

Phylogenetic analysis of mitochondrial DNA in the East Adriatic goats

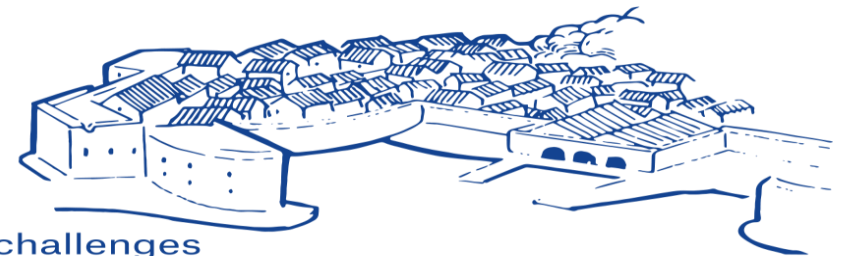
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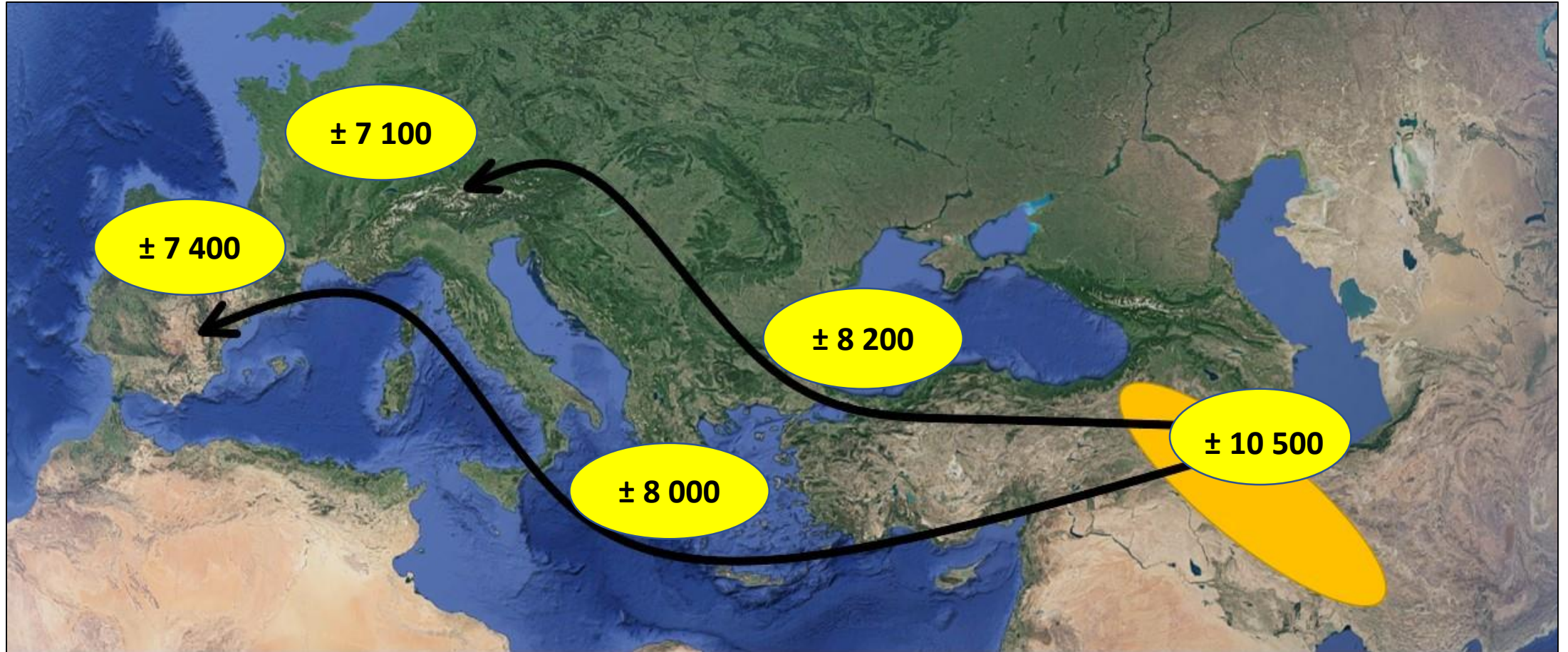
EAAP

