Recent activities at BFH-HAFL

SABRE-TP, 11. Januar 2024, ETH Zürich

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▸ Hochschule für Agrar-, Forst- und Lebensmittelwissenschaften HAFL

General

▶ «Hochschule für Agrar-, Forst- und Lebensmittelwissenschaften (HAFL)» in Zollikofen is a departement of «Berner Fachhochschule (BFH)»

▶ Faculty of agronomy, animal genetics group (led by: Dr. Hannes Jörg):

Services at BFH-HAFL

Breeding value estimation

Breeding value estimation

Sheep and horses

▶ Schweizerischer Schafzuchtverband (SSZV): Breeding values for fertility and daily gain

(Fotos: SSZV)

▶ Franches-Montagnes (Schweizerischer Freibergerverband): Breeding values for white markings, riding and driving performance and conformation

▶ Swiss Warmblood (Zuchtverband CH Sportpferde): Breeding values for jumping performance, riding performance and conformation

(Fotos: M. Rindlisbacher)   (Foto: K. Stuppia)

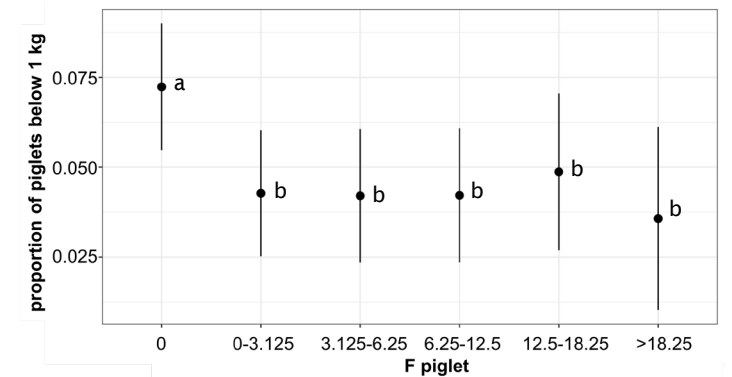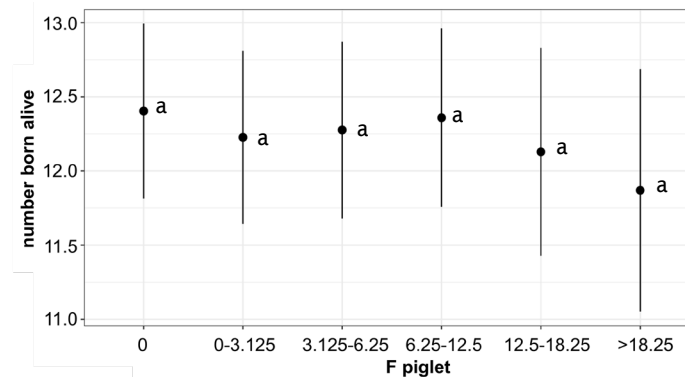# Projects at BFH-HAFL

Inbreeding depression in pig

► Data from Swiss Large White, Swiss Landrace and F1-crossbred sows:

# of records	Trait
36477	Number born alive
28891	Proportion of piglets below 1kg
35487	Piglets survival during suckling
97062	Proportion of stillbirth piglets

