Accuracy of genomic-polygenic prediction

for milk yield and fat percentage in the Thai dairy cattle population

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Genomic evaluation

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

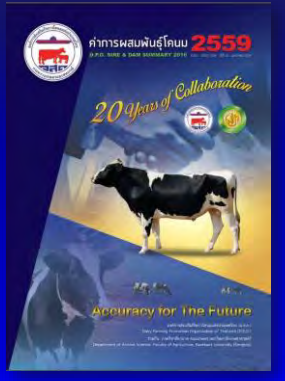
Countries	Accuracy (%)		Gain
	EBV	GEBV	
USA	35	58	23
Canada	39	63	24
New Zealand	34	67	32
Netherlands	35	61	26

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

Dairy Genomic Evaluation in Thailand

Livestock Science

Comparison of genetic evaluations for milk yield and fat yield using a polygenic model and three genomic–polygenic models with different sets of SNP genotypes in Thai multibreed dairy cattle



Objectives

- To compare prediction accuracies and animal rankings for 305 -d MY and 305-d FP using genomic-polygenic and polygenic models
- To evaluate GPEBV trends for each trait as Holstein (H) fraction increased from 0% to 100%

Dataset

Pedigree & Phenotypes

- 9,339 first-lactation cows
- 1,002 farms
- Daughters of 1,346 sires and 7,875 dams

Genotypes

- 2,661 animals (89 ♂; 2,572 ♀)
- GGP9K (n=1,412), GGP20K (n=570), GGP26K (n=540), GGP80K (n=139)

Polygenic and Genomic-Polygenic Evaluations

Phenotypes | Pedigree

9,339 first-lactation cows

Polygenic Evaluation (PEBV)

Conventional Evaluation

Blood / Semen Samples

- 2,661 animals

Genomic SNP Genotyping

- 9K, 22K, 26K, 80K

Genomic SNP Imputation

- From 9K, 22K, 26K to GGP80K
- 74,144 Actual and Imputed SNP

Genomic-Polygenic Evaluation (GPEBV)

Polygenic and Genomic-Polygenic Models

$$y = Xb + Z_h h + Za + e$$

Fixed effects

- Herd-year-season
- Calving age
- Heterosis

Random effects

- Additive genetic
- residual

$Var(a) = A * \sigma_a^2$ for polygenic model

$= H * \sigma_a^2$ for genomic-polygenic model

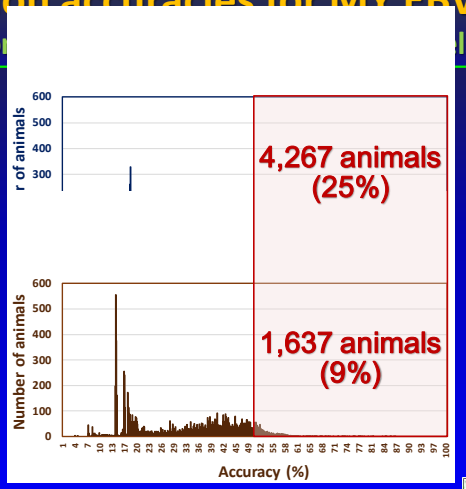
$$H = \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G_{22} - A_{22})A_{22}^{-1}G_{21} & A_{12}A_{22}^{-1}G_{22} \\ G_{22}A_{22}^{-1}A_{21} & G_{22} \end{bmatrix}$$

