Genome-wide assesment of inbreeding (F_{ROH}) in Pag sheep

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AIM & CONCLUSION

The study aimed to examine genomic inbreeding with the runs of homozygosity (ROH) in the population of Pag sheep

The results have important practical contribution - they provide the baseline for implementation of the optimum contribution selection (OCS)

Conservation of the Pag sheep - development of "pipelines" for calculation and inclusion of F_{ROH} in the routine genetic (genomic) evaluation following the basic principles of OSC

Figure 1. Pag sheep

Figure 2. Flock of Pag sheep

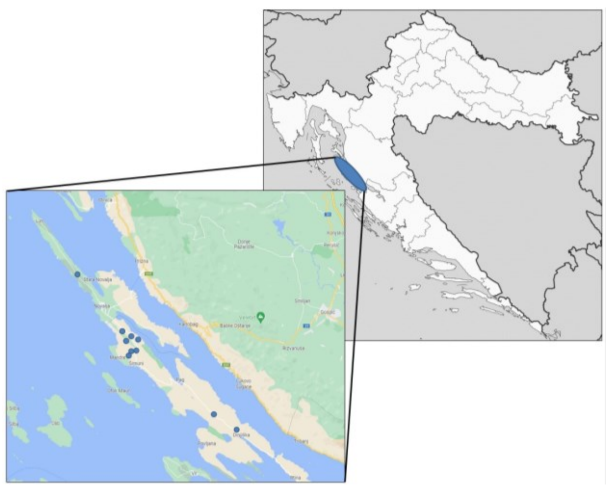

Figure 3. Sampling area (location of flocks)

MATERIAL

- Pag sheep – autochthonous breed
- 749 genotyped animals (Ovine SNP50 BeadChip) from 10 flocks
- QC: autosomal SNPs only
  call rate: SNP 0.05 & animal 0.10
  GC score: >0.7
- 705 animals and 49,079 SNPs

METHODS

- PLINK
  - Quality control analysis
  - Detection of the ROH segments with different size
  - Large ROH segments (>5Mb) considered
- R programme
  - Post hoc analysis i.e. estimation of genomic FROH (>5Mb)

$$F_{ROH(>5Mb)} = \frac{\sum_i L(ROH_i)}{L\,(total\ length\ of\ genome\ covered\ by\ SNP)}$$

RESULTS

- Individual F_{ROH} (>5Mb)
  - From 0.002 to 0.363
  - Mean – 0.026
- Mean flock F_{ROH} (>5Mb)
  - From 0.012 to 0.058

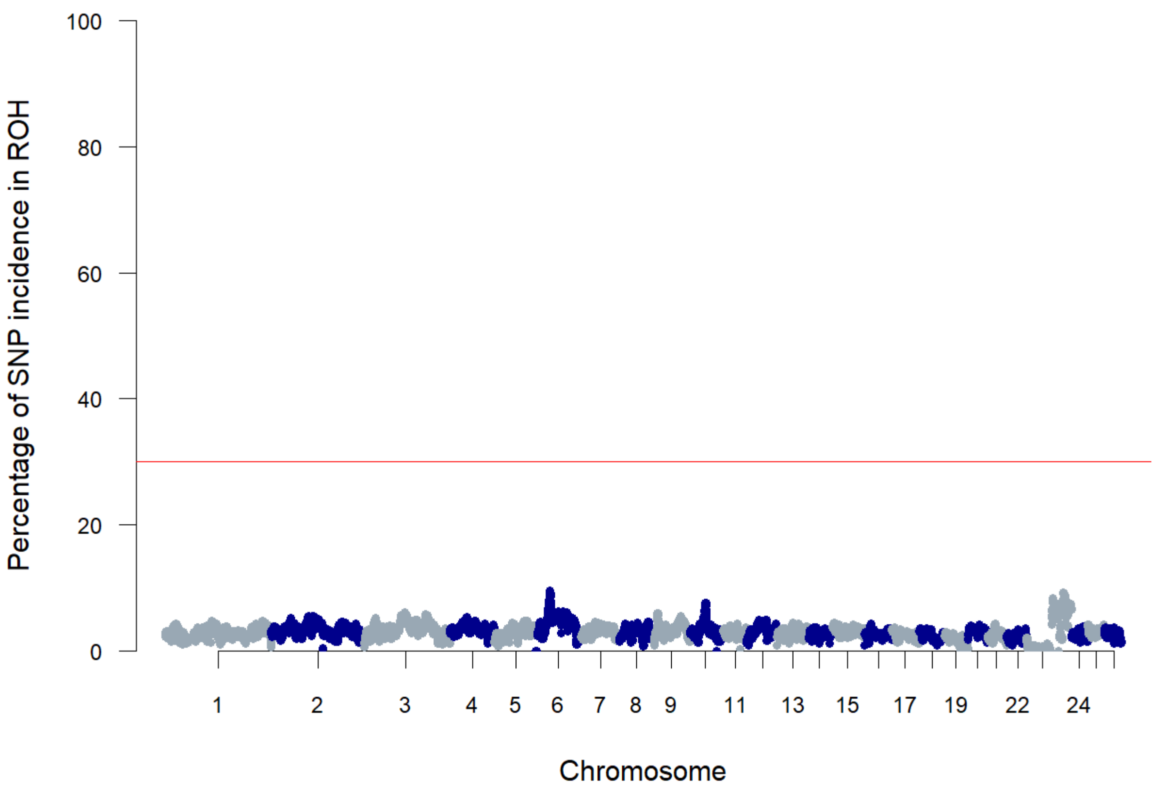

Figure 4. ROH incidence plot in Pag sheep with the threshold for SNP incidence in ROH with a p-value ≥ 0.999

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