► Inbreeding has an influence on reproductive traits
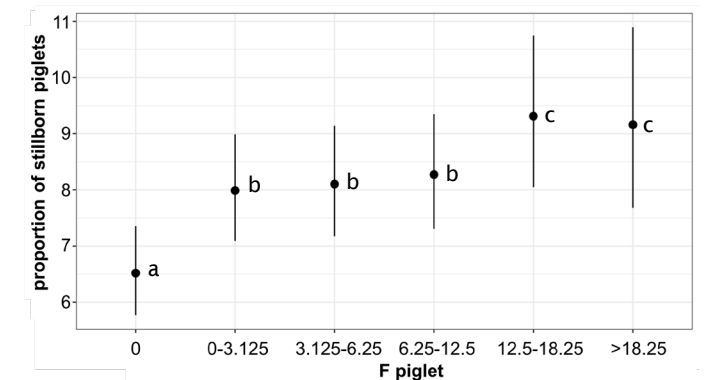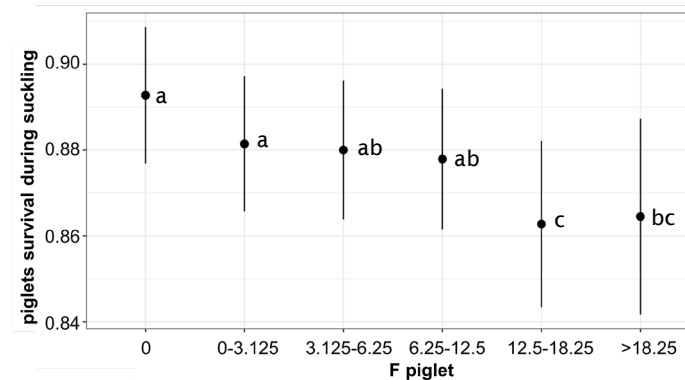
Quelle: A. Burren et al. (2023)

Importance of milke urea content for the estimation of nitrogen excretions in cattle (in collaboration with ETH Zürich)
(S. Probst, T. Kupper, M. Kreuzer, M. Terranova, A. Burren)

▶ Data available from metabolic experiments of Agroscope and ETH for:
  ▶ 604 cows from the breeds Braunvieh, Holstein, Swiss Fleckvieh and Jersey
  ▶ Live weight, milk urea content, urine nitrogen excretion

▶ 10% of data for model validation randomly excluded

▶ Mixed linear models for modelling of urine nitrogen excretion

→ the effect of the breed is significant: excretions increase less with higher milk urea content in Brown Swiss cattle than in Holstein cattle

Rätisches Grauvieh

(In collaboration with Uni Bern, Verein Rätisches Grauvieh Schweiz, ProSpecieRara, Braunvieh Schweiz; supported by BLW)

▶ SNP genotyping of the population Rätische Grauvieh

▶ Determination and conservation of genetic diversity

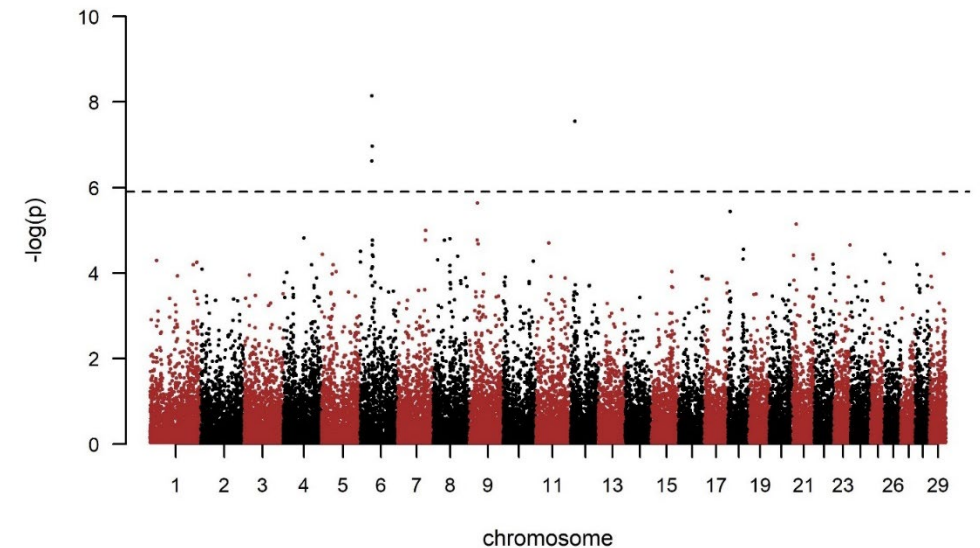▶ Genomic analysis of health traits, height, conformation, coat colour and milk protein variants

Abbildung 32: Manhatten-Plot GWAS Kreuzbeinhöhe

Quelle: Mirjam Fingerle (2023)

The relationship of local Swiss cattle populations with other local breeds from the Alps

