





69th Annual Meeting of the European Federation of Animal Science, Dubrovnik, Croatia

Collaboration of studbooks advancing development of genomic selection for sport horses

M. Wobbe^{1,2}, K. F. Stock^{1,2}, S. Neigenfind³, N. Krattenmacher³, W. Schulze-Schleppinghoff⁴, M. von Depka Prondzinski⁵, E. Kalm³, R. Reents¹, C. Kühn⁶, J. Tetens⁷, G. Thaller³

¹IT Solutions for Animal Production (vit), Verden, Germany; ²University of Veterinary Medicine Hannover (Foundation), Hanover, Germany; ³Kiel University, Kiel, Germany; ⁴Oldenburger Pferdezuchtverband e.V., Vechta, Germany; ⁵Werlhof-Institut MVZ, Hanover, Germany; ⁶Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany; ⁷University of Goettingen, Goettingen, Germany



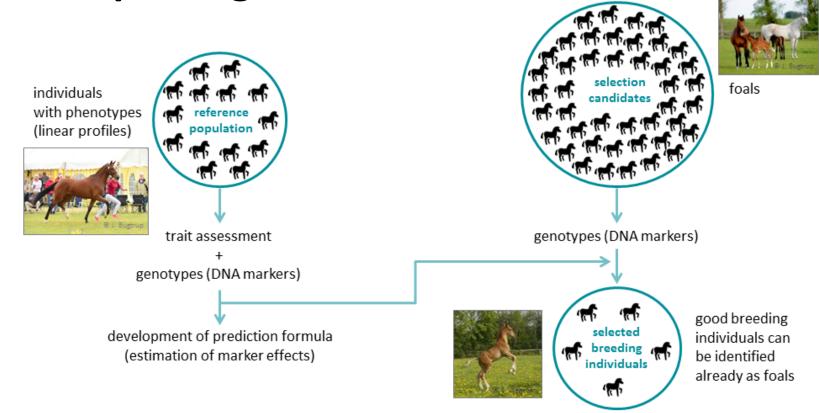
Overview

- Genomic selection how it works
- Potential of genomic selection in horses
- Requirements of implementation
- Realization
 - Collaboration (science, practice)
 - Financing
- Prospects





Principle of genomic selection





Potential of genomic selection

- long generation interval in horses
 - genomics supporting selection decisions at younger age
- challenging breeding goal traits in horses
 - low heritability and/or
 - recording with high efforts and/or
 - recording only possible late in life
 - genomics enabling better inclusion in breeding programs
- potential to accelerate and increase the breeding progress





Requirements of implementation

- appropriate target traits
- meaningful reference population
 - large enough (many horses with phenotypes + genotypes)
 - phenotypes of high quality
 - representative (no closely related individuals, ...)
- possible ways to achieve this:
 - a) own solutions (single studbook) \rightarrow efficiency? strength?
 - b) cooperation of studbooks → efficiency! strength!





Realization: Finances

- no (or hardly any) public funding for equine research
- joint studbook initiative: company formation in 2017
 - Verband der Züchter des Oldenburger Pferdes e.V. (OL)
 - Springpferdezuchtverband Oldenburg-International e.V. (OS)
 - Westfälisches Pferdestammbuch e.V. (WESTF)
 - Trakehner Verband e.V. (TRAK)
 - Verband der Züchter des Holsteiner Pferdes e.V. (HOL)
- International Association of Future Horse Breeding GmbH & Co. KG (IAFH)



Realization: Consortium



- cooperation partners from practice and science
 - Kiel University
 - University of Goettingen
 - Leibniz Institute for Farm Animal Biology, Dummerstorf
 - Werlhof Institute, Hanover
 - IT-Solutions for Animal Production (vit), Verden
- close collaboration among studbooks and of practice and science implying optimum starting point for successful introduction of genomic selection in horse breeding

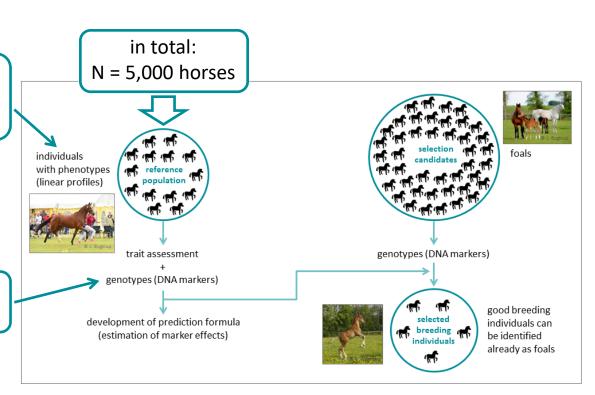


Project outline

linearly described mares (studbook inspection, performance tests)

focus on linear performance traits

SNP genotyping (medium density: 70k+)





Data collection

- high quality phenotyping of enough horses
 - joint basis for meaningful reference population
- suitable target traits
 - refined linear profiling
 - same linear scheme across studbooks within IAFH
 - conformation, gaits, jumping, behavior
 - seven-point scale from -3 to +3,
 four-point scale from 0 to +3
 for special remarks (defect traits)
 - mobile system (tablet PC)

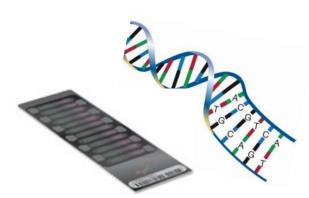






Project activities

- continuous phenotypic data screening
 - quality control
 - within and across studbooks (harmonization)
- DNA sampling and stepwise genotyping
 - favorable course of sample collection (hairs) and DNA extraction
 - \rightarrow already genotyped: 1st and 2nd cohort (approx. N = 1,300 horses)
- preliminary analyses
 - structure of the reference population (pedigree-based, genomic)
 - linking of genotypes and phenotypes (search for associations)





Prospects

- increasing number of studbooks working with linear profiling
 - in Europe and worldwide
 - regular meetings for exchange of experiences, practical training, ...
- similarity / comparability of linear traits as basis of closer collaboration in research and routine
- genomic applications as valuable tool for horse breeding
 - synergies through joint reference population and joint genomic evaluation systems
 - motivation for new approaches of collaboration













Mirell Wobbe (E-mail: mirell.wobbe@vit.de; phone: +49-4231-955185)

Kathrin F. Stock (E-mail: friederike.katharina.stock@vit.de; phone: +49-4231-955623)

Thank you!

Take home: genomic applications as motivation for new approaches of collaboration







The authors acknowledge the financial support of the H. Wilhelm Schaumann Foundation.