IT-Solutions for
Animal Production

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Session: TS 1

Setting up a female reference population for German Holsteins

Reinhard Reents, H. Alkhoder, Z. Liu, F. Reinhardt, D. Segelke, K. Stock

Vereinigte Informationssysteme Tierhaltung w. V. **vit**, Germany,
http://www.vit.de/

Future challenges in genomic evaluation (GE)

1. Bull reference populations (RP) will become less informative
   - Random progeny testing programms stopped with Genomics
   - Less daughter proven bulls
   - Genomic bulls highly preselected (1 out of 40) ➔ selection bias expected

   ➔ A random, unselected RP covering the whole genetic variability of the population, is needed

2. New traits needed in future breeding programs
   - Eg Health, claw traits, feed efficiency
   - New traits / measurements derived from sensors on farm
     (Locomotion, heat detection, rumination,….)
   - New traits derived from additional data analyzed by labs
     (Spectral data, hormons status, …)

   ➔ Quick start in GE for these new traits only possible using **genotyped animals with own performance**

Cow reference population

meets these requirements, if

- complete herds are genotyped (all females)
- additional new traits are recorded on all cows in these herds

Steps

→ Data collection for new traits
Motivation and support of farmers to participate

→ Genotyping all females and genomic evaluation

→ Linking both elements to a national cow reference population

GKUHplus Project → new traits

- German federal structure created regional pilot programs
- German Innovation Partnership linked successful regional health projects and their knowledge and expertise (national initiative)
- Partners are both breeding organisations but also DHI organisations
- Comprehensive concept of
  - On farm collected data (mainly by the farmer)
  - Data recorded by veterinarians

Deutsche Innovationspartnerschaft dipAgrar

GKUH plus
GESUNDHEITSMONITORING

The project is supported by funds of the German Government's Special Purpose Fund held at Landwirtschaftliche Rentenbank

Bundesanstalt für Landwirtschaft und Ernährung

rentenbank

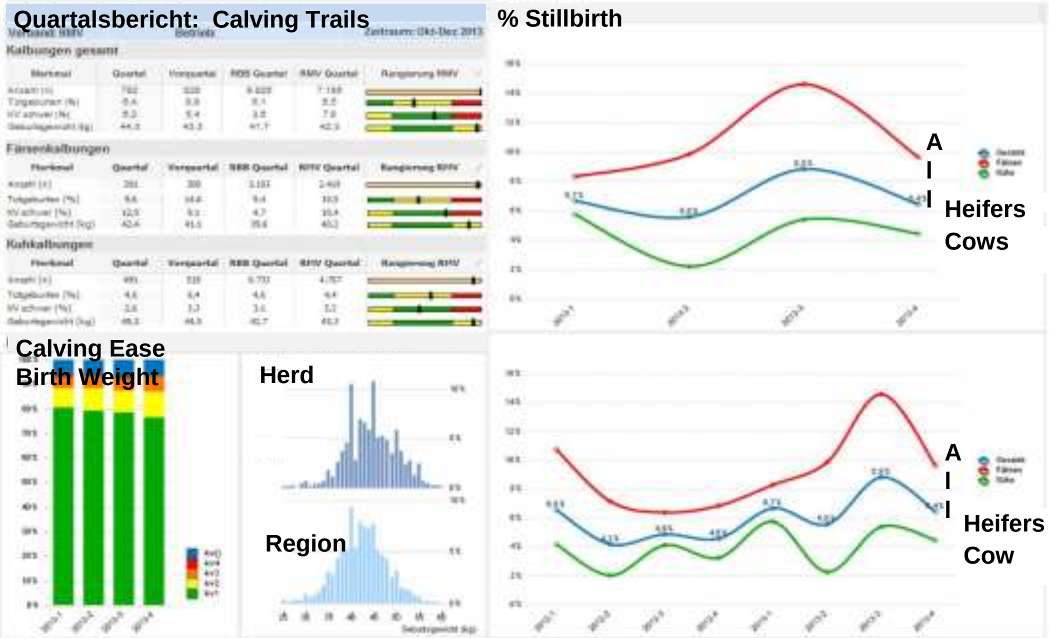
project period: 9 Jan 2014 to 30 June 2017
project coordination: vit (F. Reinhardt / K.F. Stock)

