



Genomic inbreeding between flocks in Istrian Sheep

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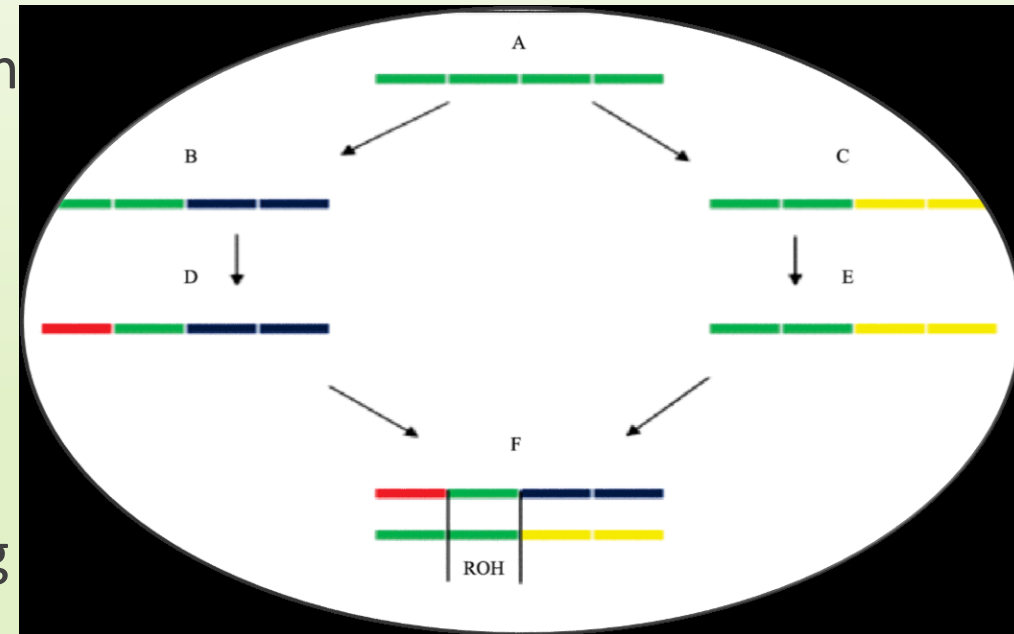
INTRODUCTION

- Istrian sheep
 - Croatian local breed
 - Milk & meat production
 - Herdbook: 1,100 animals
- Local (native) breeds
 - Genetically very diverse
 - Represent a valuable reservoir of genes
 - Often small populations → inbreeding = challenge



INTRODUCTION

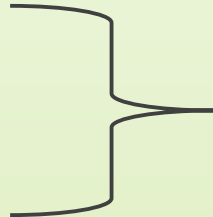
- Inbreeding
 - May affect fitness and decrease production
 - $\text{SNP} \rightarrow \text{ROH} \rightarrow F_{\text{ROH}}$
- Runs of homozygosity (ROH)
 - Useful to effectively estimate inbreeding
 - Longer ROH segments = recent inbreeding
 - Shorter ROH segments = ancient inbreeding



AIM

- Quantify genomic inbreeding of Istrian Sheep from the ROH segments at:

- Population level
- Flock level



preliminary step to optimum
contribution selection (OCS)



MATERIAL & METHODS

○ 719 Istrian sheep → 10 flocks → OvineSNP50

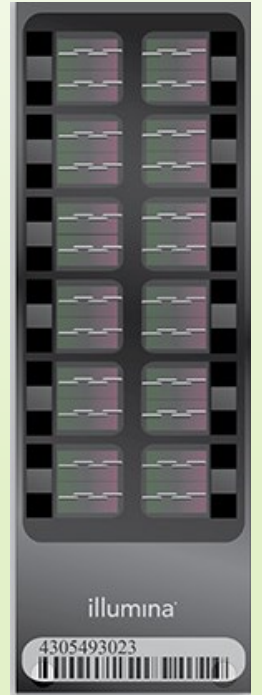
○ Quality control:

- Only autosomal SNPs were used
- GC >0.7
- GT >0.4

PLINK v1.90 software

- SNP call rate $\geq 90\%$
- Minor allele frequency (MAF) $\leq 5\%$
- Animals displaying $\geq 5\%$ missing genotypes

656 animals
38,351 SNPs



MATERIAL & METHODS

- ROH → PLINK v1.90 software
 - Sliding window (*Lencz et al. 2007, Purfield et al. 2012*)
 - No SNP window (44); No het (0) & No miss SNP (1)
- ROH identification: (*Ferenčaković et al., 2013; Meyermans et al., 2020*)
 1. The minimum length constituting ROH was set to 1 Mb
 2. At least 44 homozygous SNPs were included in a ROH
 3. The maximal gap between adjacent SNPs was 1 Mb
 4. A minimum density of a SNP per ROH was 1 SNP per every 250 Kb

$$L = \frac{\log_e \frac{\alpha}{n_s n_i}}{\log_e (1 - \text{het})}$$

MATERIAL & METHODS

- Five ROH length category (*Gorssen et.al. 2021*)
 - 1-4 Mb, 4-8 Mb, 8-16 Mb, 16-32 Mb and >32 Mb
- F_{ROH} was calculated based on the length of ROH segments

$$F_{ROH (>4Mb)} = \frac{\sum_i length (ROH_i)}{L (auto)}$$

- Results obtained from PLINK were analyzed using R (R Development Core Team, 2018)

