

Use of Young and Proven Sires with Genomic Evaluations for Improving Milk Yield in Thai Multibreed Dairy Cattle



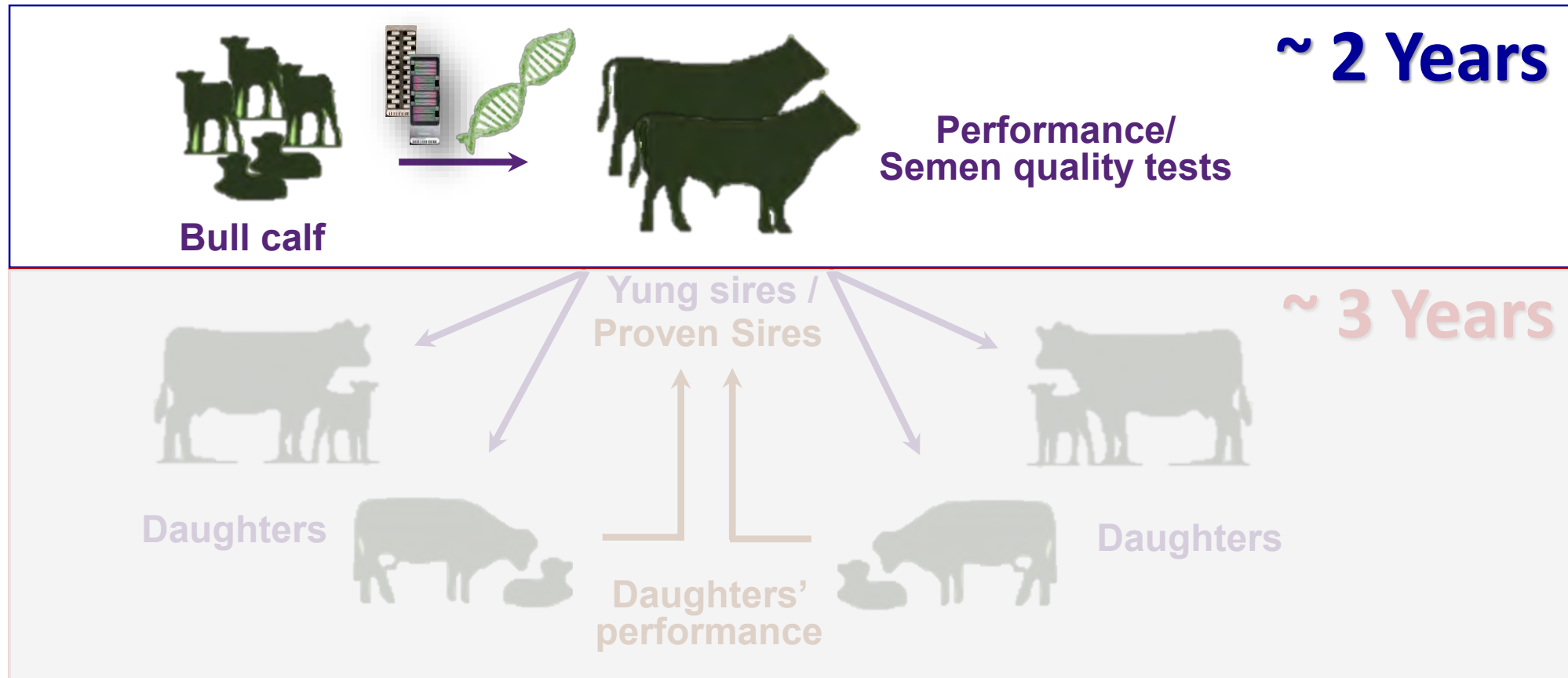
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