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Animal Production

Genomic prediction of health traits using a mixed bull and cow reference population for German Holsteins

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vit, IT Solutions for Animal Production**,** Germany, www.vit.de

Distribution of herds of the Herd Genotyping Project (KuhVision) in Germany, Austria and Luxembourg
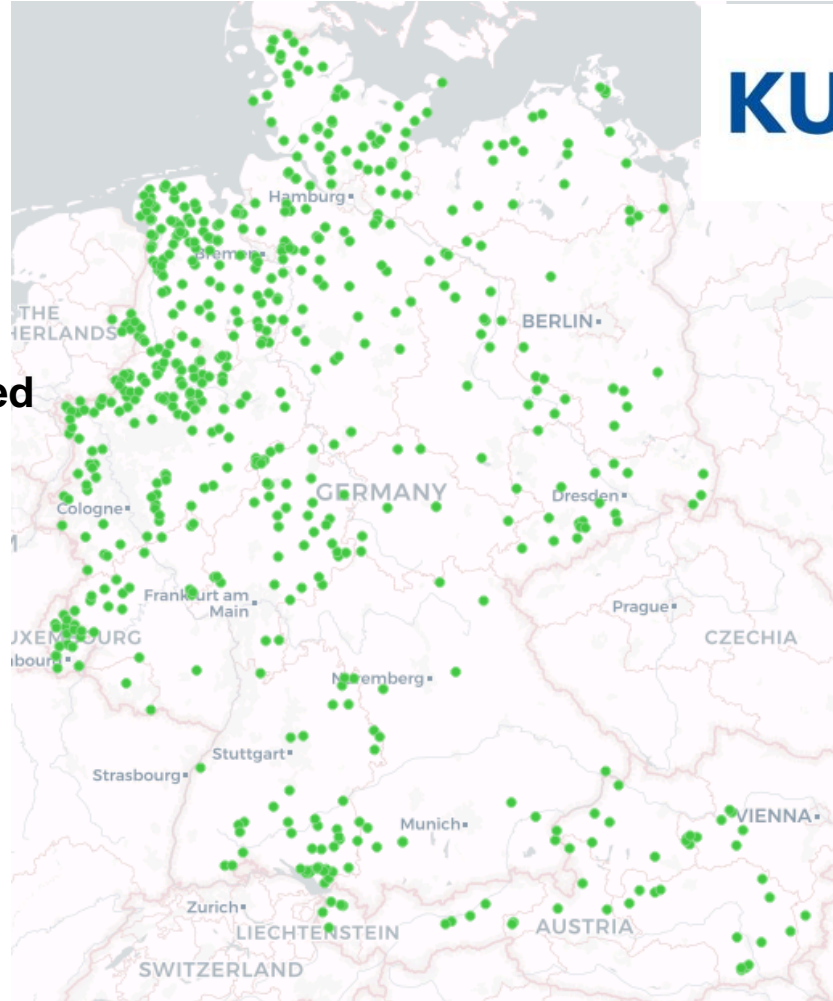
1421 herds

~13% herdbook cows

~50 herds/month added

664 herds for health traits

~379,000 females genotyped

(3 June 2019)

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Direct health traits

Trait complex	Direct health trait	h²	Index weight	h² Index	Total
Udder health	Early mastitis (DIM -10 to 50)	0.029	60%	0.080	**40**
	Late mastitis (after DIM 50)	0.072	40%		
Claw health	Digital dermatitis (Mortellaro)	0.117	30%	0.112	**30**
	Laminitis	0.030	15%		
	White line disease	0.060	15%		
	Claw ulcers	0.110	15%		
	Digital phlegmon	0.085	15%		
	Interdigital hyperplasia	0.113	10%		
Reproduction	Ovarian cycle disorders	0.058	50%	0.066	**20**
	Retained placenta	0.033	25%		
	Endometritis / Metritis	0.032	25%		
Metabolic stability	Left-displaced abomasum	0.029	50%	0.042	**10**
	Milk fever	0.041	25%		
	Ketosis	0.027	25%		

Claw health trait, **interdigital dermatitis**, will be added in genetic evaluation

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Calf fitness

- Calf fitness is defined as survival of female calves from day 3 to 458

- A multi-trait animal model with 5 intervals: day 3-14, 15-60, 61-120, 121-200, and 201-458. Genetic correlations from 0.22 to 0.87.

