The adjusted genomic relationships by allele frequencies within breeds and use in single-step GBLUP

Mahlako Makgahlela[1 2], Ismo Strandén[1 2], Ulrik Nielsen[3], Mikko Sillanpää[4 5] & Esa Mäntysaari[2]

[1]Department of Agricultural Sciences, University of Helsinki, Finland

[2]MTT Agrifood Research Finland, Biotechnology & Food Research, Biometrical Genetics, Finland

[3]Danish Agricultural Advisory Service, Aarhus, Denmark

Departments of Mathematical Science[4], Biology & Biocenter[5], University of Oulu, Finland

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- Simple allele frequencies (AF) across breeds are often used to construct genomic relationship matrix (**G**) in multi-breeds
- Ignoring differences in AF between breeds may result in distorted coefficients in **G**
- Optimal construction of **G**, and its incorporation with the numerator relationship matrix (**A**) may improve single-step GBLUP in multi-breeds

OBJECTIVES

1. To compare the effect of AF within-breeds ($\mathbf{G}_{WB}$) to AF across-breeds ($\mathbf{G}_{AB}$) on **G** in an admixed population, and to compare AF estimated from the genotyped *versus* base population
2. To compare single-step GBLUP validation reliabilties from $\mathbf{G}_{WB}$ and $\mathbf{G}_{AB}$

CONCLUSIONS

- AF within breeds reduced breed differences in **G**, while AF across breeds increased **G** coefficients, markedly for distantly related animals
- $\mathbf{G}_{WB}$ with AF from the base populations was closer to **A**, which simplified the blending of these matrices
- Validation reliabilities were unaffected by AF used to construct **G**

MATERIALS & METHODS

- 4,106 bulls (1971-2006) with genotypes for 38,194 informative markers
- Deregressed proofs (DRP) for 2,816,745 cows
- Pedigree (n=4,624,453), used to estimate bulls' breed proportions

Modification of G with AF within breeds

- Regression of bull genotype on breed proportions was fitted to obtain AF
- $\mathbf{G}_{WB} = \mathbf{ZZ}'/m, \quad \mathbf{Z}_{i,j} \Longleftarrow (u_{ij}-2p_{ij})/sqrt(2p_{ij}(1-p_{ij})),$

m is the No. of markers; u_{ij} is 0, 1 or 2 copies of the 2nd allele and p_{ij} is expected mean AF

Single-step GBLUP

- Cow DRP were fitted as data, weighted by their effective record number
- A unified matrix combined **G** (i.e., $\mathbf{G}_{AB}$ or $\mathbf{G}_{BW}$) and **A**
- Results were compared using Interbull GEBV validation test on young bulls

RESULTS

- Diagonal elements were smaller with $\mathbf{G}_{WB}$ versus $\mathbf{G}_{AB}$
- $\mathbf{G}_{WB}$ coefficients were similar within and across breeds
- $\mathbf{G}_{WB}$ was more correlated (36%) with **A** than $\mathbf{G}_{AB}$ (16%) using AF from the base populations
- Reliabilities were 1-2% higher with $\mathbf{G}_{AB}$ than $\mathbf{G}_{WB}$

