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Agroscope

Animal GenoPhenomics – Overview of current research projects

Markus Neuditschko



Current projects

- Pig – protein efficiency
(low coverage sequencing data)



- Cattle – RegioBeef
(low coverage sequencing data)



- Honey bee – Varroa resistance
(pool sequencing data)

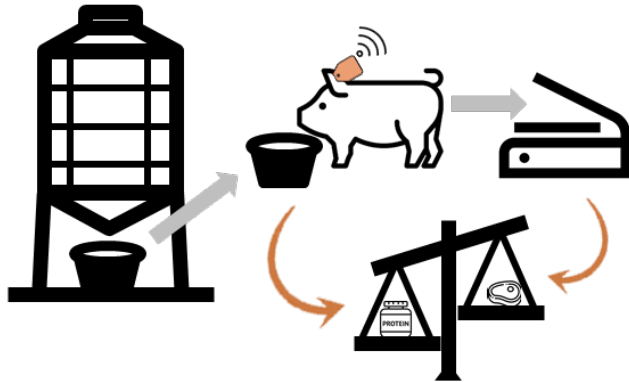


- Horse – Shape and Gaits 2.0
(high-density SNP chip data)



Pigs – protein efficiency

Phenotyping



682, ♀ & ♂



80% protein content, soy free



~100 kg live weight



**fondation
sur la croix**

Projekte Landwirtschaft

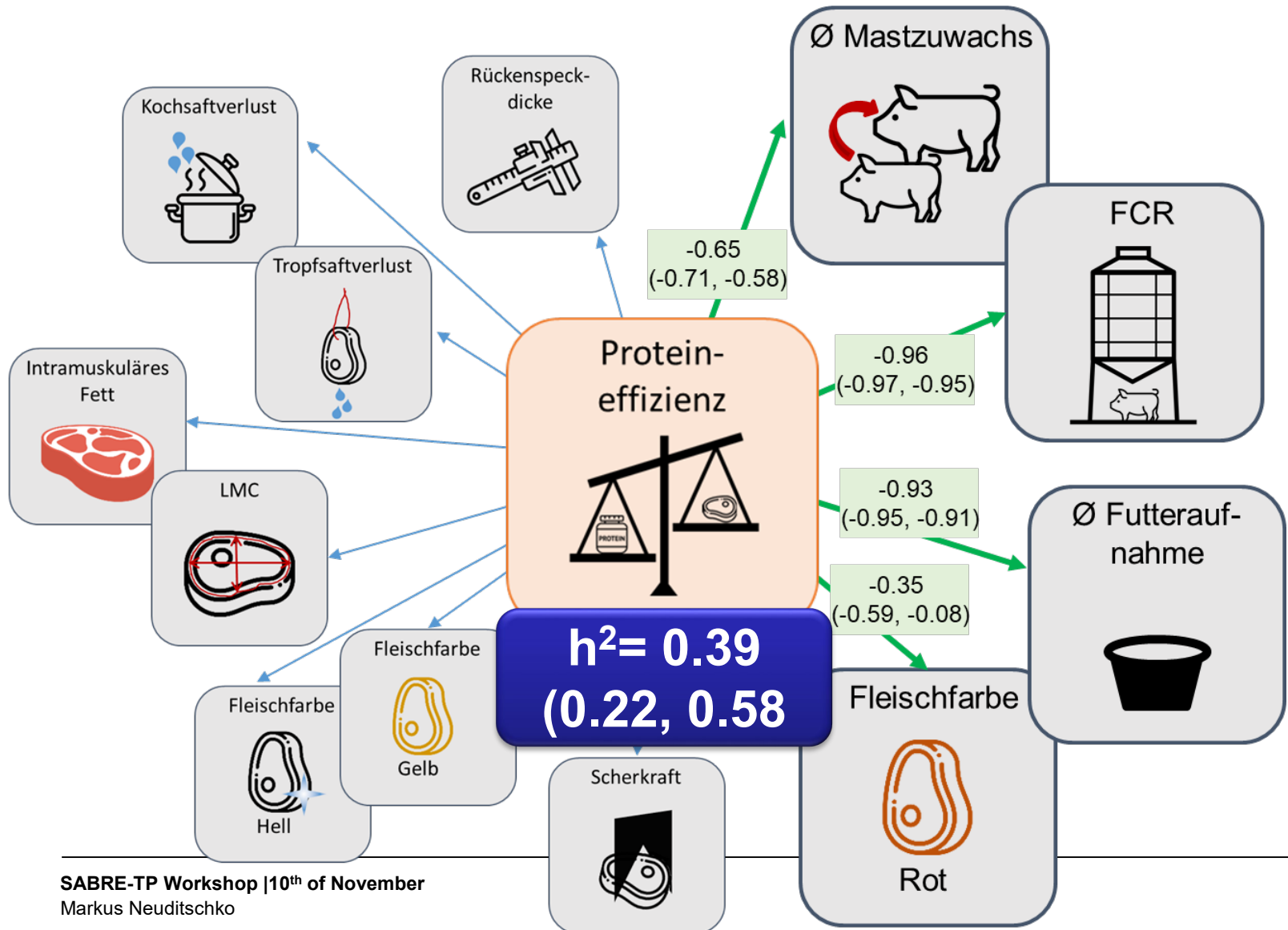
Genotyping



~ 1000 pigs (300 from previous HD genotyped and low-pass (1X) sequenced



Pigs – preliminary results





Cattle – genomic analyses

- RegioBeef – Efficiency of beef production in different production systems and cross breeds
 - **Braunvieh x Angus (95 cattle)**
 - **Braunvieh x Limousin (125 cattle)**
 - **Braunvieh x Simmental (95 cattle)**

- First sequencing batch (Neogen – skim-sequencing)
 - **Number of samples: 283 F1 crosses**
 - **Number of sites: 59 204 179**
 - **Number of biallelic SNPs: 21 345 015**

- Further sequencing of sires (32), dams (245) and remaining F1 crosses (~30)



