



IT-Solutions for
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Single step genomic evaluation for horses based on a multi-breed reference population

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Outline

- ❖ project background (collaborative initiative)
 - genomics for riding horses → multiple breeds
- ❖ material and methods (single step approach)
- ❖ validation and results of test runs
 - focus on possible breed differences
- ❖ conclusions & prospects



1

Genomics for riding horses



- ❖ riding horses → multiple breeds
- ❖ challenging requirements for implementation
 - meaningful reference population (large enough, quality of phenotypes)
 - suitable target traits
- ❖ collaborative initiative in Germany
 - consortium formation in 2017: International Association of Future Horse Breeding GmbH & Co KG (IAFH)
 - studbooks + IT service provider + scientific partners

IAFH

International Association of Future Horse Breeding GmbH & Co KG

CAU
Christian-Albrechts-Universität zu Kiel

Werlhof Institut

GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN

FBN

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2

Project outline

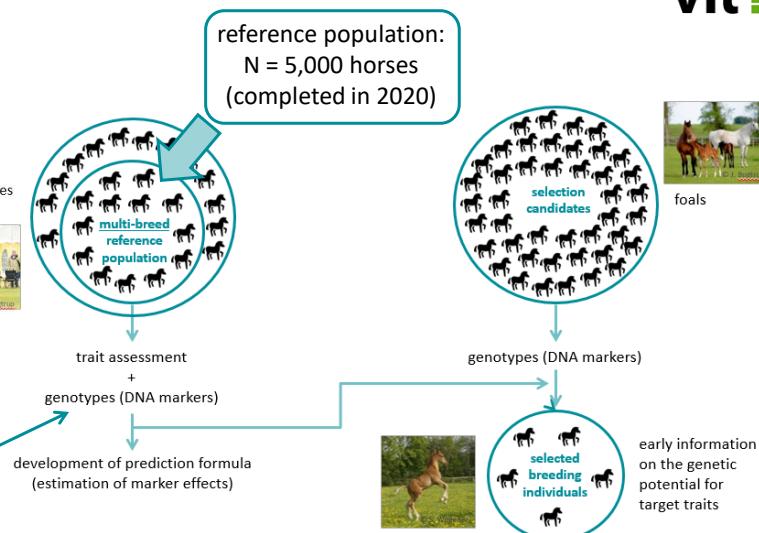


comprehensive linear profiles: conformation, gaits, jumping



balanced set of linear traits:
conformation (N=23)
performance (N=18)

whole genome SNP genotyping
(medium density: 70k+)



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3

Single-step method: Data

- ❖ phenotype data: linear profiles (foals, adult horses)
 - same linear scheme and system used across studbooks
 - approx. 61,000 linear profiles (2012-2021)
- ❖ pedigree data: phenotyped horses + 5 generations (approx. 184,000)
- ❖ genotype data: reference population
 - genotyping with GGPEquine (N=788 horses with 65,157 SNPs)
GGPEquinePlus (N=4,212 horses with 71,947 SNPs)
 - QC-criteria: MAF (0.01), CF (0.1), CR (0.05), HWE (<0.001), MSE (0.003)
 - N = 4,964 horses with 60,037 SNPs

Model

- ❖ single- / multi-trait repeatability animal model
 - as in the routine genetic evaluation for linear traits

foals:

$$Y_{ijklop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE_M_k + SEX_l + animal_o + e_{ijklop}$$

mares / sires:

$$Y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE_Y_m + PTYP_n + animal_o + pe_o + e_{ijmnop}$$

- fixed effects:
SB = studbook, EVENT-TEAM = date x location x assessment team, AGE = age (in months / years), SEX = sex, PTYP = presentation type (in hand, free, under saddle)
- random effects:
animal = additive genetic, pe = permanent environmental, e = residual

Validation

- ❖ 10-fold cross-validation: focus on possible breed differences
 - 20% of animals randomly per studbook, sex, trait (genotyped or not)
 - number of validation animals slightly different between traits and runs
 - approx. numbers of validation animals (VA) per trait complex:

group	conformation (N=23 traits)	performance (N=18 traits)			
		walk (N=2)	trot (N=6)	canter (N=4)	jumping (N=5)
VA all	3,800	4,800	6,200	3,300	1,380
VA geno	1,100	1,600	2,200	1,500	600

- ❖ forward validation: focus on quality of prediction
 - animals linearly described in 2018/2019
 - phenotype data 2020/2021 not yet considered in the validation runs



Cross-validation results

- ❖ means and ranges of GEBV correlations (Pearson) between full run and ten validation runs

group		conformation			performance			mean	min.	max.			
		all (N=23 traits)			incl. jumping (N=18 traits)								
		mean	min.	max.	mean	min.	max.						
VA non geno	all	0.79	0.73	0.86	0.81	0.76	0.87	0.83	0.77	0.87			
VA geno	all	0.85	0.80	0.88	0.83	0.79	0.88	0.84	0.79	0.88			
	OL	0.87	0.81	0.92				0.84	0.77	0.88			
	OS	0.84	0.75	0.90				0.78	0.71	0.85			
	HOL	0.83	0.72	0.90				0.77	0.70	0.82			
	TRAK	0.78	0.69	0.85				0.72	0.65	0.79			
	WESTF	0.85	0.79	0.89				0.86	0.80	0.93			

VA non geno = non genotyped validation animals, VA geno = genotyped validation animals



GEBV distribution (full run)



- ❖ subset of phenotyped horses born 2007-2017

studbook		conformation (N=23 traits)			performance (N=18 traits)		
		N	mean	std.	N	mean	std.
all	non geno	27,863	100.09	10.47	28,494	100.05	11.91
	geno	4,783	100.31	12.56	4,833	99.86	13.93
OL	non geno	11,205	100.62	10.33	11,339	99.69	10.52
	geno	1,556	100.98	12.12	1,556	100.23	12.29
OS	non geno	3,296	99.17	9.32	3,356	100.46	8.30
	geno	422	99.40	11.34	422	101.21	11.07
HOL	non geno	7,486	99.79	9.11	7,569	101.70	8.46
	geno	1,218	100.01	10.98	1,268	101.75	10.16
TRAK	non geno	1,487	100.29	14.06	1,497	94.09	11.55
	geno	763	100.07	15.02	763	93.89	12.58
WESTF	non geno	2,669	100.06	9.43	2,872	100.39	12.24
	geno	824	100.18	10.97	824	101.10	13.82

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8

Conclusions



- ❖ cross-validation
 - correlations between GEBV from 0.73-0.88
 - mostly minor differences between studbooks
 - stability of the system in genotyped horses
- ❖ around +2.0 points higher GEBV variance for genotyped horses
 - benefits of genotyping (improved individual characterization)



feasability of single-step genomic evaluation for linear traits in riding horses based on a multi-breed reference population

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9

Prospects

- ❖ routine SNP genotyping in connection with parentage control by several studbooks since 2021 (increase)
 - use of the same multi-purpose array: Equine80select Genotyping Beadchip (Illumina)
 - genome-wide SNP genotyping with 80k+ SNPs
- ❖ genomic services (genetic characteristics, etc.) as a new breeding tool for studbooks and breeders
 - first GEBVs for linear traits will become (publicly) available soon



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10



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Thank you !

