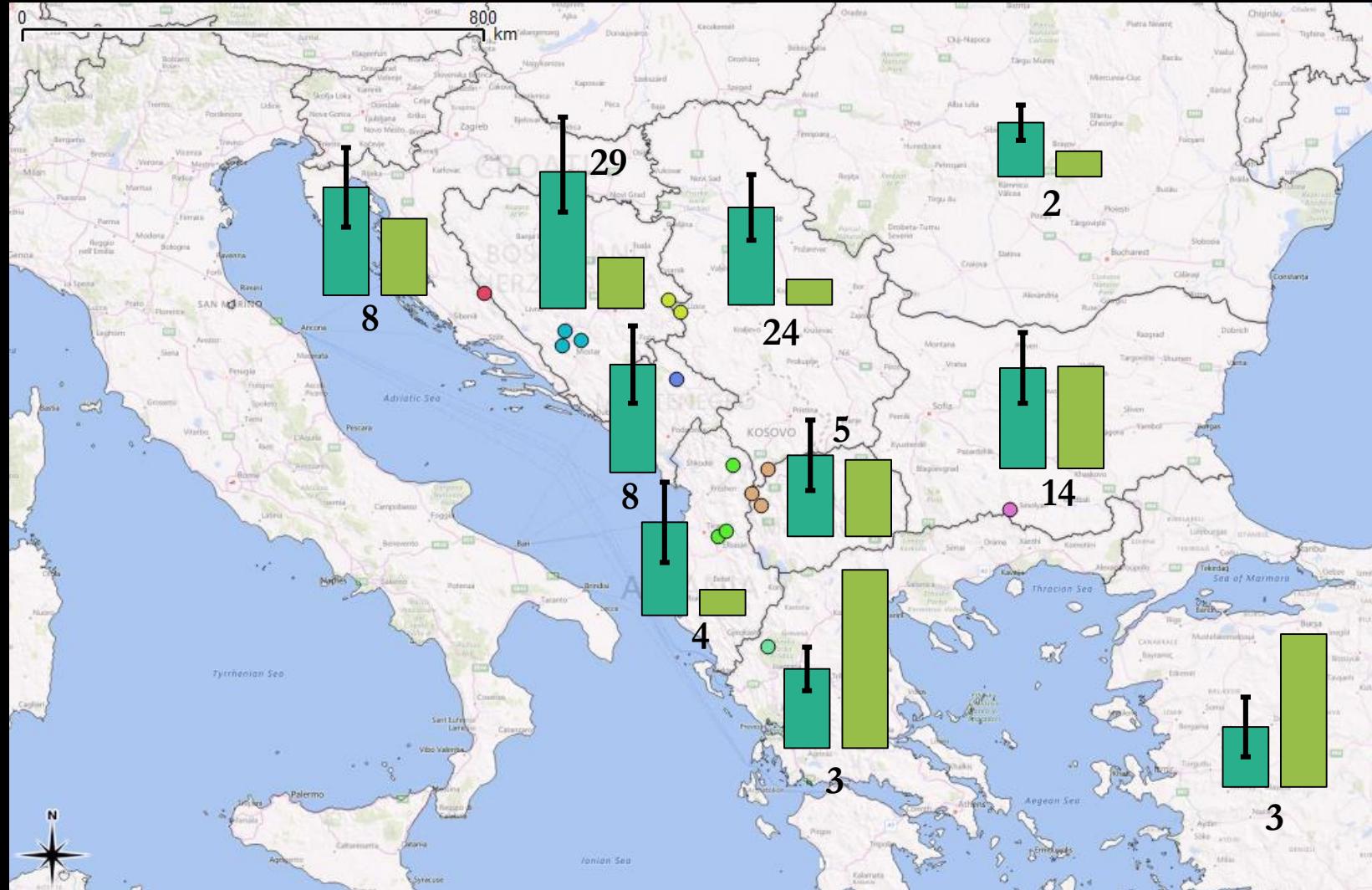


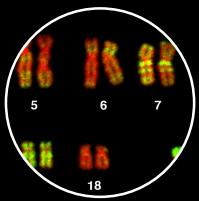
Microsatellite analysis



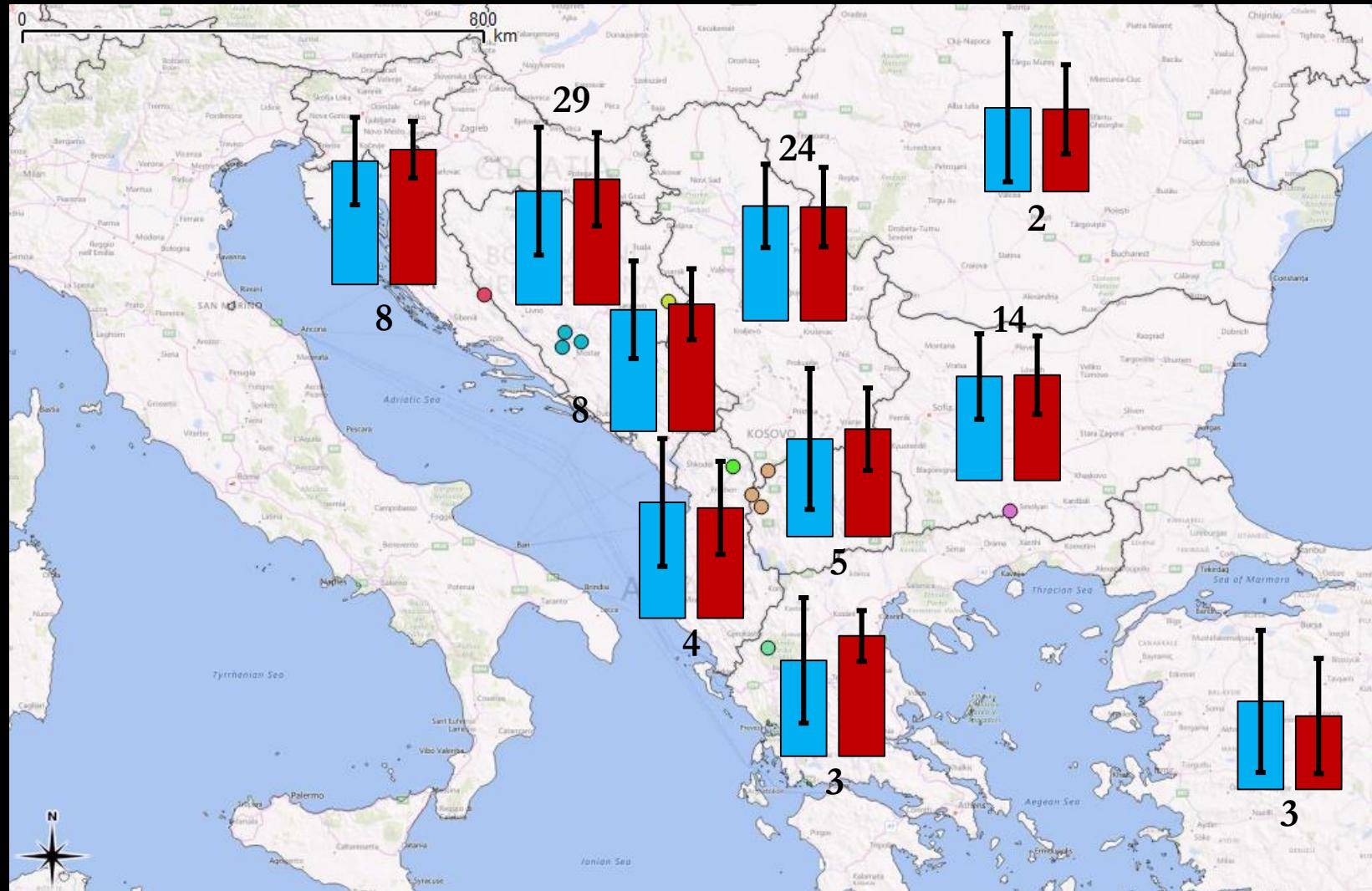


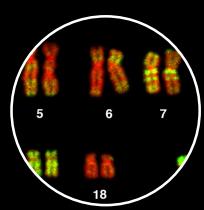
Microsatellite analysis - variability



