



## PROTOCOL 5.

# Mitochondrial DNA analysis of DNAs isolated from Balkan chamois bone remains

### Things to be done before the start:

- Dilute DNA samples down to the concentration of 1 ng/μl.
- Dilute SSR primers down to final concentration of 10 μM.
- Gradually thaw 10 x PCR Buffer and dNTPs at temperature of 4 – 8 °C.
- Prepare 5X TBE Electrophoresis Buffer (54 g Tris base, 27,5 g of boric acid and 20 ml of 0,5 M EDTA (pH 8.0) in 1000 ml distilled water).
- Prepare 6X Gel-loading Buffer (0,25 % bromphenol blue, 0,25 % xylene cyanol, 40 % (w/v) sucrose in distilled water).

### STEPS INVOLVED IN MITOCHONDRIAL DNA ANALYSIS:

PART 1. PCR AMPLIFICATION OF MITOCHONDRIAL PARTIAL CYTOCHROME B GENE AND ITS CONTROL REGION

PART 2. AGAROSE-GEL ELECTROPHORESIS OF PCR AMPLIFIED MITOCHONDRIAL REGION

PART 3. AUTOMATED DNA SEQUENCING OF PCR AMPLIFIED MITOCHONDRIAL REGION AND GEN BANK COMPARISON OF PCR AMPLIFIED REGION

### PART 1. PCR AMPLIFICATION OF MITOCHONDRIAL PARTIAL CYTOCHROME B GENE AND ITS CONTROL REGION

#### 1) DNA samples

- DNA samples were isolated from: 1) Balkan chamois molar remains (Velebit (Cro) 1893), 2) Balkan chamois maxilla remains (location and date unknown).

#### 2) PCR amplification

- PCR mix (fluorescently labelled SSR primers developed by (Radosavljević et al. 2010, 2011):

74,40 μl H<sub>2</sub>O

16,00 μl 10 x PCR Buffer (TaKaRa®)

12,80 μl dNTP (TaKaRa®)

8,00 μl mt primer L14724 (5'- CGAAGCTTGATATGAAAAACCATCGTTG -3') 10 μM

8,00 μl mt primer H15149 (5'- AAAGTGCAGCCCCTCAGAATGATATTTGTCCTCA -3') 10 μM

0,80 μl TaqHS polimerase (TaKaRa®)

120,00 μl divide in eight 0.2 ml PCR tubes (15 μl of PCR mix in each tube) and add 5 μl of each DNA (c = 0,5, 1, 5 and 10 ng/μl) to get final volume of 20 μl



➤ PCR profil

- 94 °C 4 min;
- 94 °C 30 sec, 50 °C 30 sec, 72 °C 45 sec (25 cycles);
- 72 °C 10 min;
- 12 °C (forever)

## PART 2. AGAROSE-GEL ELECTROPHORESIS OF PCR AMPLIFIED MITOCHONDRIAL REGION

- 1) Seal the edges of plastic tray to form a mold and set it on a horizontal section of the bench.
- 2) In an Erlenmeyer flask prepare 120 ml 0,5X TBE buffer and add 1,5 g agarose
- 3) Heat in a microwave oven until the agarose dissolves.
- 4) Cool the melted agarose solution to 60 °C and pour into the mold.
- 5) Set the comb and allow gel to set completely (45 minutes at room temperature).
- 6) Remove the comb carefully
- 7) Mount the gel in the electrophoresis tank and cover with 0,5X TBE buffer to a depth of ~ 2 mm.
- 8) Mix 5 µl of PCR product with 1 µl of 6X Gel-loading Buffer and load slowly this mixture into the slot of submerged gel. Load all samples and DNA size standard.
- 9) Close the lid of gel tank and attach the electrical leads so that the DNAs migrate toward the positiv anode.
- 10) Turn on Power supply (~ 120 V).
- 11) After 30 minutes turn off the electric current and immerse the gel in 0,5X TBE buffer containing gel-red dye (0,5 µg/ml) for 30 minutes.
- 12) Set the gel to UV-transiluminator of DigiGenius® Gel Documentation System and make photo using camera with orange filter and protective shield.

\* Wear nitril gloves at all times when handling liquids or gel!

## PART 3. AUTOMATED DNA SEQUENCING OF PCR AMPLIFIED MITOCHONDRIAL REGION AND GEN BANK COMPARISON OF PCR AMPLIFIED REGION

- 1) To clean-up PCR product from unincorporated primers and degrades unincorporated nucleotides prepare the following reaction mixture per each sample:
  - 5 µl PCR mixture (directly after completion of PCR)
  - 0.5 µl Exonuclease I (Exo I) (10 u)
  - 1 µl FastAP™ Thermosensitive Alkaline Phosphatase (1 u)
- 2) Mix well and incubate at 37°C for 15 min.
- 3) Stop the reaction by heating the mixture at 85°C for 15 min.
- 4) Mix 5ul of purify PCR Product and 5ul of 5uM single PCR primer.
- 5) Close 0.2 ml PCR tubes and pack in a protective cardboard box.
- 6) Make an order on Macrogen web-site ([dna.macrogen.com/eng](http://dna.macrogen.com/eng) → Order → EZ Seq).
- 7) Send samples to Macrogen Inc by DHL or Fedex.
- 8) The sequence results shall be delivered to the email address as .ab1 files
- 9) Launch Genius® software and import .ab1 files
- 10) Click two .ab1 files that represent different (complementary) strands of the same DNA sequence and assemble them in a consensus sequence.
- 11) Save consensus sequence as a .txt file
- 12) Open BLASTN (<https://blast.ncbi.nlm.nih.gov>) and paste consensus sequence.txt file.
- 13) Click BLAST and search nucleotide databases using a nucleotide query.



**Mend  
The  
Gap**



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Workshop - Archaeobotany & Integration of Genetics with Archaeobotany/12.-13.06.2017/

### References:

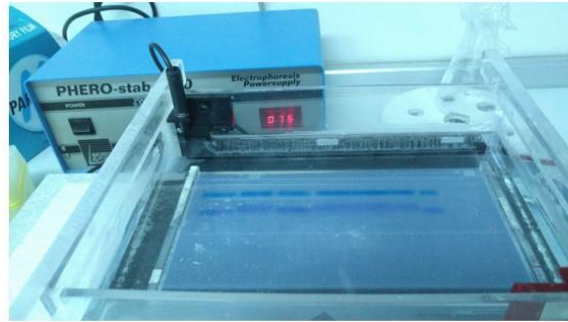
- 1) <https://blast.ncbi.nlm.nih.gov>
- 2) Rodríguez et al 2009. Cytochrome b Phylogeography of Chamois (*Rupicapra* spp.). Population Contractions, Expansions and Hybridizations Governed the Diversification of the Genus. *Journal of Heredity* 100(1):47–55.
- 3) Sambrook and Russell 2001. Detection of DNA in agarose gel. In: *Molecular Cloning – A Laboratory Manual*, Third Edition, 5.14-5.17. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.



## Laboratory equipment and accessories used for mitochondrial DNA analysis



ProFlex® PCR System



Agarose-gel Electrophoresis



Geneious® Bioinformatics Software



DigiGenius® Gel Documentation System



Micropipette Set