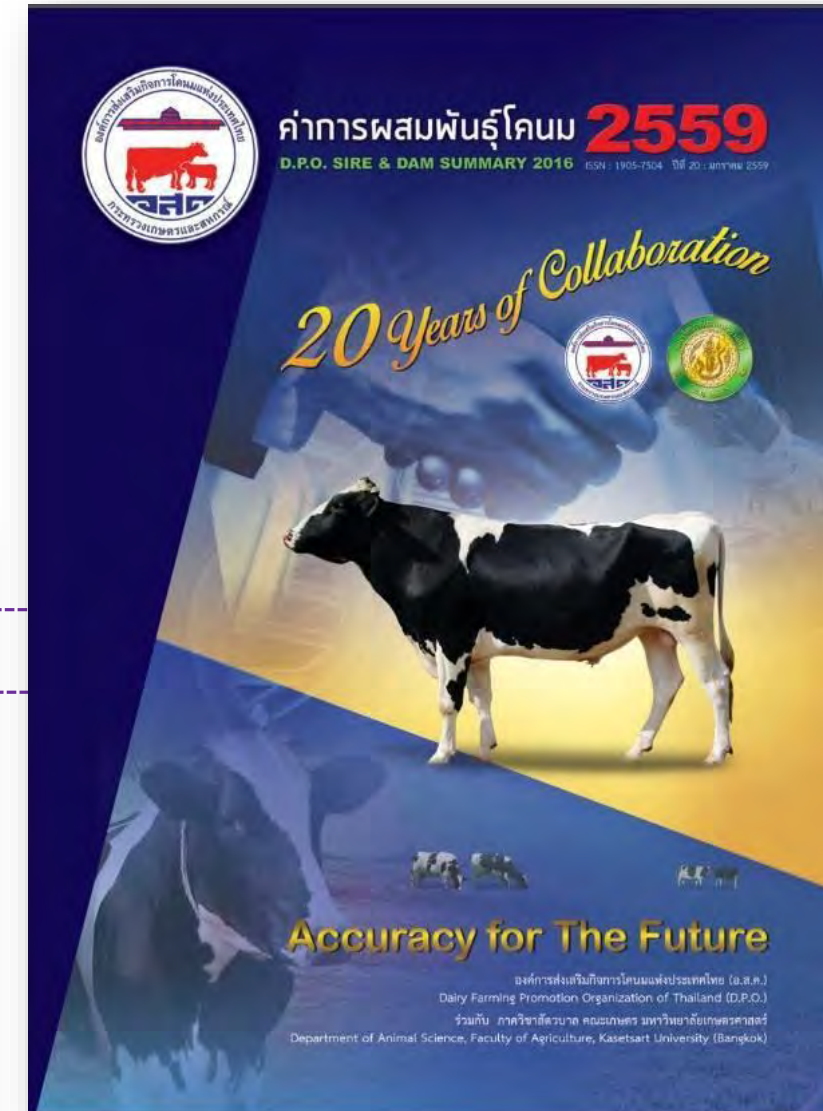
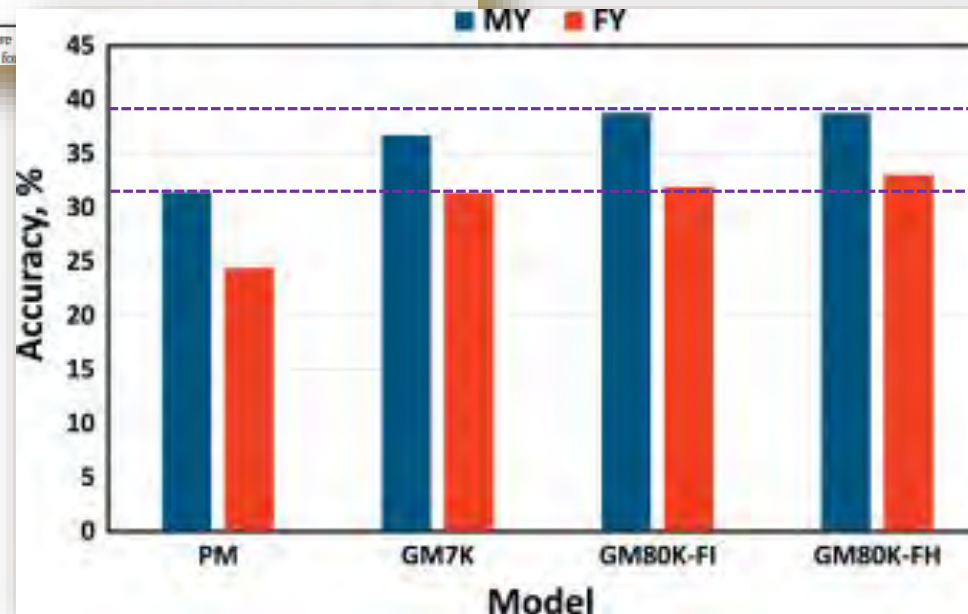
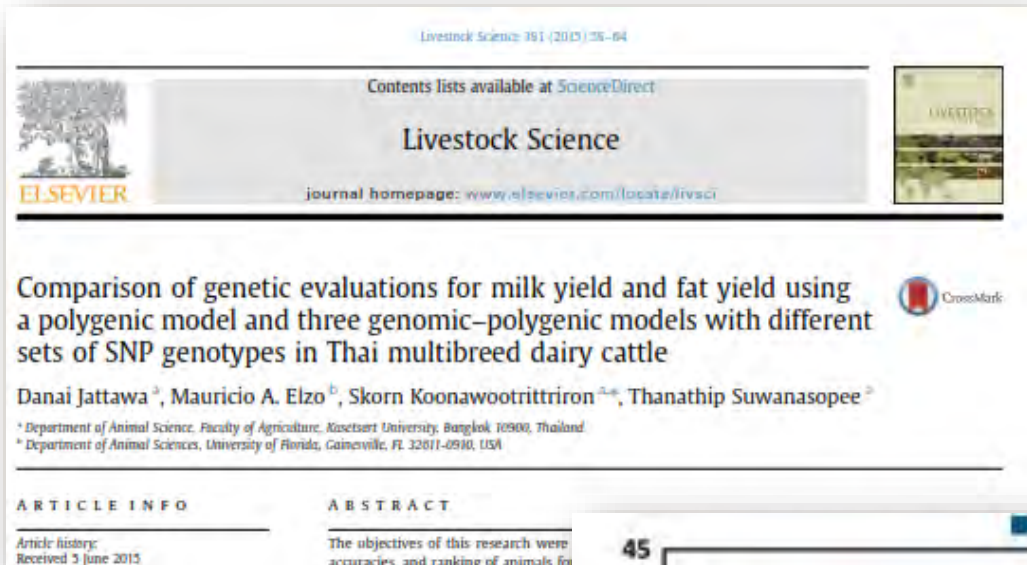
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Advantages of Genomic Evaluation



