Analysis of Subpopulation Structure in Danish Jersey

J.R. Thomasen[1,2], A.C. Sørensen[1], R.F. Brøndum[1], M.S. Lund[1] and B. Guldbrandtsen[1]

[1]Aarhus University, Department of Molecular Biology and Genetics, Denmark

[2]VikingGenetics, Denmark

jrt@vikinggenetics.com

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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?

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Objective

- 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

Divergence and Admixture

- ## 1896 – 1909
  - ~5,200 animals imported to Denmark from Jersey

- ## Mid 1960s
  - ~76,000 cows
  - Semen imported from one US bull
  -

- ## From 1985
  - More imports of US bulls

- ## 2011
  - 68,000 recorded cows
  - Admixed breed: 63% original Danish Jersey and 36% US Jersey
  - 54 bulls progeny tested

Division into Subpopulations

- ALL - 1730 animals

- DNK - 231 animals >75% DNK pedigree
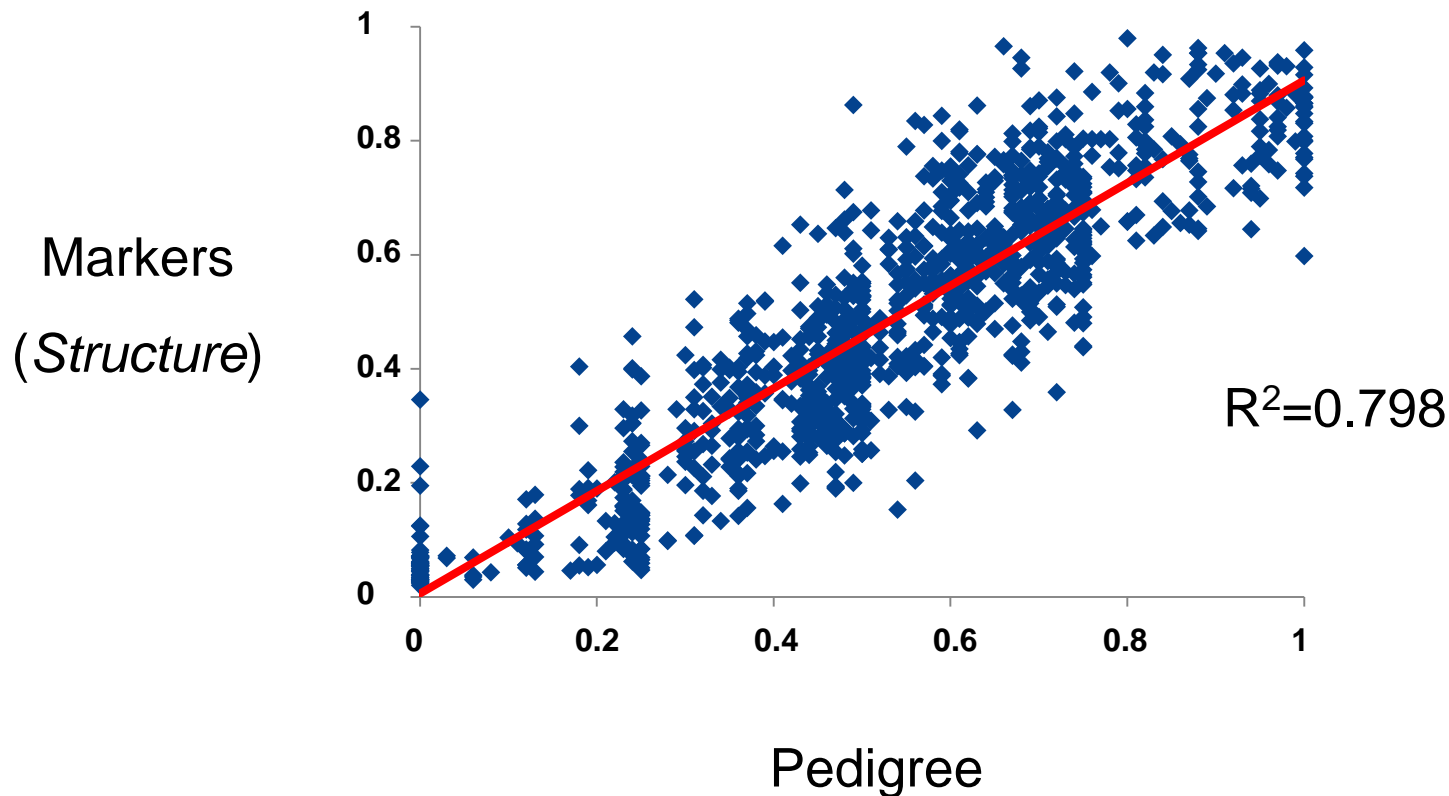
- US -   171 animals >75% US pedigree

