

Determining relatedness between South African and Australian Merino populations according to a genomic relationship matrix and its principal components

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Introduction

- Genomic prediction of breeding value takes place in Australia but not in South Africa (SA)
- Combining genomic resources across countries could benefit evaluation of Merinos in SA, depending on relatedness of reference populations in the two countries
- The relatedness of Merino populations across countries was determined by genomic methods

Methods

- Resource flocks (Elsenburg (400), Grootfontein (115), Cradock (127)) and commercial ‘Industry’ animals (41) represented SA Merinos
- Australian samples were grouped by strain: Ultrafine (270), Fine Medium 1 (224), Fine Medium 2 (133) and Strong (291)
- Recent across-country links were all in the Cradock flock
- Four Australian sires were used in 1988, 2 in 1996 and 2 Ultrafine rams in 2002-2003

Results

- Internal relationships for South African flocks were low, but positive
- Australian bloodlines were negatively related
- The highest relatedness was between the Cradock flock and the Australian Ultrafine bloodline (Figure 1)
- The first two principal components showed discernable clusters by population group
- More distant separations were seen for the Fine Medium 1 and Strong lines
- The SA Cradock flock plotted close to the Australian Fine Medium 2 and Ultrafine bloodlines (Figure 2)

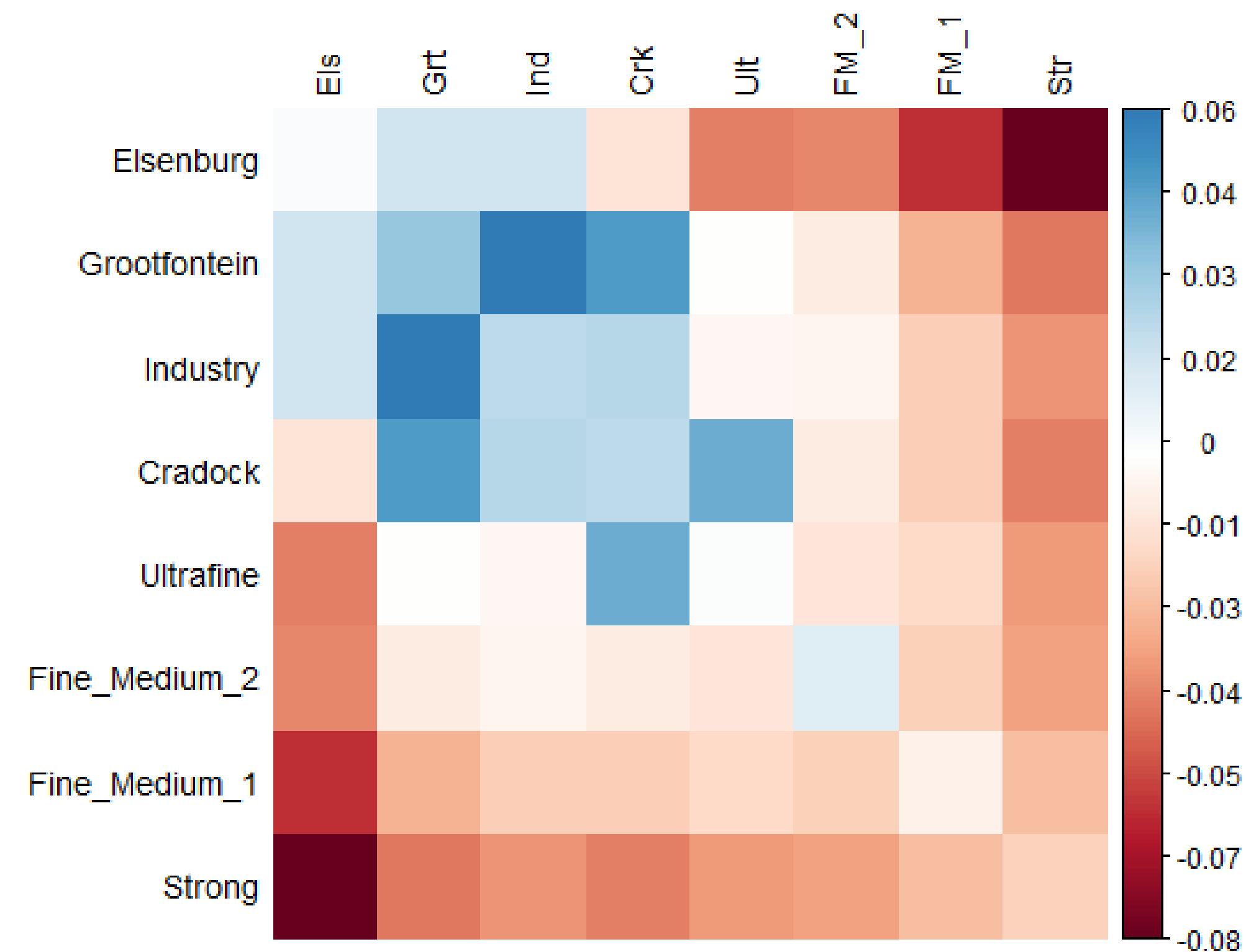


Figure 1 – Relatedness across populations according to mean values of the GRM. The diagonal of the figure represents mean relatedness to all other populations.