- Reducing generation interval
 - Increasing prediction / selection accuracies
 - Speeding up genetic progress

First Dairy Genomic Evaluation in Thailand



Dairy Genomic Evaluation System in Thailand



Pedigree

Phenotypes

~ 1,000 first-lactation cows / year

**Blood / Tissue
Samples**

~ 300 animals / year
• 15 sires
• 285 cows

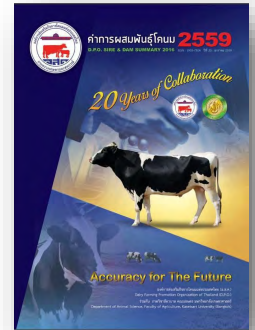
**Genomic SNP
Genotyping**

- HD chip for all sires and highly related cows
- LD chip for the rest cows
- Imputation technique

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

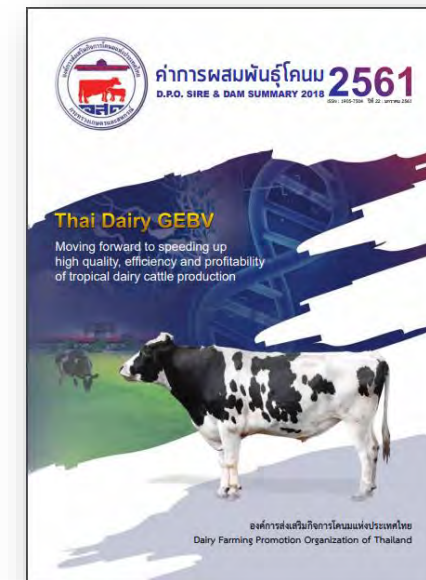
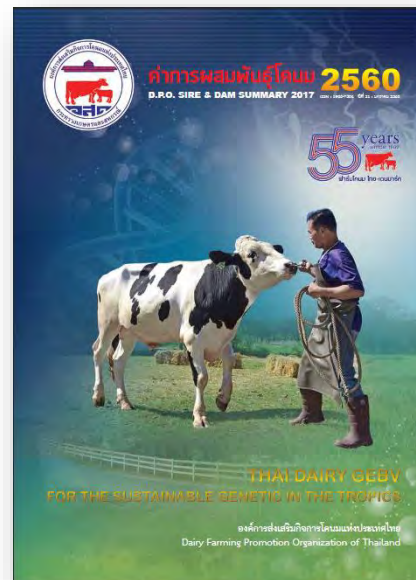
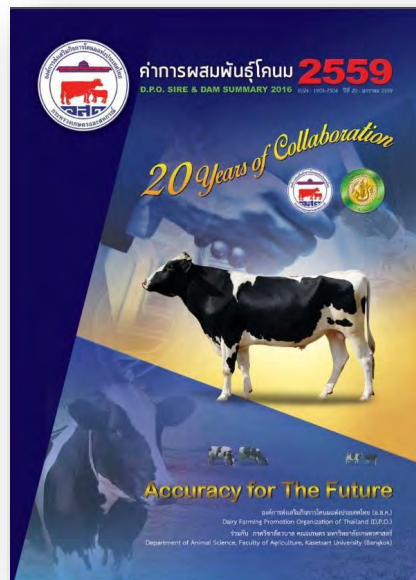
**Genomic-Polygenic Evaluation
(GEBV)**

Single-Step Genomic BLUP



Objective

To investigate the genomic estimated breeding values (GEBV) and prediction accuracy for 305-d milk yield (MY) of **young sires (had no or < 10 daughters)** and **proven sires (had ten daughters or more)** in 2016 to 2018 Thai dairy genomic evaluations



Dataset



Pedigree and phenotypes

- ❑ 11,383 first-lactation cows
- ❑ 1,121 farms
- ❑ Daughters of 9,317 dams and 1,358 sires
 - 1,140 young sires (no or < 10 daughters)
 - 218 proven sires (≥ 10 daughters)


Genotypes

- ❑ 3,261 animals
- ❑ 121 sires and 3,140 cows
- ❑ Actual and imputed 74,396 SNP
(9K, 20K, 26K were imputed to 80K)




