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Photo: M. Rindlisbacher

Genetic analyses of the Franches-Montagnes horse breed with genome-wide SNP data

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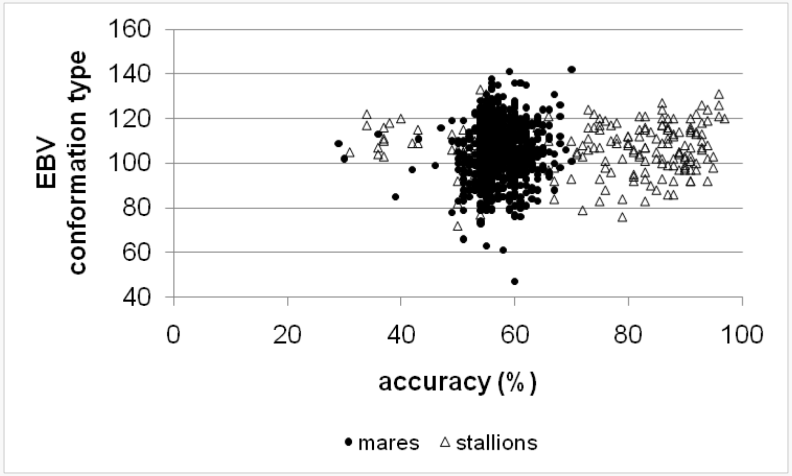
EAAP 2011, Stavanger (Norway)

Material & selection of horses

- Selection of ~1’100 horses:
    - Number of progeny
    - EBV
    - Accuracy of EBV

→214 stallions & 886 mares,
born between 1975 and 2008



Material & selection of horses

- Genotyping with the Illumina Equine SNP50k beadchip.
- 54’602 genotypes for 1’151 FM horses
- Data of ~ 70 phenotypes:
  - 43 traits out of breeding program →
  - ~ 30 traits (e.g. health traits, coat colour, vices)

Conformation	**28**
Performance (riding & driving)	**12**
White spotting	**3**

Data preparation

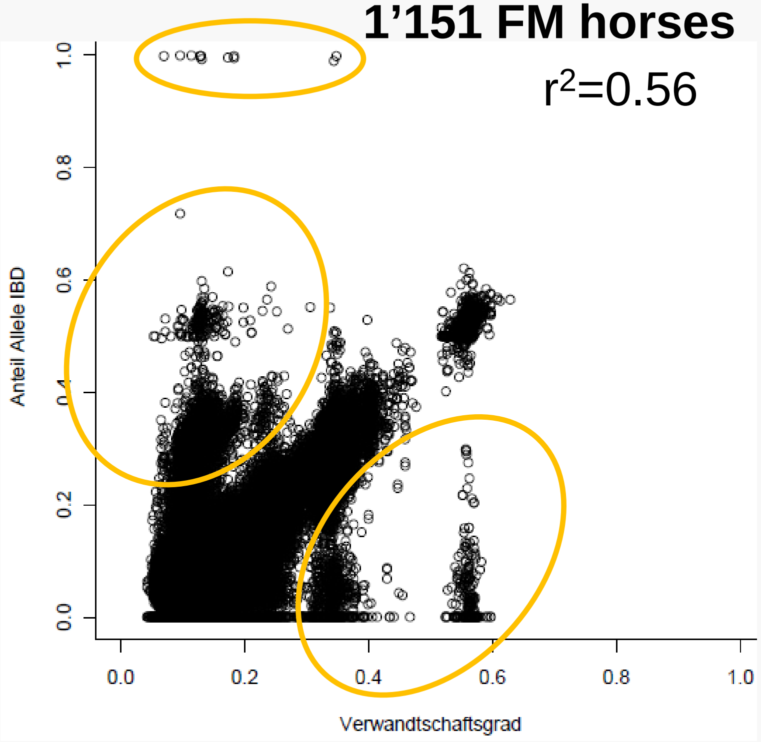
PLINK (v1.07, Purcell et al. 2007):

- Of 1’151 horses
    - 48 excluded due to sample duplication.
    - 10 removed because genotyping failed in more than 10% of the SNPs.
    - 16 excluded due to unresolved inconsistencies.
- Of 54’602 SNPs
    - 12’738 SNPs excluded due to MAF below 5%
    - 2’191 SNPs removed because more than 10% missing genotypes
    - 2’730 SNPs excluded due to deviation from HWE ($p \leq 0.0001$)