LD only persists at short distances

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

Persistence of LD

Markerinterval Distance (kb)

DNK_ALL

US_ALL
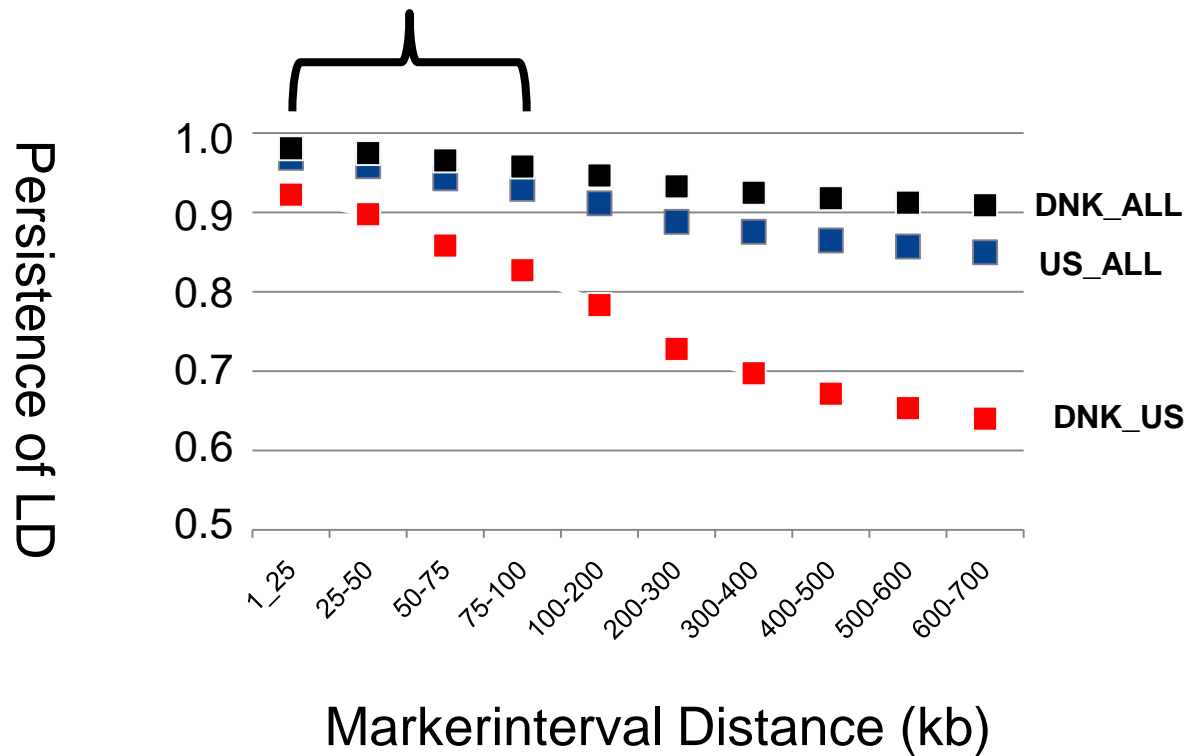
DNK_US

Markers Reflect Breed Proportions

Proportion Danish Jersey

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)

