



IT-Solutions for
Animal Production

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Impact of Genomic Selection on Organizational Structures in Milk Recording and Breeding

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- Where we came from
 - Progeny test

- *Genomic Selection 1.0*
 - Started 2009 / 2010, classical 'Interbull' traits

- *Genomic Selection 2.0*
 - started 2014-2016, Complete herd genotyping, new traits

- *Genomic Selection 3.0*
 - New sources of data

- Where do farmers want to go

- Outlook

Classical dairy cattle breeding programmes

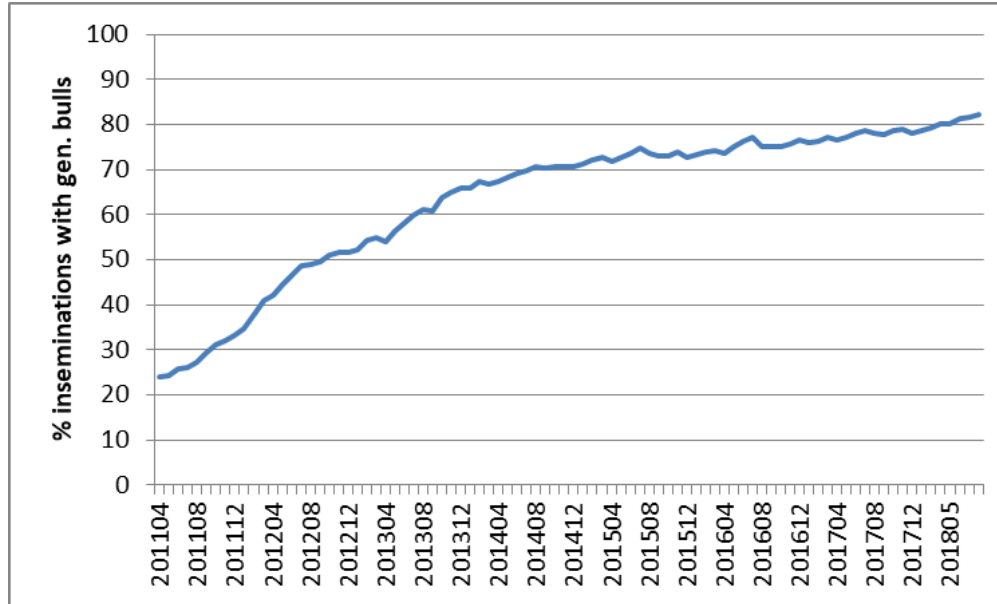
- Progeny test: size of AI breeding (testing) programs was limited by size of DHI cow population
 - International marketing of proven bulls via Interbull MACE
- *Genomic Selection 1.0* made use of large amount of historic data from progeny testing programs / DHI data
- Classical evaluation HOL Germany (April 2019):

Traits	MFP/SCC	Longevity	Fertility	Calving	Conform.	Milk.-speed
Data included >=	1990	1997	1995	2000	1998	1990
# records	420 Mio	15 Mio	43 Mio	24 Mio	2.9 Mio	8.6 Mio
# animals with rec.	22 Mio	15 Mio	29 Mio	11 Mio	2.9 Mio	2.7 Mio

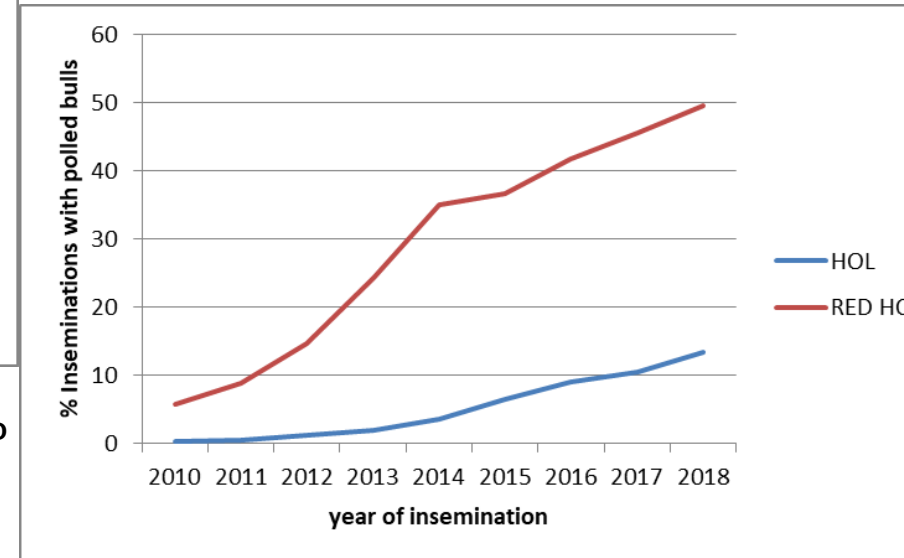
EuroGenomics reference bulls include via Interbull MACE phenotypes from about 40 Mio cows