Results and Discussion

Prediction accuracies for MY EBV
from Genomic-Polygenic and Polygenic models

Genomic-Polygenic model

Polygenic model

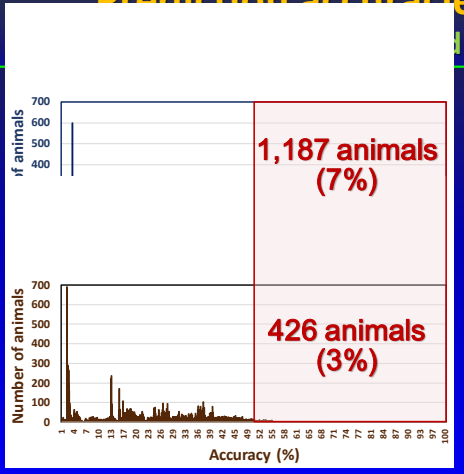


Tropical Animal Genetic Unit

Prediction accuracies for FP EBV
from Genomic-Polygenic and Polygenic models

Genomic-Polygenic model

Polygenic model



Tropical Animal Genetic Unit

Mean prediction accuracies
from Genomic-Polygenic and Polygenic models

Type of animal	n	GPM		PM		Accuracy
		MY	FP	MY	FP	Increase
All animals	17,363	38.4	27.5	33.1	23.6	4.5
Non-genotyped animals	14,702	36.7	26.4	31.1	22.5	4.8
Genotyped animals	2,661	46.2	32.5	42.6	29.1	3.5
Genotyped cows	2,572	34.5	26.2	26.9	18.9	7.5
Genotyped sires	89	64.5	43.8	59.9	43.2	2.6
Genotyped proven sires	58	69.5	47.1	67.2	49.0	0.2
Genotyped young sires	31	42.3	26.5	27.5	12.5	14.4

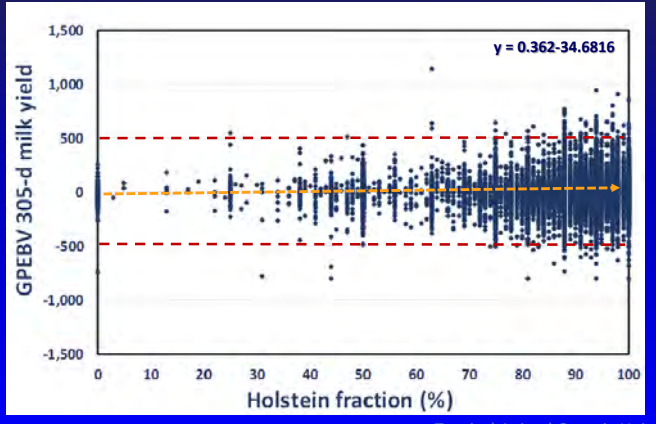
Tropical Animal Genetic Unit

Rank correlations between GPEBV and PEBV
for 305-d milk yield and 305-d fat percentage

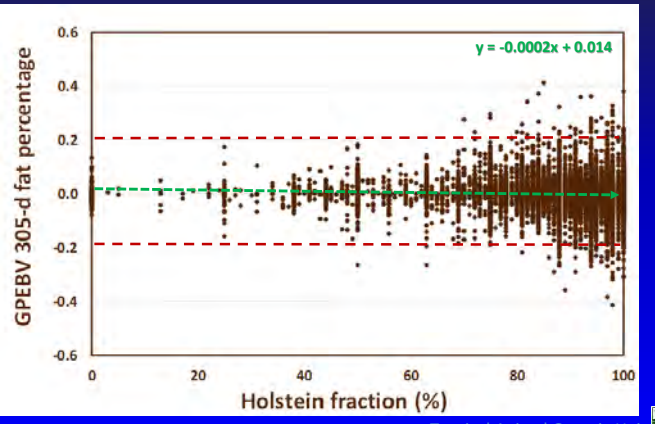
Trait	Rank correlation	P-value
All animals		
305-d milk yield	0.88	<.0001
305-d fat percentage	0.83	<.0001
Sires		
305-d milk yield	0.91	<.0001
305-d fat percentage	0.87	<.0001
Cows		
305-d milk yield	0.88	<.0001
305-d fat percentage	0.82	<.0001

Tropical Animal Genetic Unit

GPEBV as Holstein fraction increases from 0% to 100% for 305-d milk yield



GPEBV as Holstein fraction increases from 0% to 100% for 305-d fat percentage



Conclusions

- GPM yielded higher prediction accuracies than PM
- Rankings between GPEBV and PEBV were similar
- Animals with higher Holstein fraction tended to have higher GPEBV for MY, but lower GPEBV for FP than animals with lower Holstein fractions

Implications

- Selection of animals with GPEBV would be yield higher rates of genetic change than with PEBV
- GPEBV would help shorten generation interval through earlier utilization of young sires evaluated with high accuracy

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