Genomic regions underlying positive selection in local, Alpine cattle breeds

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Abstract

We used genome-wide SNP data from 18 local cattle breeds from six countries of the Alpine region to characterize population structure and identify genomic regions underlying positive selection. The geographically close breeds Evolèner, Eringer, Valdostana Pezzata Nera, and Valdostana Castana were found to differ from all other Alpine breeds. In addition, three breeds, Simmental, and Original Braunvieh from Switzerland and Pinzgauer from Austria built three separate clusters. Of the 18 breeds studied, the intra-alpine Swiss breed Evolèner had the highest average inbreeding based on runs of homozygosity (F_{ROH}) and the highest average genomic relationship within the breed. In contrast, Slovenian Cika cattle had the lowest average genomic inbreeding and the lowest average genomic relationship within the breed. We found selection signatures on chromosome 6 near known genes such as *KIT* and *LCORL* explaining variation in coat color and body size in cattle. The most prominent selection signatures were similar regardless of marker density and the breeds in the data set. In addition, using available high-density SNP data from 14 of the breeds we identified 47 genome regions as ROH islands. The proportion of homozygous animals was higher in all studied animals of local breeds than in Holstein and Brown Swiss cattle, the two most important commercial breeds in the Alpine region. We report ROH islands near genes related to thermoregulation, coat color, production, and stature. The results of this study serve as a basis for the search for causal variants underlying adaptation to the alpine environment and other specific characteristics selected during the evolution of local Alpine cattle breeds.

KEYWORDS

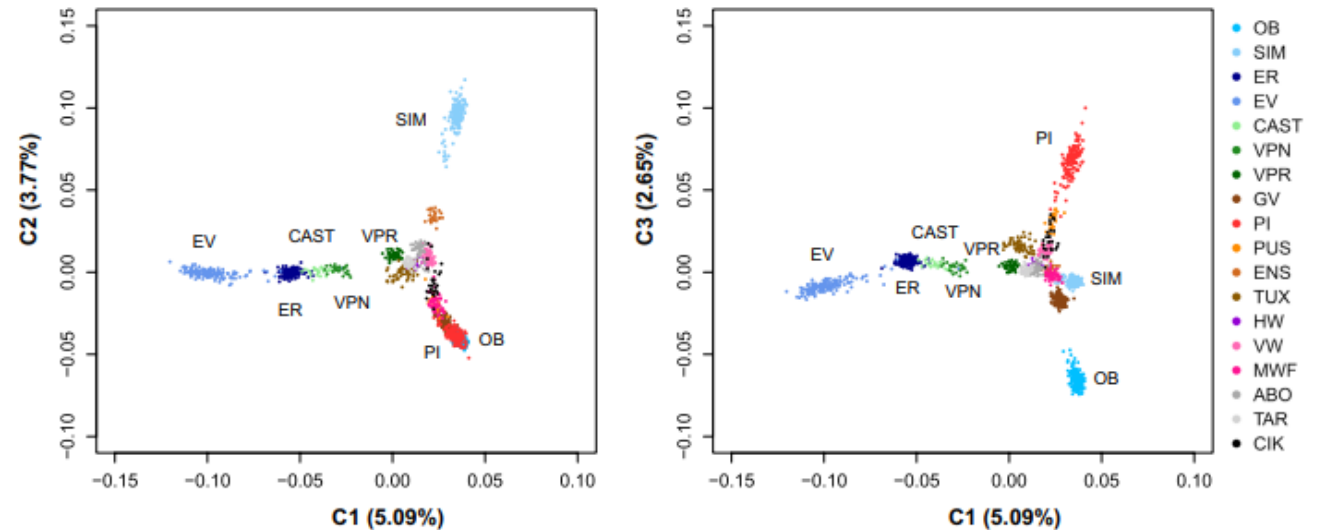diversity, selection signature, runs of homozygosity, cattle

