Admixture and Genomic Predictions in Danish Jersey

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# Genomic selection in a Small Breed

- Small breed → Small reference population

- Low reliabilities of genomic prediction
  - 0.12 – 0.47 for the traits included in NTM
  - Limited gain compared to parent index selection

- Need for improvement of genomic reliabilities

- Assume homogeneous breed

- Admixed population → Origin specific LD → Origin specific marker effect?

Objectives

- Study the subpopulation structure in Danish Jersey based on pedigree and markers

- Reconstruct the breed proportions based on the markers

- Evaluate the genomic predictions using the population structure in the model

Admixture exists in Danish Jersey

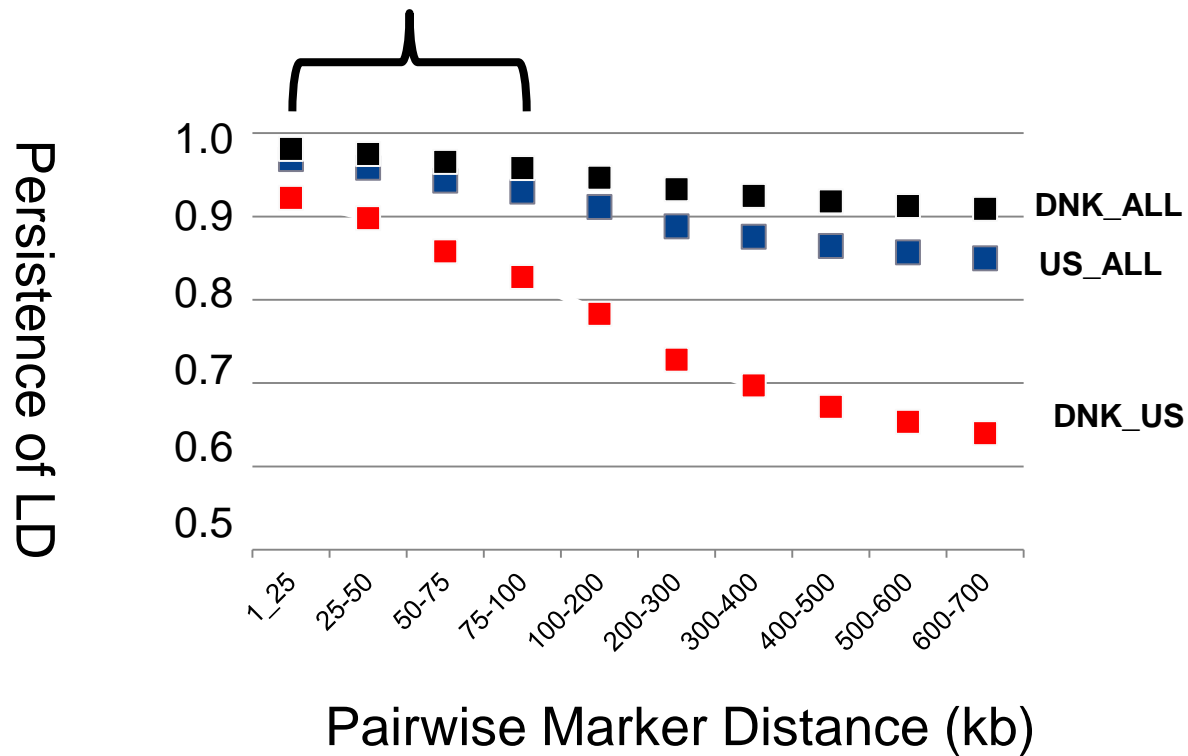Breed proportion for genotyped bulls
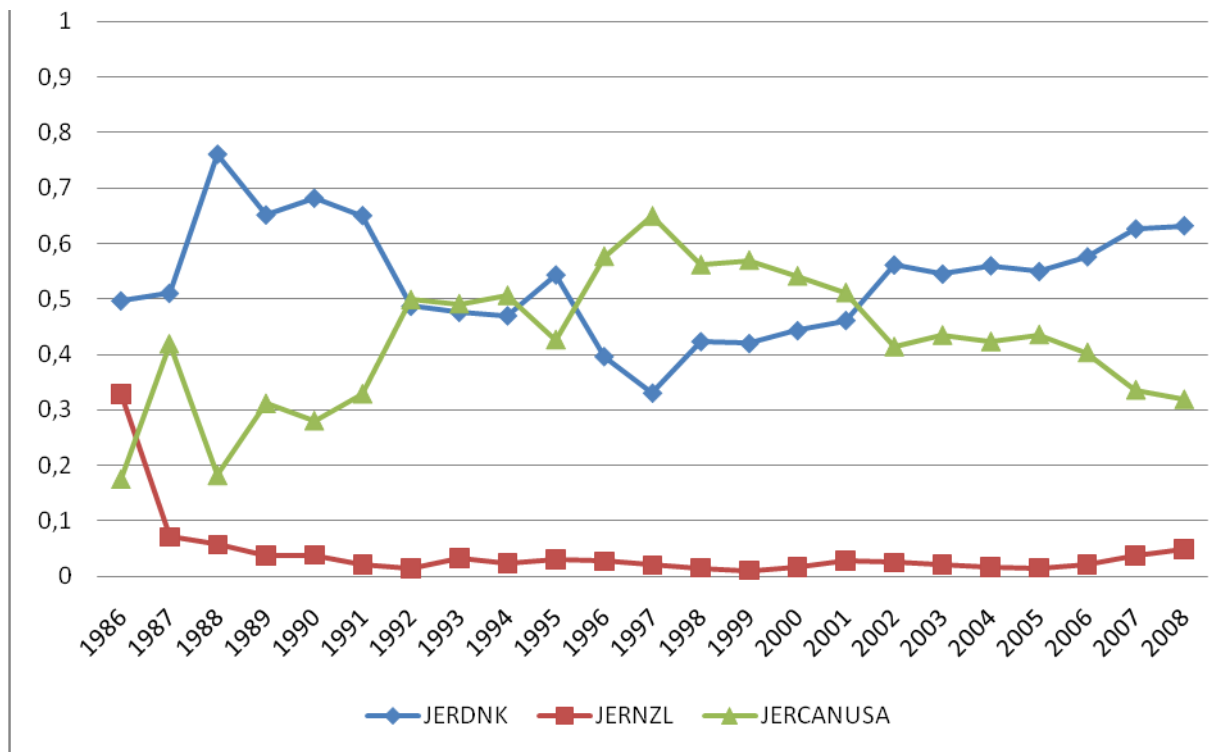
Division into Subpopulations

