



8th International Workshop on Linear Profiling in Horses
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Genomic breeding values for linear conformation and performance traits in German sport horses

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Outline

- ❖ setting the scene:
application-oriented research and development in the field of equine genomics in Germany
- ❖ description of the new routine genomic evaluation system
 - ◆ concept and data basis
 - ◆ prediction and publication of genomic breeding values (stallions, broodmares)
 - ◆ system validation
- ❖ conclusions and prospects



Collaboration as key to success |



- joint initiative to establish a genomic reference population, enable genomic selection and develop further genomic tools in horses
 - breeding organizations and vit as share holders
 - scientific partners
- research and development – short-term
 - genomic evaluation
basis of the core project: phenotypes from linear description plus withers height ('reference trait') and SNP genotypes of 5,000 horses
 - parentage testing
basis of the 'anchoring project': genotypes of microsatellite markers (short tandem repeats, STRs) as used for routine parentage control and SNP genotypes of 5,000 horses +/-
- R&D project phase 2017-2020



Collaboration as key to success II



- joint initiative to establish a genomic reference population, enable genomic selection and develop further genomic tools in horses
 - breeding organizations and vit as share holders
 - scientific partners
- research and development – long-term



- common goals as crucial link
 - ✓ strength through increased knowledge
 - ✓ competitiveness through genomic tools (improved information basis for decision making)
- challenges relating to the new / additional roles

- R&D project phase 2017-2020
 - starting point for **new, SNP-based routine applications, related R&D and continued engagement in equine genetic / genomic research as of 2021**

Genomic evaluation: core R&D of the IAFH

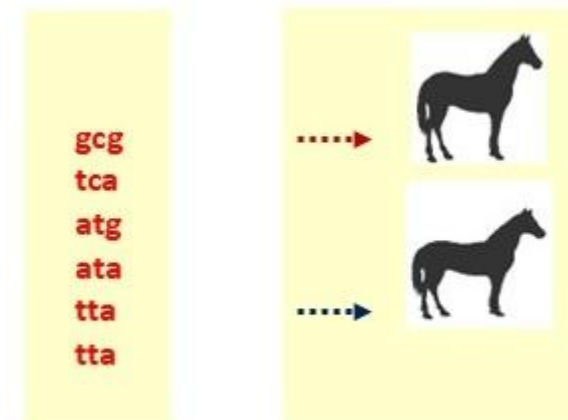
- **aim: genomic inheritance profiles** = genomic breeding values for a wider range of linear conformation and performance traits as selection tool
 - joint genomic reference population of 5,000 horses
 - single step approach for maximal / optimal use of available phenotypic data
- challenges:
 - across studbooks = across breeds (genetic exchange ↓↑)
 - sub-structures related to specialization (dressage, show-jumping)
 - heterogenous data quality
(same linear schema ≠ comparable linear profiles)
- shared R&D work with certain focus topics
 - reference trait body size (withers height)
 - conformation and movement; jumping
 - modelling suitable for routine use



Methodology I

- simple basic principle: comparison of distribution patterns
 - (1) necessary training of a prediction algorithm using horses with genome-wide marker data ('genetic fingerprint' / SNPs) and information on the target trait (phenotype)

horse	SNP1	SNP2	SNP3
1:	acggtta g ctacaattatthtaaa c gggaggaggattttattaaccag g atgtg		
2:	acggtta t ctacaattatthtaaa c gggaggaggattttattaacca a atgtg		
3:	acggtta a ctacaattatthtaaa t gggaggaggattttattaaccag g atgtg		
4:	acggtta a ctacaattatthtaaa t gggaggaggattttattaacca a atgtg		
5:	acggtta t ctacaattatthtaaa t gggaggaggattttattaacca a atgtg		
6:	acggtta t ctacaattatthtaaa t gggaggaggattttattaacca a atgtg		

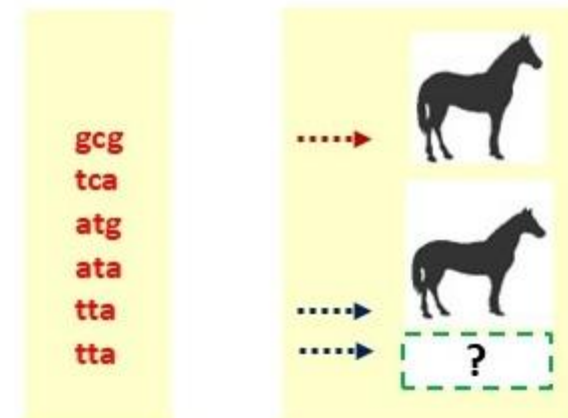


Methodology II

- simple basic principle: comparison of distribution patterns
 - (1) necessary training of a prediction algorithm using horses with genome-wide marker data ('genetic fingerprint' / SNPs) and information on the target trait (phenotype)
 - (2) practical application: reliable 'reading of the genetic fingerprint' of horses without information on the target trait

- reliable prediction of trait genetics
- also for mares and possibly already at foal age

horse	SNP1	SNP2	SNP3
1:	acggtta g ctacaattatthtaaa c gggaggagggattttattaaccag g atgtg		
2:	acggtta t ctacaattatthtaaa c gggaggagggattttattaacca a atgtg		
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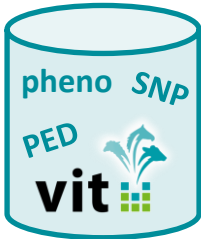


Methodology III

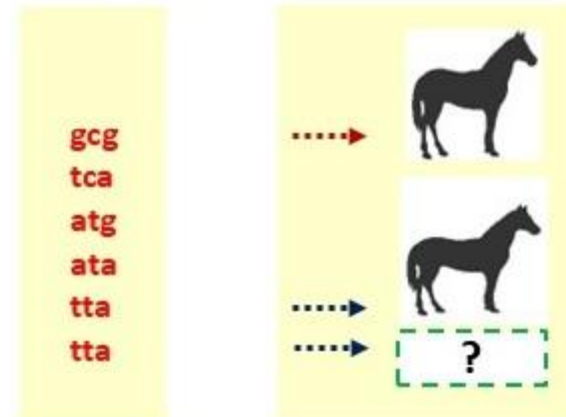


- modern / advanced systems: 'single step' = simultaneous use of all available data
 - ✓ maximal support of the prediction system by the horses with genome-wide marker data ('genetic fingerprint' / SNPs) and information on the target trait (phenotype)
 - ✓ in every prediction run comprehensive comparison of distribution patterns and reliable 'reading of the genetic fingerprint' of horses without information on the target trait

➤ reliable prediction of trait genetics
 ➤ also for mares and possibly already at foal age



horse	SNP1	SNP2	SNP3
1:	acggtta g ctacaattatthtaaa c gggaggagggattttattaaccag g atgtg		
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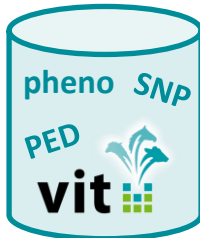


