

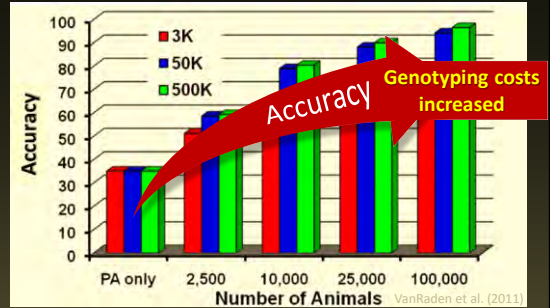
Effects of using genomic imputation on dairy genomic evaluation in Thailand



Danai Jattawa¹, Skorn Koonawootrittriron¹,
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

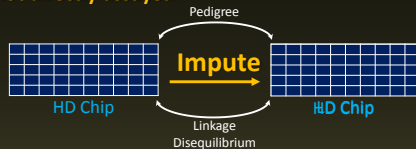
Genomic evaluation



VanRaden et al. (2011)
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Genomic imputation

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



Imputation Accuracies

Fimpute = 94%
Findhap = 85%

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Objective

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



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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



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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
- Set 1: 17,779 Actual SNP
➤ Set 2: 17,779 Fimpute imputed SNP
➤ Set 3: 17,779 Findhap imputed SNP

Genomic imputation

Reference group

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

Test group

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

7,652 SNP (Test group) **Impute** → 17,779 SNP

17,779 SNP (Reference group)

Imputation Software
✦ Fimpute 2.2
✦ Findhap 4

Single-Step genomic models

Single-Step Genomic Models

GM-Actual

+ pedigree
+ phenotypes
+ Actual SNP

GM-FI

+ pedigree
+ phenotypes
+ Impute SNP

GM-FH

+ pedigree
+ phenotypes
+ Findhap SNP

$$y = Xb + Z_g g + Za + e$$

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

$$H = \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G_{22} - A_{22})A_{22}^{-1}G_{21} & A_{12}A_{22}^{-1}G_{22} \\ G_{22}A_{22}^{-1}A_{21} & G_{22} \end{bmatrix}$$

Fixed effects


- Herd-year-season
- Calving age
- Heterosis

Random effects

- Additive genetic
- Residual

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Results and Discussion

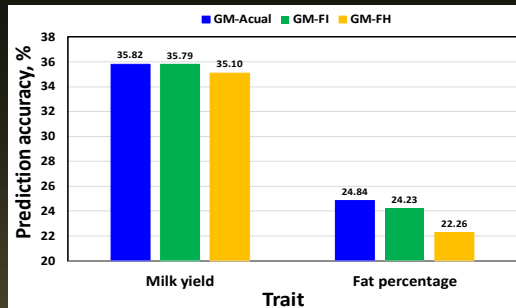
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Variance and covariance components

Parameters	GM-Actual	GM-FI	GM-FH
Additive genetic			
Var (MY)	134,020.00	133,520.00	128,150.00
Cov (MY, FP)	-15.99	-16.78	-14.38
Var (FP)	0.03	0.03	0.03
Environmental			
Var (MY)	533,510.00	533,990.00	539,440.00
Cov (MY, FP)	-44.01	-43.15	-45.58
Var (FP)	0.18	0.18	0.18
Phenotypic			
Var (MY)	667,530.00	667,510.00	667,590.00
Cov (MY, FP)	-60.00	-59.93	-59.95
Var (FP)	0.21	0.21	0.21
Heritability (MY)	0.20	0.20	0.19
Heritability (FP)	0.15	0.15	0.16

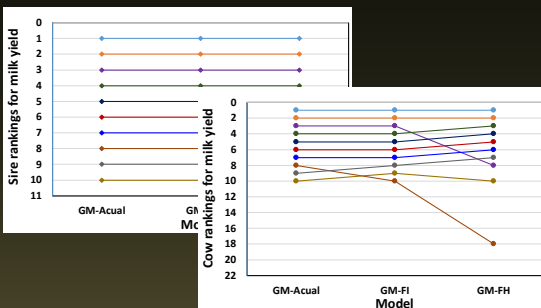
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Prediction accuracy of genomic EBV



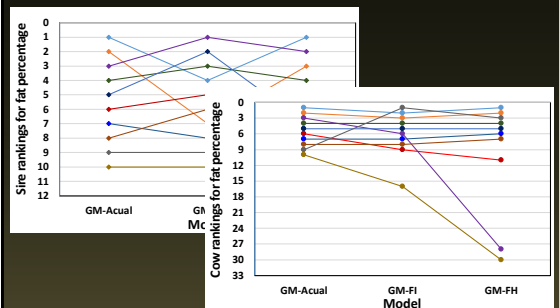
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Top 10 sire and cow rankings for MY from GM-Actual, GM-FI, and GM-FH



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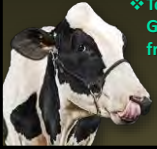
Top 10 sire and cow rankings for FP from GM-Actual, GM-FI, and GM-FH



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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-FH GEBV



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Implication

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



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Acknowledgements



Giving the scholarship



NSTDA

Providing the genomic information



Supporting the genomic evaluation training

*Thank you
for your kind attention*

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