Genomic tools for use in the New Zealand deer industry

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Introduction

- New Zealand (NZ) deer are farmed for venison & velvet.
- DNA markers have been used for NZ deer since late 1980's for breed and parentage. Deer behaviour prevents manual recording of pedigree at birth.
- Since 2017 genotyping-by-sequencing (GBS) has been used as the marker system.
- These data allow various genetic analyses.

Aim

Show how low-depth GBS data can support faster genetic progress in the New Zealand deer industry.

Methodology

- **Animals**: Invermay herd, 554 calves born 2018 plus parents. Add 109 breed standards and 4949 random industry animals for breed analysis.
- GBS:
  Hiseq2500 → UNEAK [6] → SNP catalog
  Hiseq2500 → Tagdigger [2] → Allele counts
  Check & combine results from same animal
- Population structure and breed prediction: [3,5]
  Allele counts → KGD → GRM → PCA
- Gender prediction [1] 15 Y, 1006 X SNPs
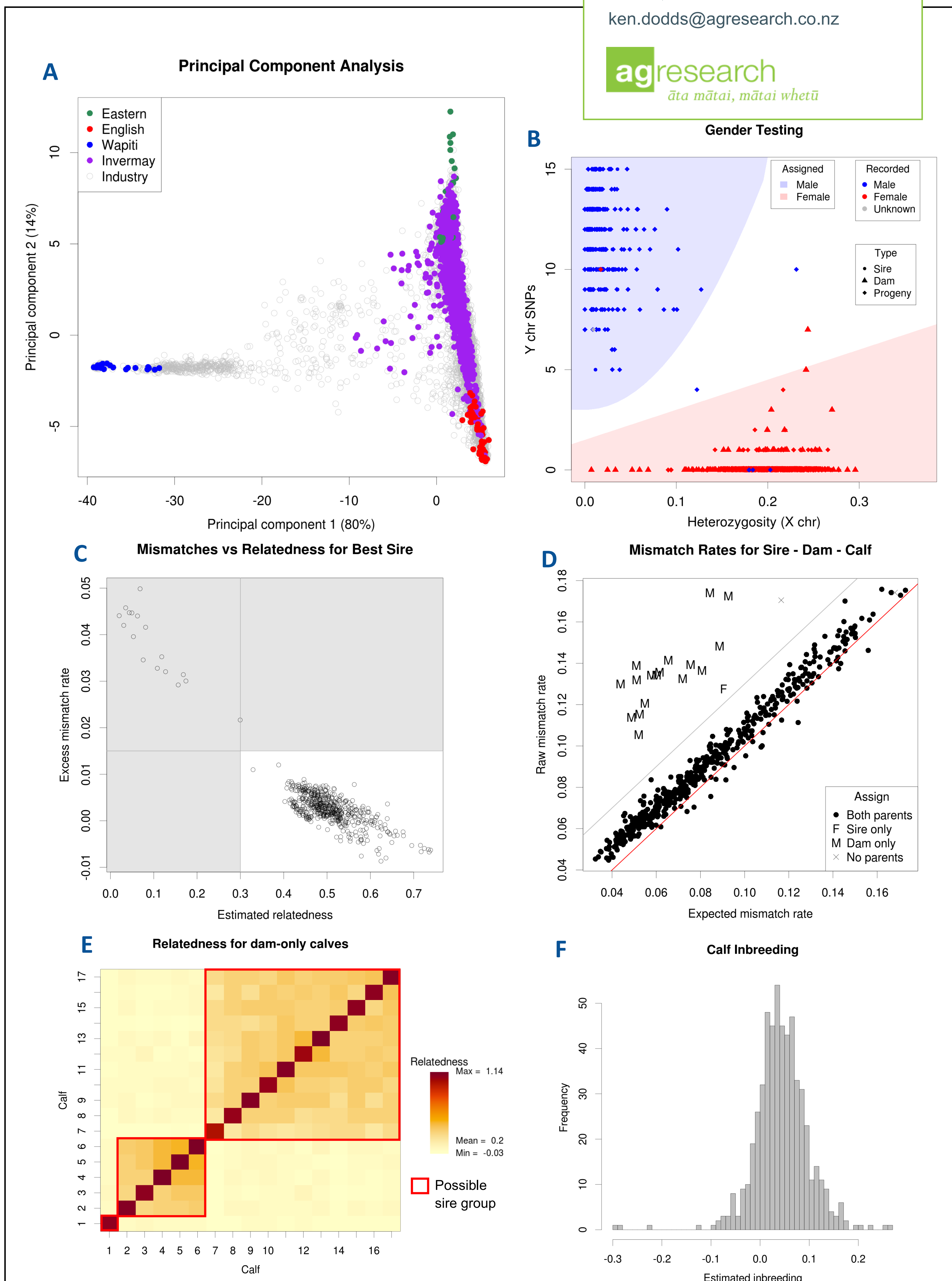- Parentage analysis [3,4] (github.com/AgResearch/KGD)

Results

- SNP catalog: 74,798 SNPs, 66,824 SNPs after filters (MAF >0.01, HW disequilibrium > -0.05). Call rate was 76.9%, mean depth was 3.37.
- PCA separates breed types (**A**). Mean (range) for Invermay animals was 58 (4-91) % Eastern, 39 (7-96) % English and 3 (0-19) % Wapiti.
- Gender (**B**): Parent gender confirmed, except 1 dam. Four calves had gender corrected (1 confirmed, 3 unavailable).
- Parentage (**C, D**). Sire + dam: 535 calves; dam only: 17 calves; sire only: 1 calf; neither parent: 1 calf.

References with doi

[1] Bilton (2019) 10.1111/age.12782
[2] Clark (2016) 0.1186/s13029-016-0057-7
[3] Dodds (2015) 10.1186/s12864-015-2252-3
[4] Dodds (2019) 10.1534/g3.119.400501
[5] Kuehn (2011) 10.2527/jas.2010-3530
[6] Lu (2013) 10.1371/journal.pgen.1003215

A — Principal Component Analysis

B — Gender Testing

C — Mismatches vs Relatedness for Best Sire

D — Mismatch Rates for Sire - Dam - Calf

E — Relatedness for dam-only calves

F — Calf Inbreeding

Discussion

- Wapiti and Red deer genetically very different (**A**). Some Wapiti ancestry in Invermay herd. Breed proportions can be used in national evaluations.
- Gender can be checked/assigned with parentage test.
- Relatedness estimates low - influenced by breeds and estimated allele frequencies; low thresholds used (**C**). Possibly 2-3 true sires missing (**E**).
- Inbreeding estimates available (**F**) - provides an alert to breeding program. Not constrained to [0,1]. Negative estimates due to parents of different breeds.
- Genomic relatedness allows genomic prediction and association analysis.

Conclusion

1988 isozymes
- breed
- parentage (from 1990)

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1994 Microsatellites
- breed
- parentage

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2017 GBS
- breed
- parentage
- gender
- GRM
- Genomic selection, GWAS ...