→ Very reliable gEBVs for the 'historic traits' for male AND female calves

Use of young genomic Holstein bulls in cow population (DEU)

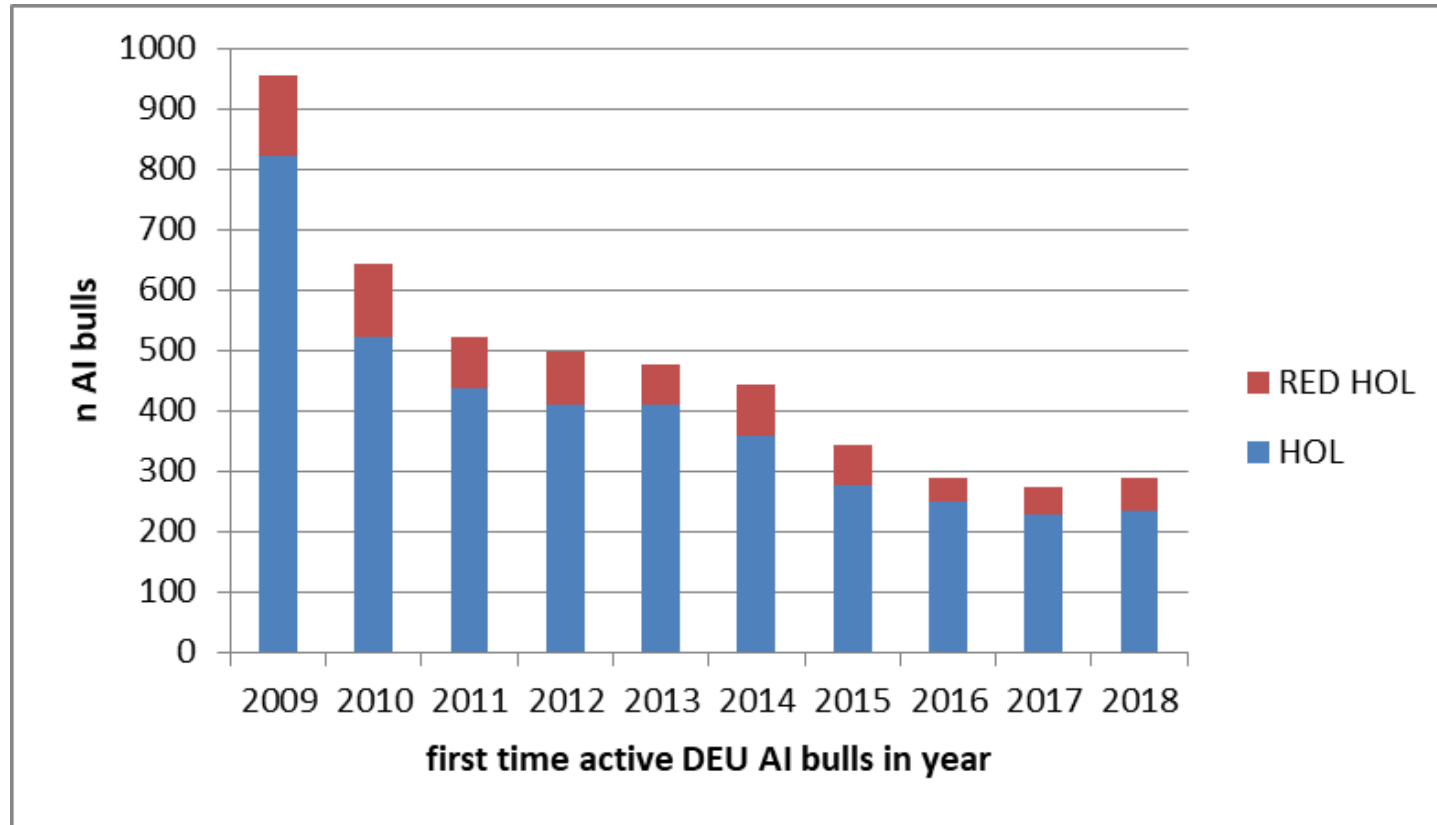


- % use of young genomic bulls now at 80%
 - Internationally 50-98%



- Increase of market for polled bulls in Germany

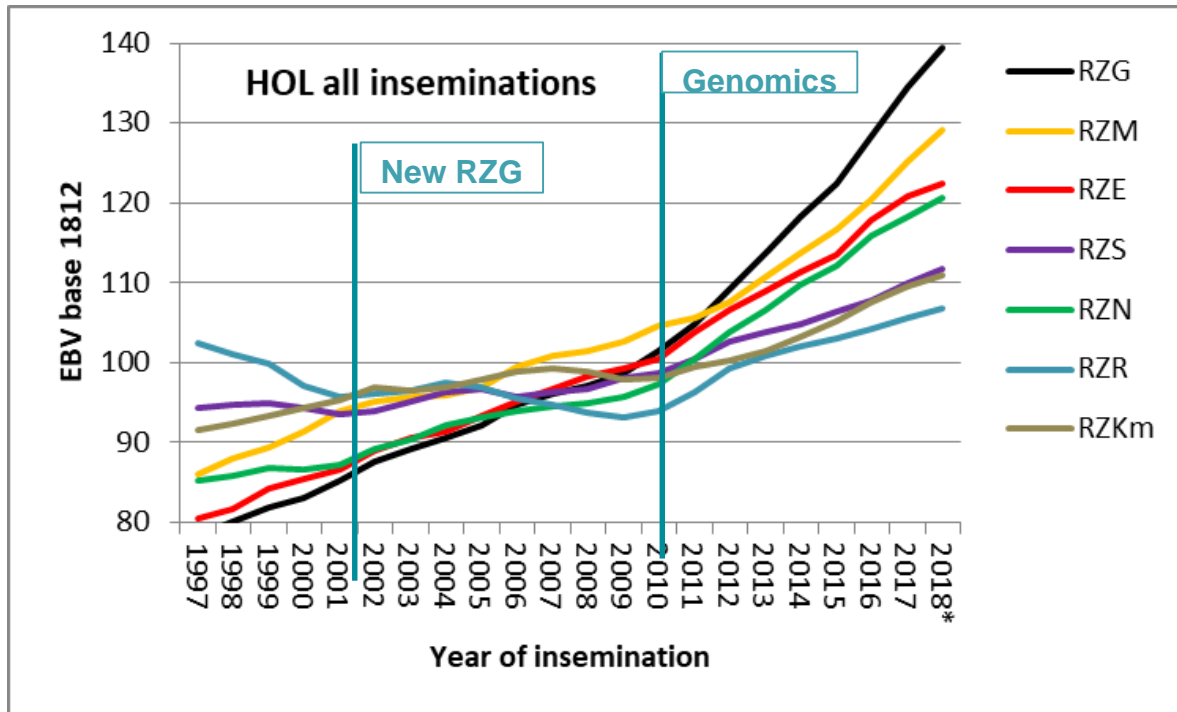
DEU: Development of number new HOL A.I. bulls per year



- But smaller number of bulls and strong preselection (1 : 40) causes problems in classical genetic evaluation ← input to bull reference population

Increased genetic progress by Genomic Selection

- EBV all used semen straws Holstein bulls in Germany, mean =100, SD = 12



HOL	Progress/year		
	1998-2001	2002-2010	2011-2018
all ins.			
RZM	1,94	1,20	3,05
RZE	1,55	1,54	2,75
RZS	-0,21	0,59	1,62
RZN	0,52	1,11	2,91
RZR	-1,68	-0,20	1,60
RZKm	0,92	0,31	1,60
RZG	1,74	1,80	4,75

