Talk outline: How selection for complex traits shapes the genome of breeding populations

* Selection is important. (Classical) selection signature analyses in livestock mostly find regions that have been relevant for domestication (coat color, olfactory genes, immune genes), insufficient resolution for a) very recent selection and b) QTL underlying complex traits
* Breeders are interested in understanding the mechanisms of selection in breeding populations – relevant scale: ongoing and past ~ 10 generations
* Genomic data provide novel opportunities to analyse selection in breeding programs on the genomic scale
* Relevant questions:
  + which traits have been under selection?
  + what is the architecture of genetic change for a given trait?
* Basic idea: Wright formula, expected change of allele frequency is a function of allelic effect
* Resulting hypotheses:

1. across all loci, effect sizes and allele frequency change are correlated under selection
2. the accumulated product a x p reflects the genetic change (results from GBLUP)
3. QTLs under selection should be marked by extreme a x p values in the region

* Proof of concept: simulation study
  + Description of simulation
  + Results for 10, 100, (1000 if available) QTLs, GWAS vs. rrBLUP – with and without correction (dot plots/contour plots and Manhattan plots)
  + Conclusions:
    - H1 confirmed, more QTLs are better, rrBLUP more powerful than GWAS, correction not helpful
    - H2 confirmed (?) need to check if realized genetic gain can be estimated that way - not sure with rrBLUP (shrinkage) – but should work.
    - H3 – for single QTL not enough power, possibly for QTL-regions/chromosomes in the cumulative function (still needs to be done)
* Application maize
  + material description (max 3 well chosen traits, how was p estimated?)
  + results
* Application chicken
  + material description (max 3 well chosen traits, Gengler-approach to estimate p )
  + results
* Discussion/outlook
  + approach works
  + little power to detect regions under selection
  + Alternative effect estimates (Bayes B/R)
  + post-processing of results (e.g. gene set enrichment analysis to identify pathways under selection)