Health data recording in practice (I)

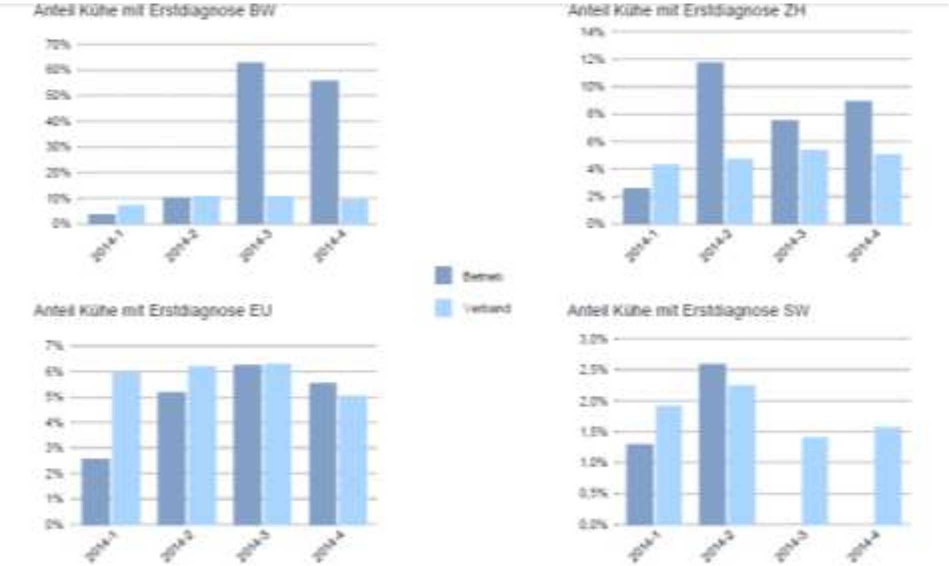
- standardization and harmonization of phenotype data collection
  - early engagement in the German dairy sector (mainly vit / VIT-PCS) for systematic recording and use of health data
  - German reference as model for international reference:
    ICAR guidelines for Recording, Evaluation and Genetic Improvement of Health Traits with ICAR Central health key (ICAR 2012)

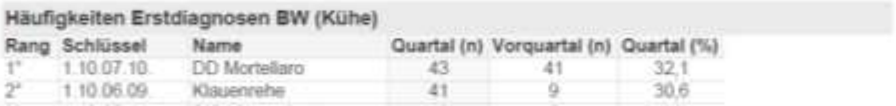
- Immediate feedback to farmers is crucial
  - central health data base (vit)
  - health reports as management tool
  - joint genetic evaluation for direct health traits in Holstein dairy cattle

Feedback to farmers



- **visible benefit** as key to success: motivation (continuity, completeness), intrinsic data quality control
  → **health reports including benchmarks**, EBV for health traits





Häufigkeiten Erstdiagnosen BW (Kühe)

Rang	Schlüssel	Name	Quartal (n)	Vorquartal (n)	Quartal (%)
1*	1.10.07.10.	DD Mortellaro	43	41	32,1
2*	1.10.06.09.	Klauenrehe	41	9	30,6

Genetic evaluation for direct health traits (GKUHplus)

- estimation basis:
  - Holstein health data from eight German federal states plus Austria (time period 01/2007 - 06/2016)
  - health events and information from routine claw trimming
  - approximately 2 million health records
  - in total about 400,000 informative lactations of 200,000 animals
- genetic evaluation:
  - multivariate linear animal model with repeated observations
  - EBV for individual health traits and derived indices

Now nearly all regional projects on one harmonised level

spectrum of health traits in the GE prototype for Holstein dairy cattle:

- udder health (early mastitis, late mastitis)
- metabolic stability (ketosis, left abomasal displacement, milk fever)
- reproduction (retained placenta, ovary cycle disturbances / sterility)
- claw health (interdigital hyperplasia, laminitis, white line disease, claw ulcers, digital phlegmona, digital dermatitis)

Genetic parameters of health traits (GKUHplus)

