

Assembly of a Complete Mitogenome of Balkan Chamois (*Rupicapra rupicapra balcanica*)

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Project: DNA as evidence of the distribution and vitality of endangered Balkan chamois

Genus *Rupicapra*

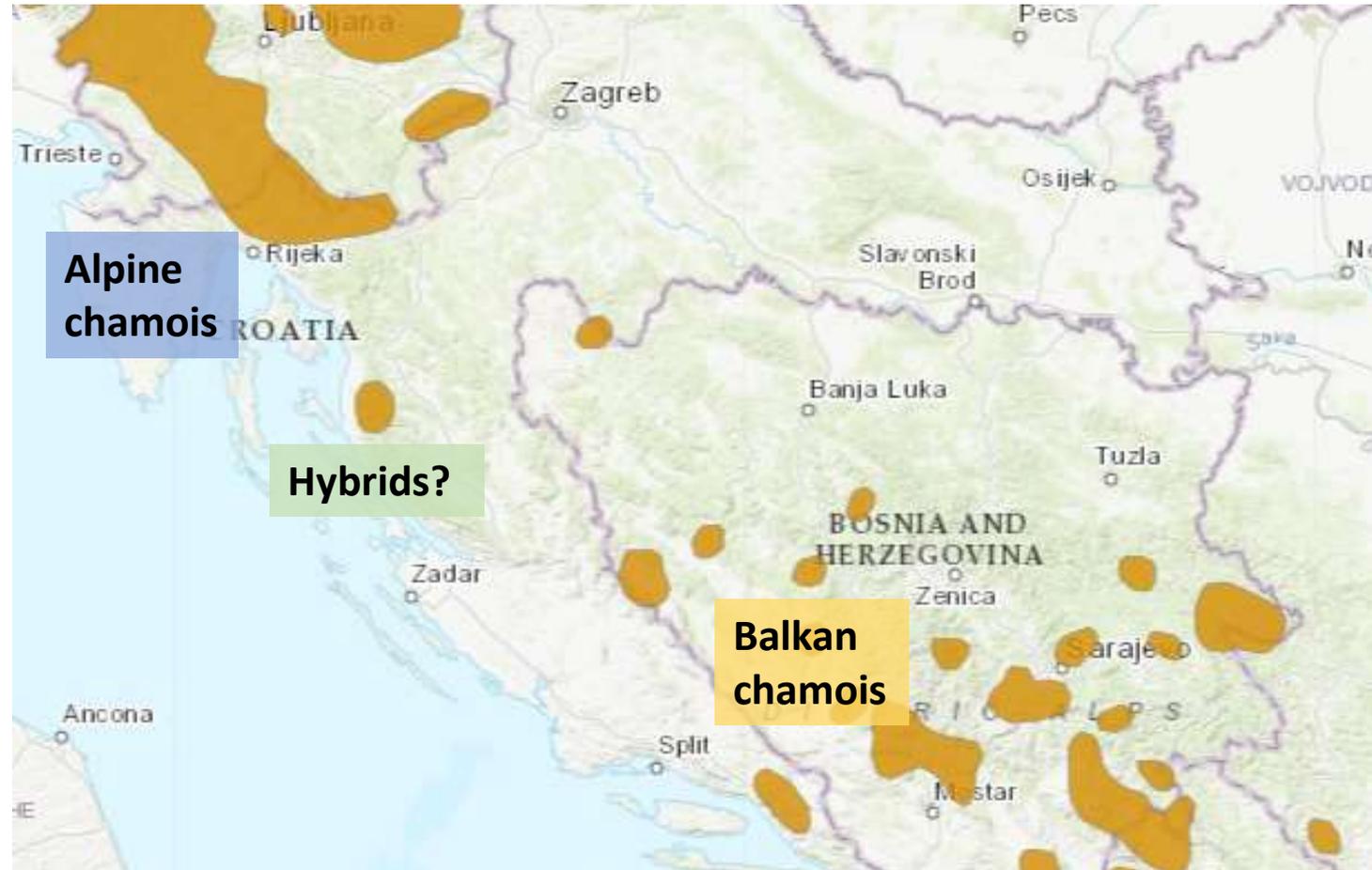
2 species: 1. *Rupicapra rupicapra*
2. *Rupicapra pyrenaica*