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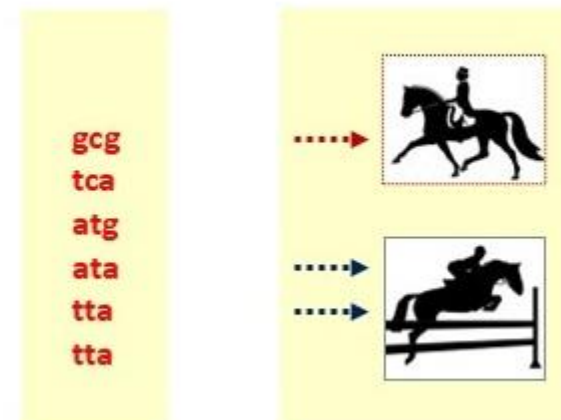
'high resolution pedigree' as universal gain of SNP genotyping

- genetic (dis-)similarity (e.g., also between full-sibs)
- better recognition of genetic differences and patterns
= better conditions for identifying associations with distribution of phenotypic data

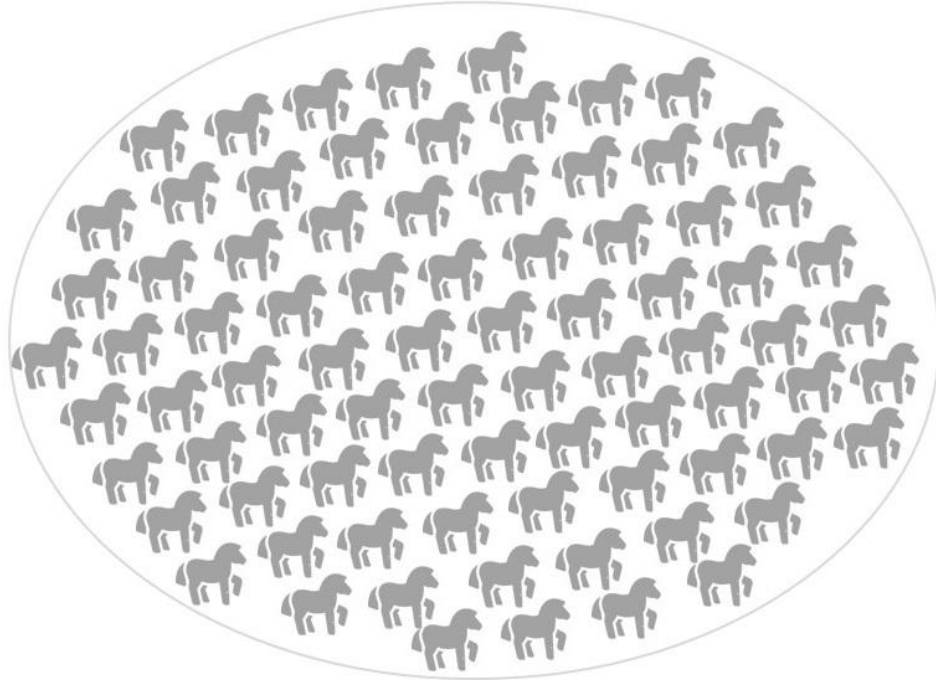
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Development concept |

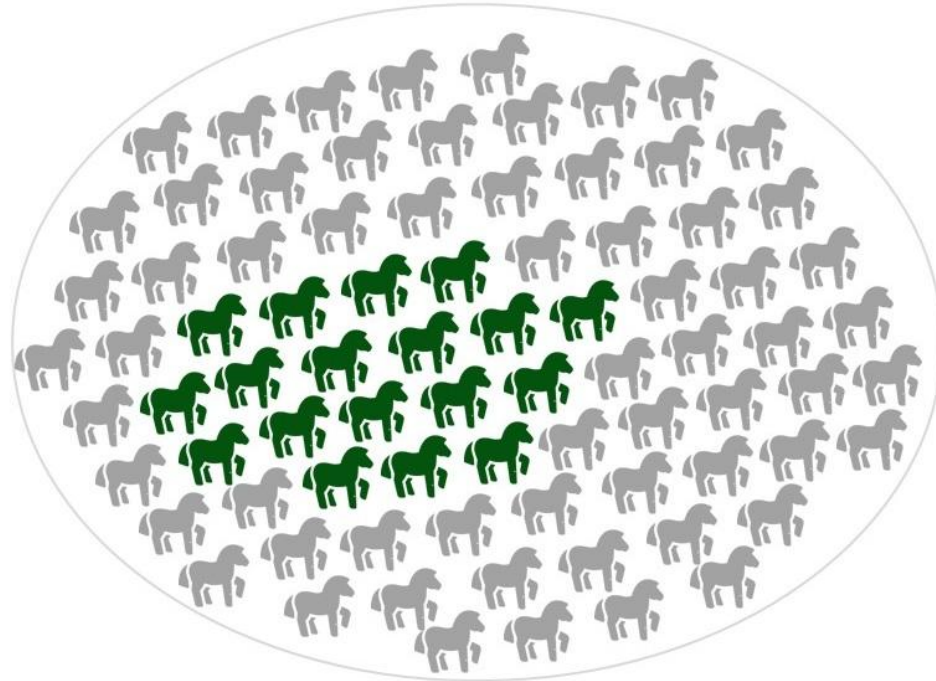


- routine linear description as phenotypic basis (target traits)

■ horse with linear description





Development concept II



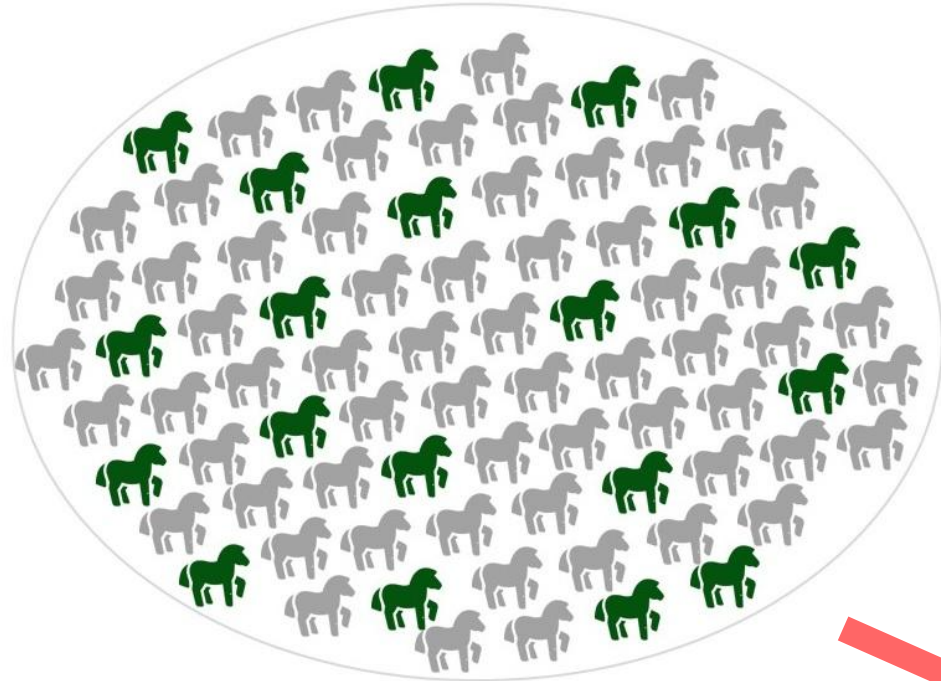
- ✓ routine linear description as phenotypic basis (target traits)
- careful checking of options for the joint reference population (= start of genome-wide SNP-genotyping)