Health Trait	N	LI [%]	h²	Index weight	Index h²
Early mastitis (-10 to 50 day in milk)	220,167	18.3	**0.04**	60%	0.10
Late mastitis (after 50 days in milk)	195,516	33.3	**0.10**	40%	
Retained placenta (* uterine disorders)	224,091	12.2	**0.04**	50% *	0.04
Sterility / ovary cycle disturbances	208,549	24.8	**0.04**	50%	
Ketosis	211,022	3.3	**0.02**	25%	0.04
Milk fever	210,044	4.7	**0.03**	25%	
Left-displaced abomasum	196,292	2.5	**0.03**	50%	
Interdigital hyperplasia	129,269	8.2	**0.15**	10%	0.08
Laminitis	137,269	13.5	**0.06**	15%	
White line disease	134,737	11.9	**0.09**	15%	
Claw ulcers	124,473	19.4	**0.09**	15%	
Digital phlegmona	119,180	15.9	**0.07**	15%	
Digital dermatitis (Mortellaro's disease)	135,196	25.8	**0.06**	30%	

$SE_{h^2} < 0.01$

Selected health traits with total number of lactations (N), lactation incidences (LI) and heritabilities (h²) from multivariate linear repeatability animal models (health data from GKUHplus project, 01/2009 to 03/2016)

Kuh-L Cow reference population

- Founded by German ministry of education and research
- Project partners
  - FBF (all German Breeding Org)
  - Uni MLU (Halle)
  - Uni Kassel
  - vit
- Main goals
  - Start of setting up a cow reference population (20,000 unselected cows)
  - in 56 contract herds (RA / RBB) with collection of health data since 2008
  - Development of GE methods based on cow RP

    VARCOMP(add., dom), estimation of SNP-effects, single step procedure, ….

Male / Female equivalence

Male EBV reliability*	Heritability				
	0.1	0.2	0.3	0.4	0.5
0.40	6.0	2.7	1.6	1.0	0.7
0.50	**9.0**	4.0	2.3	1.5	1.0
0.60	13.5	**6.0**	3.5	2.3	1.5
0.70	21.0	9.3	**5.4**	3.5	2.3
0.80	36.0	16.0	9.3	6.0	4.0
0.90	81.0	36.0	21.0	13.5	9.0

Boichard et al. (2015)

***) Based only on progeny performances**

Similar conclusion as Goddard et al., 2009

→ 5-10 times more cows than bulls in the reference population

Data for validation of GE (DGV) based on different reference populations

(Most recent data, Sept. 2016)

➔ GE with three different reference populations

1. Kuh-L, unselected cow RP (n = 18,722 cows in 56 herds)
2. Official EG-bull RP (approx. 33,000 bulls with ~40 mio daughter rec.)
3. Combined cow-RP + bull-RP (approx. 52,000)

