IT-Solutions for
Animal Production

72nd Annual Meeting of the European
Federation of Animal Science, Davos, Switzerland

Single-step genomic evaluation in German riding horses

M. Wobbe[1,2], H. Alkhoder[1], K.F. Stock[1,2], Z. Liu[1], S. Vosgerau[3], N. Krattenmacher[3], M. Von Depka-Prondzinski[4], E. Kalm[3], R. Reents[1], W. Nolte[5], C. Kühn[5], J. Tetens[6], G. Thaller[3]

[1]IT Solutions for Animal Production (vit), Heinrich-Schroeder-Weg 1, 27283 Verden, Germany, [2]University of Veterinary Medicine Hannover (Foundation), Institute for Animal Breeding and Genetics, Buenteweg 17p, 30559 Hanover, Germany, [3]Kiel University, Institute of Animal Breeding and Husbandry, Olshausenstr. 40, 24098 Kiel, Germany, [4]Werlhof-Institut MVZ, Schillerstr. 23, 30159 Hannover, Germany,
[5]Leibniz Institute for Farm Animal Biology (FBN), Institute of Genome Biology, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany,
[6]University of Goettingen, DNTW Functional Breeding, Burkhardtweg 2, 37077 Goettingen

Outline

- genomic selection principle
  - requirements for collaboration
- material and methods (single step approach)
- validation and first results
  - cross validation
  - forward validation
- prospects

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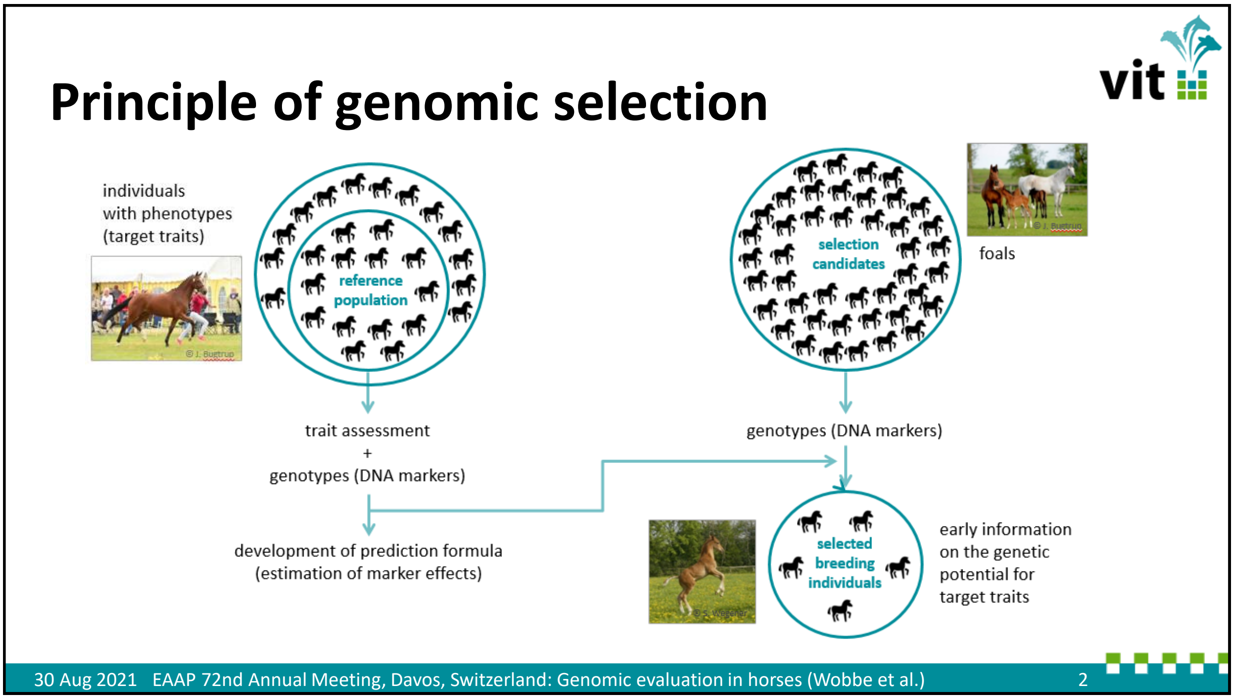

Principle of genomic selection

individuals with phenotypes (target traits)