prediction algorithm

-  horse with linear description
-  SNP genotyped horse with linear description



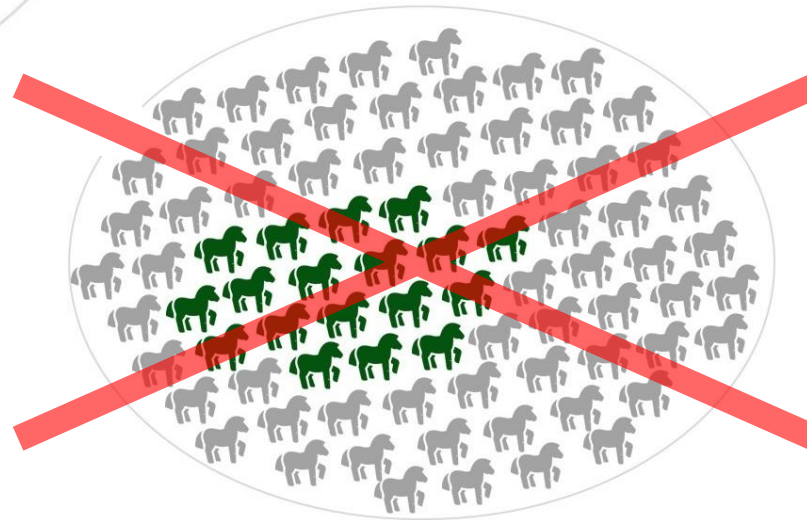
Development concept III



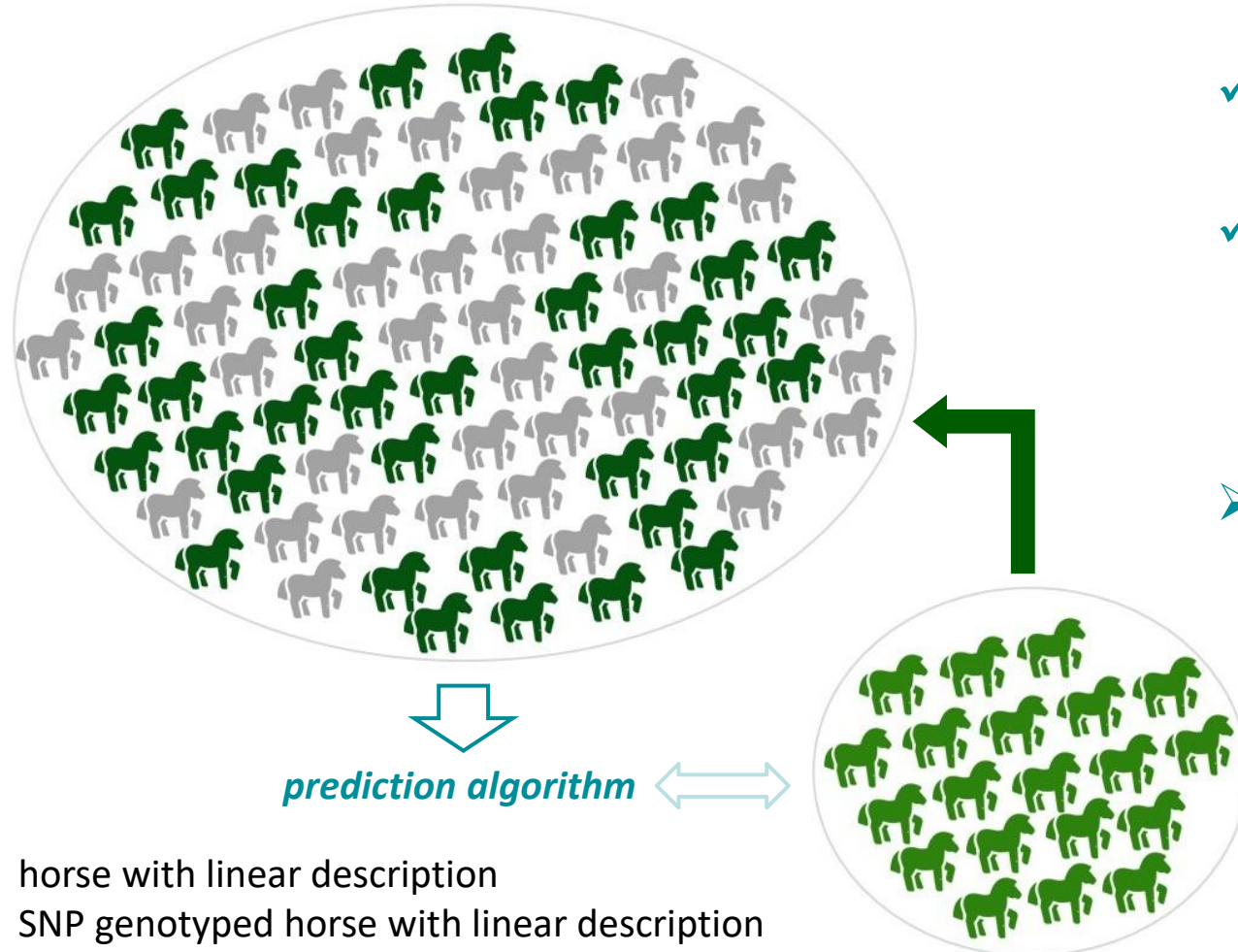
prediction algorithm

- horse with linear description
- SNP genotyped horse with linear description

- ✓ routine linear description as phenotypic basis (target traits)
- ✓ careful checking of options for the joint reference population (= start of genome-wide SNP-genotyping) → diverse, avoiding high level of pre-selection