RESULTS

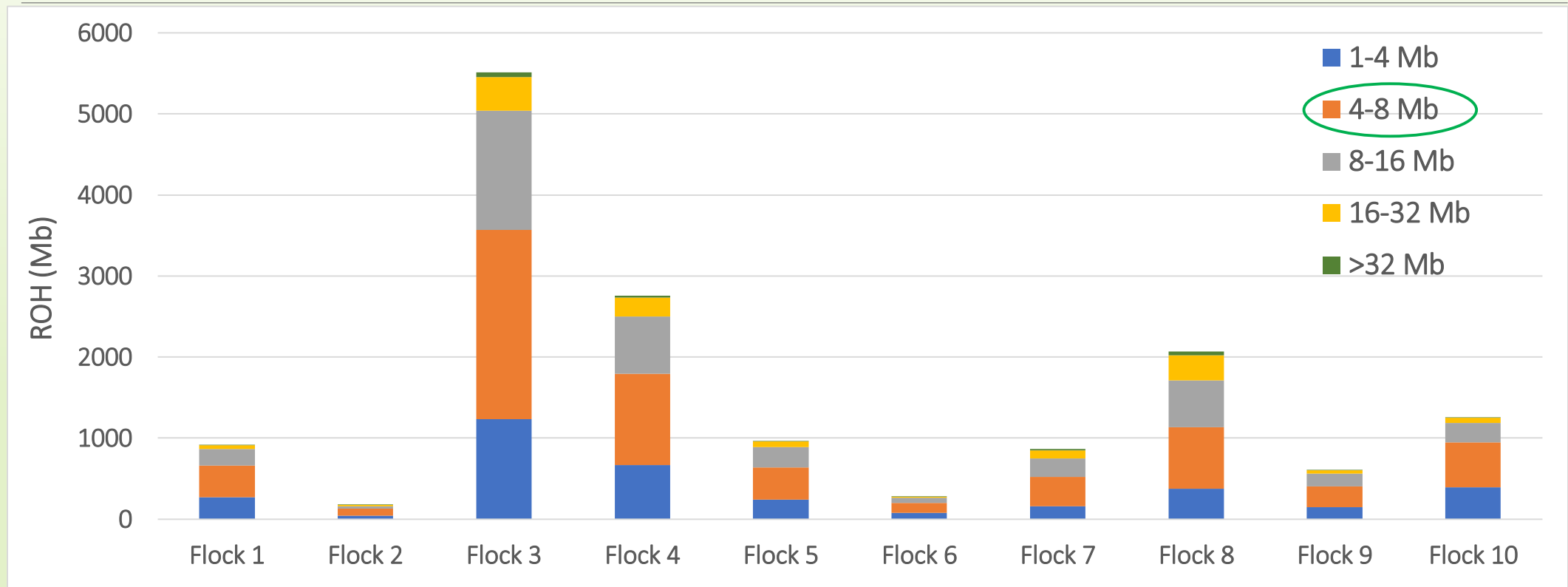
- Total of 15,817 ROH segments (average 24.11 per animal)
- Length of ROH from 1.9 to 70.1 Mb (average 8.12 Mb)

Table 1. Descriptive statistics of ROH analysis in Istrian Sheep

	ROH length categories (Mb)				
	1-4	4-8	8-16	16-32	>32
n ROH	3715	6584	4022	1327	169
% n ROH	23.48	41.63	25.43	8.39	1.07
n Animal	614	626	566	365	102
% Animal	96.6	98.5	89.0	57.4	16.1
F_{ROH}	0.007	0.022	0.029	0.028	0.024

n ROH – number of ROH segments; % – frequency distribution of ROH and animal; n Animal – number of animals; F_{ROH} – ROH coefficient of inbreeding

RESULTS



Graph 1. Classification of runs of homozygosity (ROH) size (in Mb) in five predefined categories in 10 flocks of the Istrian Sheep

RESULTS

Table 2. Genomic inbreeding coefficient F_{ROH} by predefined ROH length category (in Mb) per flock in Istrian Sheep

Flock	n	$F_{ROH\ 1-4}$	$F_{ROH\ 4-8}$	$F_{ROH\ 8-16}$	$F_{ROH\ 16-32}$	$F_{ROH\ >32}$	$F_{ROH\ All}$
Flock 1	90	0.034	0.009	0.009	0.004	0.001	0.023
Flock 2	7	0.070	0.027	0.019	0.019	0.004	0.075
Flock 3	135	0.011	0.038	0.045	0.025	0.006	0.125
Flock 4	125	0.007	0.012	0.023	0.015	0.003	0.067
Flock 5	51	0.006	0.017	0.020	0.012	0.002	0.060
Flock 6	9	0.010	0.031	0.028	0.010	0.002	0.080
Flock 7	32	0.006	0.024	0.030	0.023	0.008	0.092
Flock 8	58	0.008	0.029	0.042	0.043	0.011	0.132
Flock 9	28	0.006	0.020	0.023	0.011	0.003	0.064
Flock 10	100	0.005	0.012	0.010	0.005	0.001	0.033

n – number of individuals

CONCLUSION

- Relatively high inbreeding
 - Threatens the sustainability of long-term genetic variability
- Estimated inbreeding at the flock level = good information for implementation of OCS
- OCS should provide selection progress of dairy traits with minimal loss of genetic variability

THANK YOU FOR YOUR ATTENTION

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