

Genomic analysis of dominance and inbreeding effects on milk production traits in Pag sheep

Christina M Rochus, M Špehar, A Kasap, Z Barać, J Ramljak, I Pocrnić



THE UNIVERSITY of EDINBURGH
The Royal (Dick) School
of Veterinary Studies



Biotechnology and
Biological Sciences
Research Council

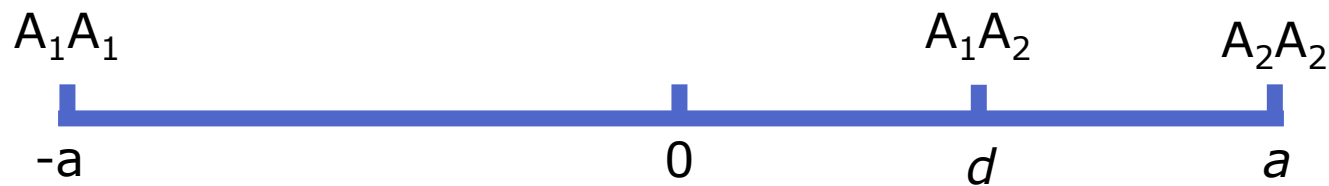
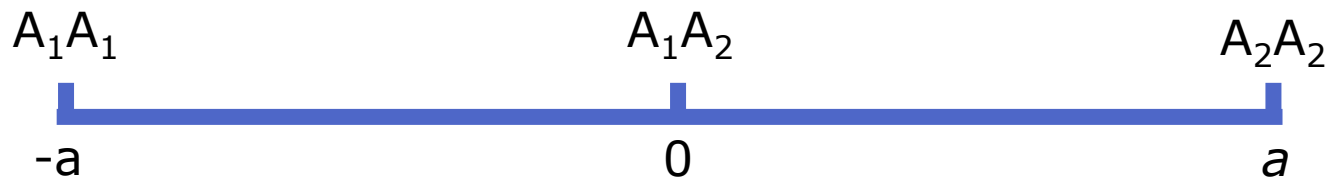


HRZZ
Croatian Science
Foundation



opti-sheep
Project: IP-2019-04-3559

Importance of including inbreeding when estimating dominance




fitness

	A_1	A_2
A_1	A_1A_1	A_1A_2
A_2	A_1A_2	A_2A_2

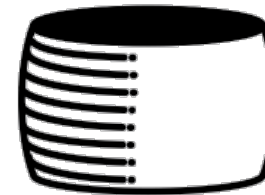
(Falconer and Mackay, 1996)

Pag sheep



Pag (Island), Croatia

Overall aim is to conserve and implement genomic selection



Objectives



For milk, fat and protein yields, and somatic cell score, estimate:

- Additive genetic variance
- Dominance genetic variance
- Genomic inbreeding



Materials and methods

50K SNP genotype data for 2134 animals

- 1744 ewes have milk records (milk, fat and protein yields (kg), and somatic cell score)

Imputation (AlphaPeel)

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

Tested four single trait models (BLUPF90+)

- REML

Backsolve to estimate SNP effects

$$g_a = \frac{1}{2 \sum p_i(1-p_i)} Z'_a G^{-1} \hat{a}$$

$$g_d = \frac{1}{2 \sum (2pq)^2} Z'_d D^{-1} \hat{d}$$

Models tested

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

Mean, parity, flock, DIM, year and season

Inbreeding (F_{ROH})

Additive (breeding) values

$$\mathbf{a} \sim N(\mathbf{0}, \mathbf{G}\sigma_a^2)$$

VanRaden (2008)

Dominance deviations

$$\mathbf{d} \sim N(\mathbf{0}, \mathbf{D}\sigma_d^2)$$

Vitezica et al. (2013)