Development concept IV

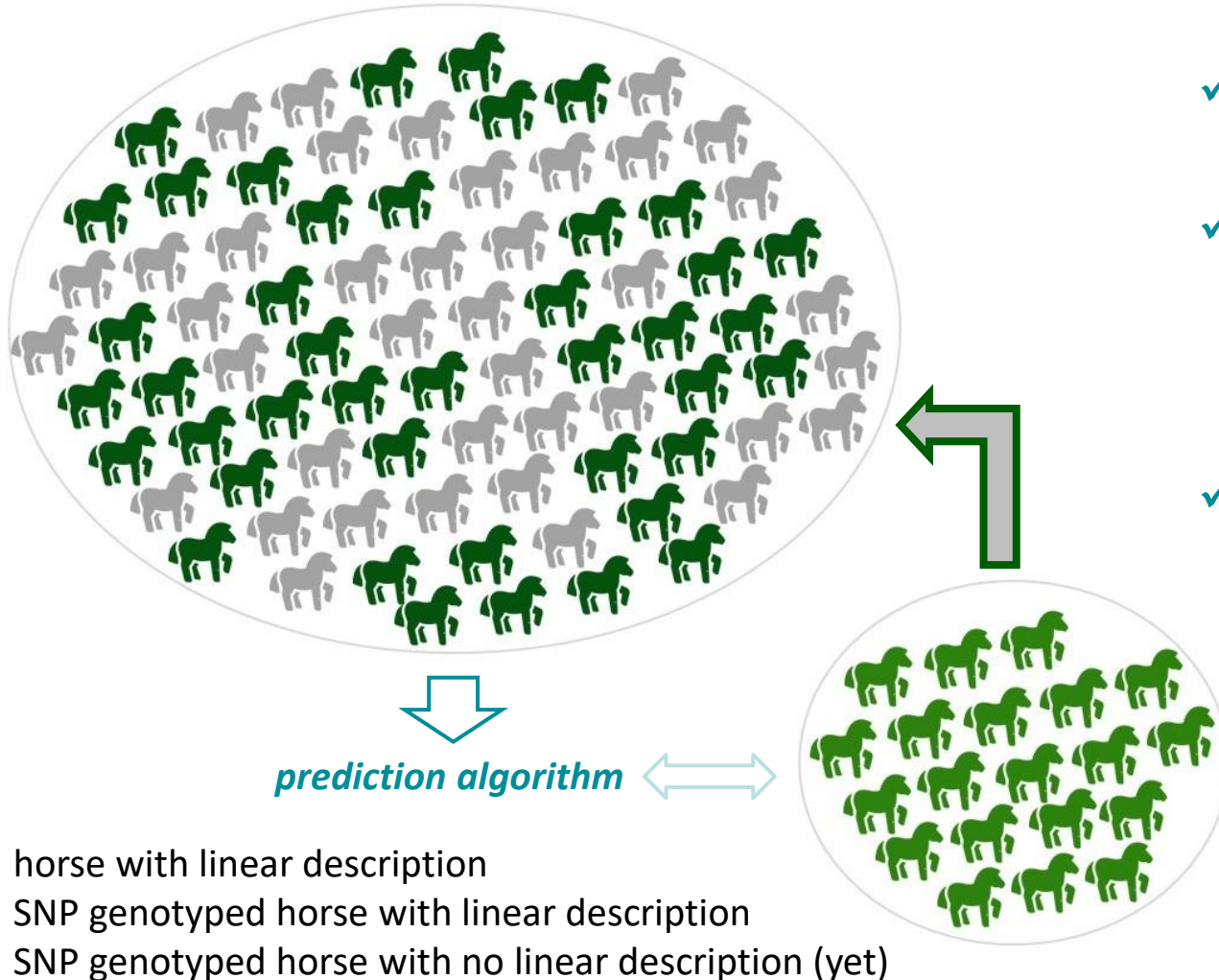


- horse with linear description
- SNP genotyped horse with linear description
- SNP genotyped horse with no linear description (yet)

- ✓ routine linear description as phenotypic basis (target traits)
- ✓ careful checking of options for the joint reference population (= start of genome-wide SNP-genotyping) → diverse, avoiding high level of pre-selection
- ensuring continued maintenance and growth (increasing number of reference animals = horses with phenotype and SNP genotype)

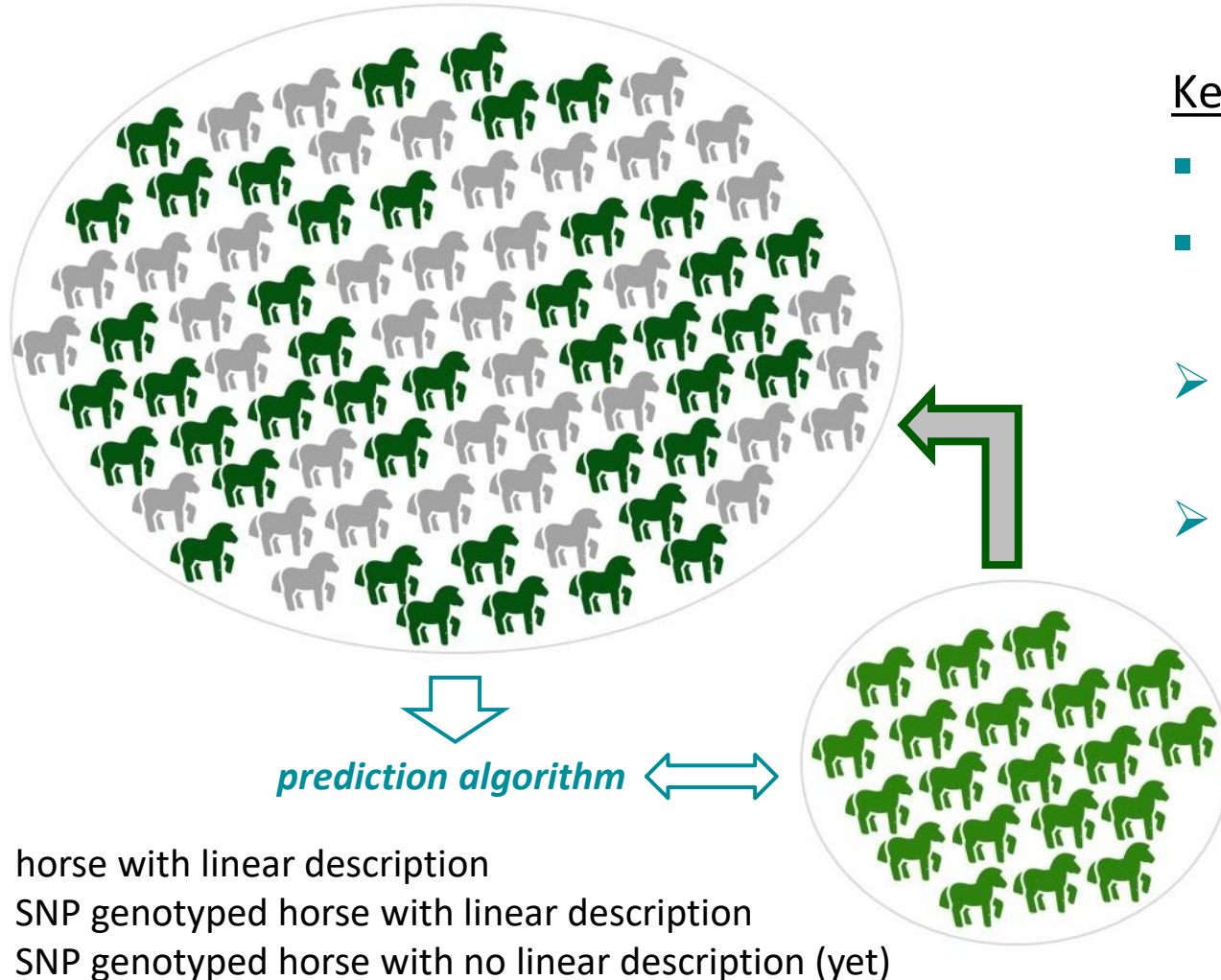
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Development concept v



- ✓ routine linear description as phenotypic basis (target traits)
- ✓ careful checking of options for the joint reference population (= start of genome-wide SNP-genotyping)
→ diverse, avoiding high level of pre-selection
- ✓ ensuring continued maintenance and growth (increasing number of reference animals = horses with phenotype and SNP genotype)
→ routine SNP genotyping with 80K for parentage control (since 2021)

