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

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The message
Crossbreeding among dairy cattle is important in New Zealand! How to get an optimal selection and taking mating decisions for crossbred cattle? Need to have advanced evaluations of the performances of crossbreds!

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

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
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)

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:

<table>
<thead>
<tr>
<th>Legendre polynomials</th>
<th>Genetic Correlations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>0.926</td>
</tr>
<tr>
<td>Linear</td>
<td>0.807</td>
</tr>
<tr>
<td>Quadratic</td>
<td>0.604</td>
</tr>
</tbody>
</table>

Genetic correlations showed genetic differences between HF and JE animals especially this indicated persistency differences between both breeds!

Crossbreds were in-between both purebreds

Heritabilities over time estimated from multi-breed model

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!