Rupicapra rupicapra

- 7 subspecies

Croatia:

Alpine and **Balkan** chamois

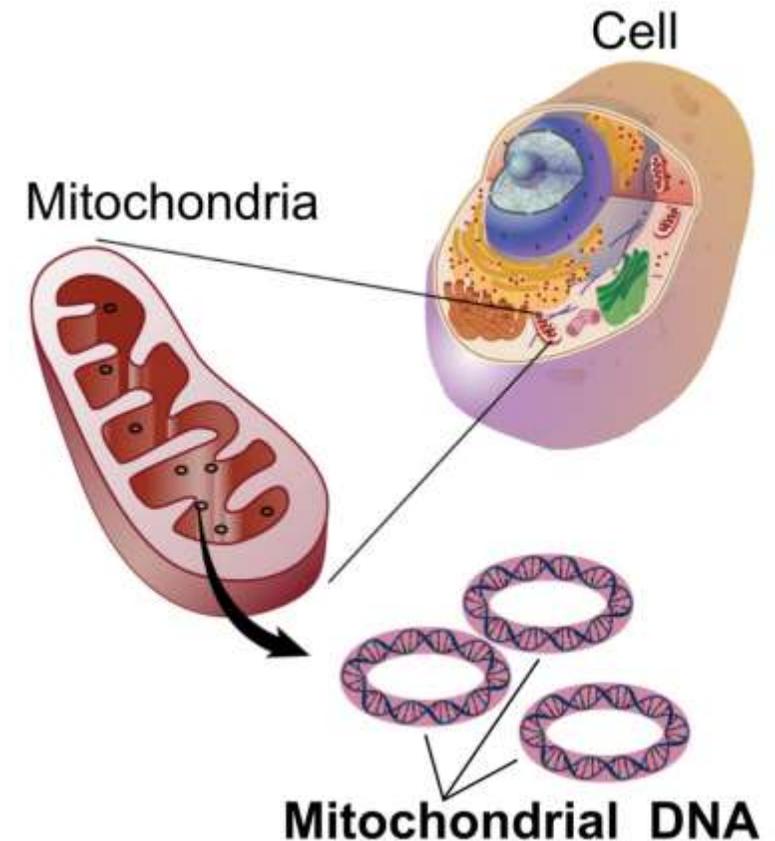
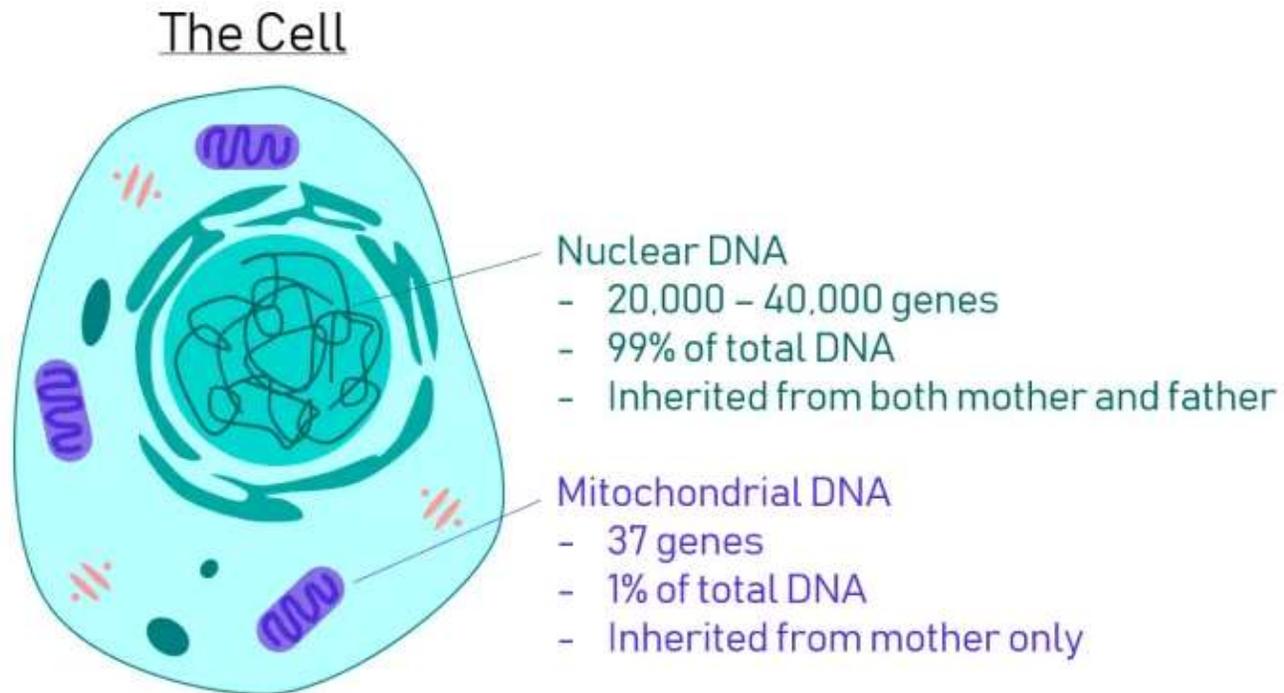