- Heritability values range from 0.5% to 0.9%. Total heritability: 1.4%

- In April 2019 conventional evaluation
  - 9.6 million Holstein female calves
  - 17 million animals in pedigree

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Genomic reference population for German Holsteins

- Reference bulls: ~ 40,000 Holstein bulls mainly from EuroGenomics
  - From 2019 onward, ~1000 USA/CAN bulls / year from birth year 2014

- All reference cows: from birth year 2011 (Kuh-L) or 2014 (KuhVision)

	Cows (milk production traits)	Cows (Type traits)	Females (Calf survival)	Cows (Clinical mastitis)	Cows (Digital dermatitis)
1804	90,737	73,614		61,550	40,915
1808	105,390	87,150		75,789	46,276
1812	117,644	97,266	262,818	87,809	57,392
1904	130,884	109,746	298,499	100,319	67,994

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Genomic reference populations for the health traits (April 2019 evaluation)

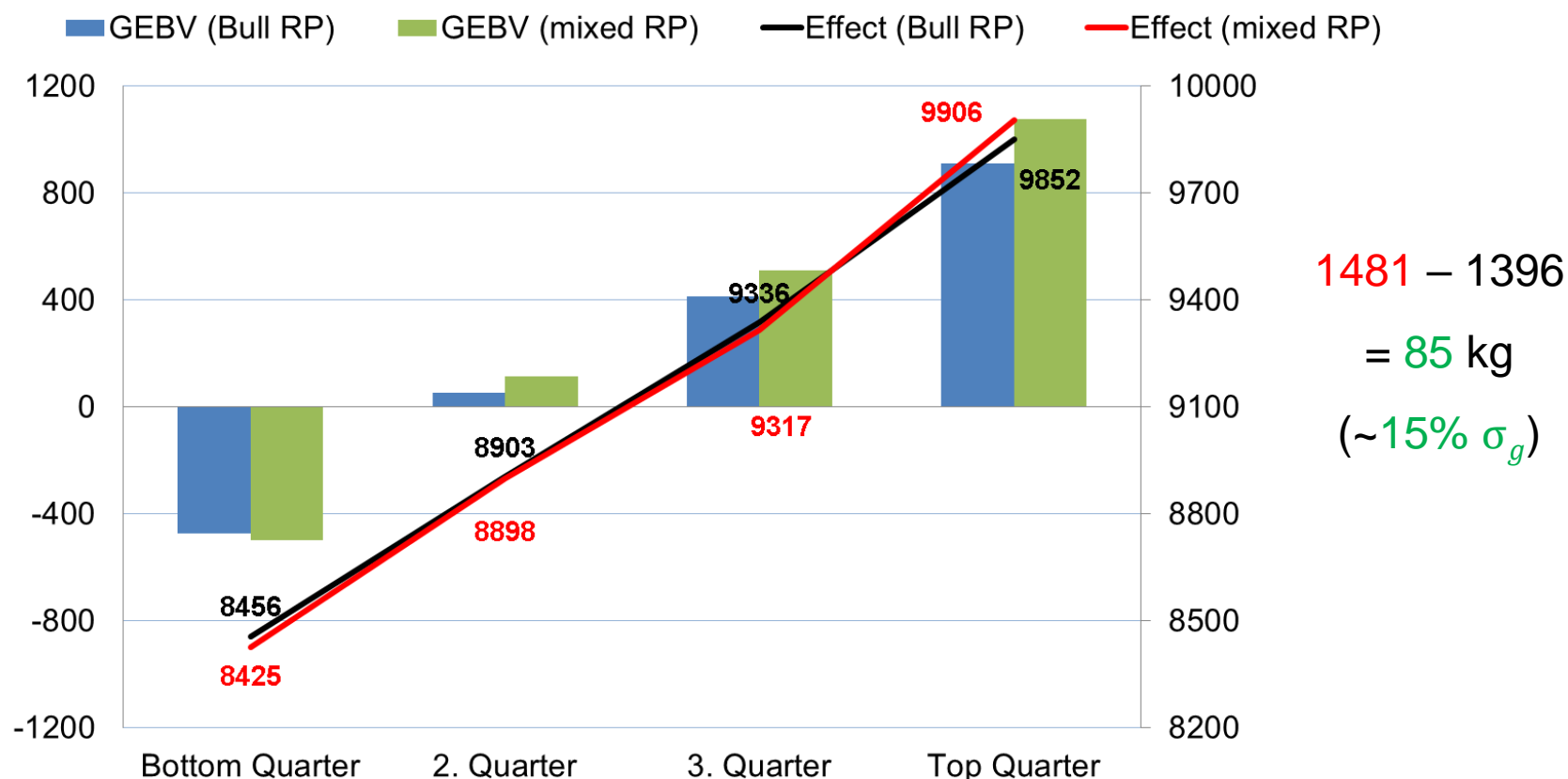| Trait		Bulls	Cows	Total
Mastitis	MAS	4998	100,319	**105,317**
Interdigital hyperplasia	LIM	4214	67,691	71,905
Laminitis	REH	4229	67,734	71,963
White line disease	WLE	4219	67,740	71,959
Sole ulcers	KGS	4045	61,118	65,163
Digital phlegmon	PAN	3974	54,037	58,011
Digital dermatitis	DDM	4140	67,994	72,134
Displaced abomasum left	LMV	4510	78,621	83,131
Ketosis	KET	4709	90,211	94,920
Milk fever	MIF	4632	86,959	91,591
Retained placenta	NGV	4873	87,585	92,458
Endometritis	MET	4413	74,197	78,610
Ovarian cycle disorders	ZYS	4355	60,625	64,980
Calf fitness	RKF	10,424	298,499	**308,923**
Indicator traits: disposal reasons for				
infertility	DR4	11,901	92,204	104,105
udder health	DR6	12,431	129,949	142,380
claw health	DR8	12,431	124,671	137,102
metabolic disorders	DRX	12,399	155,025	167,424