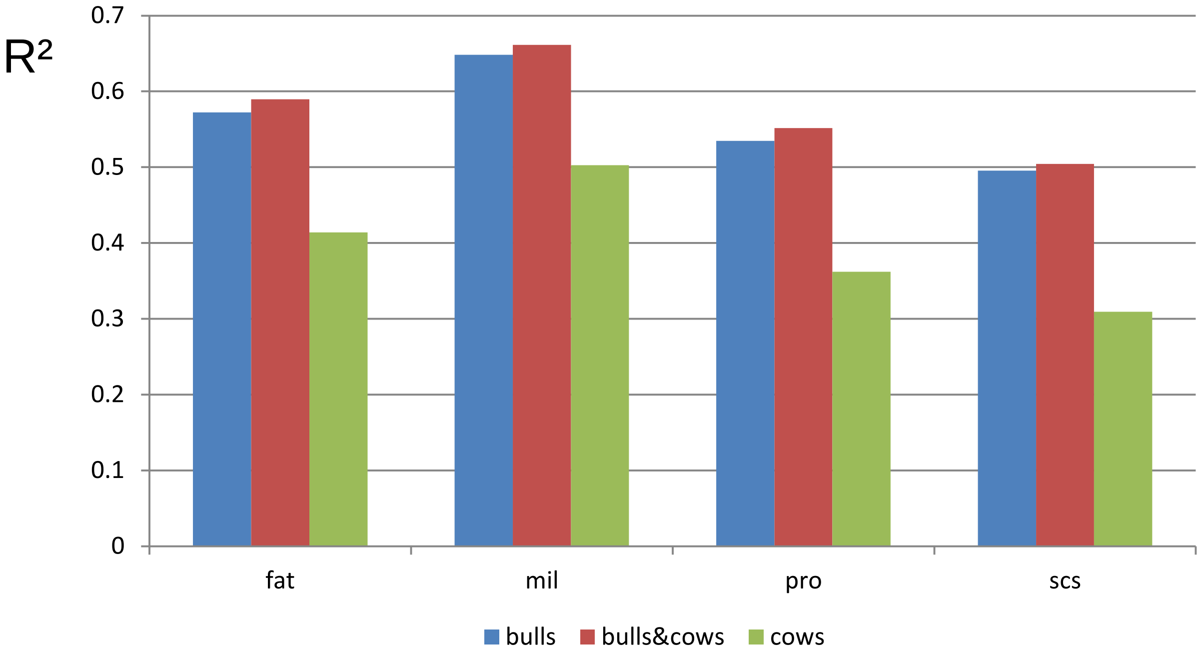
➔ Validation sample

647 German Holstein bulls

(daughters of validation bulls excluded)

Observed validation R^2 values of direct genomic values (DGV) for different reference populations

Deregressed_EBV (MACE) = $b_0 + b_1 * \text{DGV}$ N = 647 bulls



2-step procedure used:

- Estimation of SNP-effects via DRP from conv. GE according to each RP

Conclusion from the results of Kuh-L

- ➔ Information from cows leads to plausible results
  - SNP-effects, DGV
  - R² in a plausible/expected range considering size of cow RP (19.000)

- ➔ Adding unselected cows to bull RP increases accuracy of GE

- ➔ Continuous change from bull-RP to cow-RP step by step planned
  - ➔ ‚Old‘ traits slightly increase in R²
  - ➔ R² for ‚New‘ traits mainly from cow information

- ➔ Planned: Change from Two-Step to Single-Step method for combined RP

KUHVISION

KuhVision: Aims

- Set up a national cow reference population with 150.000 cows within 3 years
- Maintain reliability of old traits & have GEBVs for new traits with resonable reliability
- Recording of health data as basis for GE for health traits

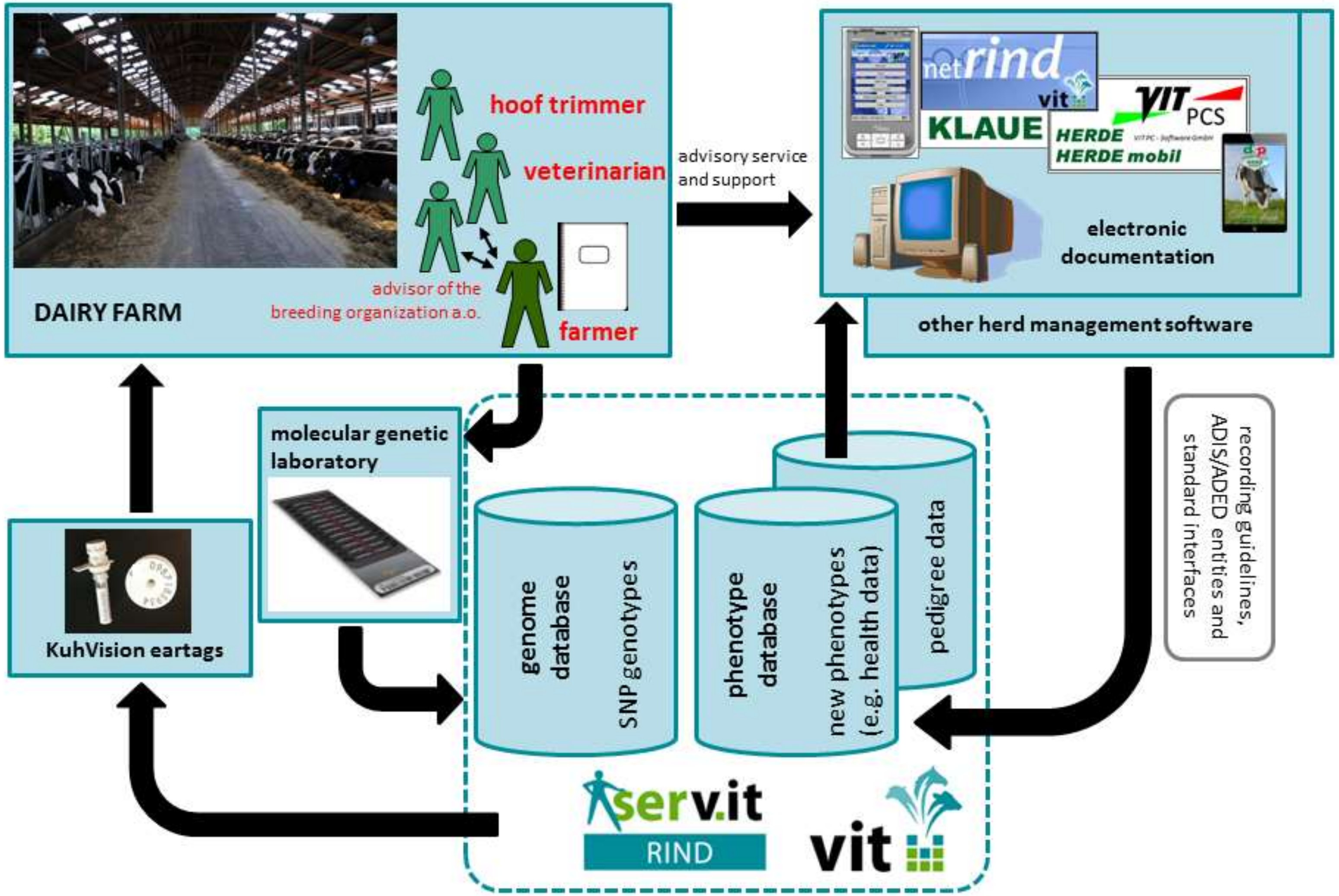
KuhVision: Organisation and current status