→ After quality control: 1’077 FM horses & 38’250 SNPs

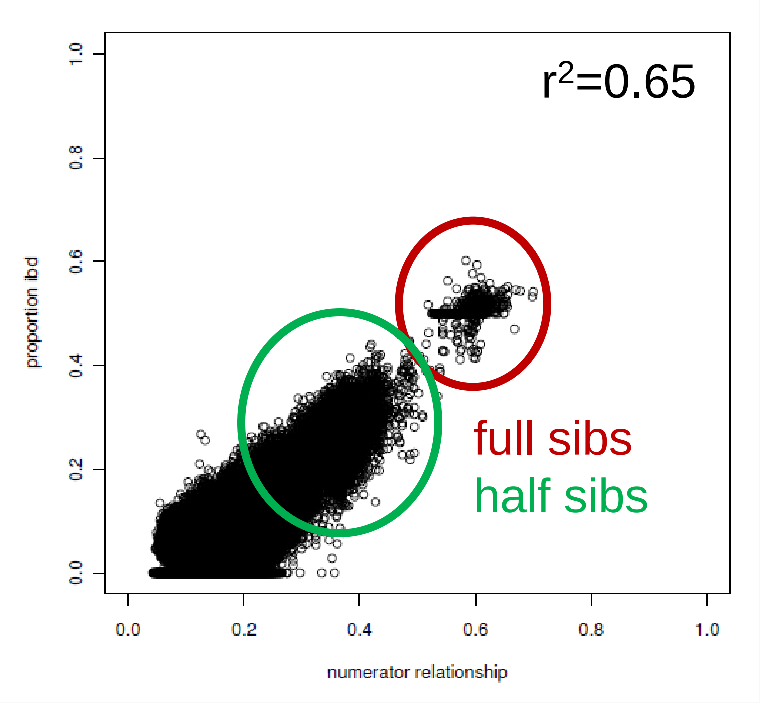
Comparing pedigree and genomic information

1’151 FM horses



Sample mixups & pedigree discrepancies

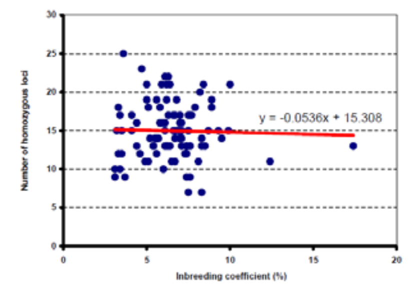
1’077 FM horses



Comparing microsatellite with SNP data

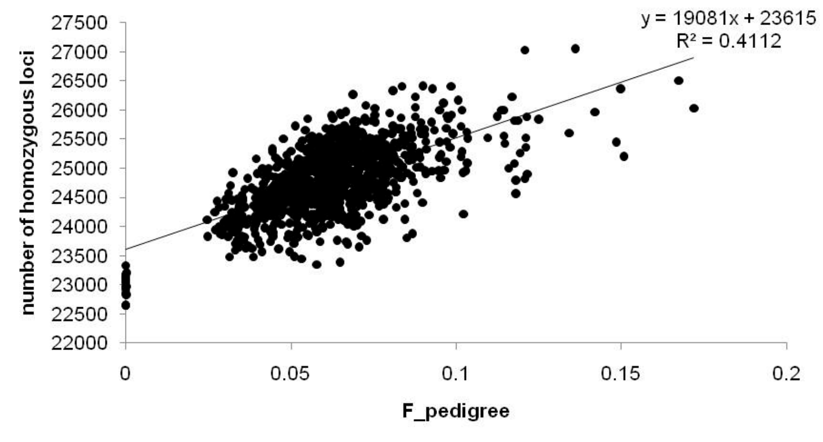
Glowatzki-Mullis et al. (2006):

- 107 FM horses
- 50 microsatellite loci
- No significant increase of the number of homozygous microsatellite loci with increasing inbreeding coefficients



Hasler et al. (2011):

- 1’077 FM horses
- 38’250 SNPs
- Increasing number of homozygous SNP loci with increasing inbreeding coefficient



Linkage disequilibrium (LD) & effective population size (N_e)

- LD measured as r^2 showed decreasing trend with increasing distance between SNPs.
- For marker pairs 0-0.05 Mb apart, average r^2 over all autosomes was 0.35.

- N_e = measure of genetic diversity
  → assessed using information coming from LD of SNPs

- According to Hill (1981):

$$\boxed{E(r^2) = \frac{1}{(1+4N_e c)} + \frac{1}{n}}$$

Effective population size (N_e)

- N_e showed a decreasing trend over the last 2’000 generations

- Average recent N_e depending on sample size:
  - Corrected for restricted sample size: 23 - 126
  - Not corrected for restricted sample size: 13 - 107

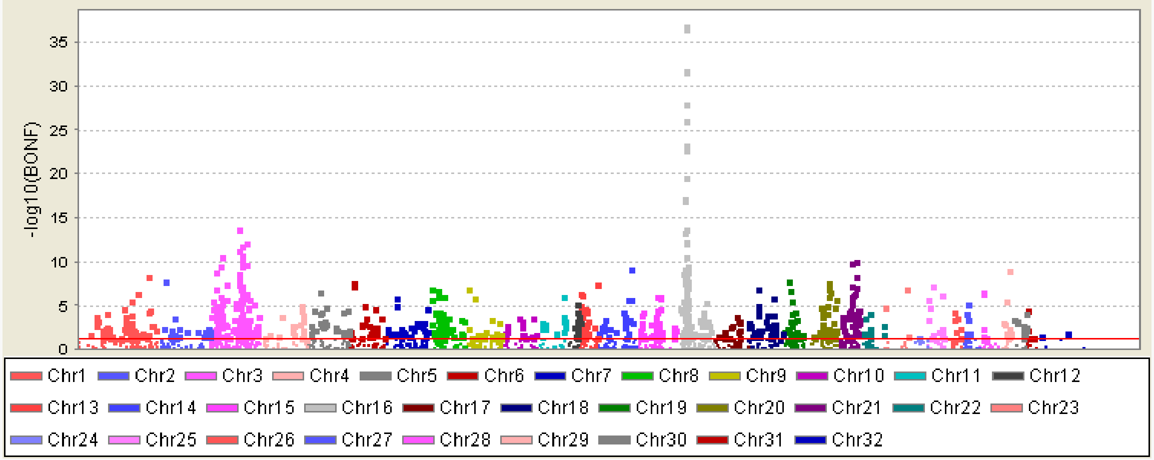
- Recent N_e based on pedigree data: 80 - 102