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Comparing the bull and mixed reference populations

- Data structures of the bull and mixed reference population differ
  - Shorter history of whole-herd cow genotyping

- Same data for a fair comparison on prediction accuracy
  - National bulls born in last two birth year as validation animals
    - 606 Holstein bulls born in 2012 and 2013
  - Daughters of these bulls removed from the mixed reference population
    - 8,415 reference cows

- Phenotype and genotype data from August 2018 routine evaluations

- Genomic evaluations using the truncated data sets for both types of reference population

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Accuracy of genomic prediction: observed correlation between DRP & GEBV of validation bulls

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GEBV test: observed R² increase from the EBV to GEBV model for the health traits with a mixed reference population

Calf fitness with a mixed reference population

Calf fitness with a bull reference population

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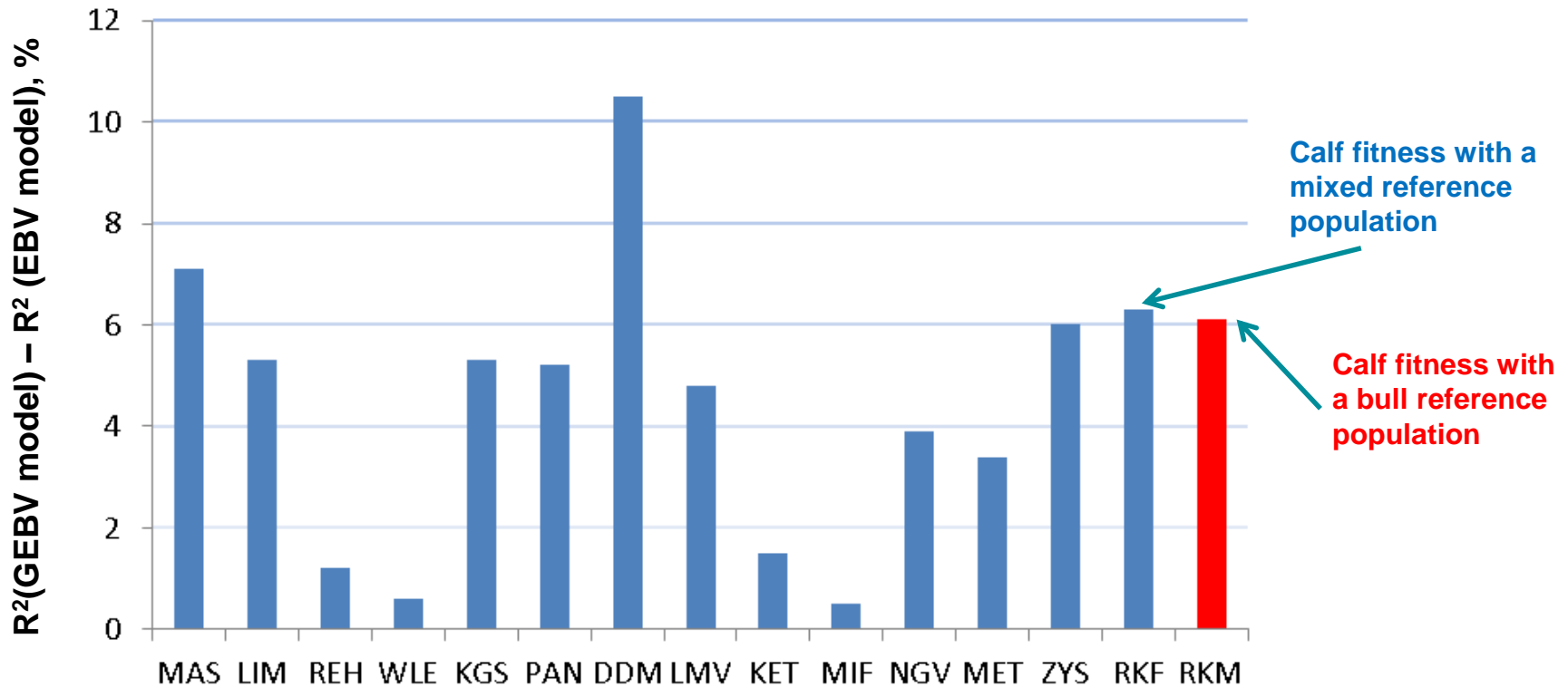
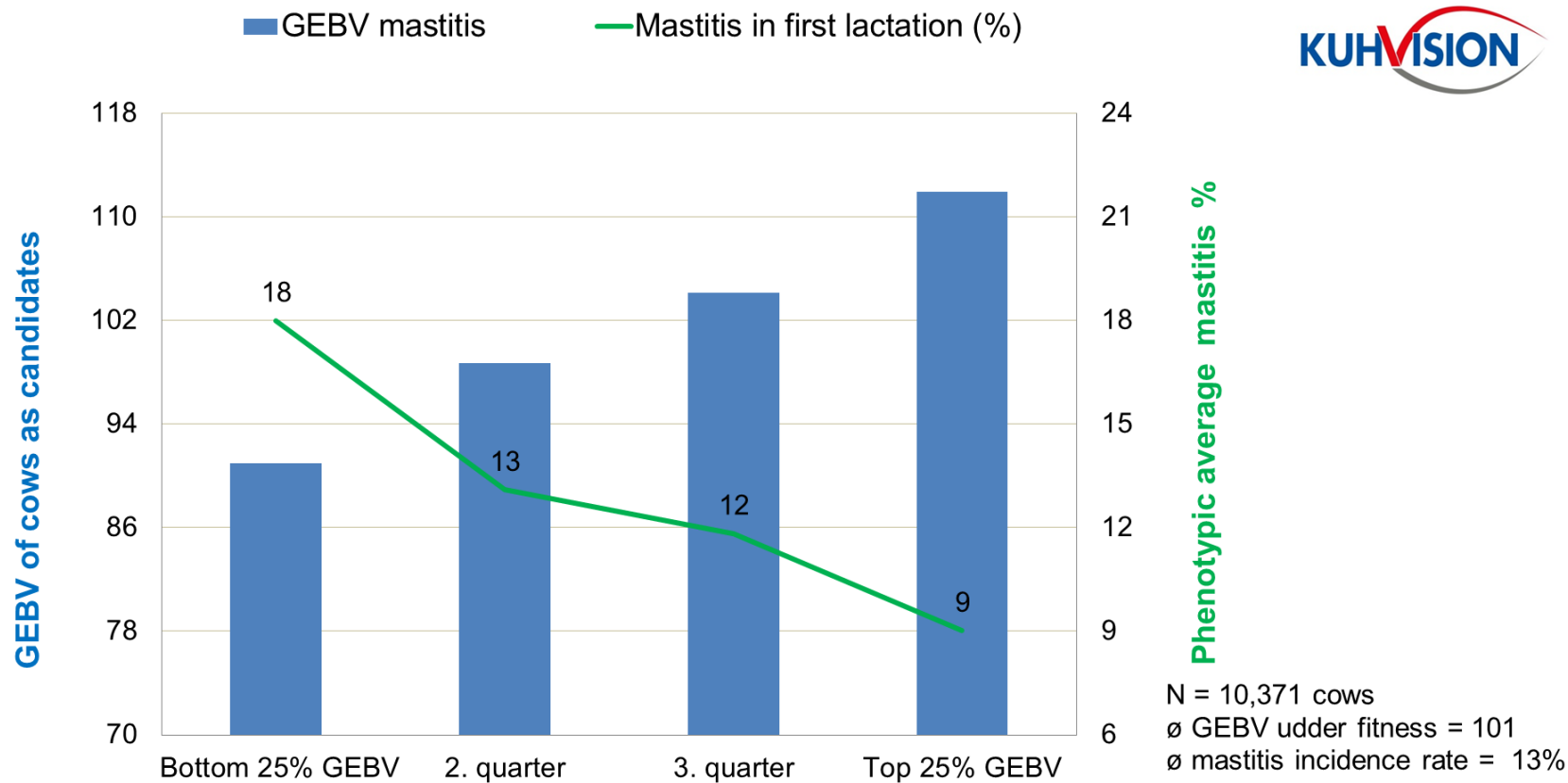# Comparison of phenotypes of validation cows using truncated data set btw. both types of reference population