Permanent environment

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

Residual

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

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

Models tested

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

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

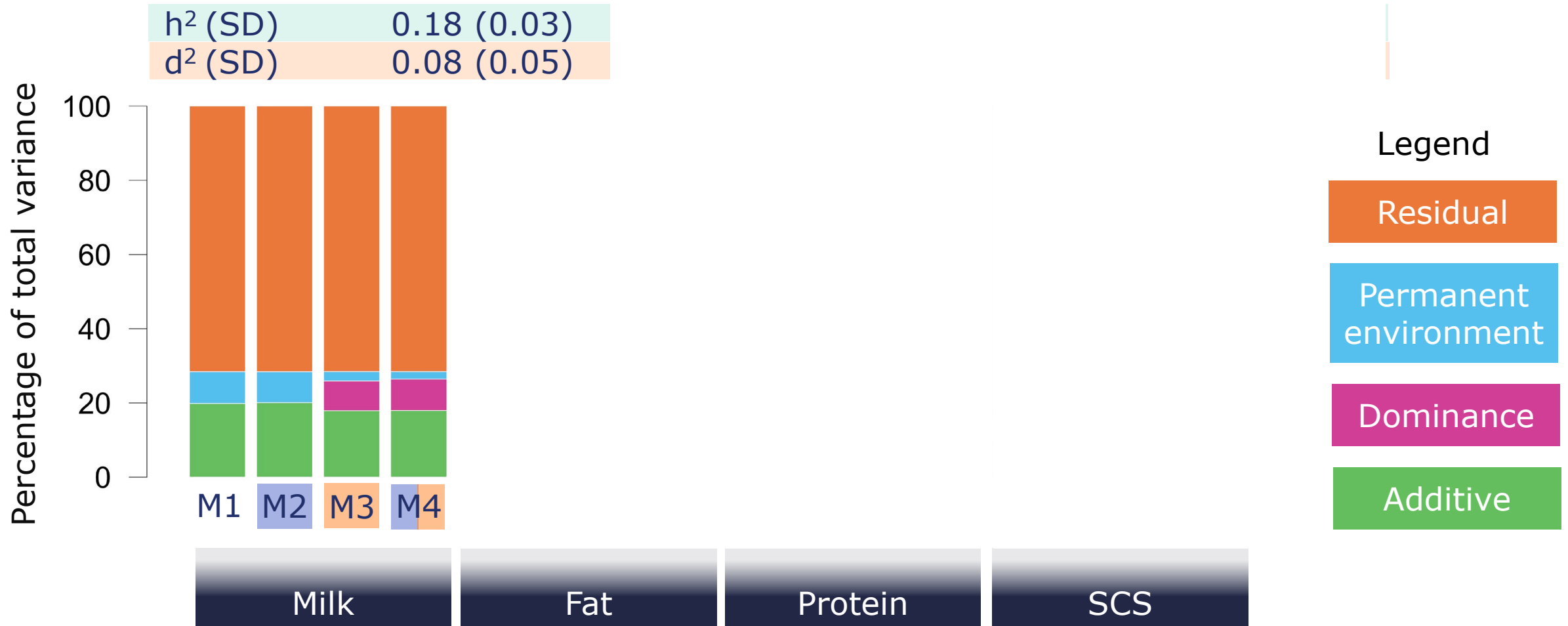
M3 $y = X\beta + Z_a a + Z_d d + Z_p pe + e$

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

Inbreeding

Dominance deviations

Variance partitioning



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

Inbreeding depression



Phenotype and
inbreeding
means

	Mean (SE)
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)
Somatic cell count (SCC)	799.3 (31.1)
F_{ROH} (%)	1.9 (0.04)