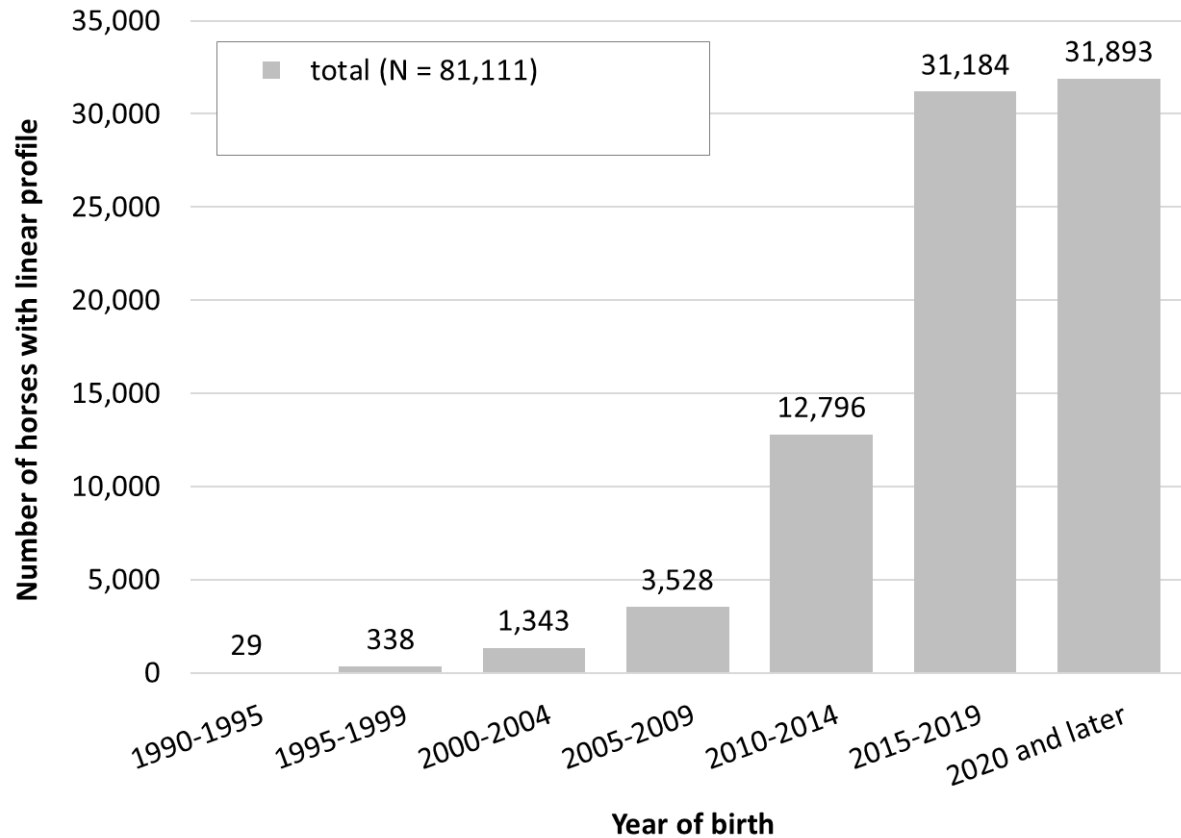
Development concept → new routine



Key figures from current routine (IAFH LIN-GE 2025)

- N= 81,111 horses with linear description
- more than 130,000 horses with 'new' parentage control, so 80K SNP genotypic data
- **more than 31,000 horses with linear description and 80K SNP genotypic data**
- across-studbook genomic evaluation system with in total more than 400,000 horses

Data basis: phenotypes

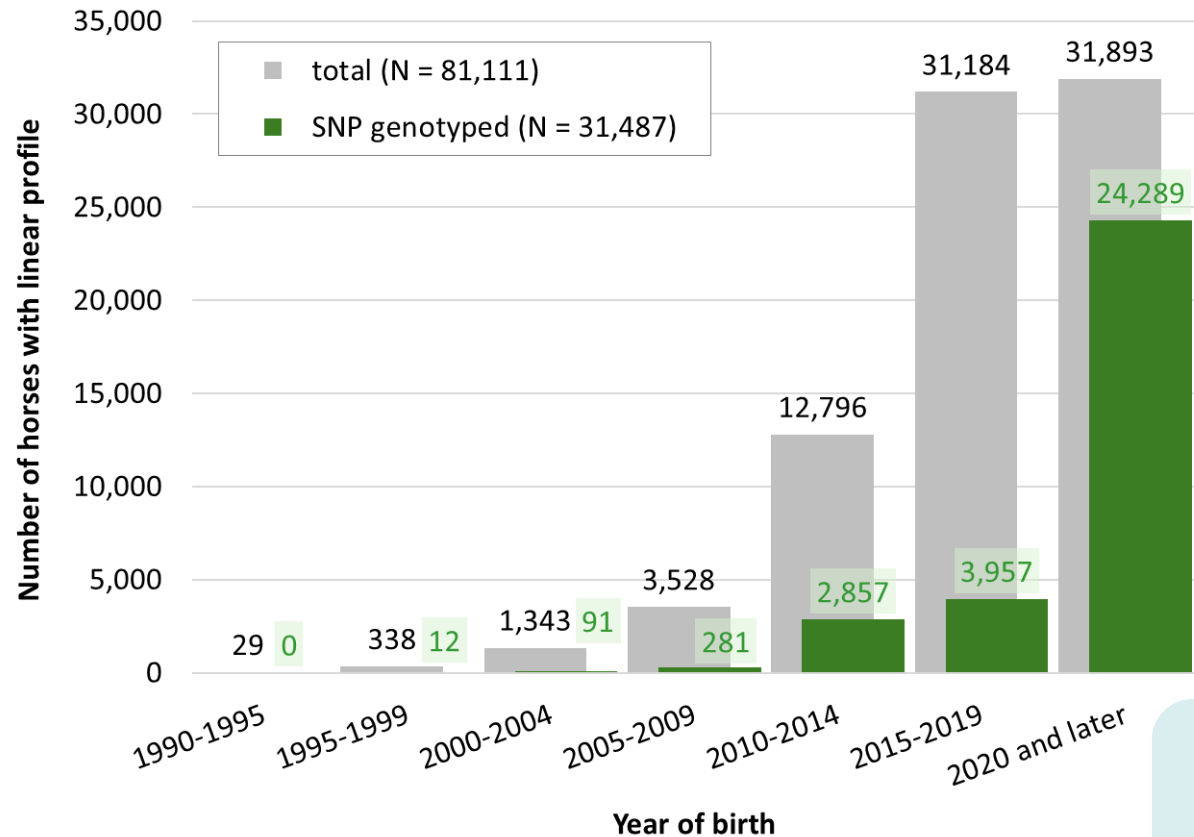


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results of linear description from 7 studbooks:
OL, OS, TRAK, HOL, WESTF, HANN, DSP-BW
(data collection 2012 - 2025, harmonized linear scheme)

Data basis: phenotypes + SNP genotypes + pedigree



Key figures from current routine (IAFH LIN-GE 2025)

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- more than 31,000 horses with linear description and 80K SNP genotypic data
- across-studbook genomic evaluation system with in total more than 400,000 horses

benefit from early investments into SNP-based routines horse genome data base, routine SNP genotyping and SNP-based parentage control of foals (via STR imputation)

Prediction of genomic breeding values



- target traits
 - standardized, comprehensive linear scheme covering major aspects of the breeding goal
 - phenotypic data recording > linear data input for genomic evaluation (data selection and processing)