- With genomic selection progress in all important traits
 - And more than doubled progress in TMI
 - Progress longevity now same as for milk production

10 Years Genomic Selection for Holstein → Breeding

- Very good selection response
 - Large databases with phenotypes from DHI
 - Combination of reference populations through Interbull MACE
- Number of new AI bulls per year
 - decreased significantly in European AI programs
 - decreased slightly in USA
- Improved international comparability of young AI bulls and females
 - Fully comparable gEBV by exchange of SNP
- High prices for elite females
 - Few individual private farmers that are still breeding AI bulls
→ many belong to AI companies or farms under contract
- New players in the AI market and increased competition
→ less AI companies

Genomic Selection for herd management

- First years of GS
 - Genotyping relatively expensive
 - Only potential elite females genotyped
 - Now
 - Genotyping cheaper (25-40 \$)
 - Higher selection intensity e.g. by use of sexed semen
 - → herd genotyping and Genomic Selection = Genomic Herd Management has become profitable for commercial dairy herds
 - e.g. in USA ca. 25% of all (new) Holsteins in DHI
 - e.g. in Germany ca. 11% of all (new) Holsteins in DHI
 - Advantages
 - Precise selection among calves (saves rearing costs)
 - Precise mating for all traits and for heifers and cows
 - Parentage verification and detection, management of genetic recessives
- on farm breeding decisions independent from phenotypes (DHI and classification)

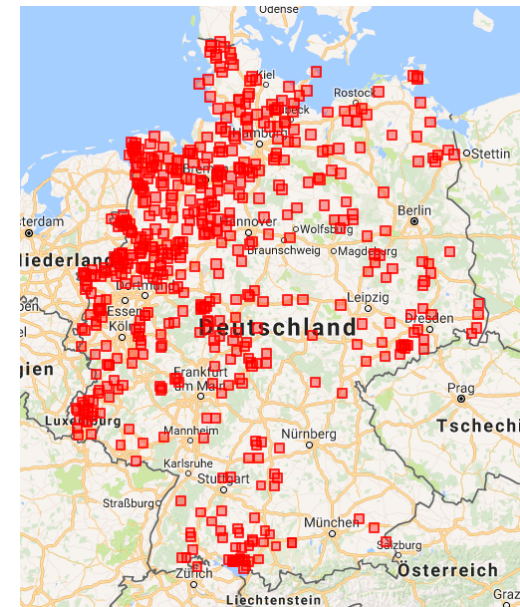
Genomic Selection 2.0

- Introduction of new traits into Genomic Selection not possible by bull reference population
 - Would take to long time
- Introduction of new traits possible by cow reference population
 - Reference cow = genotyped cow/female with phenotype
 - 3-10 reference cows same information content as one reference bull with 100 non-genotyped daughters
- for effective cow reference population just small proportion of all (DHI) cows needed
 - E.g. equivalent of 35,000 bulls = 105,000 – 350.000 reference cows
 - 3-10% of US-HOL DHI cows
 - 5-17% of DEU-HOL DHI cows
 - for Interbull traits by farms with herd genotyping already given
 - for some new traits (e.g. health traits) almost given
- Currently data recording by DHI in genotyping herds is still the base

KUHVISION : the perfect cow reference population



- Started in June 2016 as a joint project by German Holstein breeding associations with **vit**, later CONVIS (Lux.) and Holstein Austria joined
- Now a fast growing standard tool for commercial farmers
- 1,421 farms participating in whole herd genotyping / KuhVision
 - 664 farms providing data on new traits
 - 30-35 new farms every month
- milking >10% of all milk recorded HOL
- 370,000 female HOL genotyped
- >150,000 cows have already calved



3. June 2019:



Mixed cow + bull reference population health traits

- Reference cow: genotyped cow with health record
 - Health records from all lactations for genetic evaluation
- Reference bull: AI bull with daughters (non-genotyped) with health records
- Size of mixed reference population health traits (here Mastitis)