What is the relationship between subspecies?

Mitochondrial DNA (mammals) ~ 16 kb

Length of human nuclear DNA ~ 3 billion bp

Length of human mitochondrial DNA ~ 16 000 bp



Mitochondrial DNA (mammals) ~ 16 kb

Coding (conserved) parts:

- 13 protein-coding genes
- 22tRNAs
- 2 rRNAs

Non-coding region:

- Control region or D-loop (~1000 bp long)
- Controls the replication
- The most polymorphic region
- Good molecular marker for finding genetic differentiation between animal species

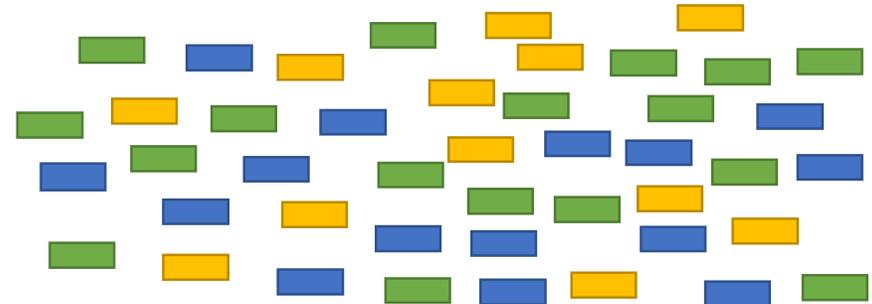
Sequencing process

Balkan
chamois
Sample 1

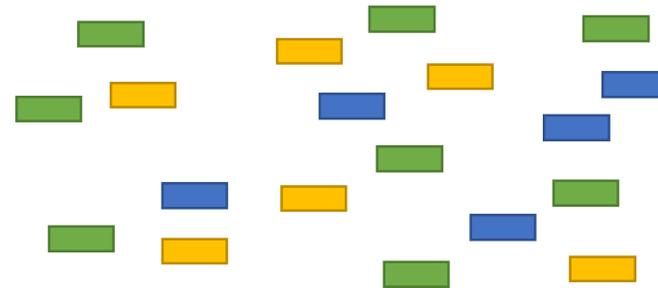
Balkan
chamois
Sample 1



1. sample: 216 million reads (150 bp length)



2. sample: 6 million reads (150 bp length)