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reference population

trait assessment
+
genotypes (DNA markers)

development of prediction formula
(estimation of marker effects)

selection candidates

foals

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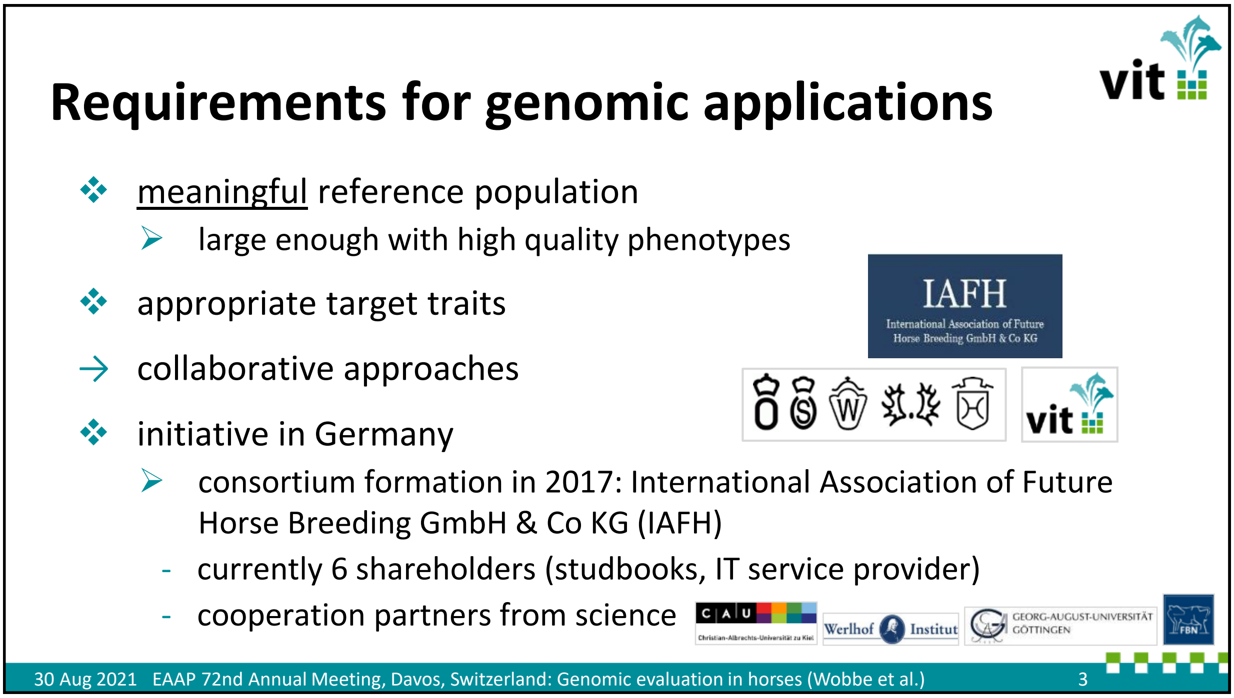
genotypes (DNA markers)

selected breeding individuals

early information on the genetic potential for target traits



Requirements for genomic applications

- meaningful reference population
  - large enough with high quality phenotypes
- appropriate target traits
- → collaborative approaches
- initiative in Germany
  - consortium formation in 2017: International Association of Future Horse Breeding GmbH & Co KG (IAFH)
    - currently 6 shareholders (studbooks, IT service provider)
    - cooperation partners from science

IAFH
International Association of Future Horse Breeding GmbH & Co KG

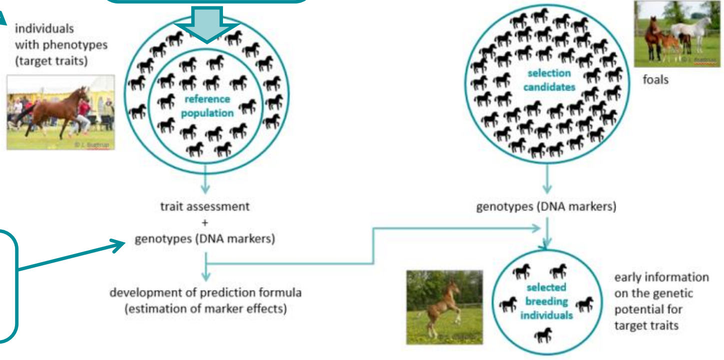
Project outline - IAFH

comprehensive linear profiles: conformation, gaits, jumping

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

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

in total:
N = 5,000 horses
(completed 2020)



