





69<sup>th</sup> Annual Meeting of the European Federation of Animal Science, Dubrovnik, Croatia

## Collaboration of studbooks advancing development of genomic selection for sport horses


M. Wobbe<sup>1,2</sup>, K. F. Stock<sup>1,2</sup>, S. Neigenfind<sup>3</sup>, N. Krattenmacher<sup>3</sup>, W. Schulze-Schleppinghoff<sup>4</sup>, M. von Depka Prondzinski<sup>5</sup>, E. Kalm<sup>3</sup>, R. Reents<sup>1</sup>, C. Kühn<sup>6</sup>, J. Tetens<sup>7</sup>, G. Thaller<sup>3</sup>

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



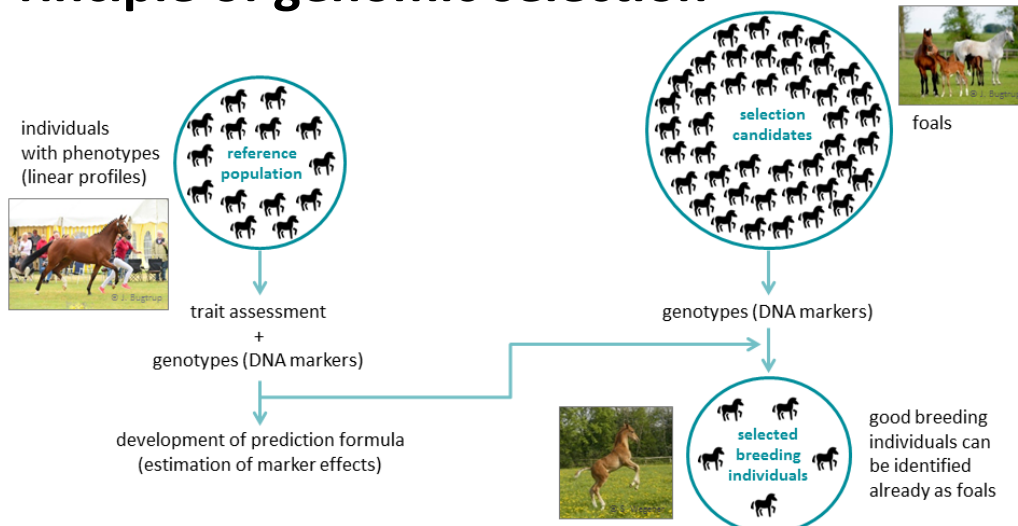
## Overview

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



29 Aug 2018 EAAP 69th Annual Meeting, Dubrovnik, Croatia: Genomic selection in sport horses (Wobbe et al.) 1

## Principle of genomic selection



29 Aug 2018 EAAP 69th Annual Meeting, Dubrovnik, Croatia: Genomic selection in sport horses (Wobbe et al.)

2

## 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



29 Aug 2018 EAAP 69th Annual Meeting, Dubrovnik, Croatia: Genomic selection in sport horses (Wobbe et al.)

3

## 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) → 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)

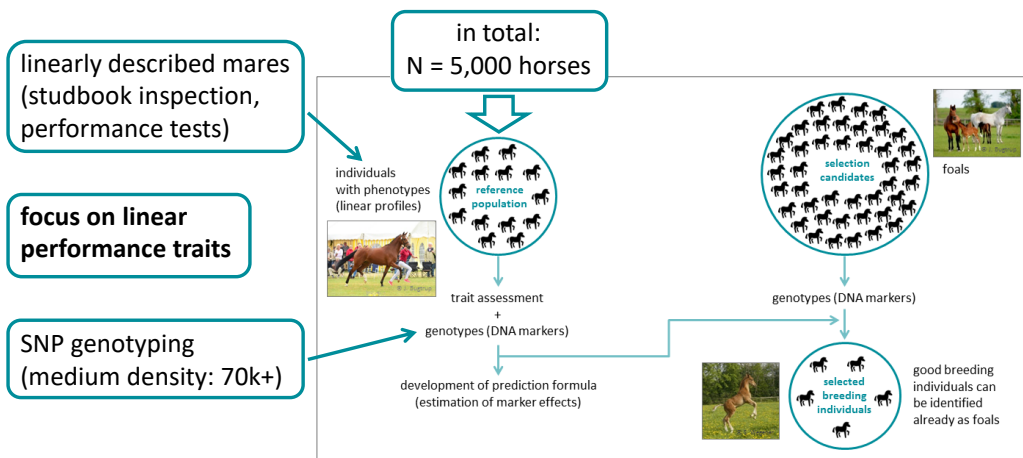


# Realization: Consortium



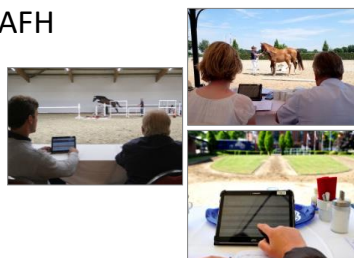
- ❖ cooperation partners from practice and science
  - ◆ Kiel University
  - ◆ University of Goettingen
  - ◆ Leibniz Institute for Farm Animal Biology, Dummerstorf
  - ◆ Werlhof Institute, Hanover
  - ◆ IT-Solutions for Animal Production (vit), Verden
- ➔ close collaboration among studbooks and of practice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

# Project outline



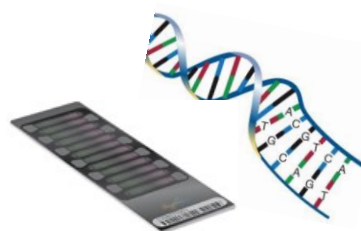
## Data collection

- ❖ 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
  - already genotyped: 1<sup>st</sup> and 2<sup>nd</sup> 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



Contact:  
 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.