Cattle – next steps

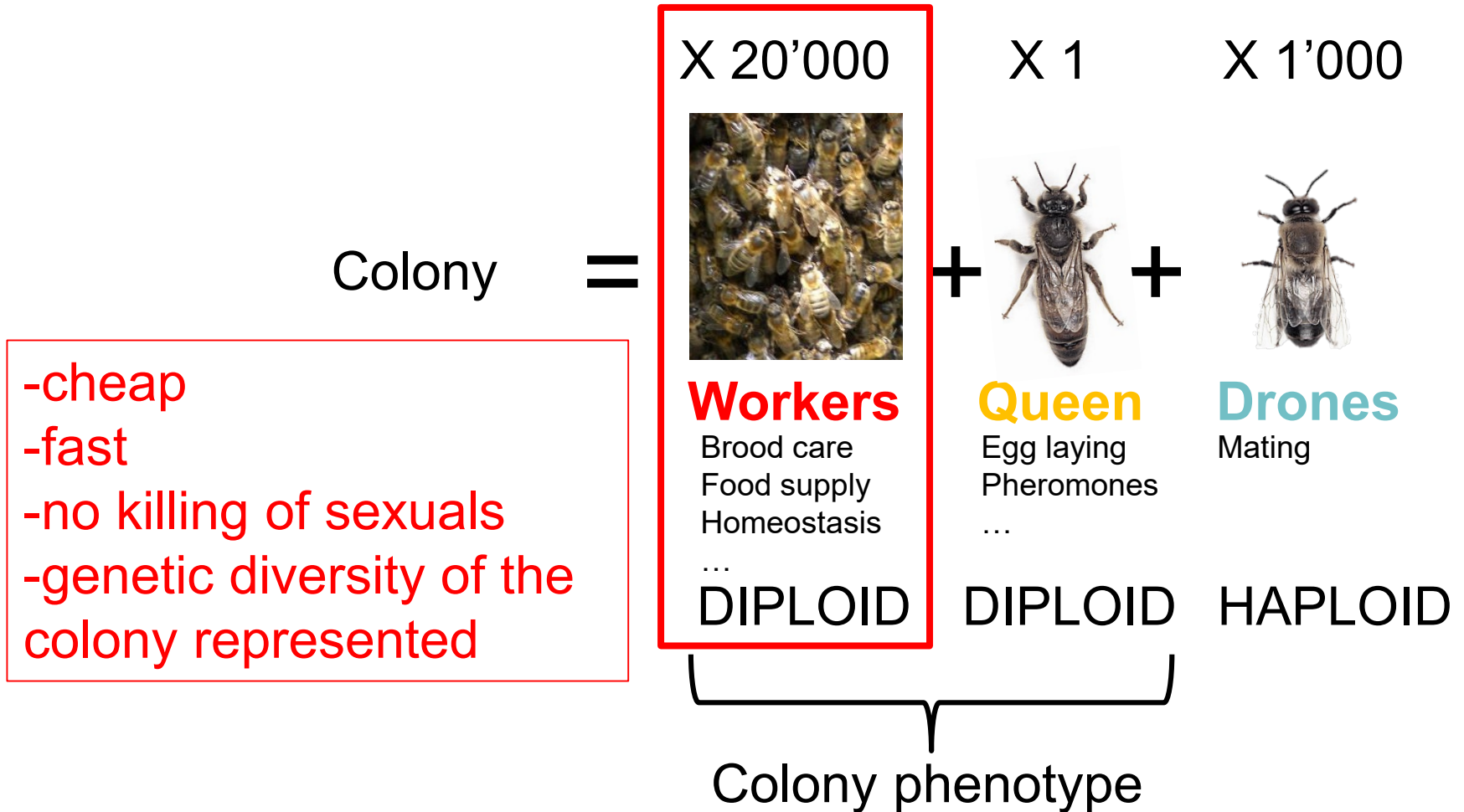
- **Concordance between array genotypes and sequencing**
(i.e., test for accuracy of skim-sequencing genotypes)

- **Test for Mendelian error rates with trio data**
(i.e., as approximation for sequencing/imputation errors)

- **Genomic analyses of F1 crosses**
 - Genetic compatibility/complementarity of different combinations of breeds
 - Identification of allele-specific expression in muscle, liver and adipose tissue (i.e., regulatory genetic changes)

Honey bee – Varroa resistance

- Using pools of workers for whole genome sequencing





Honey bee – published results



ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

SHORT COMMUNICATION

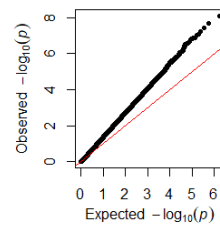
doi: 10.1111/age.13150

Two quantitative trait loci are associated with recapping of *Varroa destructor*-infested brood cells in *Apis mellifera mellifera*

M. Guichard^{*†}, B. Dainat^{*}, S. Eynard^{‡§}, A. Vignal^{‡§}, B. Servin^{‡§}, the Beestrong Consortium[¶] and M. Neuditschko[†]

