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

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Background

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Pag sheep

Pag (Island), Croatia

Overall aim is to conserve and implement genomic selection

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 $\quad \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{pe} + \mathbf{e}$

M2 $\quad \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{fb} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{pe} + \mathbf{e}$

M3 $\quad \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_d\mathbf{d} + \mathbf{Z}_p\mathbf{pe} + \mathbf{e}$

M4 $\quad \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{fb} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_d\mathbf{d} + \mathbf{Z}_p\mathbf{pe} + \mathbf{e}$

$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{fb} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_d\mathbf{d} + \mathbf{Z}_p\mathbf{pe} + \mathbf{e}$

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

Mean, parity, flock, DIM, year and season

Inbreeding (F_{ROH})

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

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

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

Residual $\quad \mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$

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

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

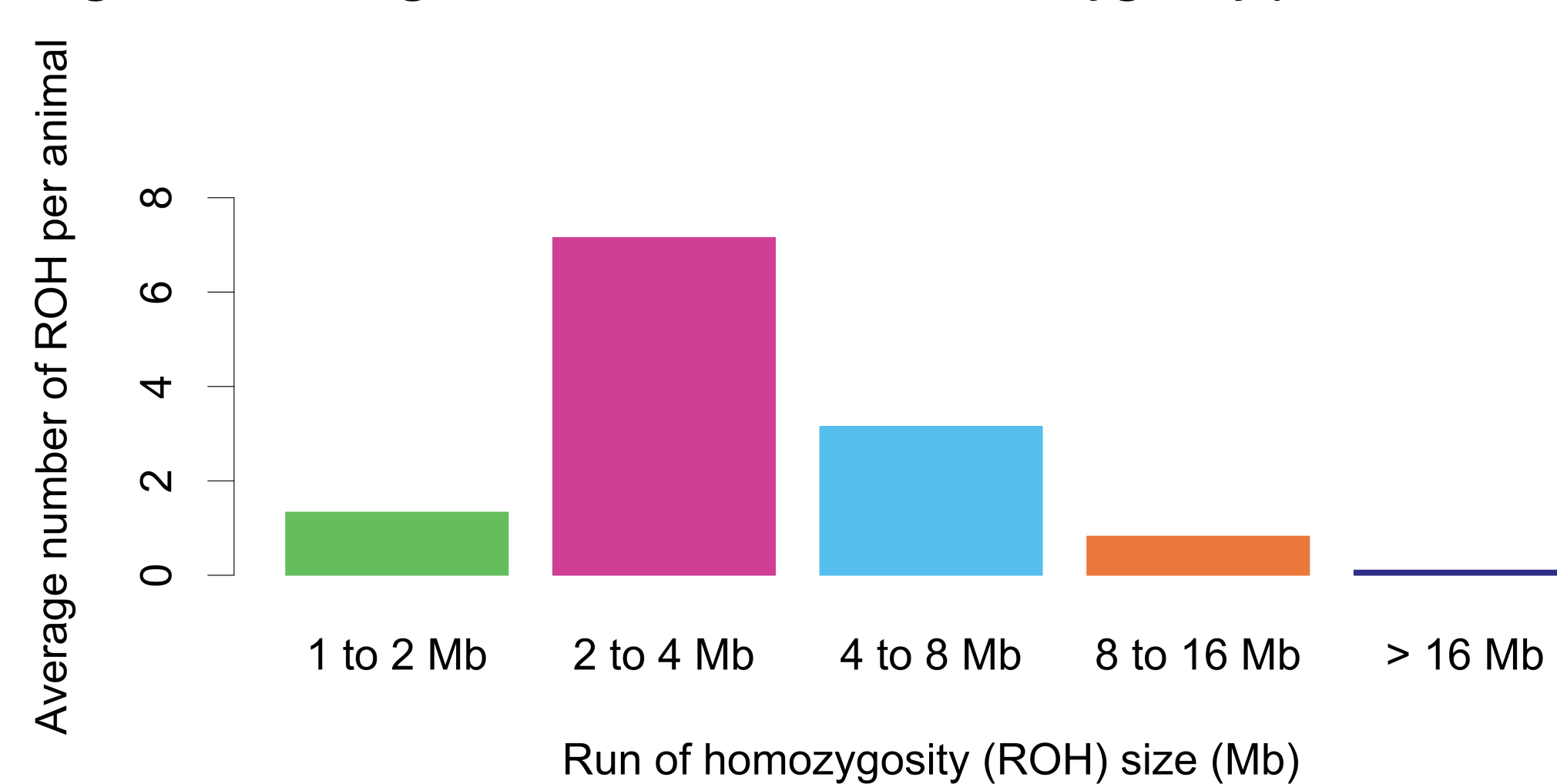Figure 1: Average number of runs of homozygosity per animal