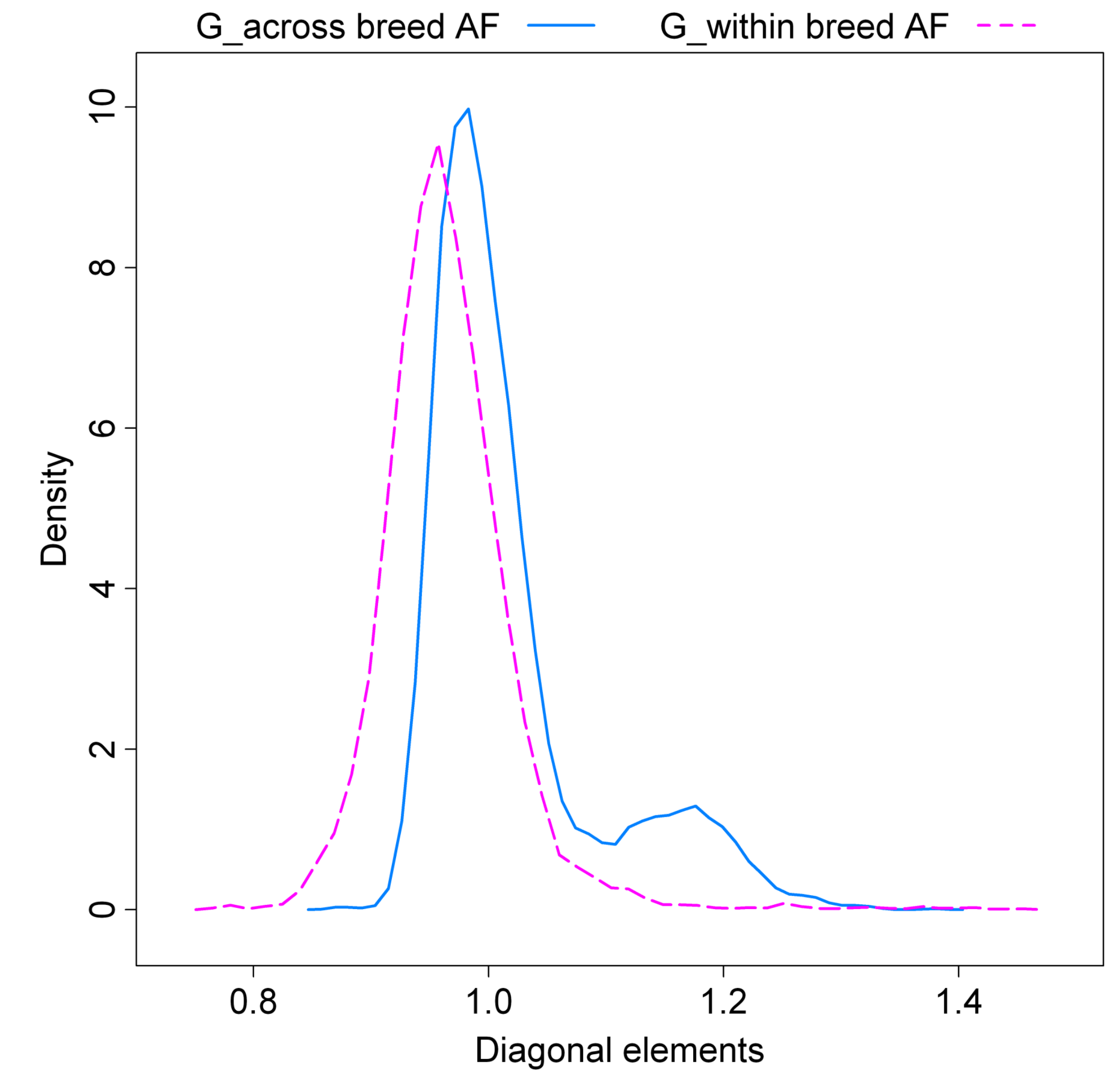

Fig. 1 Distributions of diagonal elements with allele frequencies (AF) estimated from the genotyped population