Mapping traits - white markings

Photos: Archives Haras national

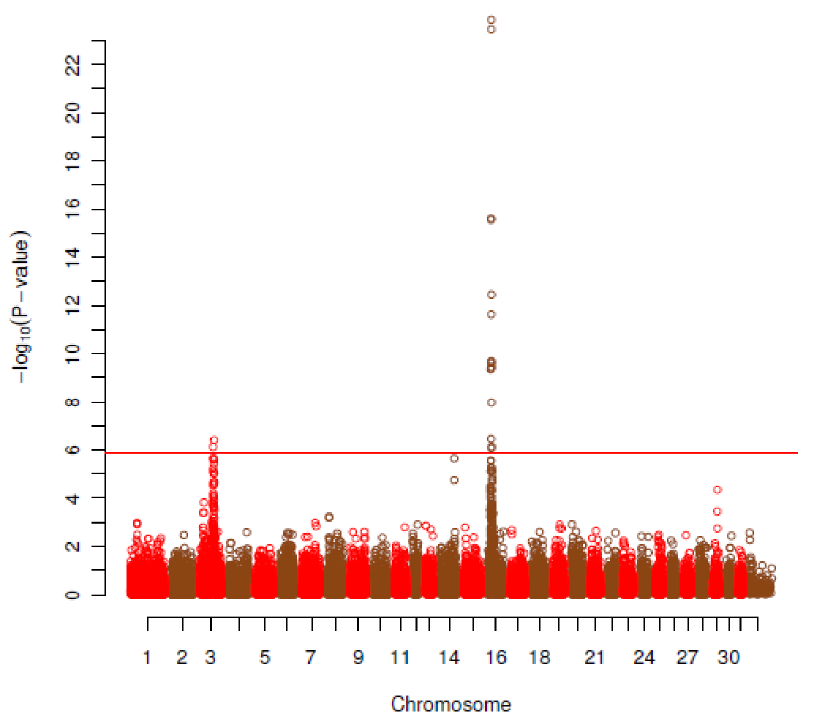
PLINK (v1.07, Purcell et al. 2007):

- Quantative association analysis for white markings head



Mapping traits - white markings

Mixed-model approach function „mmscore“ using R-package GenABEL (Aulchenko et al. 2007)



Estimation of genomic breeding values

- First results for conformation type and white markings head
- Bayes B using GenSel (Fernando and Garrick)

	Conformation type (h^2=0.27)		**White markings head (h^2=0.69)**	
	BayesBC0.2	BayesBC0.2	BayesBC0.2	BayesBC0.2
PROBFIXED	corr(ghat,y_dereg)	corr(ghat,y_ZP)	corr(ghat,y_dereg)	corr(ghat,y_ZP)
0.5	0.1497	0.5048	0.5705	0.7415
0.95	0.1185	0.4555	0.5704	0.7405
0.99	0.1012	0.4243	0.5687	0.7349

- Accuracy for actually best correlations (Hayes et al. 2009)
  - Conformation type: 0.47
  - White markings head: 0.88

Conclusion

- First experiences showed, that further processing of genotypes requires a very accurate management of samples.

- The SNP data enables the detection of pedigree inconsistencies and the deduction of relationships between individuals.

- The SNP data enables to map different traits.

Conclusion

- Due to first results, genomic breeding value estimation seems to be feasible and valuable in the Franches-Montagnes horse breed.

- Open questions:
  Acceptance?
  Implementation?
  Consequences for the current breeding programme?
  Dependency on technology?
  Dependency on one company?

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FM

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GÖTTINGEN

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- Swiss Franches-Montagnes Horse Breeders' Federation, Avenches, Switzerland
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Schweizerische Eidgenossenschaft
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Confederazione Svizzera
Confederaziun svizra

Stiftung Sur-la-Croix

FONDATION SUR-LA-CROIX

**Thank you
for your attention!**

Foto: M. Rindlisbacher

The 1’077 genotyped FM horses

Using CFC (Sargolzaei et al. 2006) to analyse pedigree data:

- Average inbreeding coefficient: 6.22%
- Average numerator relationship:14.22%
- Average pedigree completeness index (10G): 97.8%

- Horses are direct descendants from 208 sires and 883 dams