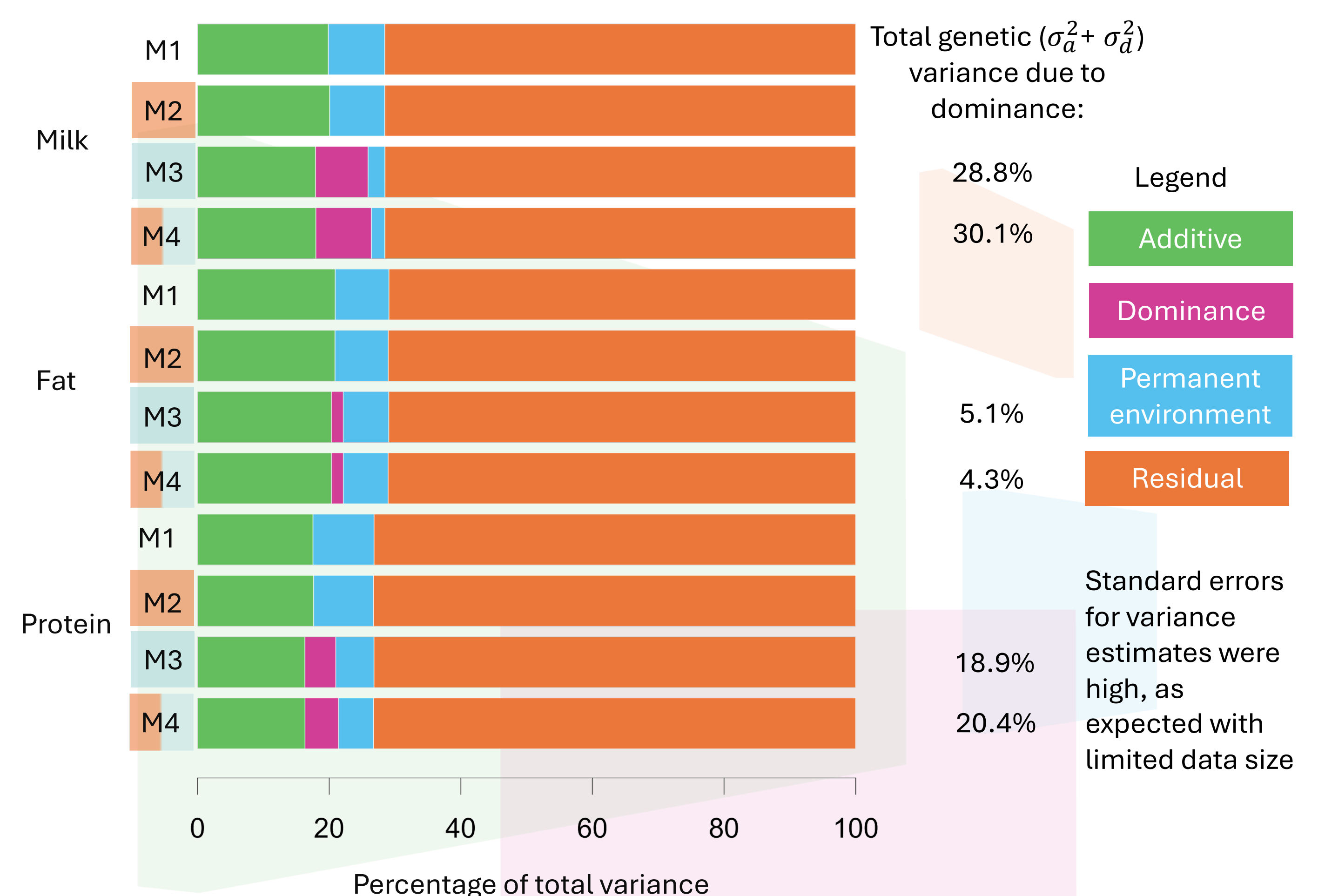Figure 2: Variance partitioning for milk, fat and protein test-day yields

Total genetic ($\sigma_a^2 + \sigma_d^2$) variance due to dominance:

28.8%
30.1%

5.1%
4.3%

18.9%
20.4%

Legend
- Additive
- Dominance
- Permanent environment
- Residual

Standard errors for variance estimates were high, as expected with limited data size

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