- Joint effort of all German Holstein Associations as members of DHV and vit
  - Size of the organisation determines
    - no of genotyped females and
    - amount of phenotypes to bring into the system
      All standard traits PLUS
      health data, claw trimming data, type classification
- Different level of subsidy according to amount of phenotypic data

- Start of the project: June 2016, status as of October 2016:

- > 330 farms participating in the project
- > 50.000 data for ear tags sent from vit to eartag supplier
- > 20.000 SNP data sets sent from lab to vit

Data flow (KuhVision project)



DAIRY FARM

hoof trimmer

veterinarian

advisor of the breeding organization a.o.

farmer

advisory service and support

electronic documentation

other herd management software

molecular genetic laboratory

KuhVision eartags

genome database

SNP genotypes

phenotype database

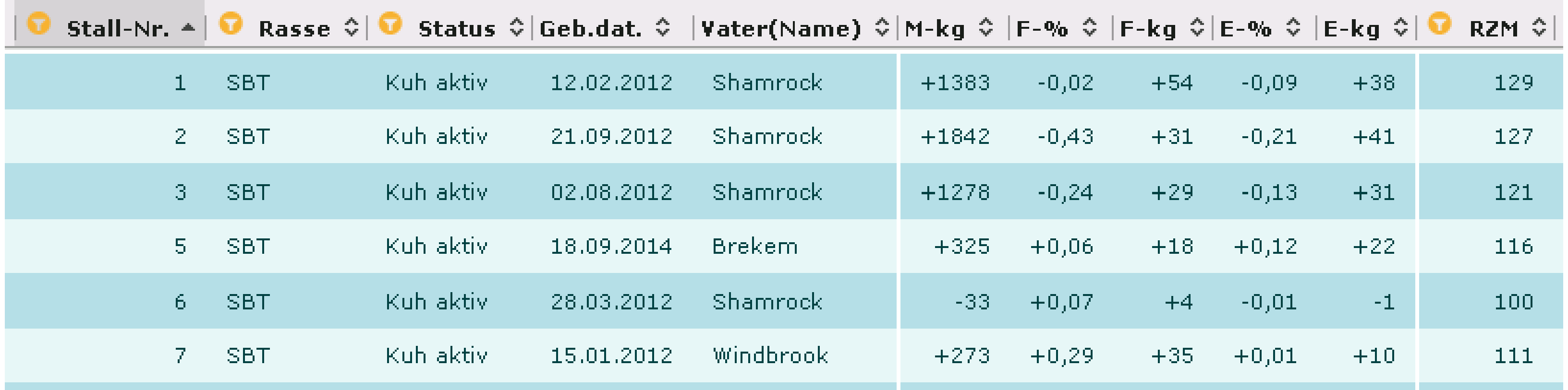
new phenotypes (e.g. health data)

