

Overview of ongoing projects at Qualitas AG

SABRE-TP Workshop, ETH Zürich November 10, 2021 urs.schnyder@qualitasag.ch

Single Step Genomic Evaluation (Adrien Butty, Mirjam Spengeler, Peter von Rohr)

- Replace the current multi-step genomic evaluation for all breed-trait combinations
- ssGTBLUP-method using MiX99-Software (Luke)
- Reliability estimation
- Include international data (MACE)
- Multi- vs single-breed analysis
- Bi-weekly routine evaluations
- Implement RRTDM for production traits in MiX99 (Madeleine Berweger, Patrick Stratz, Urs Schuler)

Efficiency – Residual Feed Intake

(Patrick Stratz)

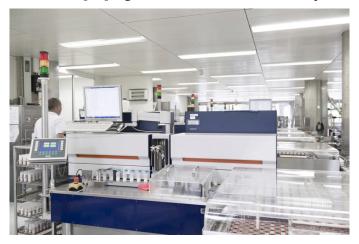
- Development of genomic evaluation for feed efficiency
 - Single Step Evaluation
- Feed intake data of 6638 Holstein cows from international collaboration (RDGP project)
 - Including data from Agroscope Posieux
 - Energy Corrected Milk (ECM), Metabolic Body Weight (MBW) and Residual Feed Intake (RFI)
- Multiple trait animal model for 2 lactation stages
 - Following Canadian implementation

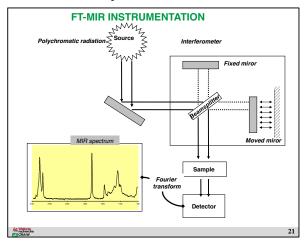
HappyMoo

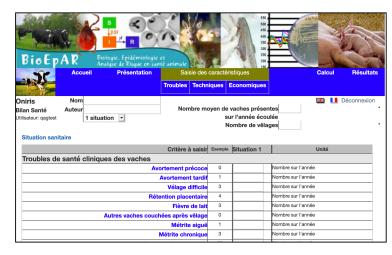
(Urs Schuler)



HappyMoo-Tool (web-based)







- Use of FT-MIR-spectra of DHI milk samples. Models for mastitis, lameness / claw health, negative energy balance and stress (acute and chronic) will be developed.
- Quantify the economic consequences of the health status in a herd.
 (Based on "Bilan de santé du troupeau laitier".)
- Embedding in the web-applications of the breeding associations possible.

HappyMoo





Mastitis prediction based on FT-MIR-spectral data

(Urs Schuler)

- Derive mastitis observations (healthy or ill) based on direct health data
 - Similar process as for the GE resistance to mastitis
 - Only observations made on herds with complete health data recording
- Assign mastitis observations to DHI milk samples
- Develop models (using FT-MIR-spectra of the milk samples) to predict the mastitis status for all DHI milk samples
- Use the predicted mastitis status in genetic evaluations

Resilience

(Beat Bapst)

- Reaction Norm Models for Heat Stress
 - Data from Milk Recording (Test Day Records)
 - Weather data from MeteoSchweiz
 - Temperature Humidity Index (THI)
- Investigation of resilience traits based on AMS data
 - Deviation from a normal lactation curve and how quickly cows can return to the normal state

SMARTER: SMAll RuminanTs breeding for Efficiency and Resilience (Beat Bapst)

- Goal: Phenotypic and genotypic characterization of resilience- and efficiency-related traits in small ruminants.
- Establishment of new breeding and management strategies
- Horizon 2020 Project: 2018 until 2023
- International consortium of 26 partners with a total budget of 7.6 million €
- Qualitas AG is subcontractor of FiBL for genetic analysis
- SZZV involved as data provider and stakeholder
- https://www.smarterproject.eu/



FiBL

SMARTER: SMAll RuminanTs breeding for Efficiency and Resilience

Swiss partners (FiBL, Qualitas) works:



Bild: FiBL

Dairy sheep

- Phenotyping of at least 1200 Lacaune sheep with respect to gastrointestinal parasite infestation
- Estimation of variance/covariance components and genetic parameters
- BLUP breeding value estimation
- Collaboration: SMG/BGK

Goats

- Genetic background of parasite resistance
 - Based on existing studies (Heckendorn et al., 2017)
 - SNP genotyping of approximately 1,250 goats with phenotypes; ssGBLUP, GWAS
- Feasibility study regarding the international comparability of ebvs, analogous to Interbull
- Collaboration: SZZV
- data provider: Uni Bern, HAFL



Bild: SZZV



Beef Production Model

(Jessica Gearing)

- Economic Weights for Beef Production Traits
- ECOWEIGHT (Wolfova et al. 2005)
- Collection of input data
 - Production costs, prices, culling and conception rates, ...
- Various Production Systems
 - SwissPrimBeef, NaturaBeef
- Expand to Beef-on-Dairy

Mating Decisions based on SD of Gamete DGVs

(Franz Seefried)

- Increase probability of superior offspring
- DGVs for chromosome segments (haplotypes)
- Recombination hotspots
- Sampling of possible combinations
- Implementation in Optimum Genetic Contribution concept

Prediction of expected genetic variation within groups of offspring for innovative mating schemes

<u>Dierck Segelke</u> □, <u>Friedrich Reinhardt</u>, <u>Zengting Liu</u> & <u>Georg Thaller</u>

Genetics Selection Evolution 46, Article number: 42 (2014) | Cite this article

Other Projects

- Ecobreed Agroscope Tänikon (Simon Schlebusch)
- Longevity Project FiBL
- Resilient Dairy Genome Project (Canada)
- GWAS 1k Bull Run 7 (Mirjam)
- Composite Conformation Scores
- Influence of THI on Male Fertility (Swissgenetics, Beat)