Implementation of genomic selection

- single-step method
  - integration of all available data
  - phenotype data: linear profiles (foals, adult horses)
    - same linear system used across studbooks
    - approx. 41,500 linear profiles (2012-2019)
  - pedigree data: phenotyped horses + 5 generations (approx. 116,500)
  - genotype data: reference population (N = 4,964 after QC)
- use of MiX99 solver (M.Lidauer, K. Matilainen, I. Stranden)
- single- / multi-trait repeatability animal model

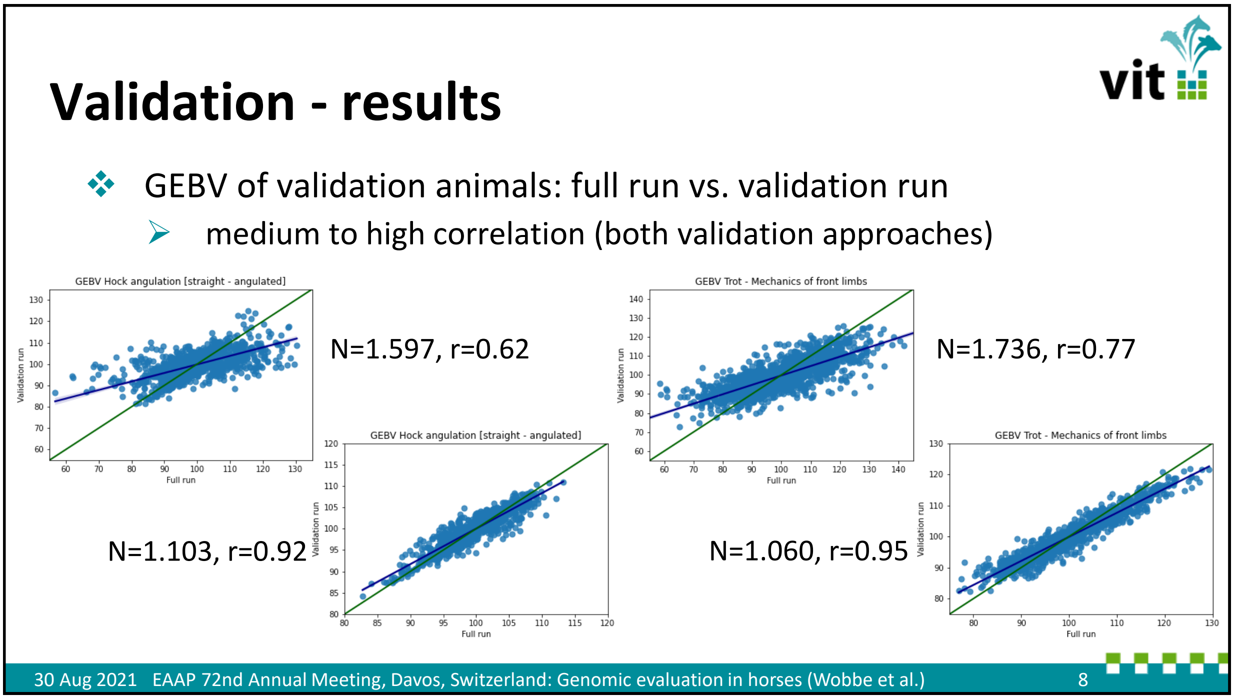
MiX99
Solving Large Mixed Model Equations

Model

- as in the routine genetic evaluation for linear conformation and performance traits
  - foals:
    $y_{ijklop} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE\_M}_k + SEX_l + animal_o + e_{ijklop}$
  - mares / sires:
    $y_{ijmnop} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE\_Y}_m + PTYP_n + animal_o + pe_o + e_{ijmnop}$
    - 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

- cross-validation
  - 10 runs, for each run randomly choosen validation animals
  - 15% of animals per studbook, sex, trait (genotyped / non-genotyped)
    - number of validation animals slightly different between the runs
    - conformation: approx. 2.140 horses
    - performance: approx. 2.800 / 3.700 / 2.600 / 1.000 horses (gaits & jumping)
- forward validation
  - animals linearly described in 2018 or later as validation animals
    - conformation: 2.700 horses
    - performance: 2.671 / 2.796 / 2.072 / 1.395 horses (gaits & jumping)