- balanced set of traits
 - N = 28 conformation traits
 - N = 31 performance traits

Trait group		Number of traits (gEBV)	
		foals	adult horses *
conformation		28	28
movement	special remarks	1	1
	walk	4	4
	trot	7	7
	canter	-	7
jumping		-	12
total		40	59

* definition of sub-groups of adult horses for performance-related linear traits (separate analyses, combination of distinct gEBV to an adult horse index)

Prediction of genomic breeding values

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Conformation traits (N = 28)

- ranges of heritabilities:
F $h^2 = 0.021 - 0.377$
A $h^2 = 0.061 - 0.337$
- add. gen correlation:
0.482 - 0.901

Movement traits (N = 19)

- ranges of heritabilities:
F $h^2 = 0.056 - 0.354$
A $h^2 = 0.038 - 0.262$
- add. gen correlation:
0.646 - 0.937

Jumping traits (N = 12)

- range of heritabilities:
A $h^2 = 0.052 - 0.329$

* definition of sub-groups of adult horses for performance-related linear traits (separate analyses, combination of distinct gEBV to an adult horse index); indicated genetic parameters referring to the core group of adult horses incl. linear data of 5 studbooks)

Prediction of genomic breeding values II

- target traits
 - standardized, comprehensive linear scheme covering major aspects of the breeding goal
 - phenotypic data recording > linear data input for genomic evaluation (data selection and processing)

➤ balanced set of traits

- N = 28 conformation traits
- N = 31 performance traits

■ single step genomic evaluation

- multivariate linear animal models
- accounting for data structure (foals, groups of adult horses; fixed and random effects)
- Mix99 software

Trait group		Number of traits (gEBV)		Published gEBV total index (F+A)
		foals	adult horses *	
conformation		28	28	28
movement	special remarks	1	1	1
	walk	4	4	4
	trot	7	7	7
	canter	-	7	7
jumping		-	12	12
total		40	59	59

foals:

$$Y_{ijklop} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE_M}_k + \text{SEX}_l + a_o + e_{ijklop}$$

adult horses:

$$Y_{ijmnop} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE_J}_m + \text{PTYPE}_n + a_o + pe_o + e_{ijmnop}$$

SB = studbook, EVENT-TEAM = date x place x evaluator x assistance, AGE_M = age of foals in months, AGE_J = age of adult horses in years, SEX = sex of foals, PTYPE = presentation type (in hand, free, under rider), pe = permanent environmental effect, a = additive genetic effect, e = error

Publication of genomic breeding values |

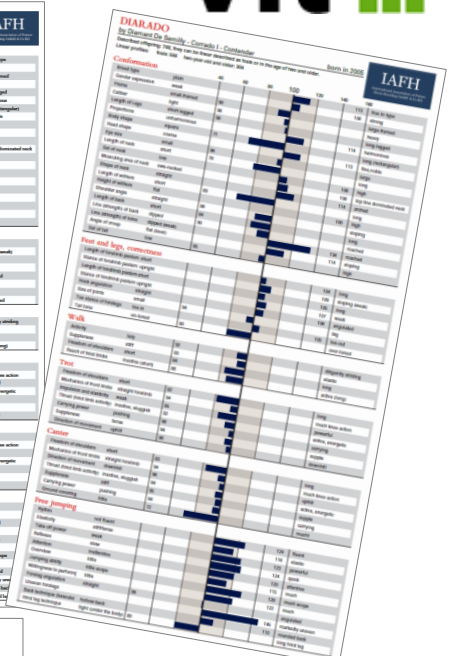
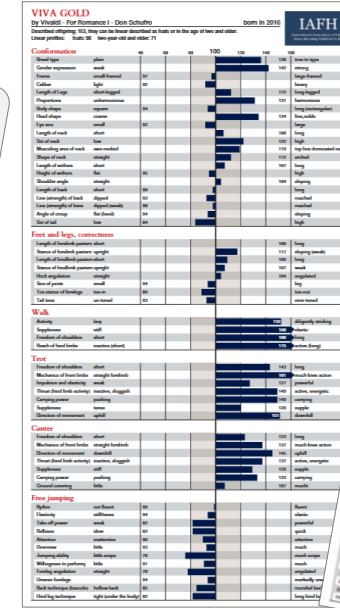
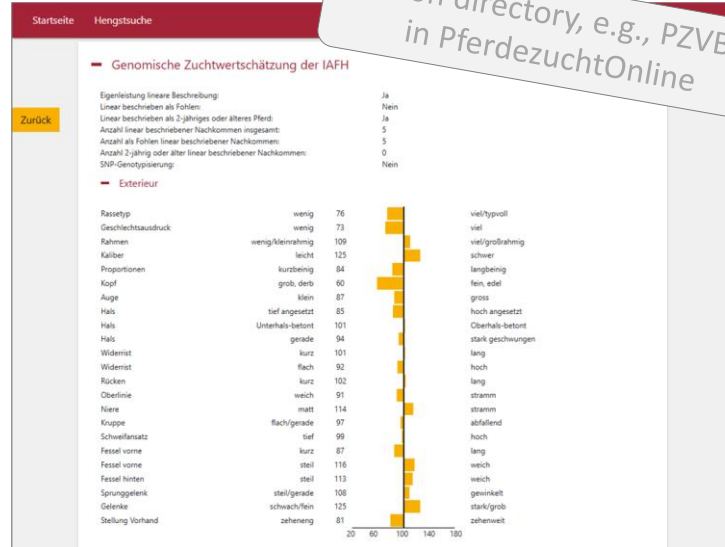
- basis and standardization of gEBV → relative breeding values
 - mean of 100 (basis: 1,381 stallions born 1995 and later with at least 3 linearly described progeny)
 - genetic standard deviation of 20
- inheritance profile with 40 or 59 traits depending on information density (F, A)



Trait group		Published gEBV total index (F+A)
conformation		28
movement	special remarks	1
	walk	4
	trot	7
	canter	7
jumping		12
total		59

Publication of genomic breeding values

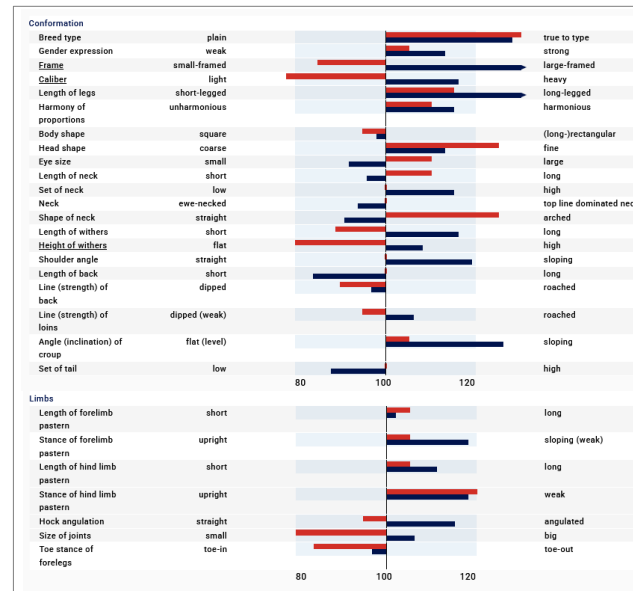
Stallion directory, e.g., PZVBW) in PferdezeitungOnline