Inbreeding
depression
estimates

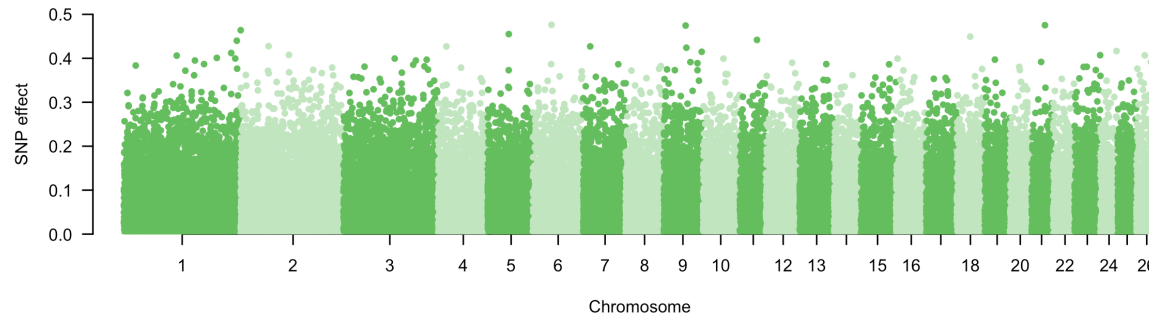
	Model	For 1% inbreeding, test-day (1 day)	For 1% inbreeding, whole lactation (150 days)
Milk yield (g)	M4	-3.7	-555
Fat yield (g)	M4	-0.3	-45
Protein yield (g)	M4	-0.2	-30
SCC	M4	1.0	NA

Genome-wide association analyses

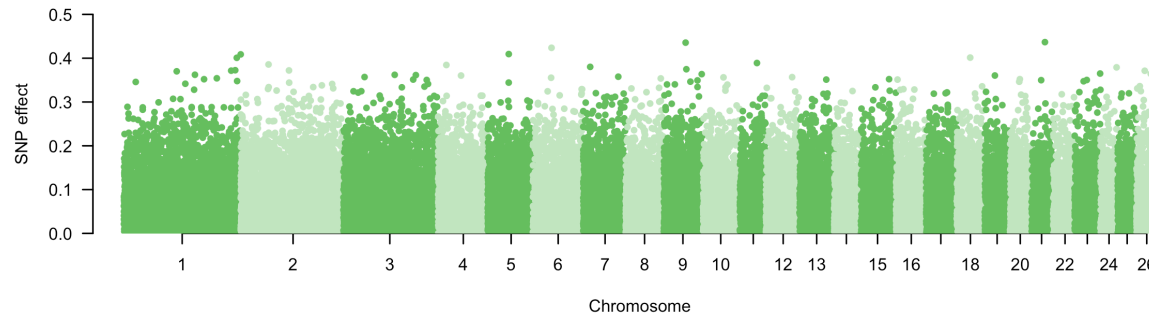


Milk yield

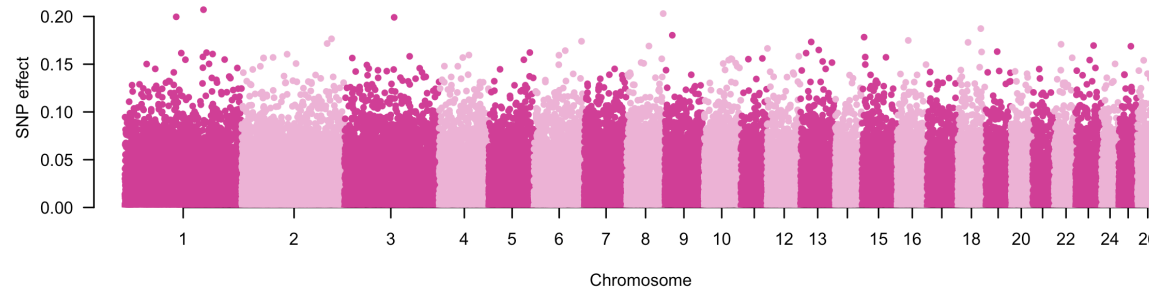
M1
Additive



M4
Additive



M4
Dominance



Future studies:

- GWAS with ROH
- Follow-up all GWAS to identify significant SNPs, and candidate genes
- Investigate impact of dominance on prediction accuracy
- Provide guidance for developing genomic selection and mate allocation programs

Summary

Estimated additive and dominance variance and inbreeding

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



Photos provided by Opti-sheep project



Christina Rochus
crochus@ed.ac.uk 11