- ALL - 1730 animals

- DNK - 231 animals >75% DNK pedigree

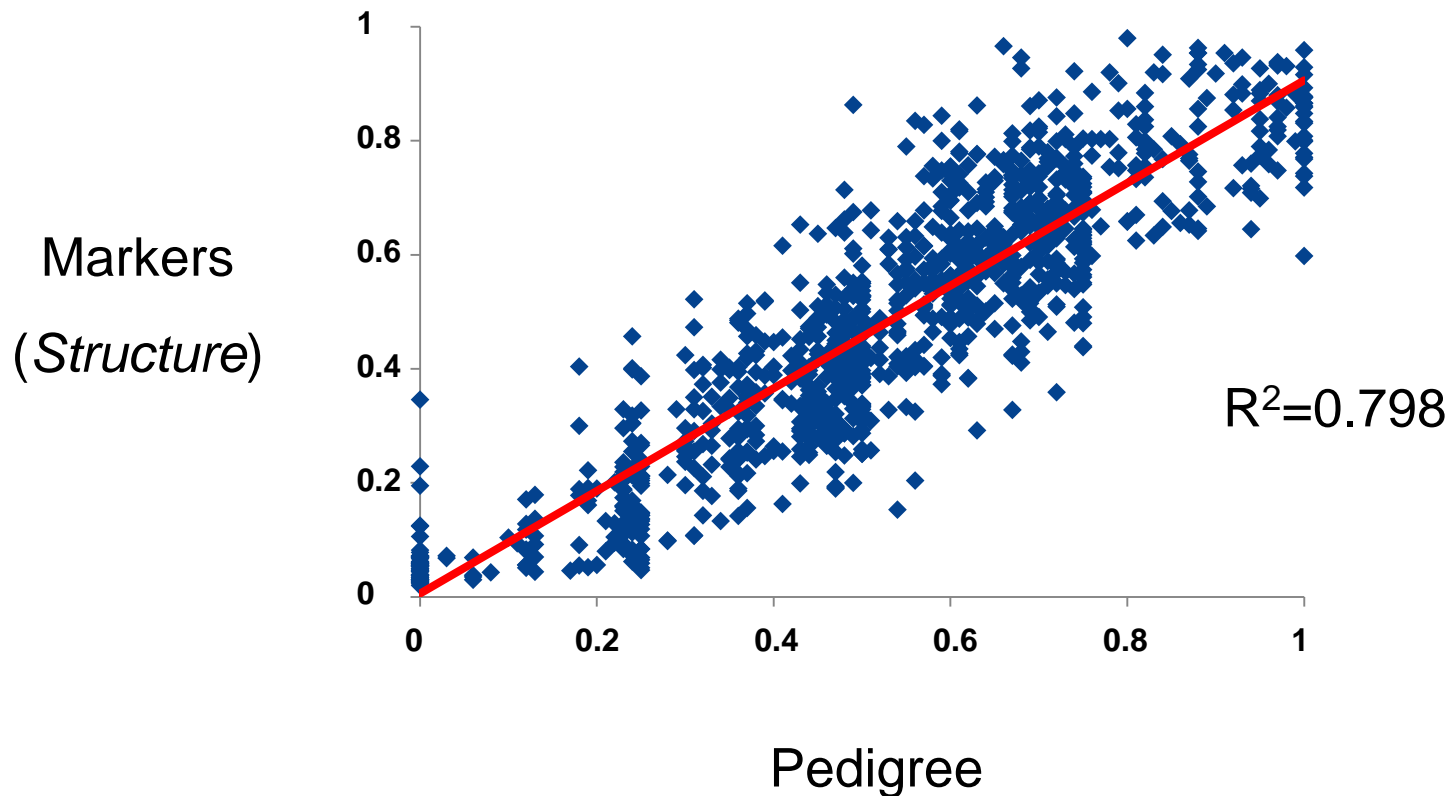- US -   171 animals >75% US pedigree

LD only persists at short distances

DNK/US	US/ALL	DNK/All
0.87	0.95	0.97

Persistence of LD

Pairwise Marker Distance (kb)

DNK_ALL

US_ALL

DNK_US

Markers Reflect Breed Proportions

Proportion Danish Jersey