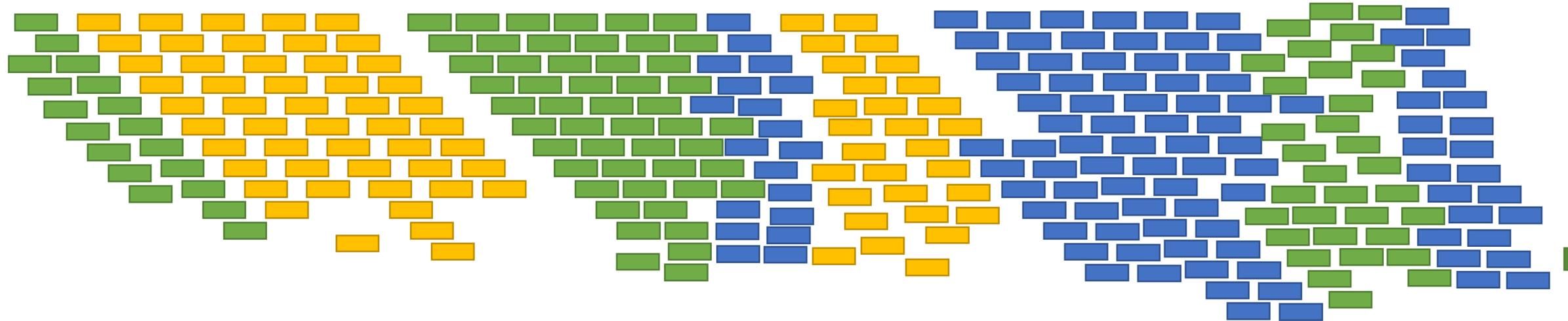


Assembly step

- Reference-based genome assembly
- De Novo assembly

Reference:

Rupicapra mitochondrion from NCBI

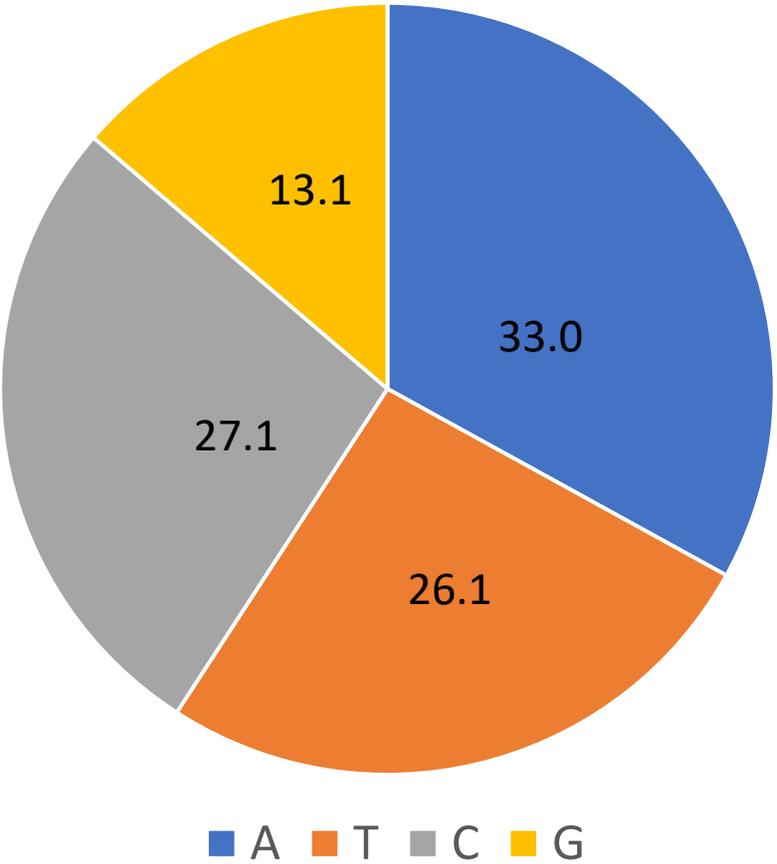


Newly assembled mitogenome:



Results: 16433 long sequence

Nucleotide composition (%)



Adenin=5429
Cytosine=4461
Guanine=2250
Thymine=4293

G+C=40.83%
A+T=59.17%

Annotation of assembled mitogenome

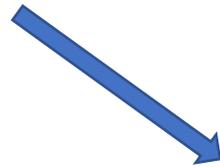
- Genome annotation is the process where biological information is attached to genome sequences (automated or manually)