	RP cows	RP bulls	RP total
04-2018 (test)	61,550	5,574	67,124
08-2018 (test)	77,029	6,159	83,188
12-2018 (test)	87,809	6,337	94,146
04-2019	ca. 100,000	ca. 6,500	ca. 106,500

Reliability (rel) of gEBV health traits

- Data just from new cow reference population

Trait	Weight in RZhealth	Without culling reasons		
		rel. P.I.	rel. dGV	rel. gEBV
RZudderfit	0.40	0.13	0.43	0.48
DDcontrol		0.14	0.46	0.51
RZhoof	0.30	0.13	0.41	0.46
RZrepro	0.20	0.12	0.43	0.48
RZmetabol	0.10	0.13	0.39	0.43
RZhealth		0.13	0.42	0.47

- Reasonable reliabilities for gEBV all 4 health trait indices and RZhealth

Improved reliability (rel) of gEBV health traits

- By information from national DHI recording of culling reasons

Trait	Weight in RZhealth	Without culling reasons			gen. corr.	Incl. culling reason	
		rel. P.I.	rel. dGV	rel. gEBV		rel. gEBV	rel. gain
RZudderfit	0.40	0.13	0.43	0.48	0,85	0.61	(+0.13)
DDcontrol		0.14	0.46	0.51			
RZhoof	0.30	0.13	0.41	0.46	0,60	0.51	(+0.05)
RZrepro	0.20	0.12	0.43	0.48	0,55	0.52	(+0.04)
RZmetabol	0.10	0.13	0.39	0.43	0,80	0.55	(+0.12)
RZhealth		0.13	0.42	0.47		0.57	(+0.10)

- Higher reliabilities for gEBV all 4 health trait indices and RZhealth

Classes of gEBV claw ulcer ⇔ % incidence



N = 9821

ø gZW-KGS = 106

ø KGS-Inzidenzrate% = 11%

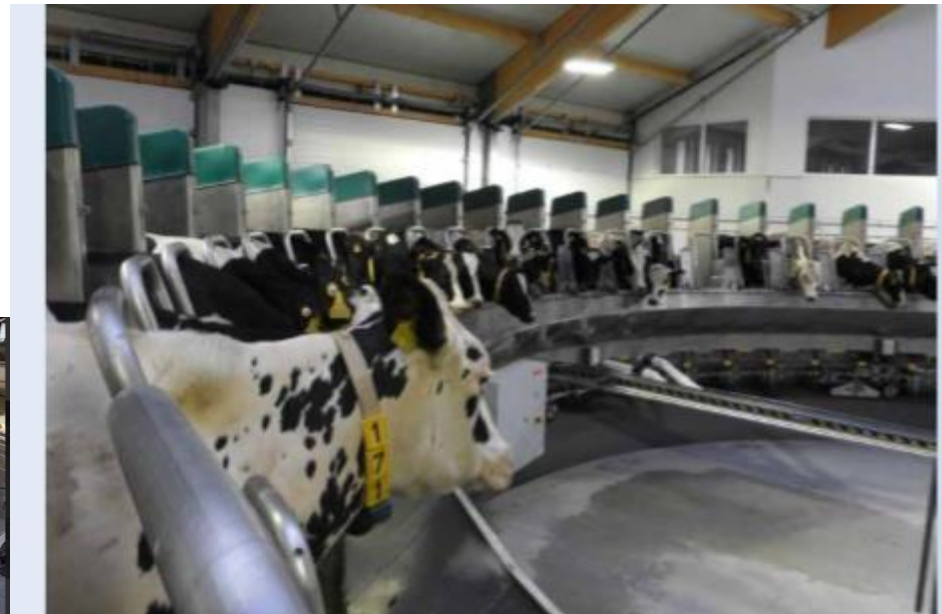
Genomic Selection 3.0

- New traits based on new ways of data recording
 - on farm (and often independent from DHI)
- i.e. (mass) data recording by sensors
- Dynamic developments driven by
 - Market for dairy management solutions
 - Breeding programs, too
- From the viewpoint of breeding programs
 - Possibility to differentiate from competitors not just by the better bull for same trait → more by new important traits
 - But investment of breeding programs needed in own data recording systems in cooperation with innovative farms
- First results are in the market