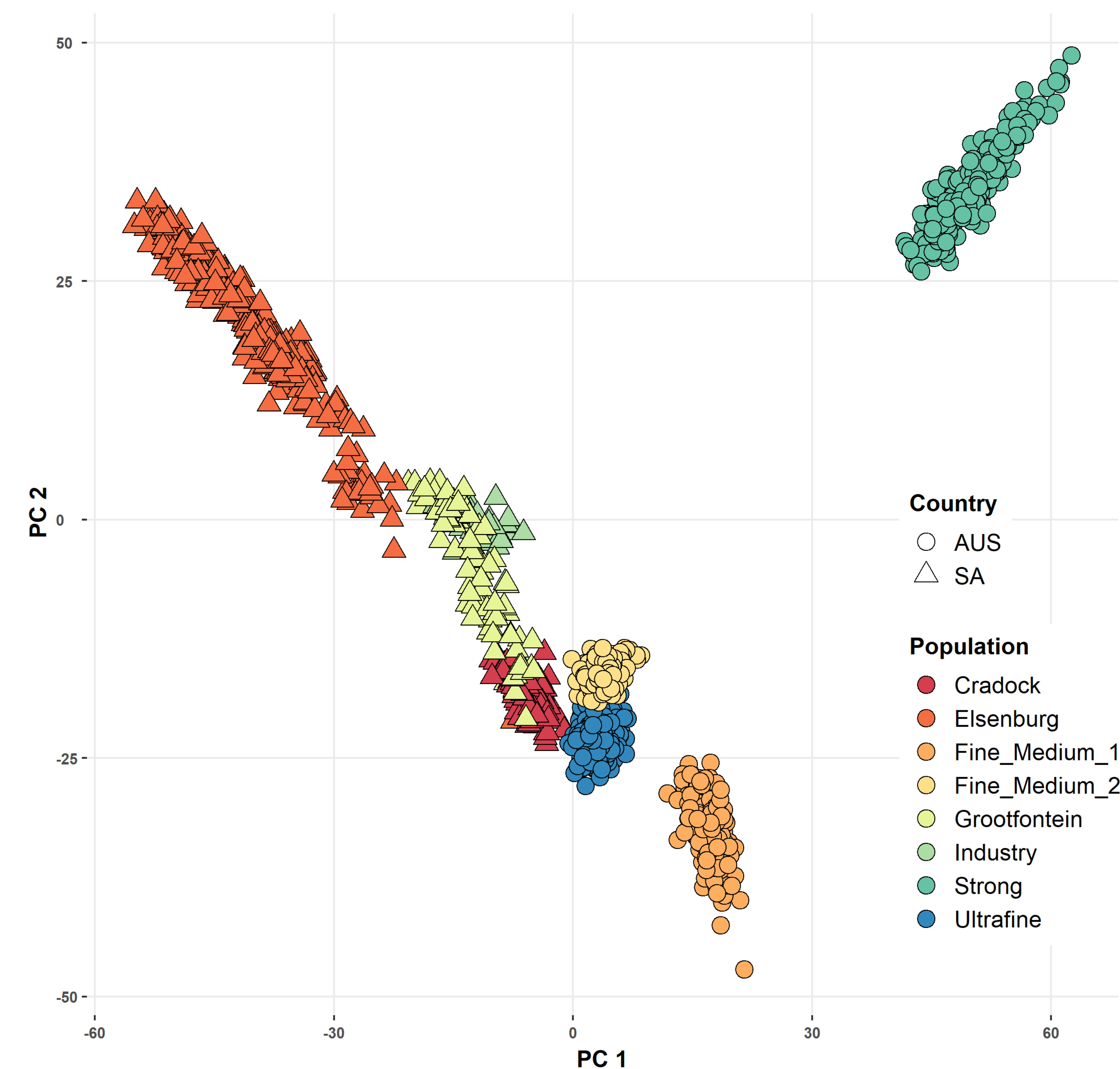


Figure 2 – The first (PC1) and second (PC2) principal components of the GRM with animals identified by flock and country of origin.

Conclusions

- The relatedness among Merinos by country and subpopulation expanded knowledge of within-breed genetic variation
- Across country relationships between un-linked flocks were generally low, and cases of recent linkage was an important factor in these measures of relatedness
- Research in across-country genomic prediction is recommended