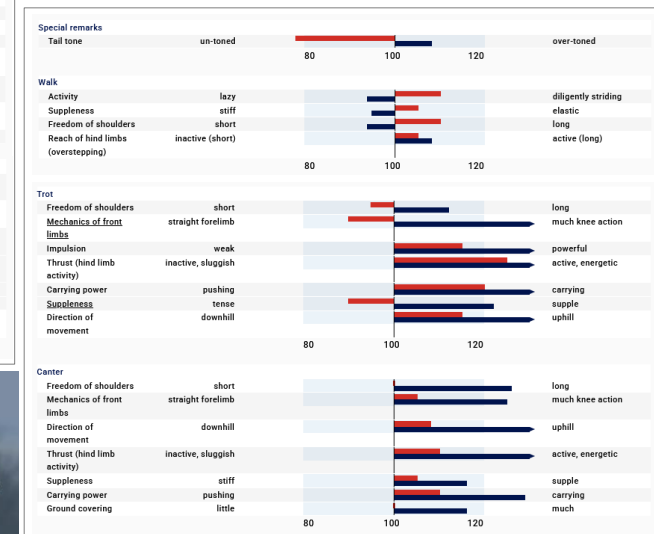
- publication of results
 - stallion directories of individual studbooks
 - IAFH genetic profiles (675 stallions)



Publication of genomic breeding values III



Mating program (pairing program),
e.g., in the OL-Account



- publication of results
 - stallion directories of individual studbooks
 - IAFH genetic profiles (675 stallions)
 - mating program in the individual online account of studbook members: 1,288 stallions and own mare(s)
 - digital support of mating planning

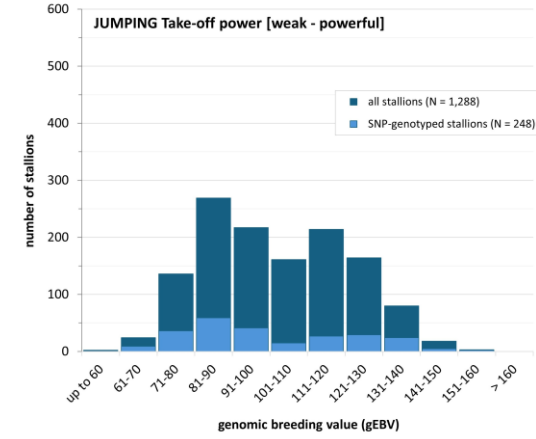
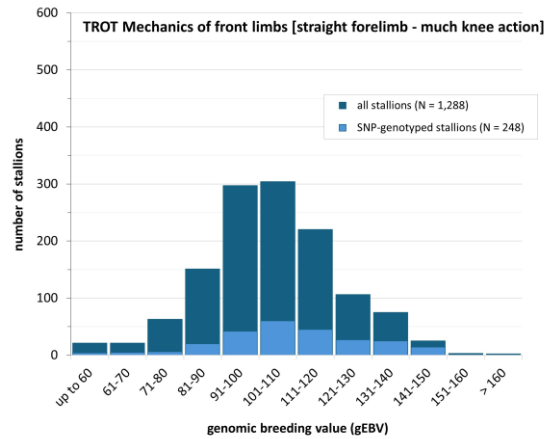
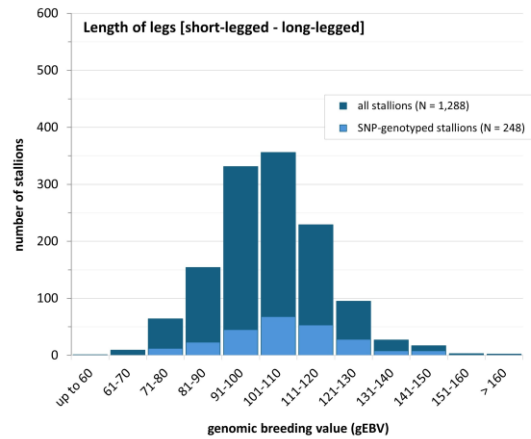


publication criteria (mating program) based on own linear profile (LIN) and number of linearly described progeny (pLIN):
stallions (N = 1,288) – at least 8 pLIN or LIN and at least 5 pLIN; mares (N = 34,805) – at least 3 pLIN or LIN(F) and at least 1 pLIN or LIN(A)

Performance of the genomic evaluation system

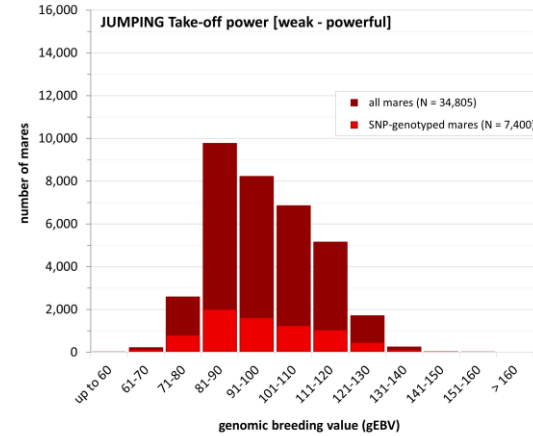
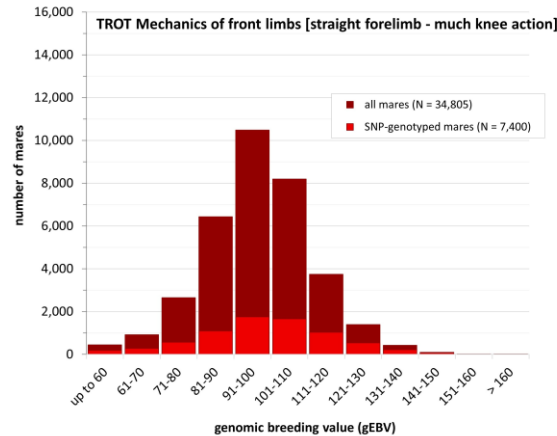
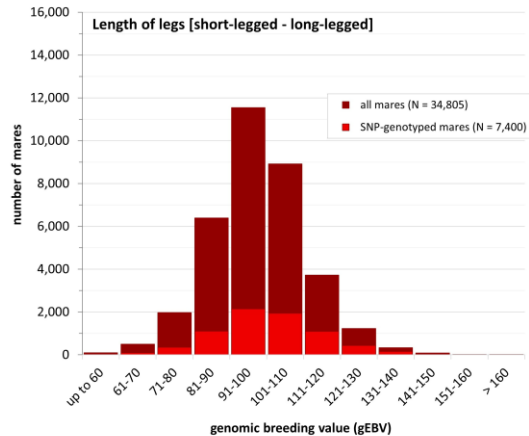


(1) distributions of genomic breeding values (gEBV) → gEBV distribution patterns



stallions
(N = 1,288)

- ✓ different levels of pre-selection in breeding stallions and active broodmares
- ✓ specialization effects