- In principal: if sensors can record data on challenging new trait, they can do for classical traits, too

Automatic Milking Systems (AMS) / Robots

- Increasing use in dairy farms
- Reduced time for visual inspection of animals
 - Interest in sensor data for
 - Milkability, Temperament
 - Udder health
 - Volume and content of milk
 - Further traits



Technical drawing of a square plate with the following dimensions and features:

- Overall width: 150
- Overall height: 125
- Inner square area (yellow): 80 x 80
- Outer square area (green): 130 x 130
- Four green circles (radius 27) located at the corners of the green area.
- Four orange circles (radius 27) located at the corners of the yellow area.
- Four grey circles (radius 27) located at the corners of the overall square plate.

- Actual teat location based on successful attachment
- Can we improve trait heritability?

Study from the Netherlands, Lely AMS

70 herds, 20.000 cows, h^2



Udder conformation traits

	h^2 ams	h^2 class.	r_s
Front teat distance	0.66	0.46	-0.96
Rear teat distance	0.56	0.45	-0.97
Udder depth	0.74	0.49	0.91
Distance front-rear	0.69		Not corrected for stature!
Udder balance	0.48		
Udder balance left-right	0.03	Low heritability Less useful trait	
Unevenness	0.45		

AMS

Objective (exact) score
Measuring multiple times
Easy to measure extra traits



Classifiers

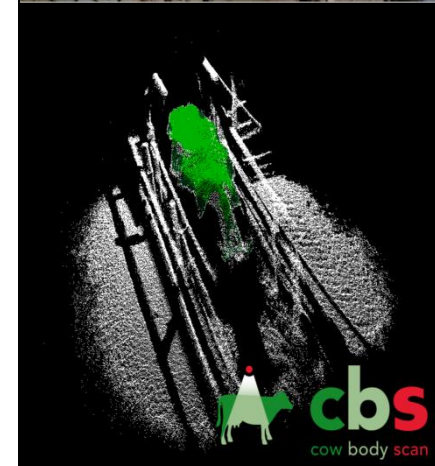
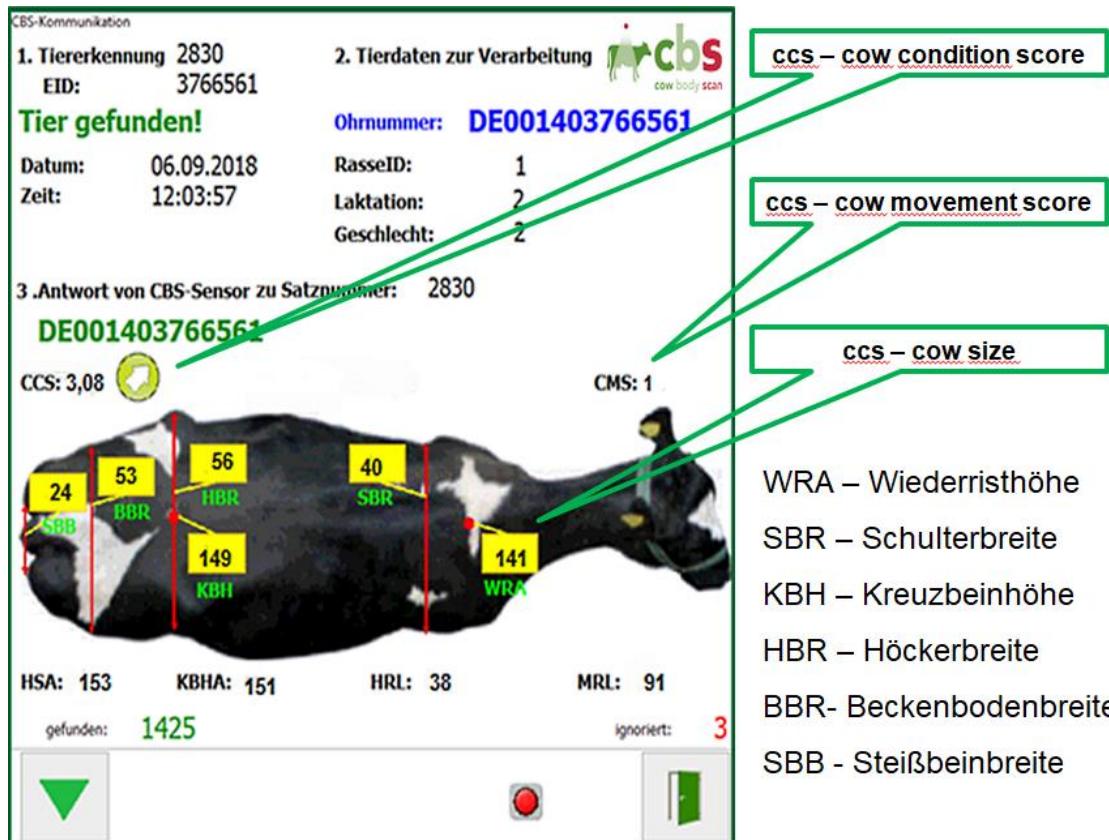
Subjective score
Measuring only once

