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Genomic estimation of dominance variance and inbreeding depression in a local sheep breed

Background



Pag sheep
Pag (Island), Croatia
Overall aim is to conserve and implement genomic selection



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Objectives

Estimate additive and dominance genetic variances and genomic inbreeding for milk traits

Materials and methods

50K SNP genotype data, 2134 Pag sheep

- After quality control, 1744 ewes with test-day milk records (milk, fat and protein yields (g))

Imputation (AlphaPeel)

Runs of homozygosity (ROH) with PLINK 1.9 and estimated inbreeding (F_{ROH})

Tested four single trait models (BLUPF90+)

- REML

$$M1 \quad y = X\beta + Z_a a + Z_p pe + e$$

$$M2 \quad y = X\beta + fb + Z_a a + Z_p pe + e$$

$$M3 \quad y = X\beta + Z_a a + Z_d d + Z_p pe + e$$

$$M4 \quad y = X\beta + fb + Z_a a + Z_d d + Z_p pe + e$$

$$y = X\beta + fb + Z_a a + Z_d d + Z_p pe + e$$

Milk records (milk, fat and protein yields in g)

Mean, parity, flock, DIM, year and season

Inbreeding (F_{ROH})

Additive (breeding) values $a \sim N(0, G\sigma_a^2)$ VanRaden (2008)

Dominance deviations $d \sim N(0, D\sigma_d^2)$ Vitezica et al. (2013)

Permanent environment $pe \sim N(0, I\sigma_{pe}^2)$

Residual $e \sim N(0, I\sigma_e^2)$

Table 1: Phenotype and inbreeding means

	Mean	Standard error
Test-day milk yield (g)	818.5	4.2
Test-day fat yield (g)	58.6	0.3
Test-day protein yield (g)	47.7	0.2
F_{ROH} (%)	1.9	0.04

Acknowledgements

Conclusions

Genomic data allowed us to estimate additive and dominance variance and inbreeding

Results contribute to developing sustainable genomic selection programmes for small livestock populations