Markers (*Structure*)

Pedigree

$R^2 = 0.798$

Different Genetic Levels in DNK and US

	DNK	US
Milk	106	114
Fat	107	98
Protein	109	108
Udder health	103	95
Fertility	100	96

Interbull breeding values 2010 (NAV, 2011)
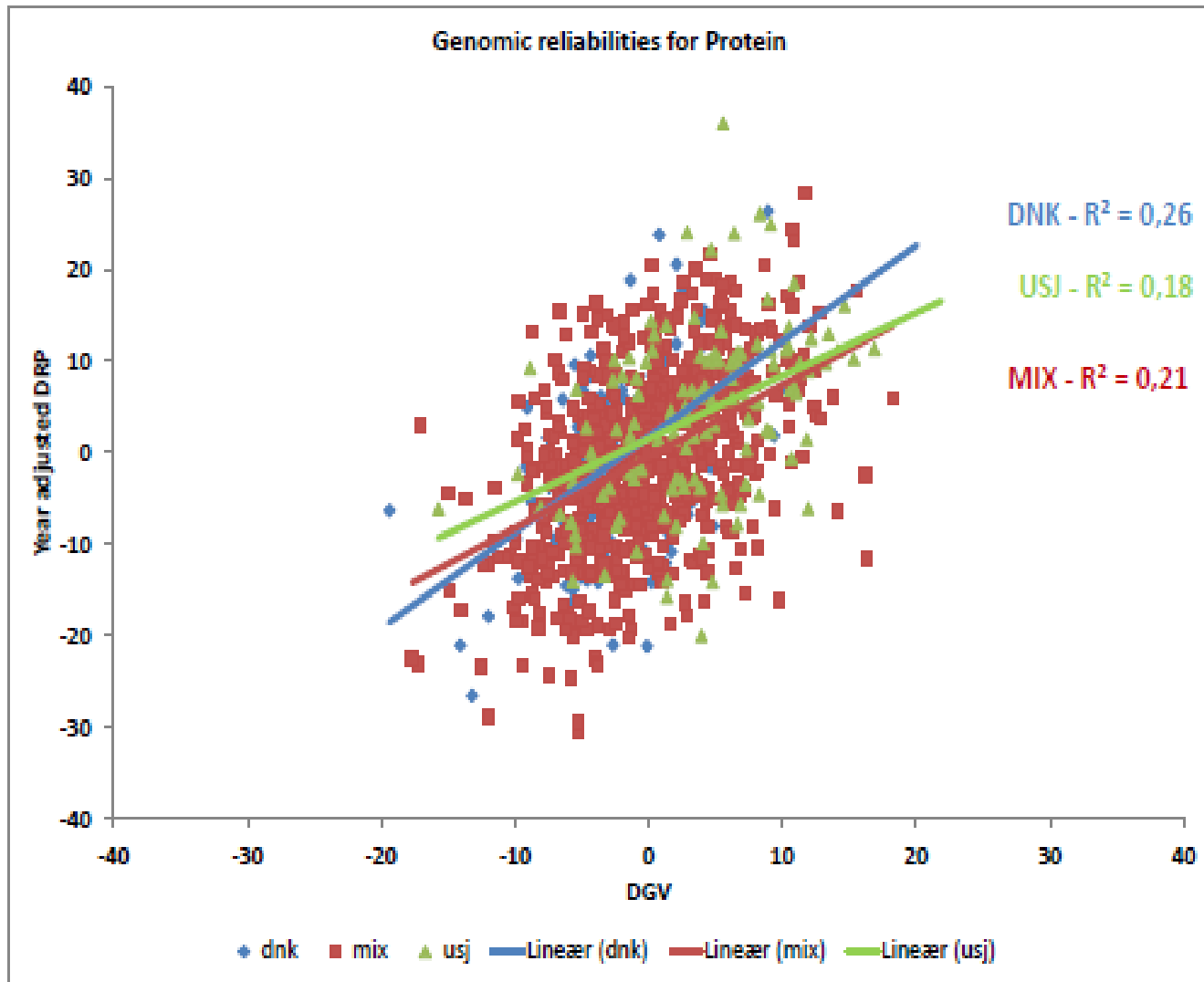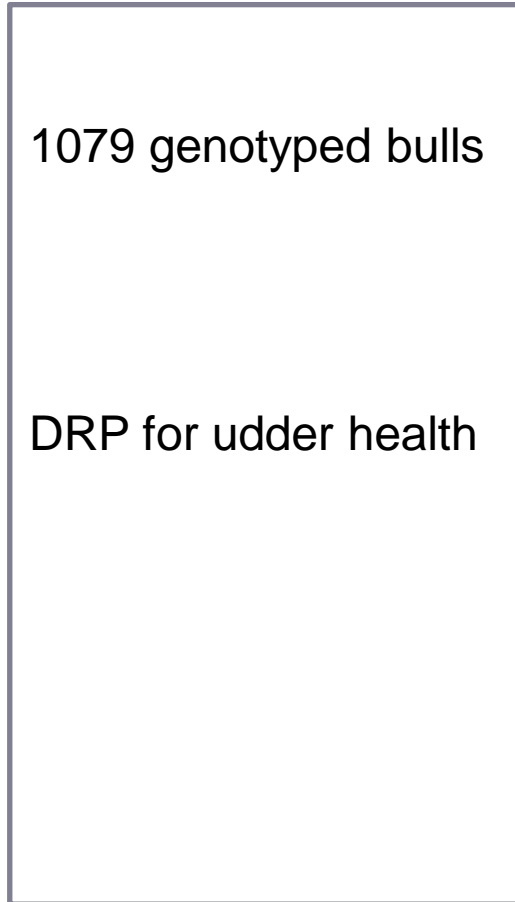
Population Structure using Random Regression