69th ANNUAL
MEETING
Dubrovnik, Croatia
27th to 31st August 2018



Conventional and traditional livestock production systems – new challenges

Goat domestication routes



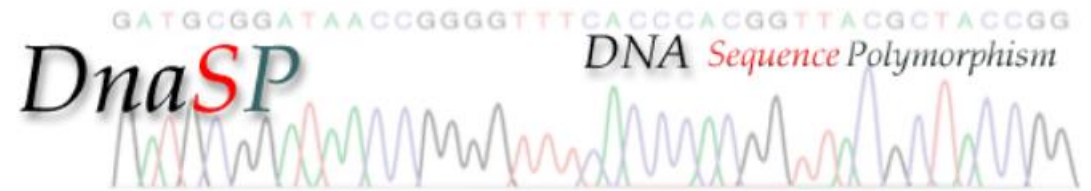
Adopted by S.Naderi

Material and methods

- 25 Croatian spotted goats
- 65% of the breeding area
- 1435 heads (HPA, 2017) under selection



Material and methods



- 660 bp D-loop fragment
- Goat, ancient goat and sheep sequences from Genbank



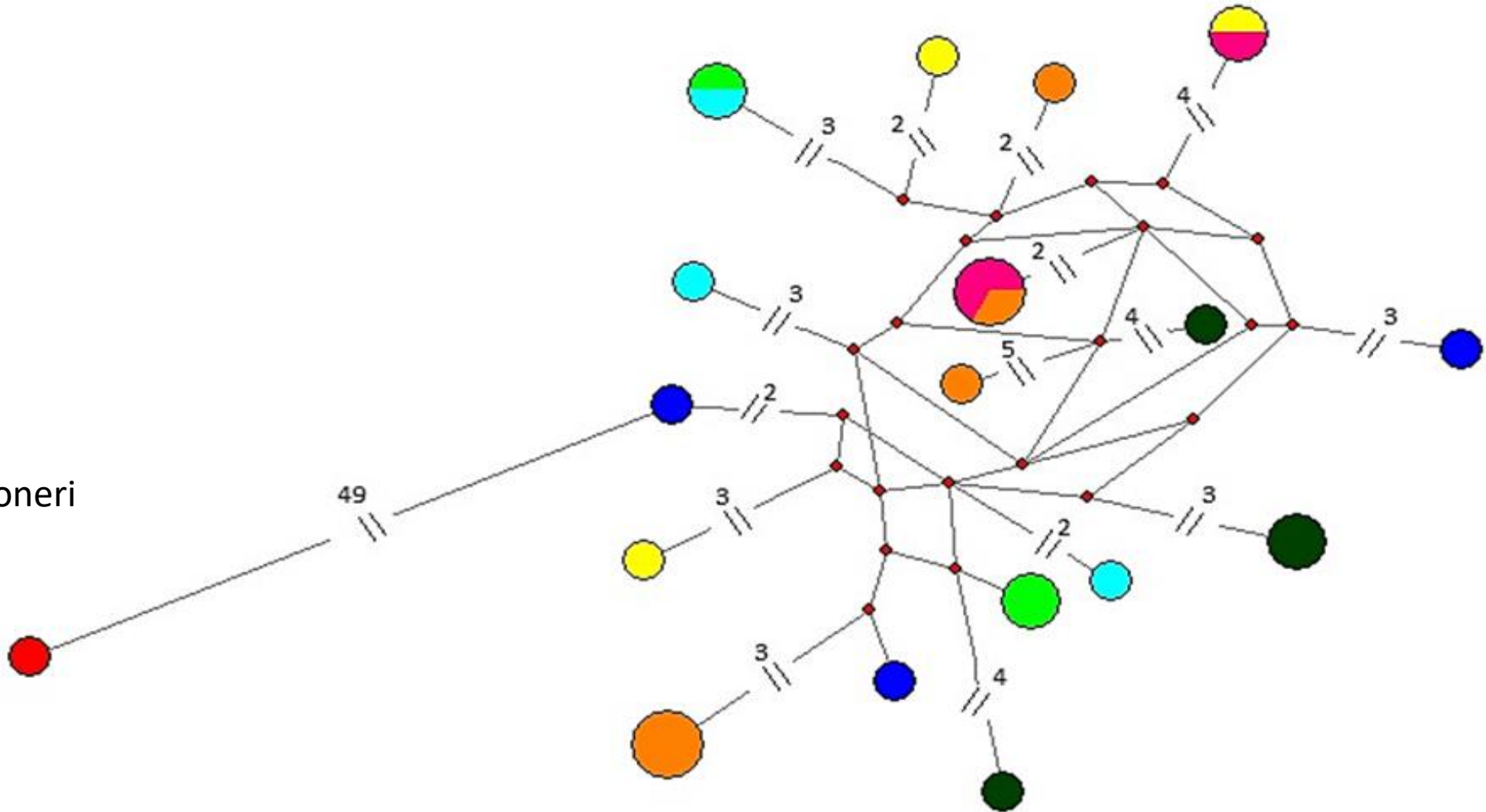
Beast2

Bayesian evolutionary analysis by sampling trees

Results

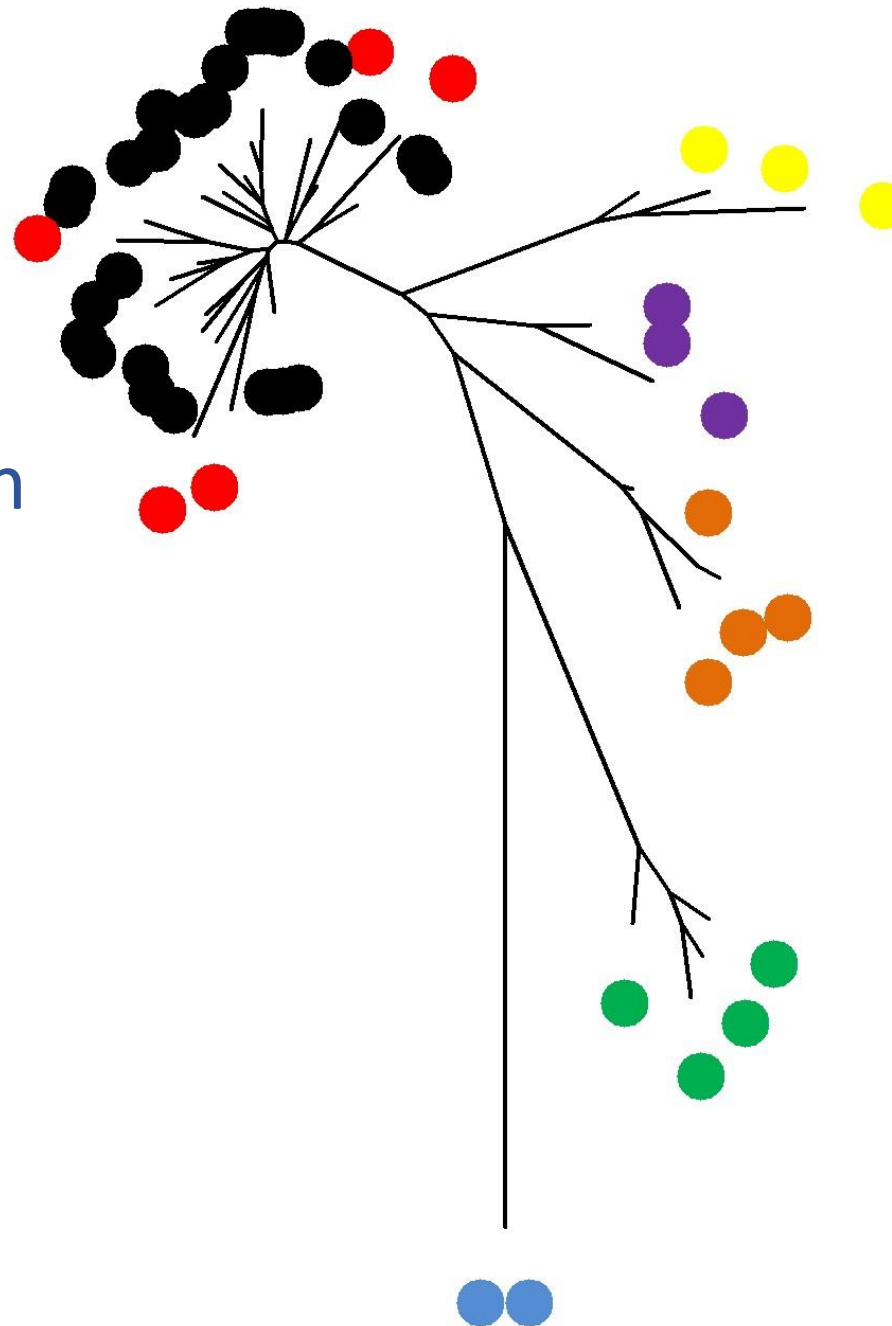
Median-joining tree of Croatian Spotted Goat