NAD4L CYTB Dloop 12S RNA
NAD5 NAD6 16SRNA
NAD2 NAD4 NAD1 ATP8
NAD3 COX1
COX3 ATP6
COX2

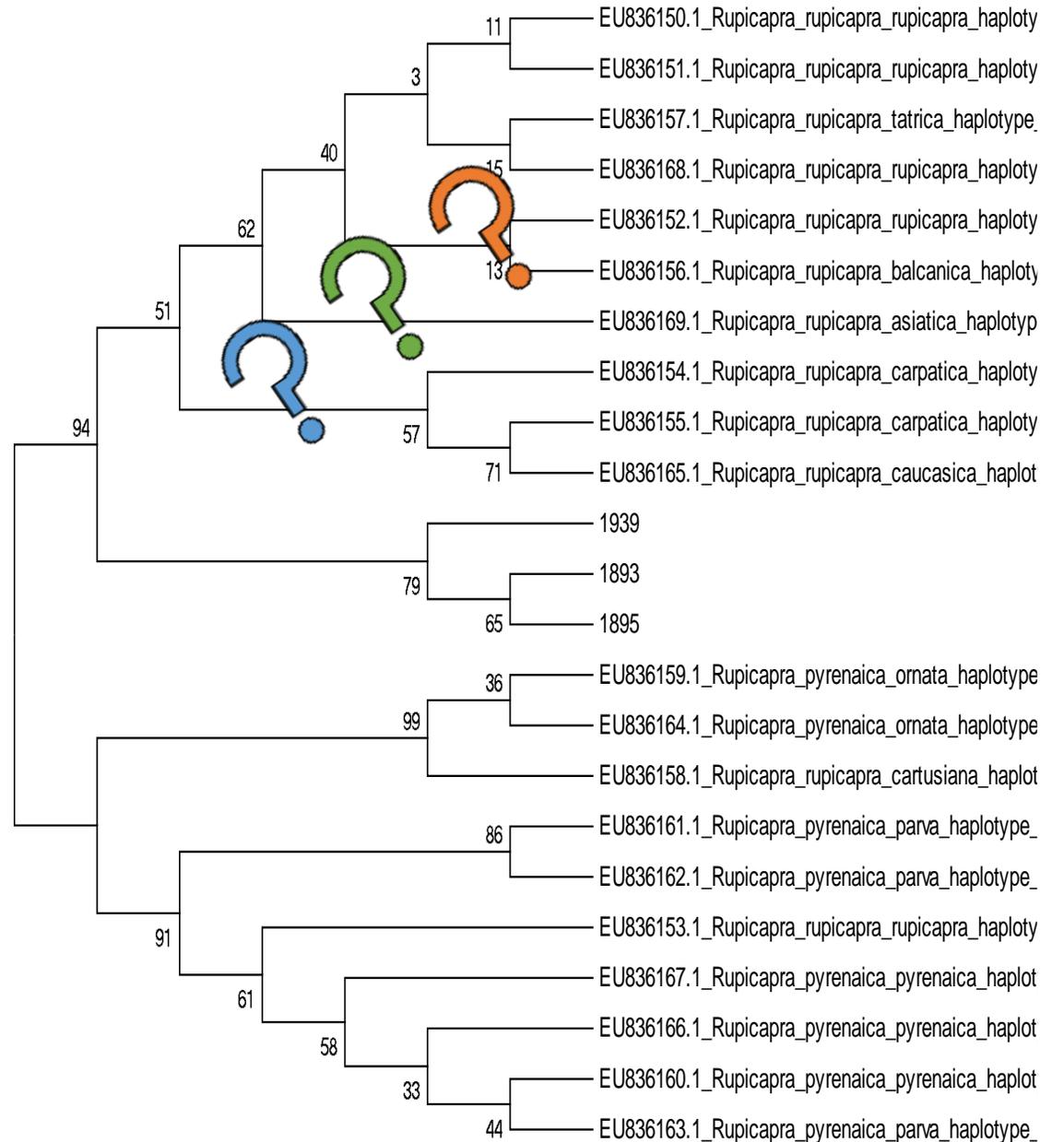
Automated annotation with software:

- Mitos online server
- MitoZ tool
- tRNAscan-SE Search Server



What is next?

- Collect samples of all subspecies
- Assemble new mitogenomes
- Resolving the taxonomy of the Genus *Rupicapra*



Thank You for Your Attention!



ACKNOWLEDGMENTS

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