$$y_i = \mu + \beta w_i + a_{0i} + w_i a_{1i} + e_i$$
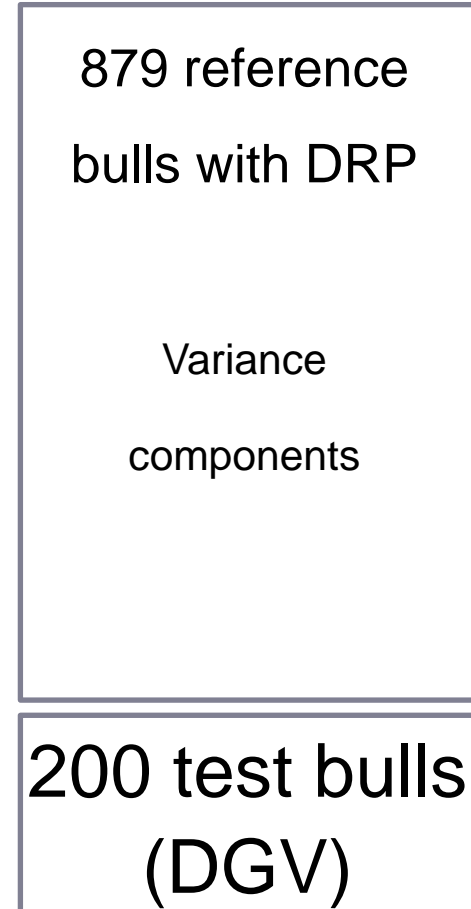
DRP   DGV for animal i

Udder health

w_i Breed proportion from *Structure* or pedigree

Covariance structure : Genomic or pedigree relationship

Dataset

Predictions

1079 genotyped bulls

DRP for udder health

$\longrightarrow$

879 reference

bulls with DRP

Variance

components

200 test bulls
(DGV)

Reliability=$r^2_{DRP,DGV}$/Rel$_{DRP}$

VIKINGGENETICS

AARHUS
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vikinggenetics.com

Gains due to G-BLUP and structure

Model	Reliability
Basic animal model	0.24
Basic genomic model	0.34
RR-genomic model – structure	0.33
RR-genomic model - pedigree	0.33

Conclusions

- Population structure in Danish Jersey exist

- Population structure modeled in the random regression model did not improve predictions compared to a basic genomic model

Why?

- The population structure modeled well by genomic relationship matrix

- Structure/pedigree information based on average marker information across the entire genome

Current improvement

- Cluster markers based on effect size and origin