Estimation of (co)variance components across breeds by a test-day model adapted to New Zealand dairy cattle

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1 The message

Crossbreeding among dairy cattle is important in New Zealand!

How getting an optimal selection and taking mating decisions for crossbred cattle ?

Need to have advanced evaluations of the performances of crossbreds!

2 Objective

Modelling of breed specific additive genetic effects

To define overall additive breeding values as a function of breed composition

In this study: used to estimate (co)variance components

3 Methods

Only Holstein-Friesian (HF) and Jersey (JE) animals in production used to estimate (co)variance components:

1. Inside breeds using a simplified random regression test-day model

   1. breed specific (co)variances

Results allowed to tranform Legendre polynomials into new independent regressions

2. Across breeds with a "multi-breed model":

   1. regressions specific to breeds

   2. allowed modelling evolution of lactation across breed types

   3. taking account of genetic and non-genetic differences between breeds as functions of HF and JE contributions (breed composition)

4 Results

Differences between HF and JE breeds were shown by the single breeds analyses !

The multi-breed analyse confirmed these differences and allowed estimation of additive genetic correlations:

Genetic correlations showed genetic differences between HF and JE animals

Legendre polynomials	Genetic Correlations
Constant	0.926
Linear	0.807
Quadratic	0.604

Especially this indicated persistency differences between both breeds!

Crossbreds were in-between both purebreds

Heritabilities over time estimated from multi-breed model
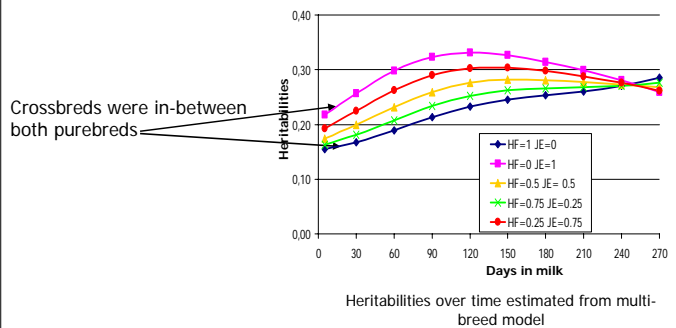
5 Conclusions

The proposed multi-breed model allowed to model additive genetic differences between HF and JE breeds

Therefore also able to provide breed specific or dependent additive breeding values!