pedigree data

recording guidelines, ADIS/ADED entities and standard interfaces

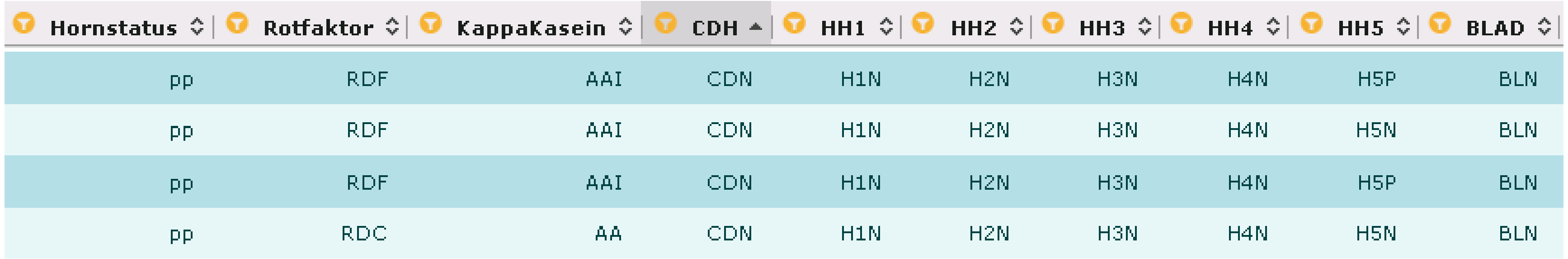
Benefits for farmers:
Additional web-tools for herd management & selection
Improved mating program

- Genomic breeding values



Stall-Nr.	Rasse	Status	Geb.dat.	Vater(Name)	M-kg	F-%	F-kg	E-%	E-kg	RZM
1	SBT	Kuh aktiv	12.02.2012	Shamrock	+1383	-0,02	+54	-0,09	+38	129
2	SBT	Kuh aktiv	21.09.2012	Shamrock	+1842	-0,43	+31	-0,21	+41	127
3	SBT	Kuh aktiv	02.08.2012	Shamrock	+1278	-0,24	+29	-0,13	+31	121
5	SBT	Kuh aktiv	18.09.2014	Brekem	+325	+0,06	+18	+0,12	+22	116
6	SBT	Kuh aktiv	28.03.2012	Shamrock	-33	+0,07	+4	-0,01	-1	100
7	SBT	Kuh aktiv	15.01.2012	Windbrook	+273	+0,29	+35	+0,01	+10	111