- Farm 1
- Farm 2
- Farm 3
- Farm 4
- Farm 5
- Farm 6
- Farm 7
- Outgroup *C. Falconeri*



Haplogroup determination

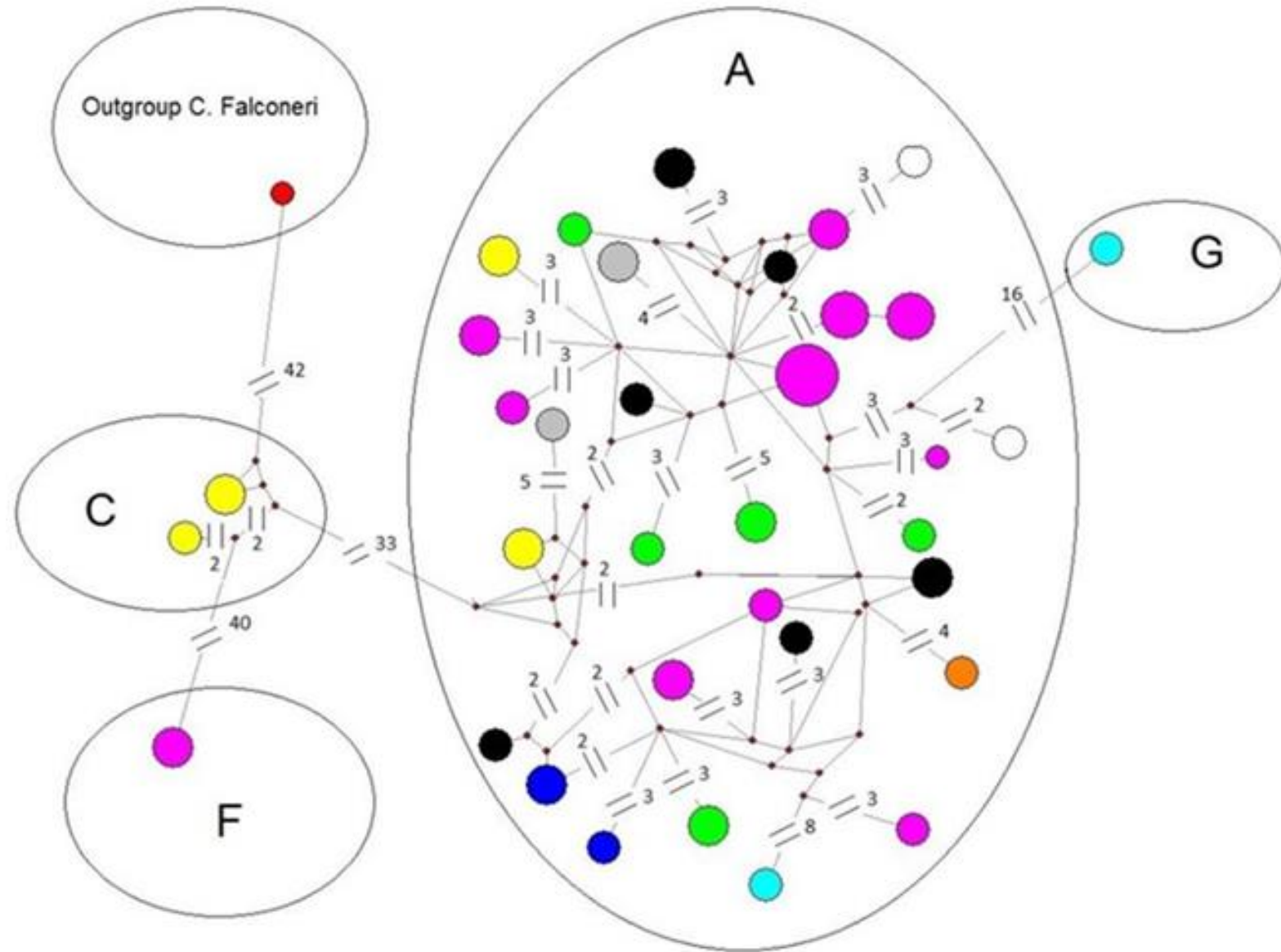
- Croatian Spotted Goat
- Haplogroup A
- Haplogroup B
- Haplogroup C
- Haplogroup D
- Haplogroup F
- Haplogroup G



