Effects of using genomic imputation on dairy genomic evaluation in Thailand

Danai Jattawa¹, Skorn Koonawootitririon¹, Mauricio A. Elzo² and Thanathip Suwanasopee¹

¹Department of Animal Science, Faculty of Agriculture, Kasetsart University, Thailand
²Department of Animal Sciences, University of Florida, Gainesville, Florida USA

Genomic imputation

Imputation is a technique for predicting genotypes that are not directly assayed

Imputation Accuracies
- FImpute = 94%
- Findhap = 85%

To investigate the effects of using genomic imputation on Thai dairy genomic evaluations for 305-d milk yield and 305-d fat percentage

Objective

Dataset

- Pedigree & Phenotype
  - 8,361 first-lactation cows
  - 810 farms
  - Daughters of 1,210 sires and 6,992 dams

- Genome
  - 1,244 animals were genotyped
  - 84 sires and 1,160 cows
  - 17,779 SNP were used
  - All SNP had MAF ≥ 0.01 and call rate ≥ 0.9

- Reference group
  - 912 animals (born before or in 2009)
  - 17,779 SNP

- Test group
  - 332 cows (born in 2010 and later)
  - 7,652 SNP

Genomic evaluation

- Accuracy increased with increased genotyping costs
- Accuracy = 94% for FImpute
- Accuracy = 85% for Findhap

Genetic imputation

- FImpute 2.2
- Findhap 4

Imputation Software

- genDiff = 17,779 actual SNP
- genDiff = 17,779 imputed SNP
- genDiff = 7,652 SNP

Reference group
- 7,652 SNP
- Impute = 17,779 SNP
- Impute Software
  - FImpute 2.2
  - Findhap 4
Single-Step genomic models

\[ y = Xb + Zg + Za + e \]

\[ \text{Var}(a) = H * \sigma_a^2 \]

\[ H = [A_{11} + A_2A_2G_{11} - A_2G_{11}A_{11} - A_2G_{11}A_{11}] \]

**Fixed effects**
- Herd-year-season
- Calving age
- Heterosis

**Random effects**
- Additive genetic
- Residual

---

### Variance and covariance components

<table>
<thead>
<tr>
<th>Parameters</th>
<th>GM-Actual</th>
<th>GM-FI</th>
<th>GM-FH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Additive genetic</td>
<td>134,020.00</td>
<td>133,520.00</td>
<td>128,150.00</td>
</tr>
<tr>
<td>Cov (MY, FP)</td>
<td>-15.99</td>
<td>-16.78</td>
<td>-14.38</td>
</tr>
<tr>
<td>Var (FP)</td>
<td>0.03</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>Environmental</td>
<td>533,510.00</td>
<td>533,990.00</td>
<td>539,440.00</td>
</tr>
<tr>
<td>Cov (MY, FP)</td>
<td>-44.01</td>
<td>-43.15</td>
<td>-45.58</td>
</tr>
<tr>
<td>Var (FP)</td>
<td>0.18</td>
<td>0.18</td>
<td>0.18</td>
</tr>
<tr>
<td>Phenotypic</td>
<td>667,530.00</td>
<td>667,510.00</td>
<td>667,590.00</td>
</tr>
<tr>
<td>Cov (MY, FP)</td>
<td>-60.00</td>
<td>-59.93</td>
<td>-59.95</td>
</tr>
<tr>
<td>Var (FP)</td>
<td>0.23</td>
<td>0.23</td>
<td>0.23</td>
</tr>
<tr>
<td>Heritability (MY)</td>
<td>0.15</td>
<td>0.15</td>
<td>0.16</td>
</tr>
<tr>
<td>Heritability (FP)</td>
<td>0.20</td>
<td>0.20</td>
<td>0.19</td>
</tr>
</tbody>
</table>

---

### Prediction accuracy of genomic EBV

**Milk yield**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Prediction accuracy, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>GM-Acual</td>
<td>35.82</td>
</tr>
<tr>
<td>GM-FI</td>
<td>24.84</td>
</tr>
<tr>
<td>GM-FH</td>
<td>35.79</td>
</tr>
<tr>
<td>Fat percentage</td>
<td></td>
</tr>
<tr>
<td>GM-Acual</td>
<td>24.23</td>
</tr>
<tr>
<td>GM-FI</td>
<td>22.26</td>
</tr>
<tr>
<td>GM-FH</td>
<td>22.26</td>
</tr>
</tbody>
</table>

---

### Top 10 sire and cow rankings for MY

from GM-Actual, GM-FI, and GM-FH
Conclusion

- Variance components and heritabilities from GM-Actual and GM-FI were nearly identical, but differed slightly from GM-FH
- Prediction accuracies for GM-Actual and GM-FI were similar, but somewhat higher than for GM-FH
- Top 10 sires and cows ranked using GM-Actual GEBV and GM-FI GEBV were similar but different from GM-FI GEBV

Implication

- The advantage of using SNP imputation to obtain highly accurate genomic predictions
- High prediction accuracies with FlImpute make this program for genomic evaluation in the Thai dairy population

Acknowledgements

- Giving the scholarship
- Providing the genomic information
- Supporting the genomic evaluation training

Thank you for your kind attention