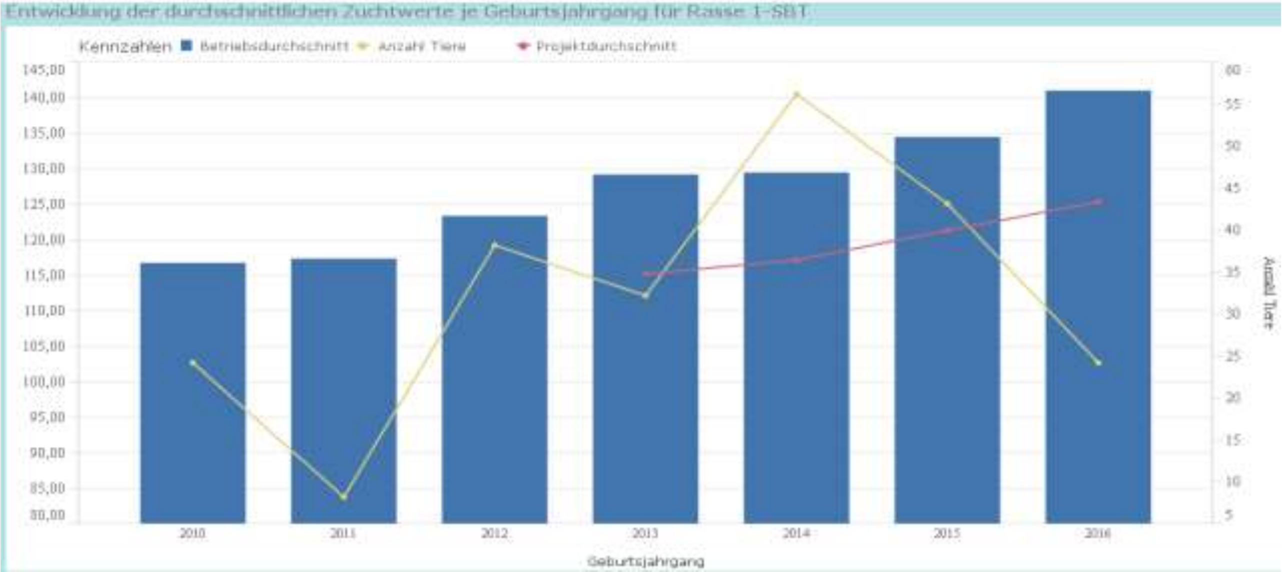
- Genetic characteristics



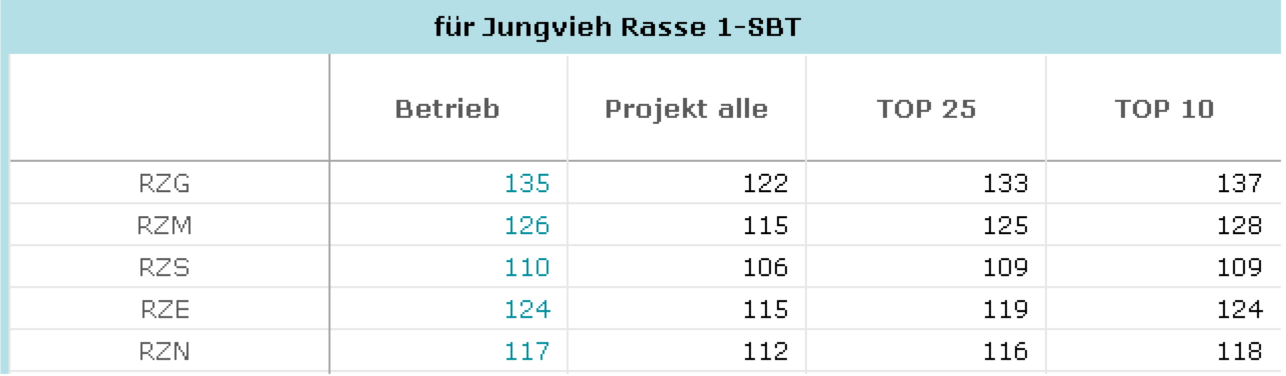
Hornstatus	Rotfaktor	KappaKasein	CDH	HH1	HH2	HH3	HH4	HH5	BLAD
pp	RDF	AAI	CDN	H1N	H2N	H3N	H4N	H5P	BLN
pp	RDF	AAI	CDN	H1N	H2N	H3N	H4N	H5N	BLN
pp	RDF	AAI	CDN	H1N	H2N	H3N	H4N	H5P	BLN
pp	RDC	AA	CDN	H1N	H2N	H3N	H4N	H5N	BLN

Benchmarking of GEBVs at herd level

Genetic trend: Mean breeding values of cows over birth years



Comparison herds, TOP25 & TOP10% of all KuhVision farms



für Jungvieh Rasse 1-SBT

	Betrieb	Projekt alle	TOP 25	TOP 10
RZG	135	122	133	137
RZM	126	115	125	128
RZS	110	106	109	109
RZE	124	115	119	124
RZN	117	112	116	118

Conclusion KuhVision

- Considering current milk market situation more participating herds than expected
- Additional herds without subsidies
- Routine recording of health traits via herd management software
- Logistic for genotyping in place
  - Additional feature is pedigree checking incl. parentage discovery
- Evaluation procedures developed in R&D-Projects Kuh-L and GKUHplus will be the start for genomic evaluation of KuhVision data

Thanks for your attention!

vit

IT-Solutions for Animal Production