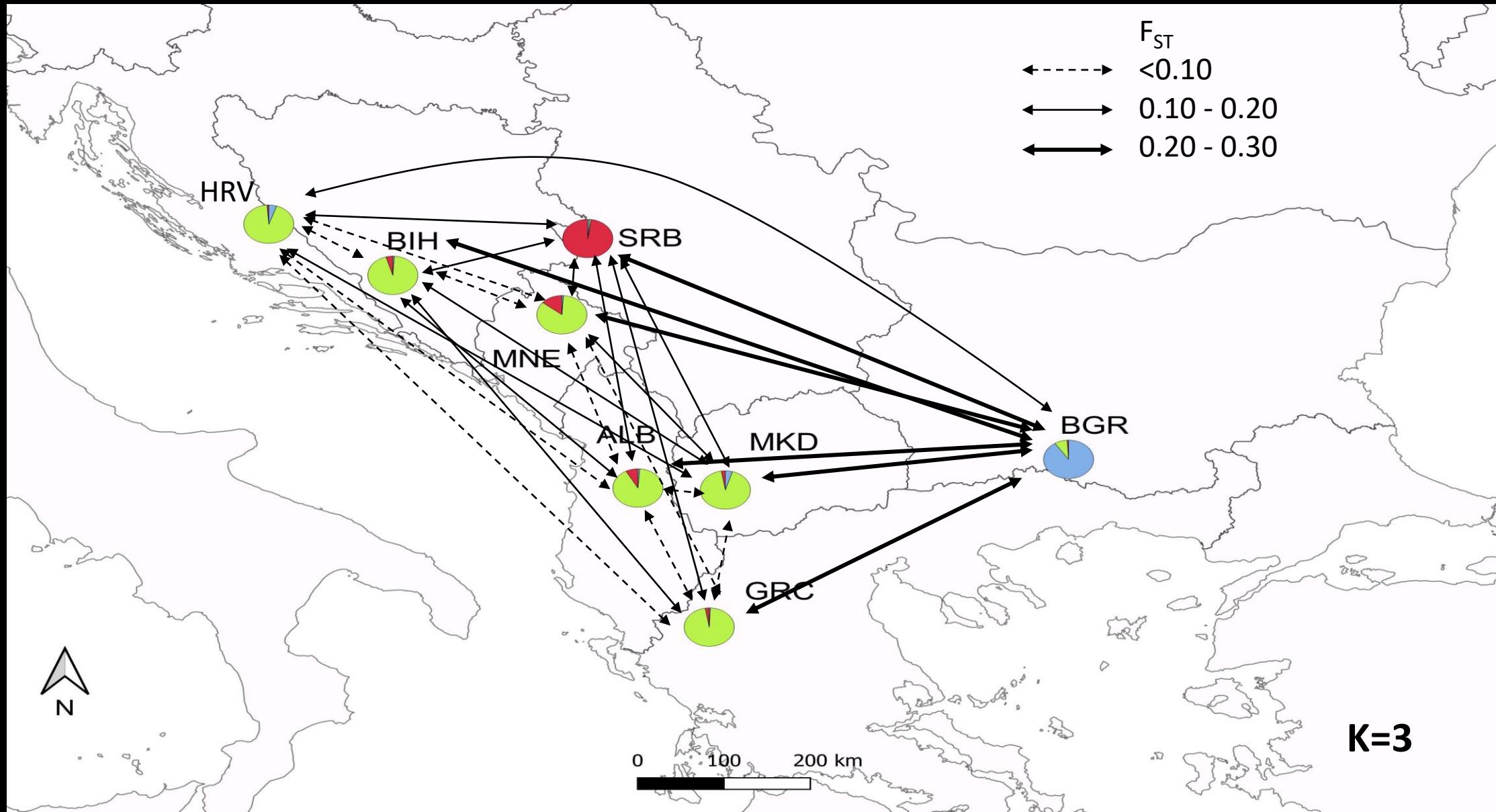


Microsatellite analysis - variability





Microsatellite analysis – Population structure



Conclusions



mtDNA shows past connectivity among areas and confirms the poly-phylogeny of the Genus

Microsatellites highlight the presence of isolated areas





ACKNOWLEDGEMENTS
**DNA as evidence of distribution
and vitality of endangered Balkan
chamois – BalkCham**
IP-2016-06-5751