Higher heritability for AMS traits



Type traits collected by cameras

- Movement scores
- Cow condition scores and cow size



New data sources arrive rapidly

- From big manufacturers (blue, grey, red)
- Specilised Manufacturers (eg acivity sensors)
- From startups
 - Using the camera of a regular smartphone
- Many more



Low activity
High activity

Body condition score

COW DATA

Feed consumption
Visits to feed station

Milking interval
Flow
Milk yield

Gate passages

LDH **SCC**
BHB
Progesterone
Urea

Body weight

Electrical conductivity
Colour / blood

How do practical farmers look onto this?

- Looking for some examples that have made use of these new possibilities
- Opinion on future development

Herd management in times of GS and sensor data

Two examples from US and Germany:

- No-Fla Holsteins, Florida/USA
(owner Don Bennink)



- Benninghoff Holsteins, North Germany
(owner Marc Benninghoff)



Herd management in times of GS and sensor data

Two examples from US and Germany:

	No-Fla	Benninghoff
HOL milking cows	6,500	1,200
Herd genotyping	since 2014	since 2016
Use genomic bulls	>90%	100%
Cows/heifers with embryos	50%	25%
Heifers as donors	90%	100%
Use beef bulls	0%	25%
DHI participation	yes	yes

What changed ?

	Selection/Breeding
Before Genomics	DHI results, pedigree, conformation (<u>on cows</u>)
Current	Genomics, pedigree, conformation (<u>on calves/heifers</u>)
	Management decisions
Before	Daily milk yield, monthly DHI results (SCC)
Current	No-Fla: Daily milk yield, monthly DHI results (SCC) Benninghoff: Daily milk yield, activity data, SCC from DHI
Future	More on-farm measures (fat, prot., SCC, ketosis, progesteron)
	Value of DHI
Before	Monthly data recording, statistics (actions, benchmarking)
Current	Statistics (actions, benchmarking)
Future	Statistics and advise based on combination of all (central and on-farm recorded) data

Summary

- Genomic Selection based on bull reference populations
 - changed Holstein breeding programs
 - increased genetic progress
 - Increased competition among AI breeding programs
 - ➔ some impact on organizational structures in breeding
 - ➔ no impact on structures of DHI
- Genomic Selection based on female reference populations
 - Needs only data from small proportion of cow population/herds
 - Offers opportunities for new important traits
 - Genomic data is already given by herd genotyping for management
 - Sensor data are on the way to provide (all) necessary data
 - ➔ impact on organizational structures in breeding
 - ➔ possibly severe impact on structures of DHI
 - ➔ possibly severe impact on structures of (national) genetic evaluations



Outlook

- Genotyping of all females will become a well used standard tool
- Farmers will use more technical devices in **day to day** management
→ big role/task for ICAR to evaluate the properties of this new data
- Herd Genotyping AND new on-farm tools are a big threat to traditional farmer owned service organisations
- Progressive farmers:
 - Role of DHI / Labs with more flexible test plans (early lactation)
 - Benchmarking
 - Use of spectral data
 - AI and DHI → jointly help them to integrate data from different sources
→ iDDEN
 - Farmers are willing to share on farm data if the novel services are of value to them

vit



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