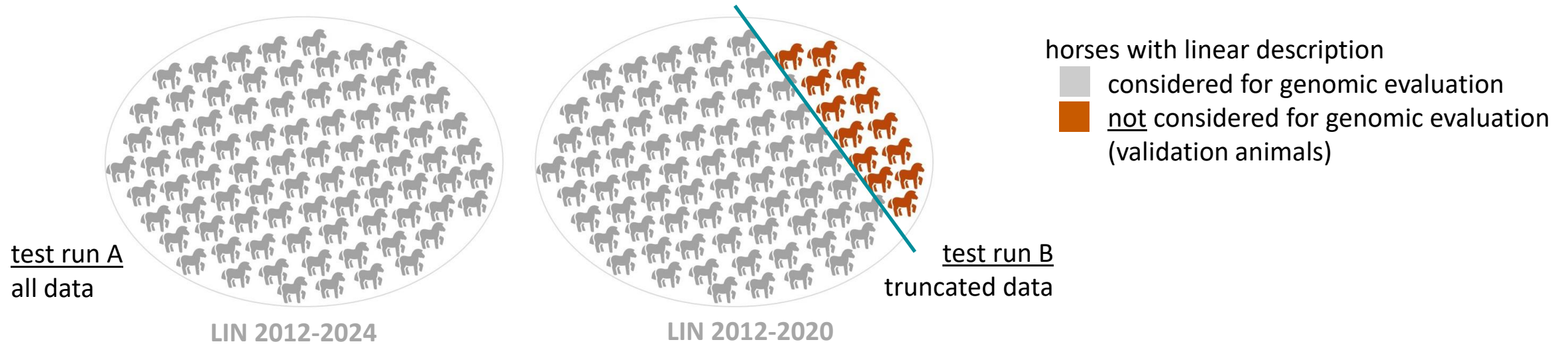


mares
(N = 34,805)



Performance of the genomic evaluation system II

- (1) distributions of genomic breeding values (gEBV) → gEBV distribution patterns
- (2) validation → gEBV stability? gEBV as predictors of future phenotypes?



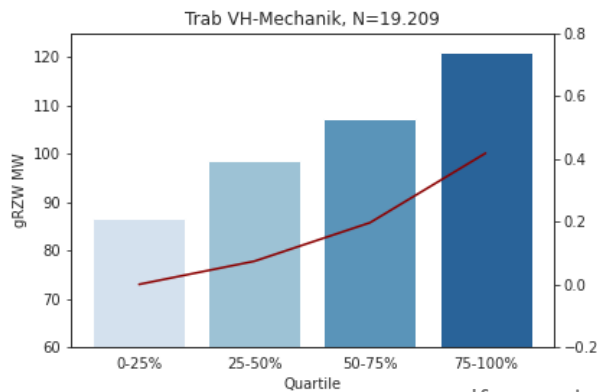
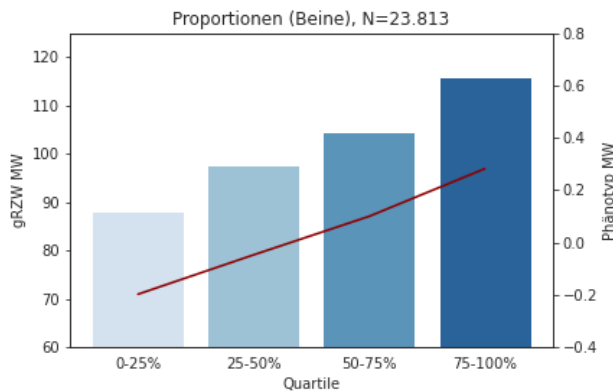
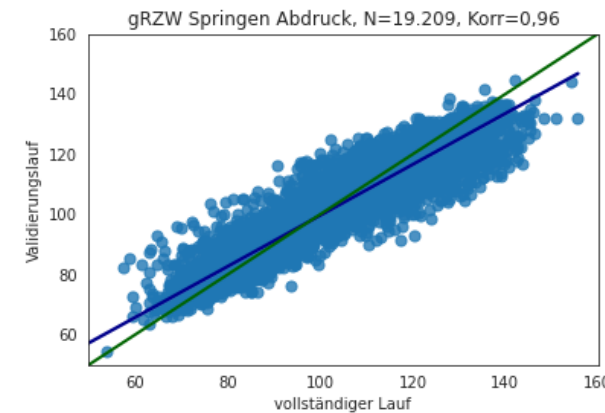
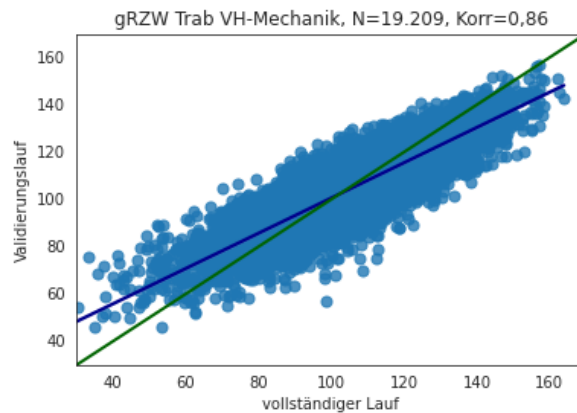
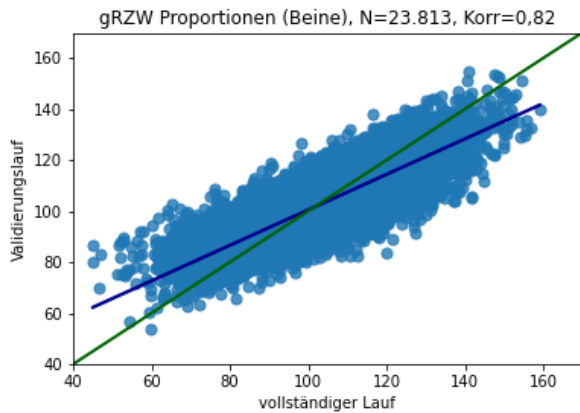
- correlations between results of genomic evaluation test runs A and B
- gEBV vs. phenotype statistics for validation animals (gEBV from test run B)

'forward validation' similar to the routinely used Interbull method (dairy cattle)

Performance of the genomic evaluation system III



- (1) distributions of genomic breeding values (gEBV) → gEBV distribution patterns
- (2) validation → gEBV stability? gEBV as predictors of future phenotypes?



- ✓ moderate to high gEBV correlations (truncated vs. all data): Pearson correlation coefficients (r) of $r_{\text{conformation}} = 0.83$, $r_{\text{movement}} = 0.88$, and $r_{\text{jumping}} = 0.92$
- ✓ distributions of predicted gEBV resembling distributions of (later) phenotypes

'forward validation' similar to the routinely used Interbull method (dairy cattle)

Conclusions and prospects

- information gain through the new joint genomic evaluation of the IAFH: qualitative and quantitative 'upgrade' of inheritance profiles (genetic profiles)
 - genomic breeding values
 - information basis and numbers of horses ↑
 - spectrum of linear conformation and performance traits ↑
- immediate practice transfer: digital tools for breeders for decision support and informed mating planning
- continued R&D on genomic applications
 - new traits in genomic evaluation (sport performance, health, behavior)
 - genetic and genomic background of specific traits of interest (e.g., ECVM)

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qualitative and quantitative 'upgrade' of inheritance profiles (genetic profiles)
- immediate practice transfer:
digital tools for breeders for decision support and informed mating planning
- continued R&D on genomic applications

Thank you !

IAFH

International Association of Future
Horse Breeding GmbH & Co KG