A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	
SNP	NAME	Chromosome	Position	SNP	ILMN	Str	Customer	No	Call	Alt	Freq	A	Freq	B	Freq	MAF
1	ARS-BFGL-NGS-108995	0	0	[T/C]	TOP	TOP	1020	90	0.9389	0.2863	0.488	0.2157	0.5353	0.4847	0.4847	
2	ARS-BFGL-NGS-114435	0	0	[A/G]	TOP	TOP	1083	27	0.9757	0.2327	0.5042	0.2632	0.4848	0.5152	0.4848	
3	ARS-BFGL-NGS-2467	0	0	[T/C]	TOP	TOP	1073	37	0.9667	0.1445	0.4846	0.3709	0.3868	0.6132	0.3868	
4	ARS-BFGL-NGS-30261	0	0	[G/C]	TOP	TOP	1098	12	0.9052	0.3452	0.4982	0.1566	0.5943	0.4057	0.4057	
5	ARS-BFGL-NGS-72955	0	0	[T/C]	TOP	TOP	1085	25	0.9755	0.5806	0.3244	0.0949	0.7429	0.2571	0.2571	
6	BTB-40029-no-s	0	0	[T/C]	TOP	TOP	1096	14	0.9874	0.3285	0.4681	0.2035	0.5625	0.4375	0.4375	
7	BTB-0179304	0	0	[A/G]	TOP	TOP	1058	52	0.9532	0.3705	0.4745	0.135	0.6078	0.3922	0.3922	
8	Hapmap19620-BTA-11785	0	0	[A/C]	TOP	TOP	1095	15	0.9805	0.4064	0.4575	0.1361	0.6352	0.3648	0.3648	
9	ARS-USMARC-Parent-AY781125-r12903723	1	1,275,408	[T/A]	TOP	TOP	1092	18	0.9838	0.1882	0.5284	0.2885	0.4473	0.5527	0.4473	
10	BTB-114834-no-s	1	1,127,408	[T/A]	TOP	TOP	1093	17	0.9847	0.4227	0.4483	0.129	0.6468	0.3532	0.3532	
11	ARS-BFGL-NGS-107347	1	936,034	[C/G]	TOP	TOP	1080	30	0.973	0.3333	0.4806	0.1861	0.5736	0.4264	0.4264	
12	ARS-BFGL-NGS-70523	1	1,511,408	[T/G]	TOP	TOP	1066	44	0.9604	0.3931	0.4512	0.1557	0.6187	0.3813	0.3813	
13	ARS-BFGL-NGS-13683	1	1,366,408	[C/G]	TOP	TOP	1092	18	0.9838	0.1676	0.5128	0.3196	0.424	0.576	0.424	
14	Hapmap45471-BTA-11783	1	403,785	[G/C]	TOP	TOP	1093	107	0.9836	0.2353	0.4995	0.2652	0.485	0.515	0.485	
15	ARS-BFGL-NGS-111885	1	958,937	[T/A]	TOP	TOP	1093	17	0.9847	0.269	0.4959	0.2351	0.5169	0.4831	0.4831	
16	ARS-BFGL-BAC-11044	1	1,280,548	[T/C]	TOP	TOP	1094	16	0.9856	0.6444	0.3208	0.0947	0.8048	0.1952	0.1952	
17	ARS-BFGL-BAC-11193	1	2,930,548	[T/C]	TOP	TOP	1096	14	0.9874	0.3577	0.4854	0.1569	0.6004	0.3996	0.3996	
18	ARS-BFGL-BAC-11750	1	1,970,880	[T/C]	TOP	TOP	1103	7	0.9937	0.1396	0.4742	0.3862	0.3767	0.6233	0.3767	
19	ARS-BFGL-BAC-12579	1	393,878	[T/C]	TOP	TOP	1094	26	0.9766	0.321	0.4751	0.2639	0.5066	0.4934	0.4934	
20	ARS-BFGL-BAC-15578	1	2,015,340	[T/C]	TOP	TOP	1101	9	0.9919	0.0563	0.5515	0.5932	0.2321	0.7679	0.2321	
21	ARS-BFGL-BAC-18144	1	1,136,408	[A/G]	TOP	TOP	1094	16	0.9856	0.1335	0.4744	0.2211	0.5507	0.4493	0.4493	
22	ARS-BFGL-BAC-27364	1	943,730	[A/C]	TOP	TOP	1055	55	0.9905	0.0919	0.4114	0.4967	0.2976	0.7024	0.2976	
23	ARS-BFGL-BAC-31122	1	874,470	[A/G]	TOP	TOP	1094	16	0.9856	0.2185	0.5046	0.277	0.4777	0.5223	0.4777	
24	ARS-BFGL-BAC-34208	1	963,590	[A/G]	TOP	TOP	1098	12	0.9892	0.1466	0.4863	0.367	0.3898	0.6102	0.3898	
25	ARS-BFGL-BAC-4996	1	3,909,944	[A/C]	TOP	TOP	1093	7	0.996	0.3619	0.4889	0.4892	0.4904	0.5096	0.4904	
26	ARS-BFGL-BAC-7198	1	1,254,408	[A/G]	TOP	TOP	1096	14	0.9874	0.0438	0.3558	0.6804	0.2217	0.7783	0.2217	
27	ARS-BFGL-NGS-100206	1	1,356,408	[T/C]	TOP	TOP	1057	53	0.9523	0.2479	0.5421	0.21	0.5189	0.4811	0.4811	

Genomic Evaluations





Genotypes

- 3,261 animals
- 121 sires and 3,140 cows
- Actual and imputed 74,396 SNP (9K, 20K, 26K were imputed to 80K)



Pedigree and phenotypes

- 11,383 first-lactation cows
- 1,121 farms
- Daughters of 9,317 dams and 1,358 sires
 - 1,140 young sires (no or < 10 daughters)
 - 218 proven sires (≥ 10 daughters)



2016

- Pedigree and Phenotypes**
- 9,339 first-lactation cows
- Genotypes**
- 2,661 animals