Legend: GEBV (Bull RP) | GEBV (mixed RP) | Effect (Bull RP) | Effect (mixed RP)

Chart values:
- Bottom Quarter: 8456 (black), 8425 (red)
- 2. Quarter: 8903 (black), 8898 (red)
- 3. Quarter: 9336 (black), 9317 (red)
- Top Quarter: 9906 (red), 9852 (black)

$$1481 - 1396$$
$$= 85 \text{ kg}$$
$$(\sim 15\% \ \sigma_g)$$

6,992 validation cows (daughters of validation bulls)
First lactation milk yield (kg)

$$y = herd + GEBV\_group + error$$
Phenotypic std dev = 893 kg

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Routine verification of candidate GEBV of cows by comparing their phenotypes between cow groups (I)

N = 10,371 cows
ø GEBV udder fitness = 101
ø mastitis incidence rate = 13%

3

Cows were not included in genomic reference population

Summary and Conclusions (I)

- Genomic selection since 2010 has doubled genetic progress
  - >80% semen from young genomic bulls on the national level
  - EuroGenomics bull reference population led to an already high accuracy

- KuhVision project for a mixed bull and cow reference population
  - >370,000 female calves genotyped
  - Genomic reference population increased fast

- Higher accuracy of genomic prediction using a mixed reference population than a bull reference population
  - No decrease in accuracy found in any trait
  - Also for low heritability traits

- Validation cows showed more variation in (later) phenotypes based on (early) GEBV from a mixed than a bull reference population

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Summary and Conclusions (II)

- Application of GEBV test to the new traits
  - Reasonable increase of R^2 values from the EBV to GEBV model despite of using national phenotypes only

- For the early trait calf survival, no difference in accuracy found between bull and mixed reference population
  - Though some female calves not genotyped within first 2 weeks

- Official introduction of the mixed reference population in April 2019 in German Holsteins
  - For all current regular traits, and
  - For the new health traits

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Thanks for your attention!

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Disposal reasons as indicators for direct health traits

- Routine recording of disposal reasons for a long time

- Genetic correlated with direct health traits

- Four disposal reasons for
    - Infertility (DR4, h^2=0.041) → indicator for reproduction sub-index (r_g = 0.55)
    - Udder health (DR6, h^2=0.049) → indicator for mastitis (r_g = 0.85)
    - Claw (DR8, h^2=0.053) → indicator for claw health sub-index (r_g = 0.60)
    - Metabolic disorders (DRX, h^2=0.024) → indicator for metabolic stability sub-index (r_g = 0.80)

- (G)EBV of 4 disposal reasons blended to 4 direct health sub-indices

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Phenotypes of cows for genomic evaluation

- National conventional evaluation for all traits (April 2019)

Regular Trait	Cows with data (number of records)	Novel Trait	Cows with data
Production & SCS	21,984,517 (420,238,055 test-day records)	Calf fitness	9,558,532 female calves
Type & Workability	2,856,592 (8,591,548 workability records)	Claw health	424,240
Longevity	14,735,985	Mastitis	659,870
Fertility	19,825,324 heifers or cows	Metabolic diseases	526,432
Calving	30,424,609 calves or cows	Reproduction	611,492