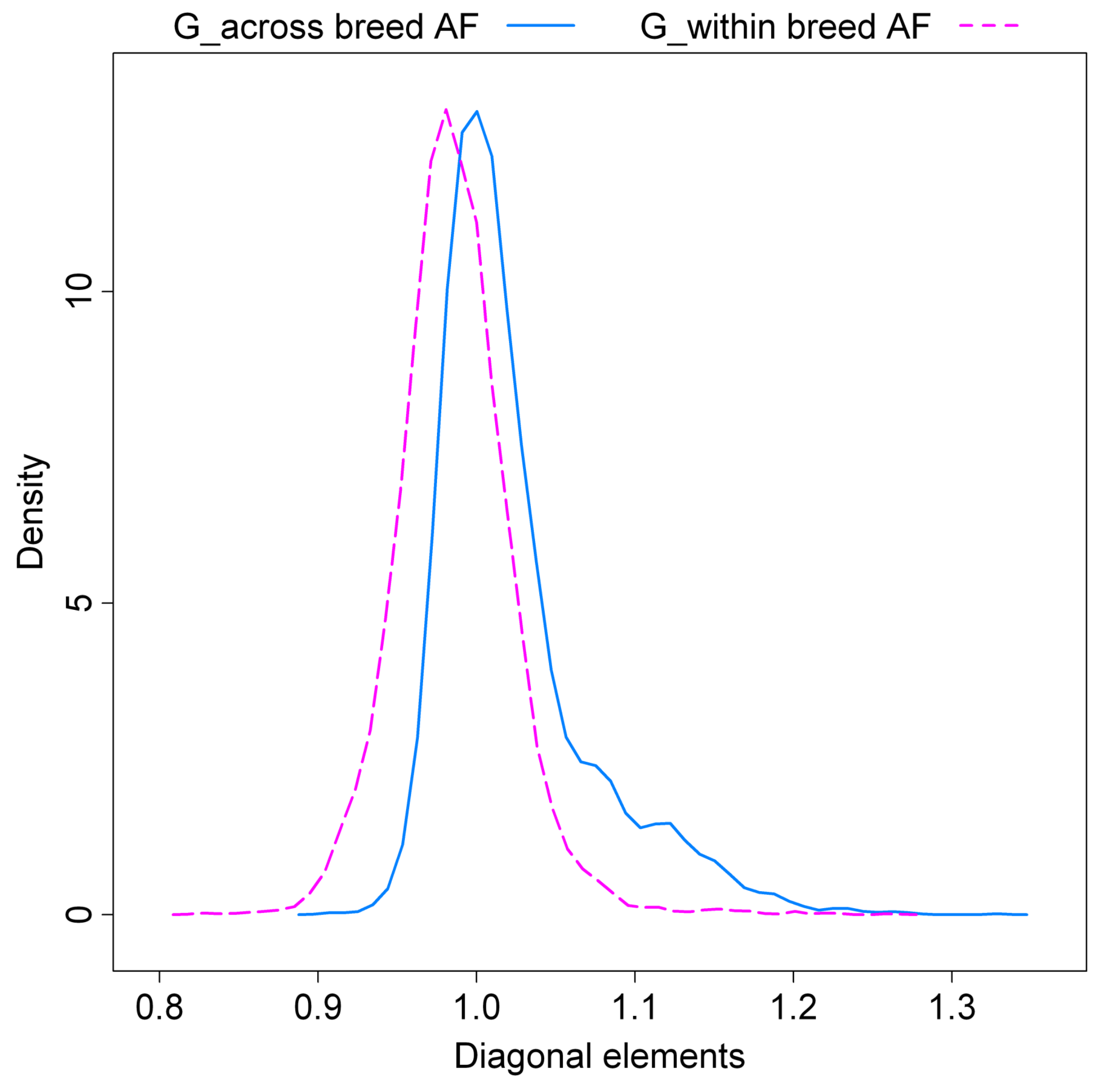

Fig. 2 Distributions of diagonal elements with allele frequencies (AF) estimated from the base population

Validation reliabilities (R^2_{BV}) and regression coefficients (b_1) of breeding values

Method	Milk		Protein	
	b1	R^2_{BV}	b1	R^2_{BV}
Genotyped AF				
$\mathbf{G}_{AB}$	0.77	0.37	0.90	0.40
$\mathbf{G}_{WB}$	0.75	0.36	0.88	0.39
Base AF				
$\mathbf{G}_{AB}$	0.76	0.37	0.86	0.40
$\mathbf{G}_{WB}$	0.72	0.36	0.78	0.38

Reference: Makgahlela et al. (2013) J. Dairy Sci. 96:5364-5375