Median-joining network

● Croatia

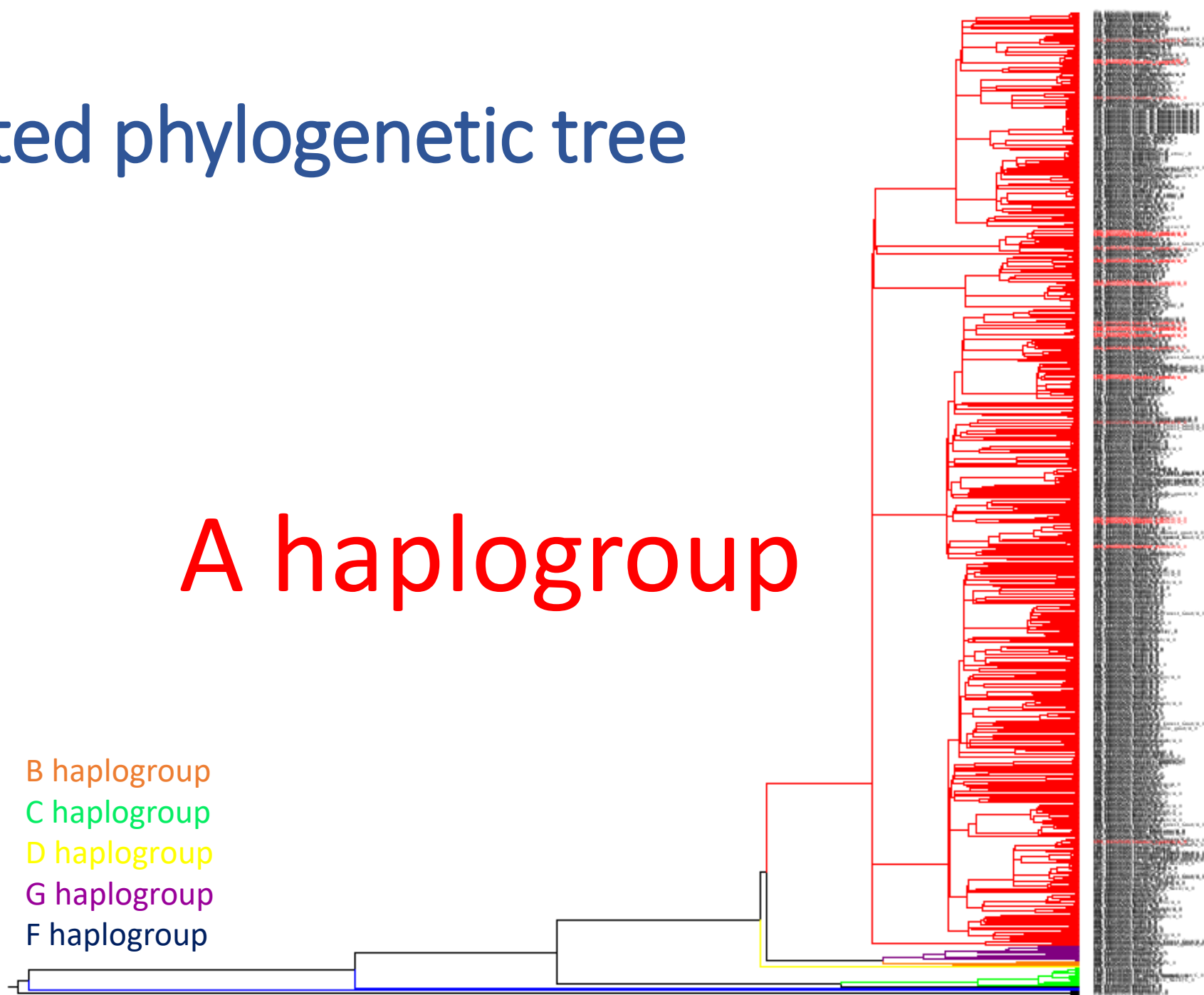
- Albania
- Greece
- Switzerland
- Italy
- Egypt
- Romania
- Spain
- Austria
- Outgroup C. Falconeri