- De-regression of cow EBV and calculation of effective record contribution

2

A new genomic evaluation system

- **Reference population much bigger than bull reference population**
  - SNP effect estimation more time consuming
  - SNP effect estimation in parallel, with traits distributed to multiple servers optimized via UC4
  - Within two days (starting Thursday afternoon, ending on Saturday)

- **A weekly routine genomic evaluation**
  - Deadline for genotype submission is Thursday 18:00
  - Genomic evaluation during weekend (ending on Friday evening)
  - Monday for results analyses and possible repeating
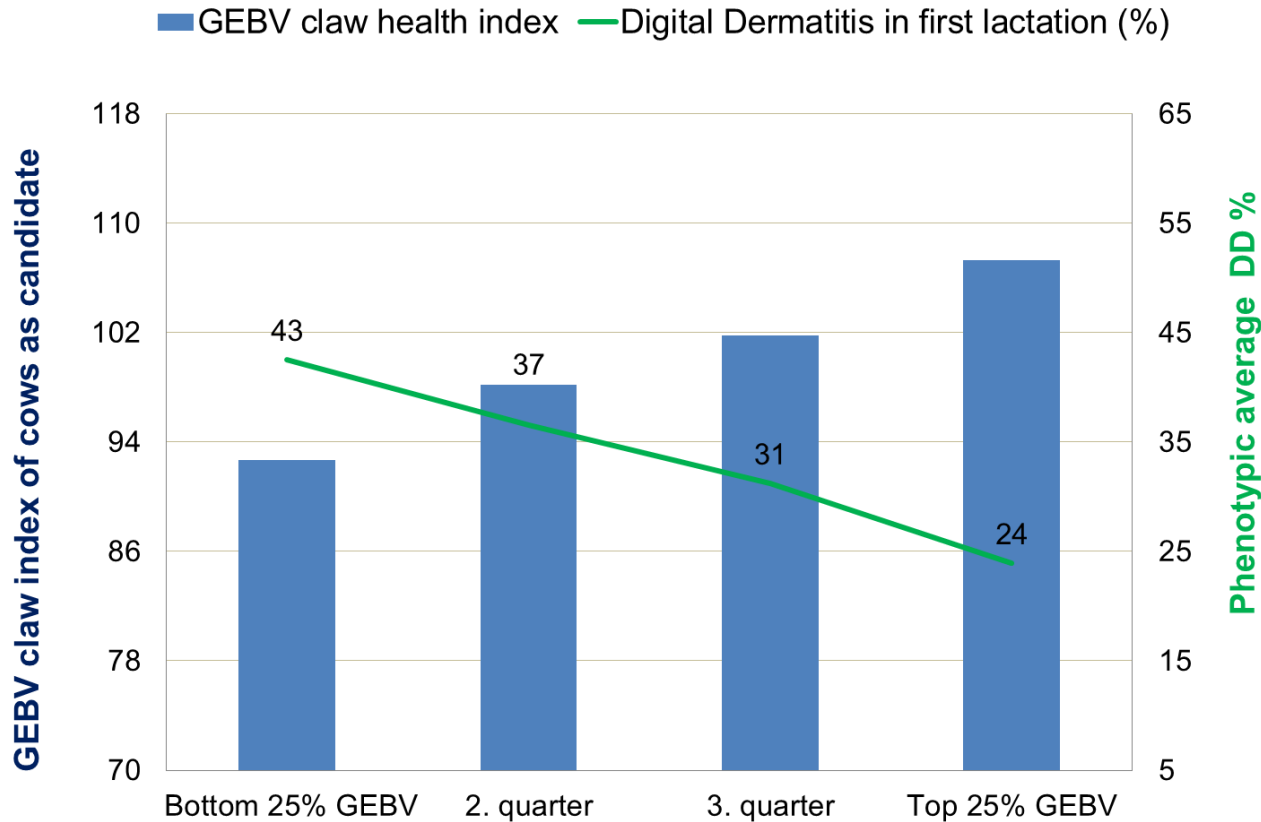 - Official publication on Tuesday morning

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Routine verification of candidate GEBV of cows by comparing their phenotypes between cow groups (II)

N = 3,998 cows
ø GEBV claw index = 100
ø DD incidence rate = 33%

Cows were not included in genomic reference population