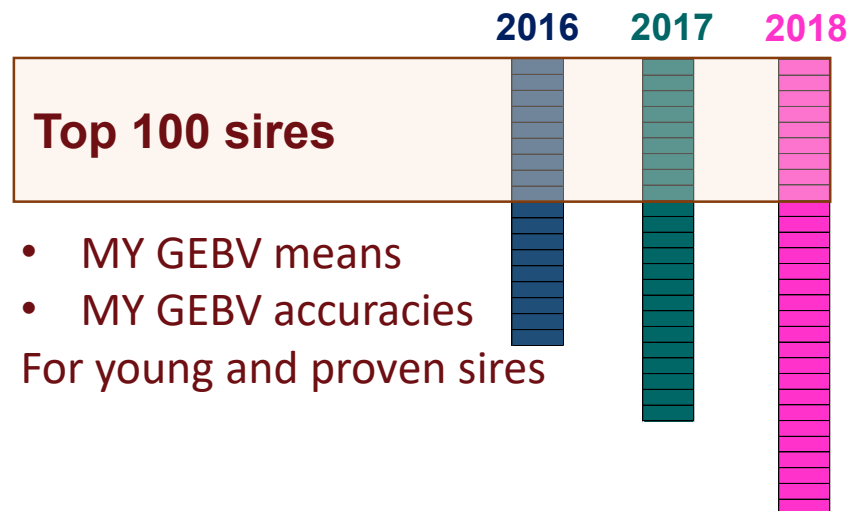
2017

- Pedigree and Phenotypes**
- 10,345 first-lactation cows
- Genotypes**
- 2,961 animals



2018

- Pedigree and Phenotypes**
- 11,383 first-lactation cows
- Genotypes**
- 3,261 animals



