





Genomic inbreeding in Istrian sheep – baseline for optimum contribution selection

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INTRODUCTION

- Istrian sheep (native)
 - Milk & meat production
 - Herdbook (N=1,302)
 - Dairy production traits

Runs of homozygosity (ROH)

- Stretches of homozygous genotypes \rightarrow inhereted from commom ancestor
- Segments size:
 - Long (recent) vs. Short (ancient)







AIM

- Estimate genomic inbreeding (F_{ROH}) in Istrian sheep:
 - Individual level F_{ROH}
 - Overall population F_{ROH}
 - Within flock F_{ROH}

MATERIAL & METHODS (1)

• 719 Istrian sheep \rightarrow 11 flocks \rightarrow OvineSNP50 BeadChip



- PLINK software
 - Autosomes
 - Quality control: _
 MAF<0.05
 Call rate: SNP 0.10 & animal 0.05

GC>0.7, GT>0.4

& animal 0.05 656 sheep 38,351 SNPs

MATERIAL & METHODS (2)

• Defining sliding window (Lencz et al. 2007, Purfield et al. 2012)

- No SNP window (44); No het (0) & No miss SNP (1)
- Identifying ROH (Ferenčaković et al., 2013; Meyermans et al., 2020)

 $log_{e} \overline{n_{s} n_{i}}$

- Homozyg Length (1 Mb); SNP ROH density (1 SNP/250 Kb)
- SNP gap (1 Mb);
 Homozyg minSNP (44)
- Homozyg het (0);
 Homozyg miss SNP (0)

• $F_{\text{ROH (>4Mb)}} = \frac{\sum_{i} lenght (ROH_i)}{L (total length of genome covered by SNP)}$

RESULTS

• F_{ROH (Individual)} = 0.002-0.382

- F_{ROH (breed)} = 0.068
- $F_{\text{ROH (flock)}} = 0.024 0.124$
 - $-F_{ROH} = 0.114$



$RESULTS \rightarrow \text{next step...}$

genomic inbreeding → checking inbred segments → signals of selection



CONCLUSION

- Istrian sheep $F_{ROH} \rightarrow 6.8\%$
 - close conventionally accepted level 6.25%
- First insights into genomic inbreeding \rightarrow
 - a clue to search selection signals
 - to set up the baseline for the Optimum Contribution Selection
 - (selection progress & minimall loss of genetic diversity)



This research was funded by the Croatian Science Foundation (Genomic characterization, preservation, and optimum contribution selection of Croatian dairy sheep, OPTI-SHEEP), under grant number IP-2019-04-3559.



Thanks to Department of Agriculture of Republic of Croatia, Regional office HAPIH Pazin, AZRRI, and Istrian sheep breeders