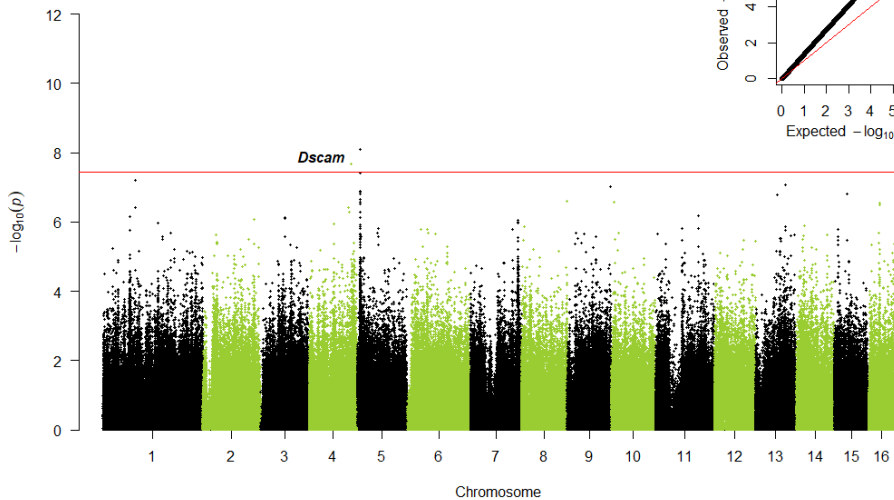
^{*}Agroscope, Swiss Bee Research Centre, Schwarzenburgstrasse 161, Bern 3003, Switzerland. [†]Agroscope, Animal GenoPhenomics, Rte de la Tioleyre 4, Posieux 1725, Switzerland. [‡]GenPhySE, INRA, INPT, INPENVT, Université de Toulouse, Castanet-Tolosan 31320, France. [§]UMT PrADE, Protection des Abeilles Dans l'Environnement, Avignon 84914, France. [¶]Labogena, Domaine de Vilvert Bat 224 CS80009, Jouy-en-Josas CEDEX 78353, France.

Summary



Recapping of *Varroa destructor*-infested brood cells is a trait that has recently attracted interest in honey bee breeding to select mite-resistant *Apis mellifera* colonies. To investigate the genetic architecture of this trait, we evaluated a sample of *A. mellifera mellifera* colonies ($N = 155$) from Switzerland and France and performed a genome-wide association study, using a pool of 500 workers per colony for next-generation sequencing. The results revealed that two QTL were significantly ($P < 0.05$) associated with recapping of *V. destructor*-infested brood cells. The best-associated QTL is located on chromosome 5 in a region previously found to be associated with grooming behaviour, a resistance trait against *V. destructor*, in *A. mellifera* and *Apis cerana*. The second best-associated QTL is located on chromosome 4 in an intron of the *Dscam* gene, which is involved in neuronal wiring. Previous research demonstrated that genes involved in neuronal wiring are associated with recapping and varroa sensitive hygiene. Therefore, our study confirms the role of a gene region on chromosome 5 in social immunity and simultaneously provides novel insights into genetic interactions between common mite resistance traits in honey bees.

Keywords ataxin-10, *Dscam*, genome-wide association study, honey bee, pool sequences, recapping, Wnt7





Horse – Shape and Gaits 2.0

- Study to improve the assessment of conformation and gait traits in the Franches-Montagnes (FM) horse breed
- **Three steps**



Step 1:
photographs and
hair samples
(genotyping)



Step 2:
equipping the horse,
measure limb length



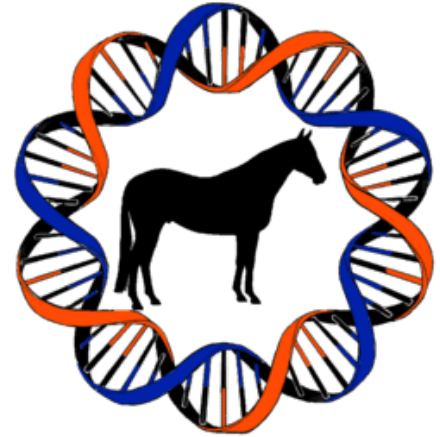
Step 3:
Walk and trot horse



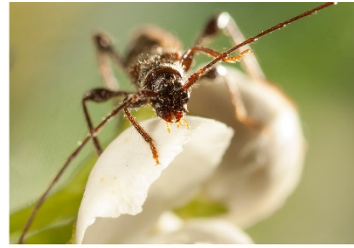
Horse – current database



EquiMoves



- 620 FM
 - 487 stallions (1940 – 2018)
 - 70 mares (2004 – 2018)
 - 63 geldings (2009 – 2018)
- 234 FM
 - 178 3 year-olds
 - 56 older stallions
- 1618 FM
 - 1077 50K SNP
 - 30 sequences
 - 511 670K SNP



Thank you for your attention

Markus Neuditschko

Markus.Neuditschko@agroscope.admin.ch

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