

Genomic and conventional polygenic evaluations for milk yield and fat yield of dairy cattle in a Thai Holstein upgraded population



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Genomic evaluation

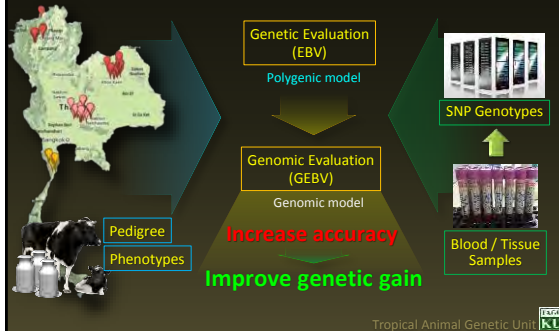
- ❖ Genomic evaluation combines pedigree, phenotypes, and genotypes to evaluate the animals
- ❖ Genomic evaluation can increase prediction accuracy and rate of genetic progress

Countries	Accuracy (%)		Gain
	EBV	GEBV	
USA	35	58	23
Canada	39	63	24
New Zealand	34	67	32
Netherland	35	61	26

Harris et al., 2008; De Roos et al., 2009;
Schenkel et al., 2009; VanRaden et al., 2009

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Dairy genetic evaluation in Thailand



Objectives

To compare variance components, genetic parameters, prediction accuracies, and ranking of animals for 305-d MY and 305-d FY using two genomic and a polygenic models



Dataset

Pedigree & Phenotype

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

Genome

- ❑ 2,661 animals (89 ♂; 2,572 ♀)
- ❑ GGP9K (n=1,243)
- ❑ GGP20K (n=570)
- ❑ GGP26K (n=540)
- ❑ GGP80K (n=139)



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Genomic data

Two sets of SNP genotypes were constructed

- ❑ Set 1: Using SNP in common among GGP9K, GGP20K, GGP26K, and GGP80K
- ❑ Set 2: Using imputed SNP from GGP9K, GGP20K and GGP26K to GGP80K

SNP deletion criteria

- ❖ Located on Y-, mitochondrial and unknown chromosome positions
- ❖ MAF lower than 0.04
- ❖ Call rate lower than 0.9

Set 1: included 7,656 SNP
Set 2: included 74,144 SNP

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Animal Mixed Models

Polygenic model (PM)

- Utilized pedigree + phenotype

Genomic model 7K (GM7K)


- Utilized pedigree + phenotype + SNP set 1
7,656 SNP

Genomic model 80K (GM80K)

- Utilized pedigree + phenotype + SNP set 2
74,144 SNP

These three models
were used to compare

- VCE and parameters
- Prediction ACC
- Animal rankings

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Animal Mixed Model

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

$$\begin{aligned} \text{Var}(a) &= A * \sigma_a^2 \text{ for polygenic model} \\ &= H * \sigma_a^2 \text{ for genomic models} \end{aligned}$$


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

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

Variance components	GM80K	GM7K	PM
Additive genetic			
Var (MY)	172,190	126,480	100,030
Cov (MY, FY)	4,148	3,264	3,057
Var (FY)	230	184	177
Environmental			
Var (MY)	500,420	542,750	565,990
Cov (MY, FY)	16,125	16,955	17,099
Var (FY)	1,039	1,083	1,085
Phenotypic			
Var (MY)	672,610	669,230	666,030
Cov (MY, FY)	20,273	20,219	20,156
Var (FY)	1,269	1,266	1,262

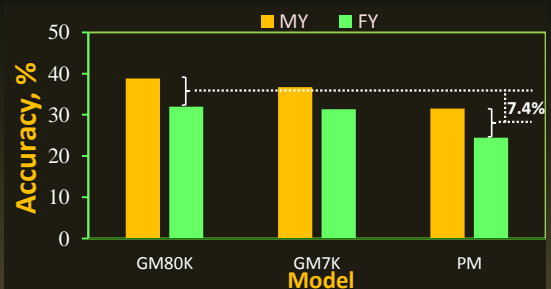
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Heritabilities and Correlations

Parameters	GM80K	GM7K	PM
Heritability (MY)	0.26	0.19	0.15
Heritability (FY)	0.18	0.15	0.10
Genetic corr (MY, FY)	0.66	0.68	0.70
Environmental corr (MY, FY)	0.71	0.70	0.70
Phenotypic corr (MY, FY)	0.69	0.69	0.70

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Prediction accuracy



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