Sire rankings
for MY GEBV

Standardized
MY GEBV

Single-Step Genomic Models

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

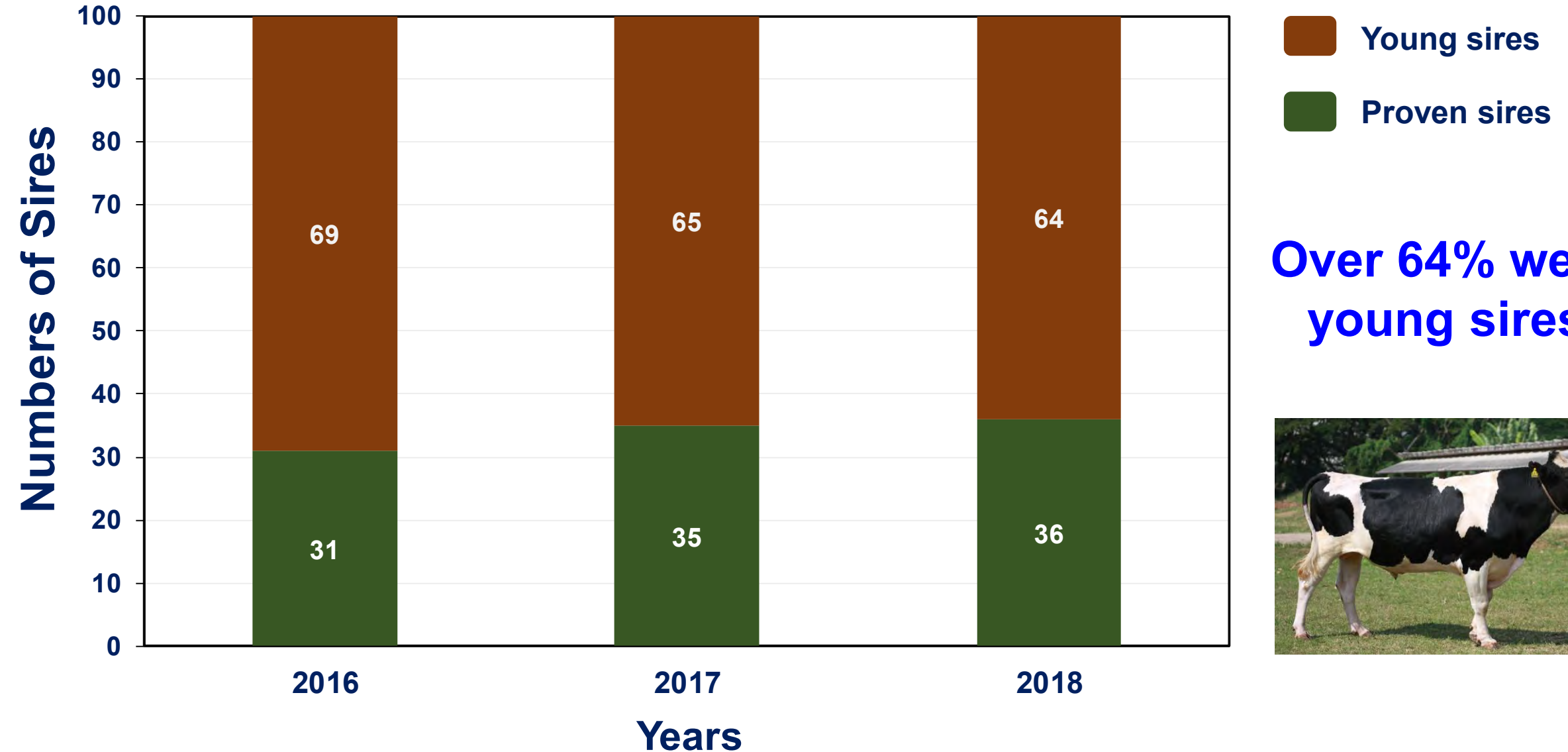
Fixed effects

- Herd-year-season
- Calving age
- Heterosis

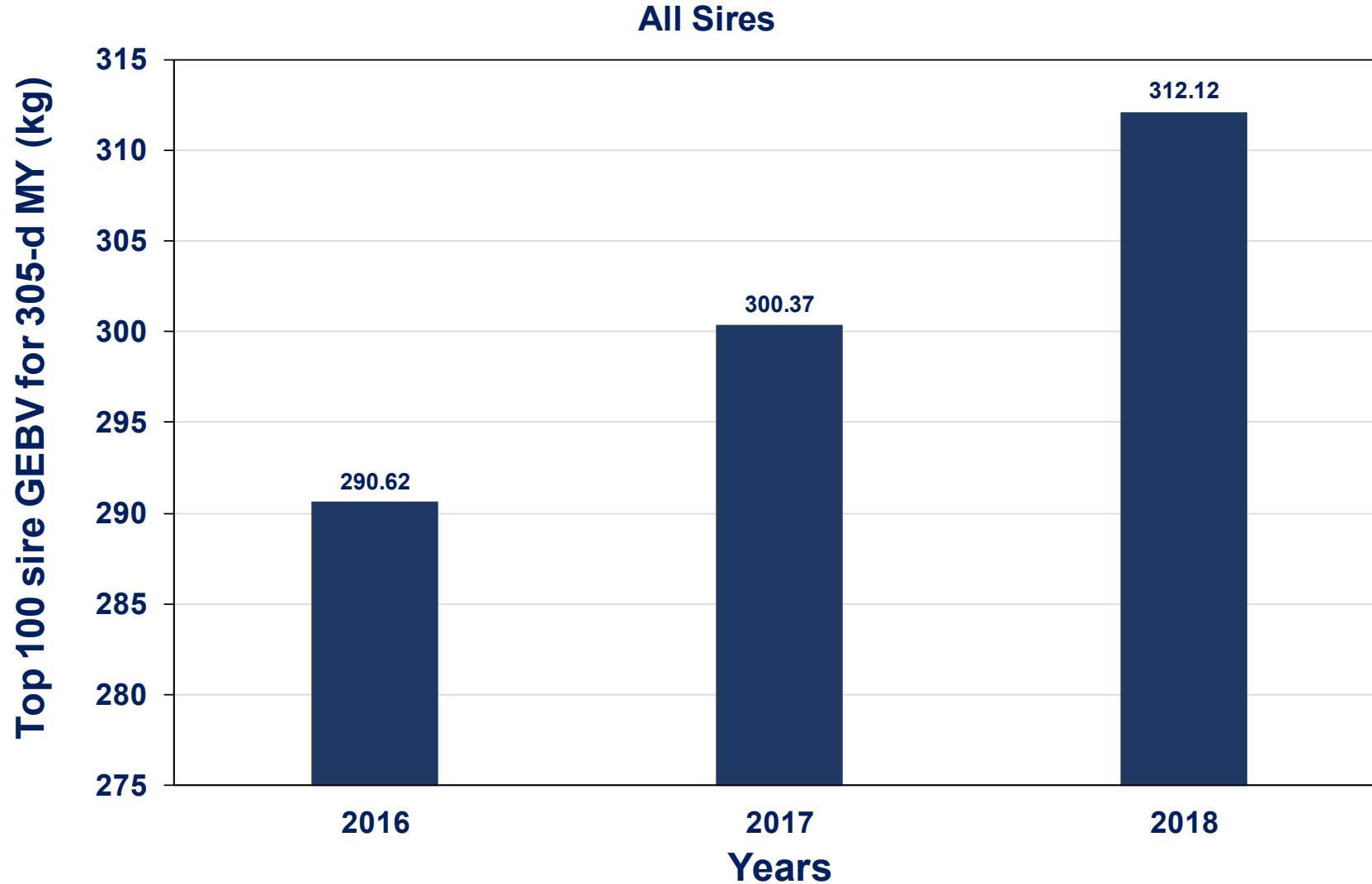
Random effects

- Additive genetic
- residual

Numbers of Young and Proven Sires in Top 100 Rankings

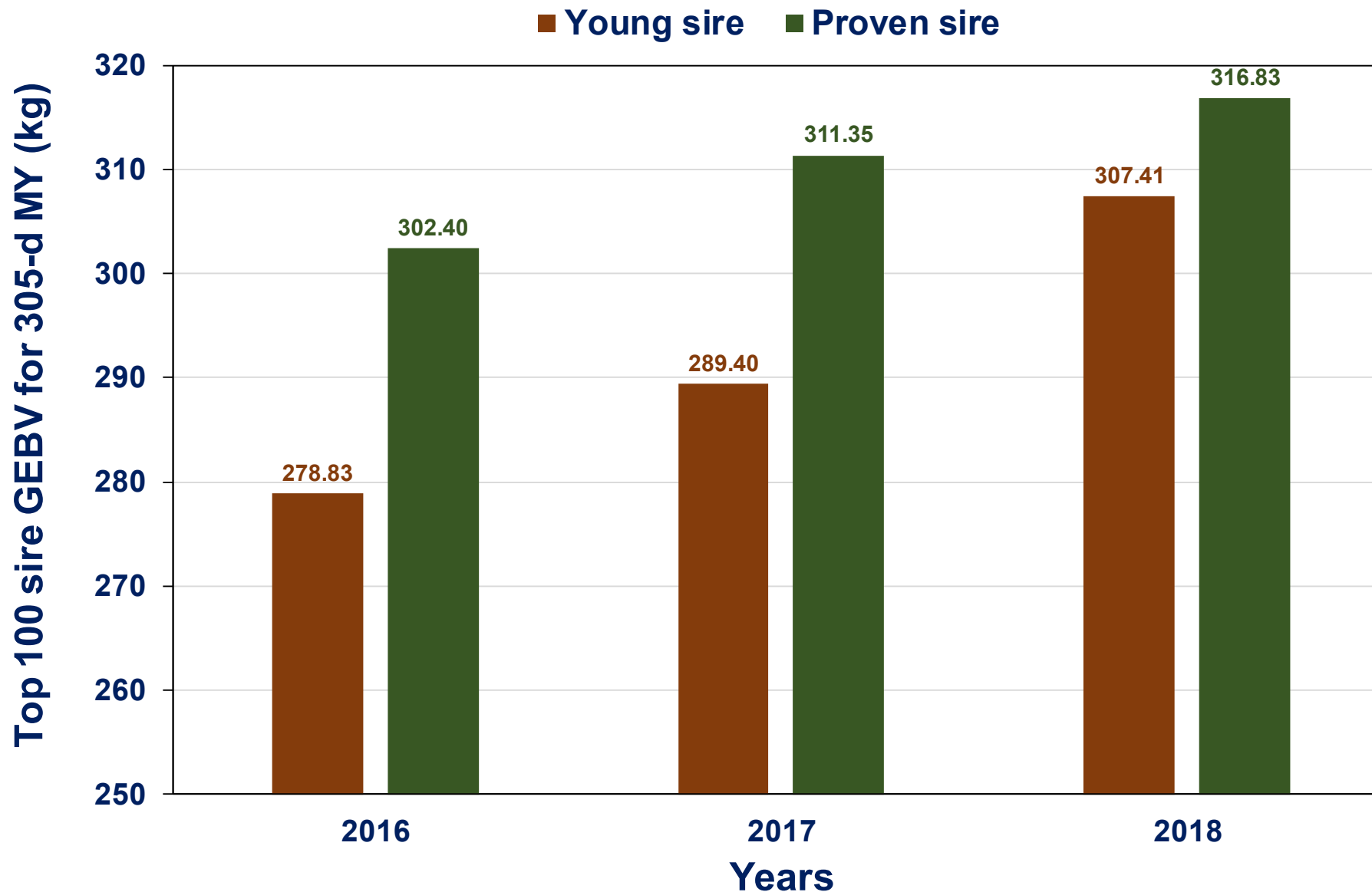


Genomic EBV for Top 100 Sires

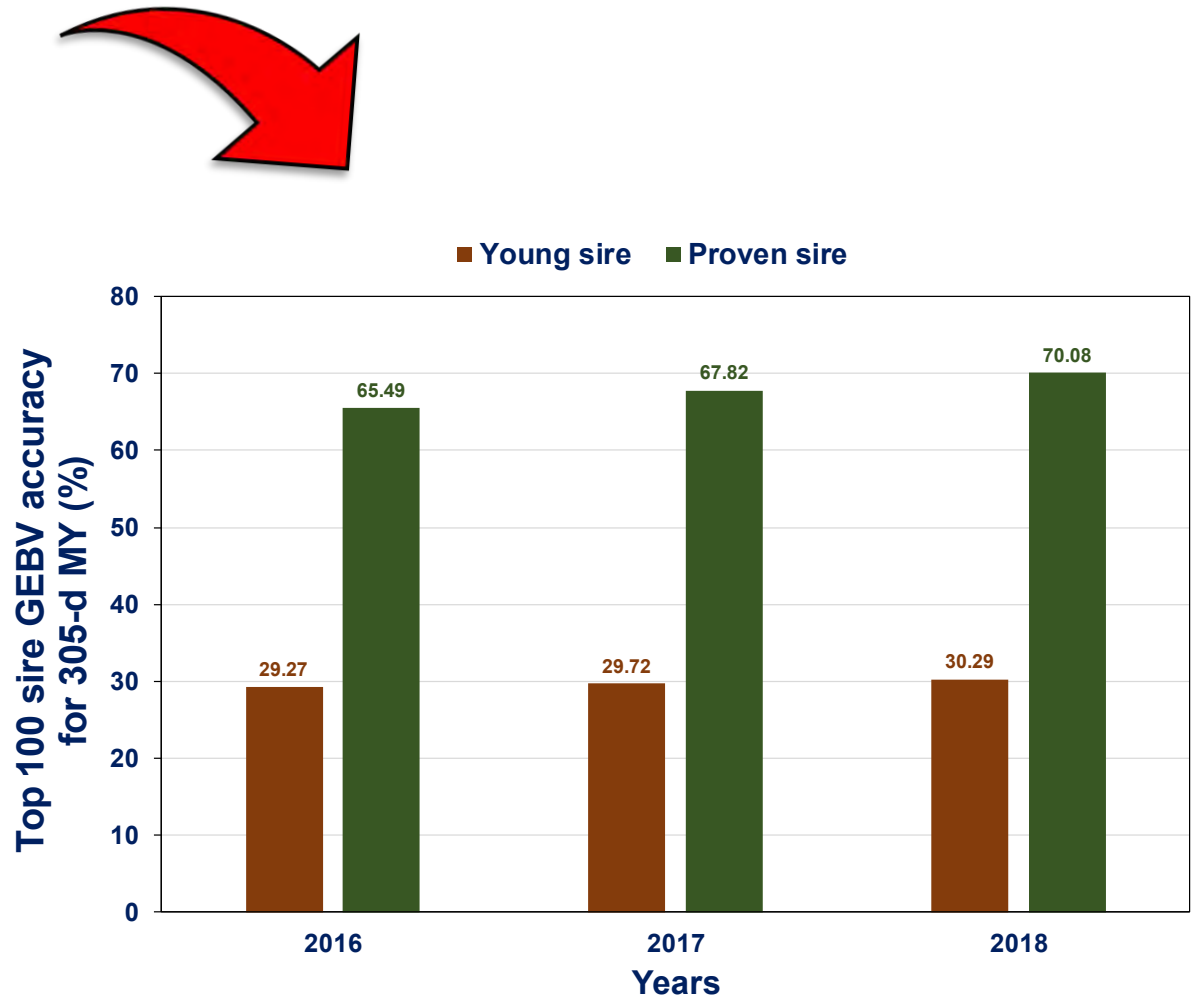
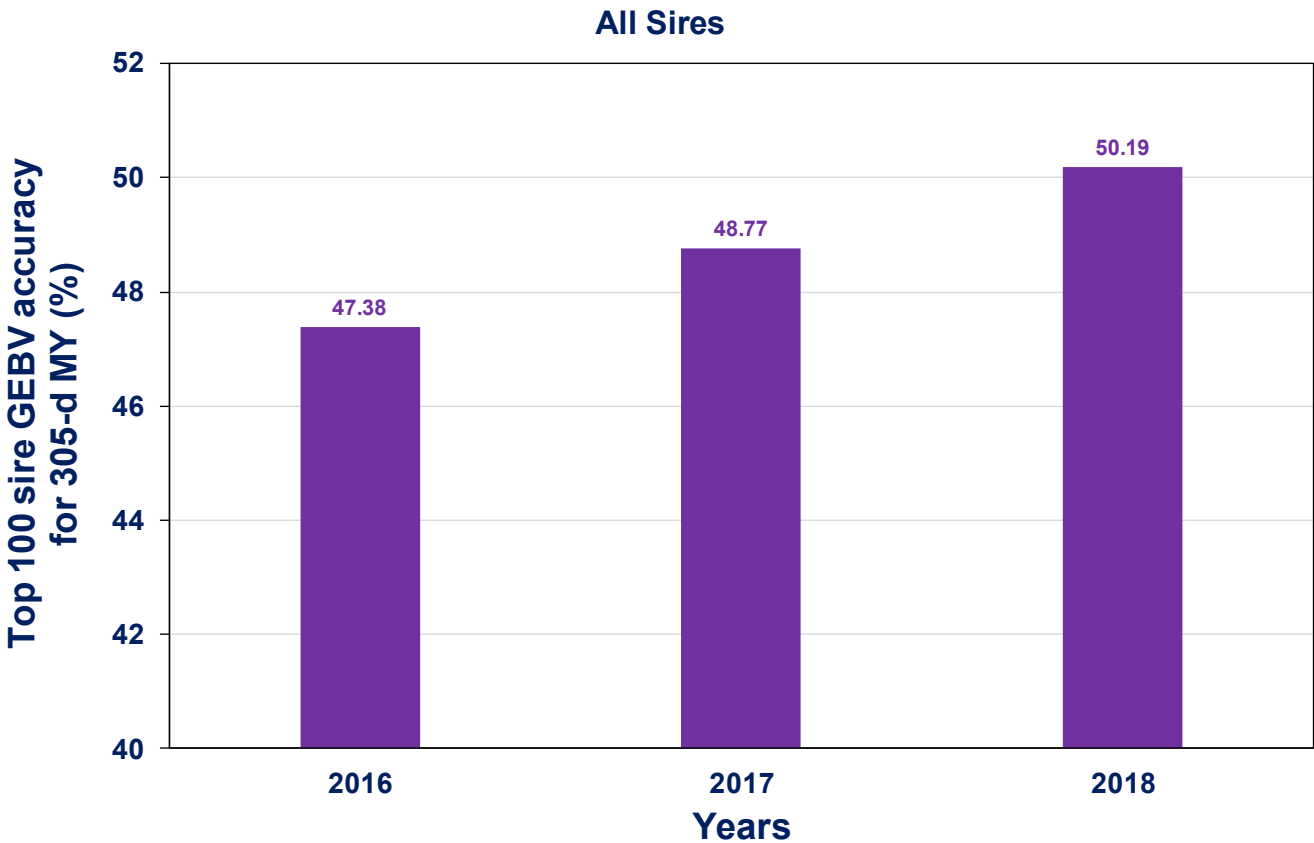


GEBV LSmeans for top 100 sires trended to increase from 290 kg to 312 kg

Genomic EBV for Top 100 Young and Proven Sires



Genomic EBV Accuracy for Top 100 Young and Proven Sires



Conclusions

- ❖ Over 64% of sires that were ranked in top 100 for MY in 2016, 2017 and 2018 were young sires
- ❖ GEBV means for MY trended to increase from 278 kg (2016) to 307 kg (2018) for young sires and 302 kg (2016) to 316 kg (2018) for proven sires
- ❖ GEBV accuracy for MY trended to increase from 29.27% (2016) to 30.29% (2018) for young sires and 65.49% (2016) to 70.08% (2018) for proven sires

Wider utilization of superior sires would help speed up genetic progress for MY in Thai dairy population



Acknowledgements

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Genomic and phenotypic data support



Research collaboration



*Thank you
for your kind attention*



Tropical Animal Genetic Unit

Genomic EBV Accuracy for Top 100 Young and Proven Sires

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

Jattawa et al., 2016