Results

Figure 1: Average number of runs of homozygosity per animal

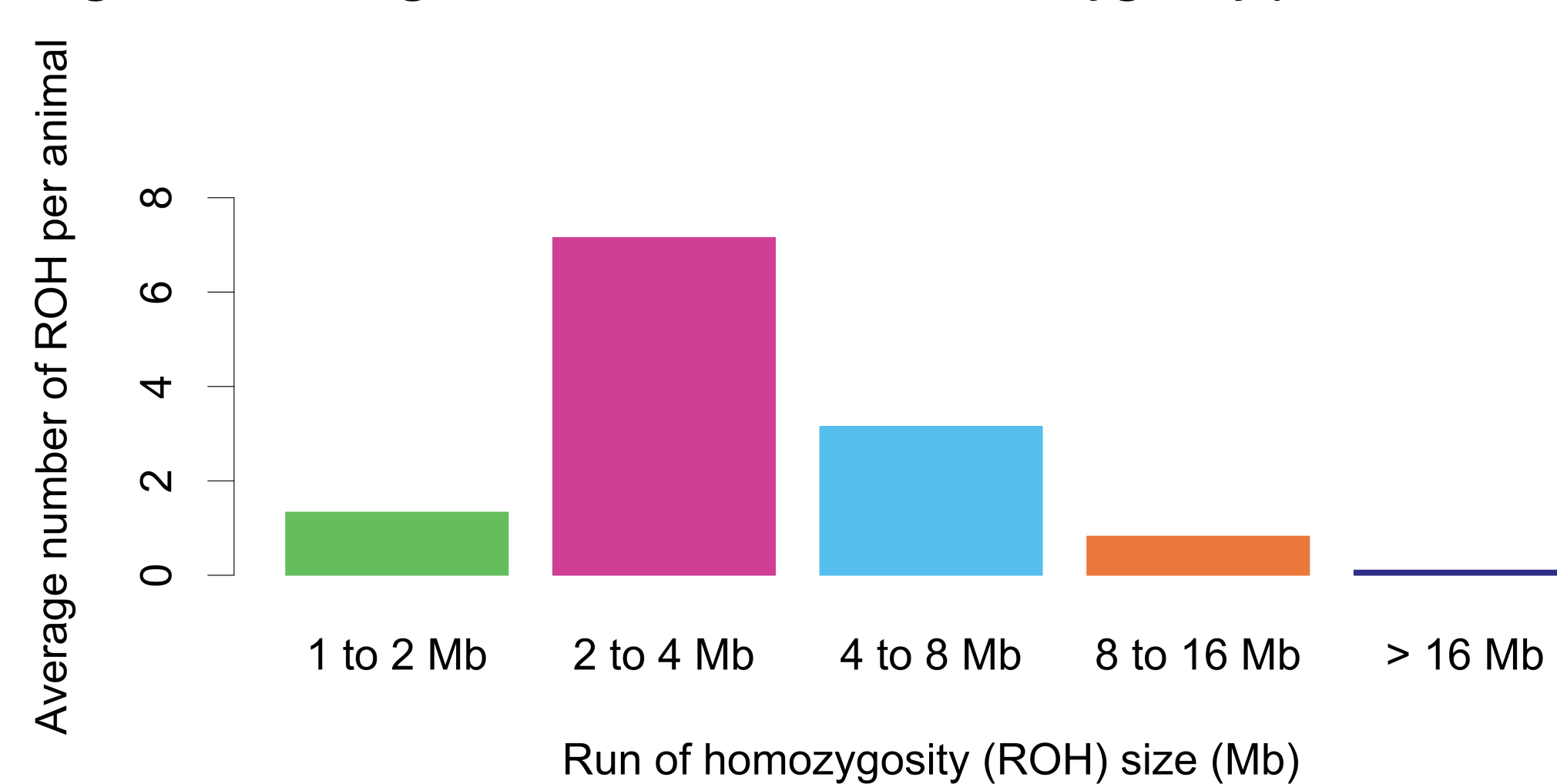


Figure 2: Variance partitioning for milk, fat and protein test-day yields

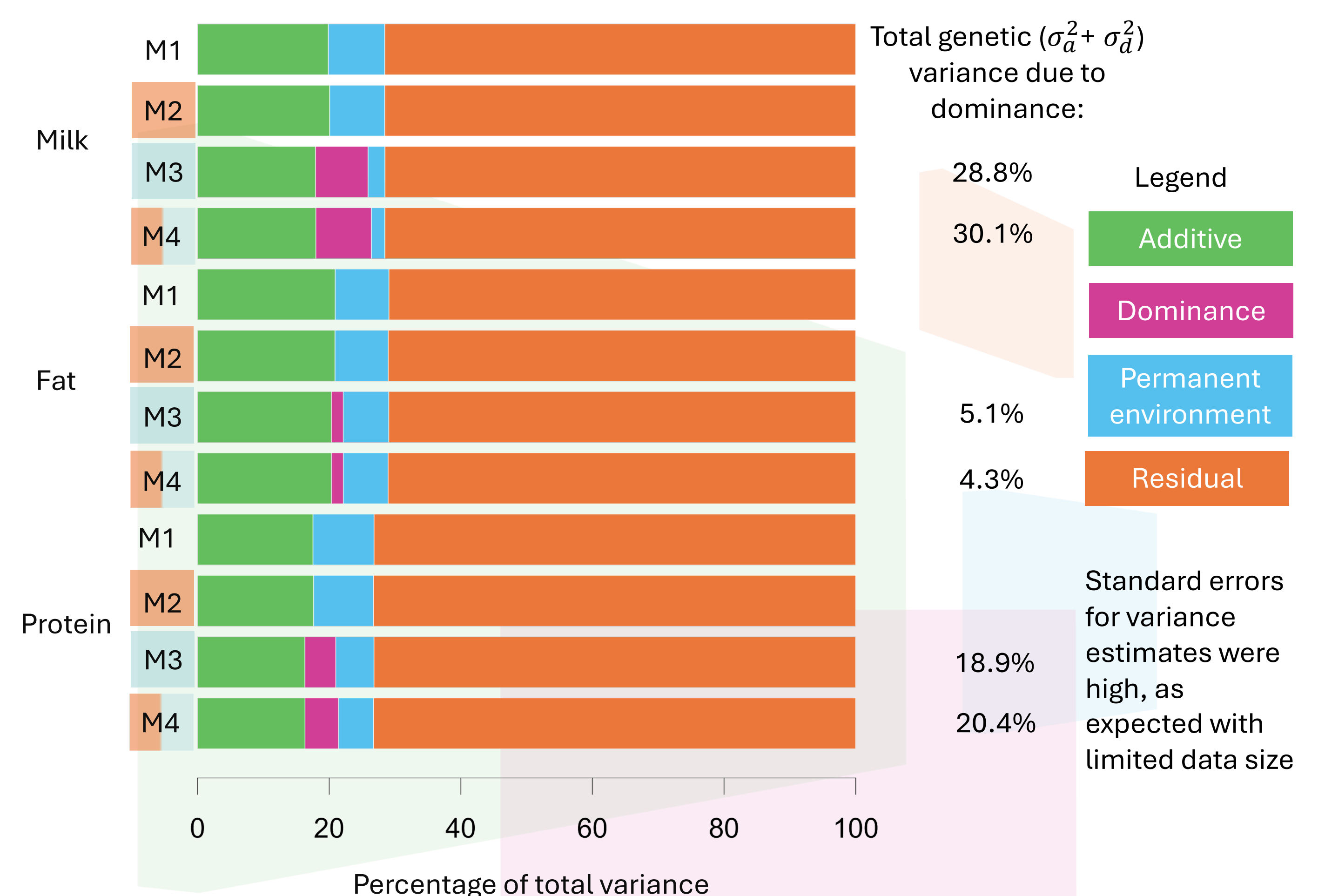


Table 2: Inbreeding depression estimates

	Model	For 1% inbreeding, test-day (1 day)	For 1% inbreeding, whole lactation (150 days)
Milk yield (g)	M2	-2.8	-420
	M4	-3.7	-555
Fat yield (g)	M2	-0.2	-30
	M4	-0.3	-45
Protein yield (g)	M2	-0.2	-30
	M4	-0.2	-30

Work in progress

Understand the genomic landscape of inbreeding through genome-wide association analyses including dominance and ROH

Provide guidance for optimal contribution selection

Investigate impact of dominance on prediction accuracy