Validation - results

- GEBV of validation animals: full run vs. validation run
  - medium to high correlation (both validation approaches)

N=1.597, r=0.62

N=1.736, r=0.77

N=1.103, r=0.92

N=1.060, r=0.95

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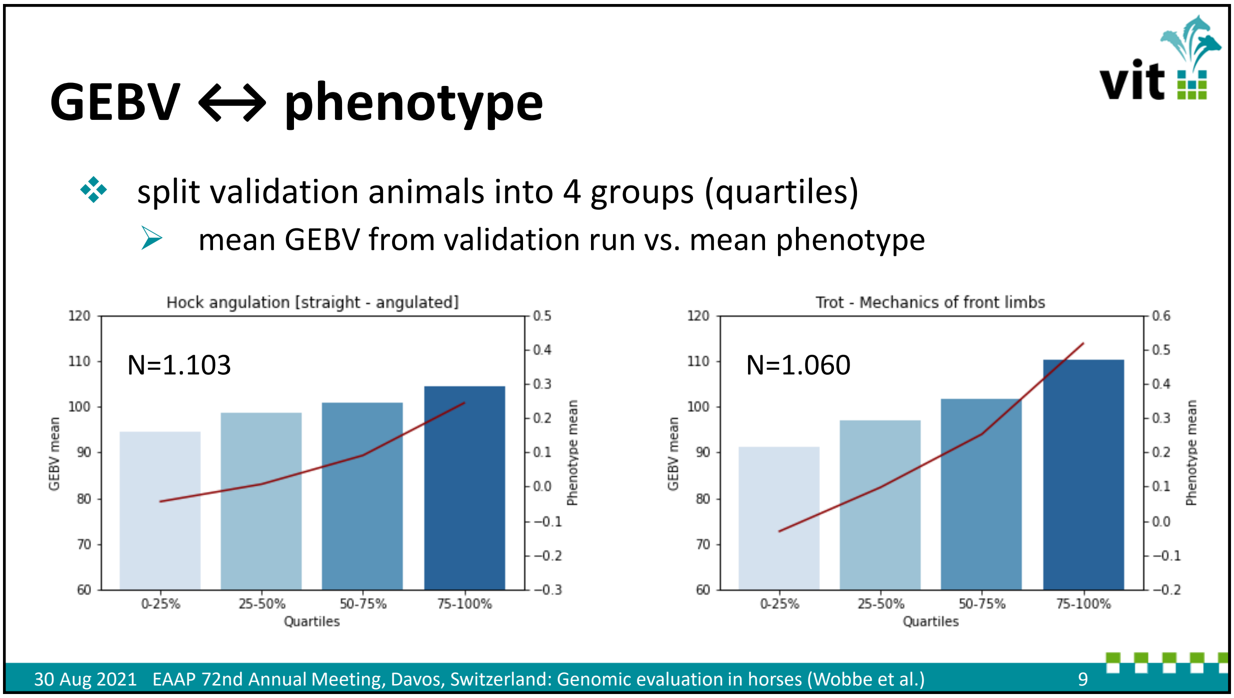

GEBV ↔ phenotype

- split validation animals into 4 groups (quartiles)
  - mean GEBV from validation run vs. mean phenotype

N=1.103

N=1.060

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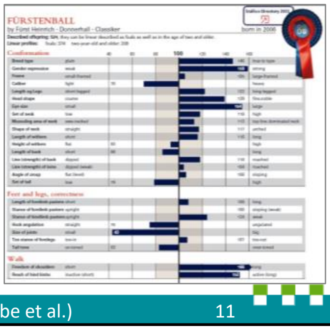
Summary & Conclusions

- both validation approaches:
  - medium to high GEBV correlations between validation and full runs
  - indicating stability of the system
- cross validation: differences between studbooks
  - highest correlations for Oldenburg and Westphalian studbook
  - slightly lower correlations for Trakehner
- work in progress: genomic reliabilities

Prospects

- routine SNP genotyping by the studbooks (IAFH) since 2021
  - coverage of the population
- new routinely used SNP Array (Equine80select Beadchip, Illumina)
  - parentage testing, genetic characteristics, genomic evaluation, etc.
- information of breeders and support of using genomic applications in sport horse breeding

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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 !

information of breeders and support of using genomic applications in sport horse breeding

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