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• **Conclusion**

- Danish Jersey consists of two subpopulations

- Different genetic levels in DNK and US

- Current genomic predictions assume homogeneous breed

• **Hypotheses**

- Differences in marker allele effects exist due to difference in origin of allele (DNK versus US)

- Use of genomic structure based on the information from markers/pedigree improves prediction of genomic breeding values

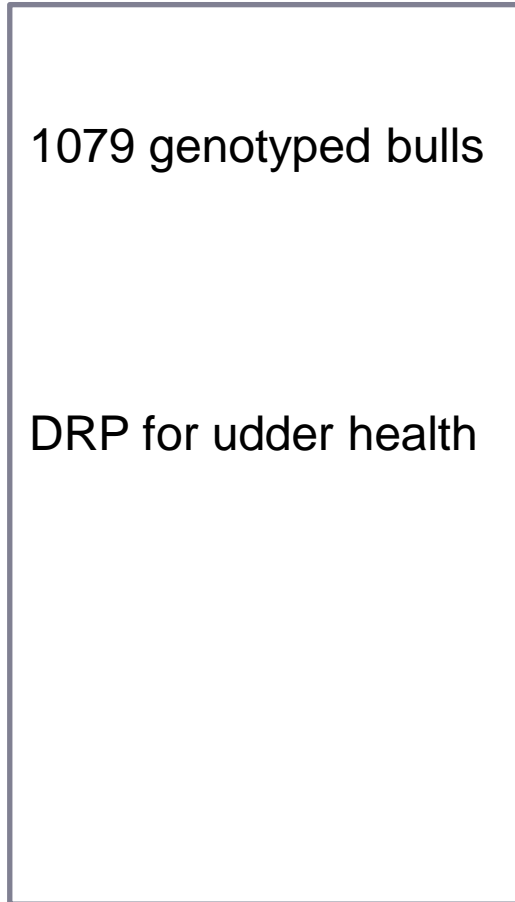# Population Structure using Random Regression

$$y_i = \mu + \beta w_i + a_{0i} + w_i a_{1i} + e_i$$

DRP   DGV for animal *i*

Udder health

w_i Breed proportion from *Structure* or pedigree

Covariance structure : Genomic or pedigree relationship

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Dataset

1079 genotyped bulls

DRP for udder health

→

Predictions

879 reference bulls with DRP

Variance components

200 test bulls (DGV)
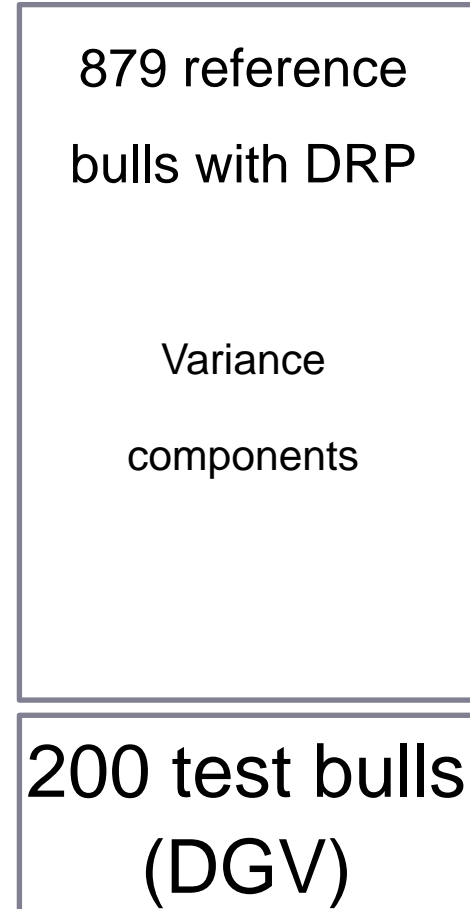
$$\text{Reliability} = r^2_{DRP,DGV} / Rel_{DRP}$$

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

Future improvement

- Cluster markers based on effect size and origin