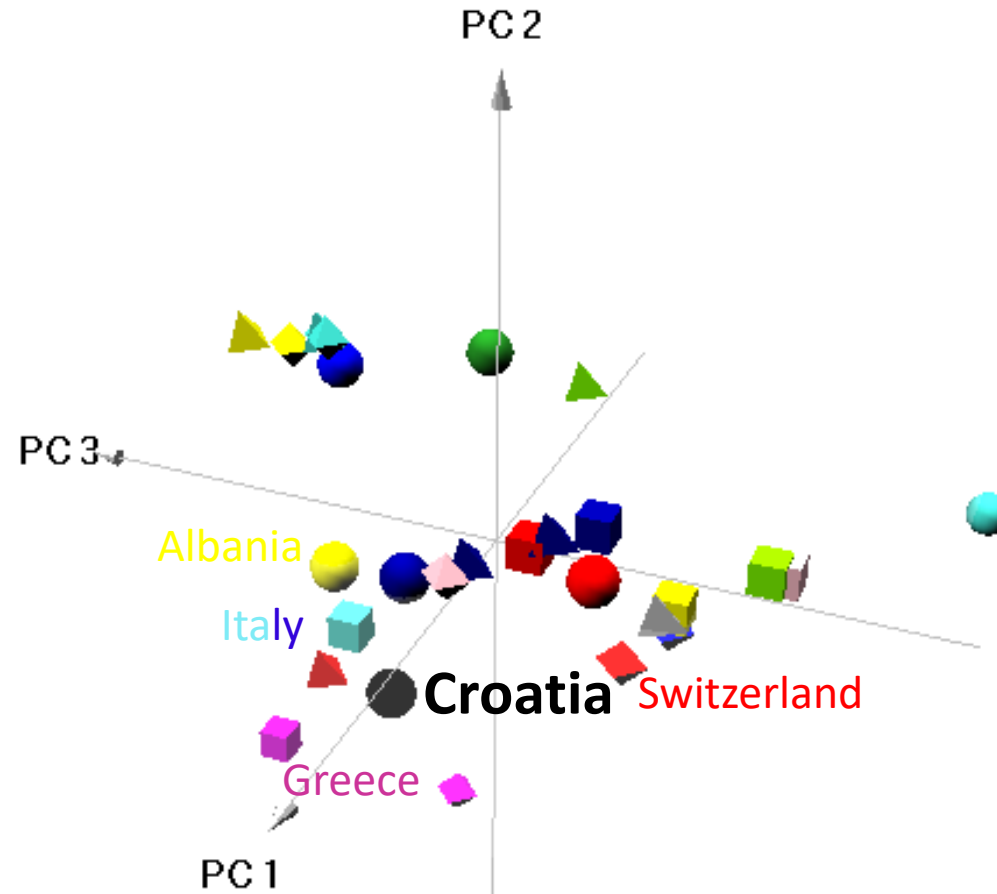
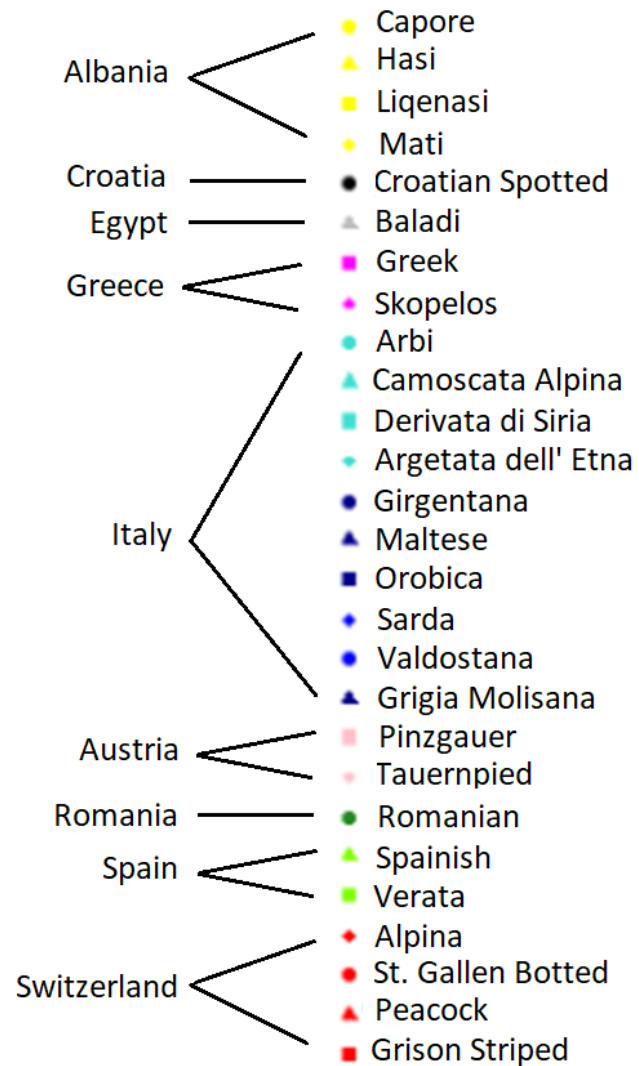
Calibrated phylogenetic tree

A haplogroup

- B haplogroup
- C haplogroup
- D haplogroup
- G haplogroup
- F haplogroup



Principal component analysis



Conclusion

Croatian Spotted goat

- has preserved high genetic diversity
- has high heterogenic origin
- is closest to Albanian, Greece and Italian goats by mtDNA
- has low phylogeographic structure characteristic to all goats

Thank you for your attention!