FIGURE 1 PCA-plot showing population structure based on the first (C1) and second (C2) components (left) and on the first (C1) and t (C3) components (right) of the 18 local Alpine cattle breeds. The first principal component (C1) explains 5.09%, the second (C2) 3.77%, and t third (C3) 2.65% of the observed variation.
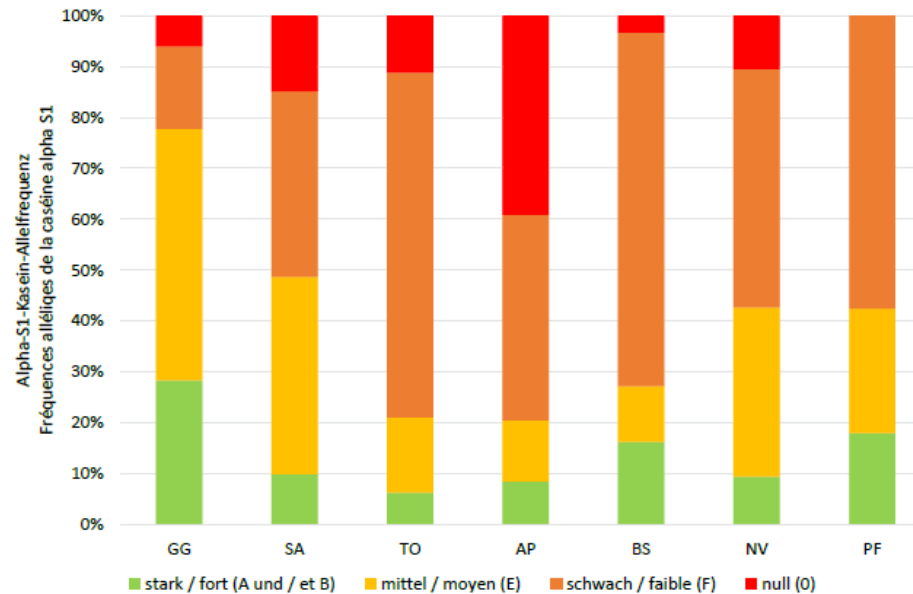
Alpha-S1-Kasein in goats

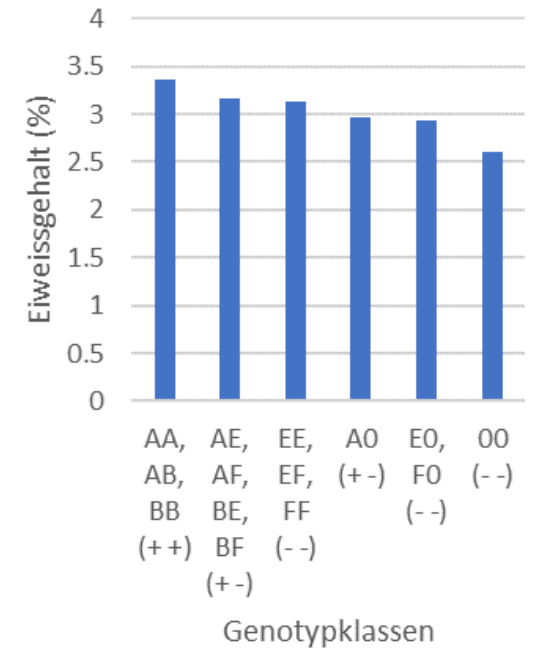## (In collaboration with Uni Bern, Qualitas and SZZV; supported by BLW)

▶ **Alpha-S1-Kasein has an influence on cheesemaking characteristics**

Foto: S. Zahnd

stark / fort (A und / et B) mittel / moyen (E) schwach / faible (F) null (0)

Quelle: Forum 12/2023

Sheep

Foto: ProSpecieRara

▶ Students work of Laurin Vogel on tail length in Engadine sheep (in collaboration with Uni Bern, SSZV, Schweizerischer Engadinderschaf Zuchtverein)

Spiegelschaf
(Foto: ProSpecieRara)

Causse du lot
(Foto: Wikipedia)

Kärntner Brillenschaf
(Foto: Wikipedia)

Jezersko-Solcava
(Foto: Wikipedia)

▶ Master thesis work of Dorothee Neururer on the genetic diversity of Spectacled sheep from Switzerland, France, Germany, Austria, Italy and Slovenia based on SNP data (in collaboration with Uni Bern)

Thanks!