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IAFH
International Association of Future
Horse Breeding GmbH & Co KG


Quelle: Sascha Schulz

8th International Workshop on Linear Profiling in Horses
on April 14-15, 2026, in Adelheidsdorf and Celle, Germany

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

photo: OLDArt

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

International Association of Future Horse Breeding GmbH & Co KG (IAFH)
and its scientific collaboration 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

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- <u>research and development</u> – 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

- <u>aim:</u> **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)


photo: Lafrentz


photo: Lafrentz

- ➢ shared R&D work with certain focus topics
  - ➢ reference trait body size (withers height)
  - ➢ conformation and movement; jumping
  - ➢ modelling suitable for routine use

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Genomic evaluation

Methodology

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

Genomic evaluation

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) <u>and</u> information on the target trait (phenotype)
  (2) practical application:
  reliable 'reading of the genetic fingerprint' of horses <u>without</u> information on the target trait

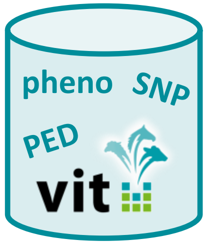
> ➢ reliable prediction of trait genetics
> ➢ also for mares and possibly already at foal age

horse	SNP1 SNP2 SNP3	
1:	acggttagctacaattatttaaacgggaggagggattttattaaccagatgtg	gcg
2:	acggttatctacaattatttaaacgggaggagggattttattaaccaaatgtg	tca
3:	acggttaactacaattatttaaatgggaggagggattttattaaccagatgtg	atg
4:	acggttaactacaattatttaaatgggaggagggattttattaaccaaatgtg	ata
5:	acggttatctacaattatttaaatgggaggagggattttattaaccaaatgtg	tta
6:	acggttatctacaattatttaaatgggaggagggattttattaaccaaatgtg	tta

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



Genomic evaluation

Methodology IV

- modern / advanced systems: 'single step' = simultaneous use of all available data

'high resolution pedigree' as universal gain of SNP genotyping

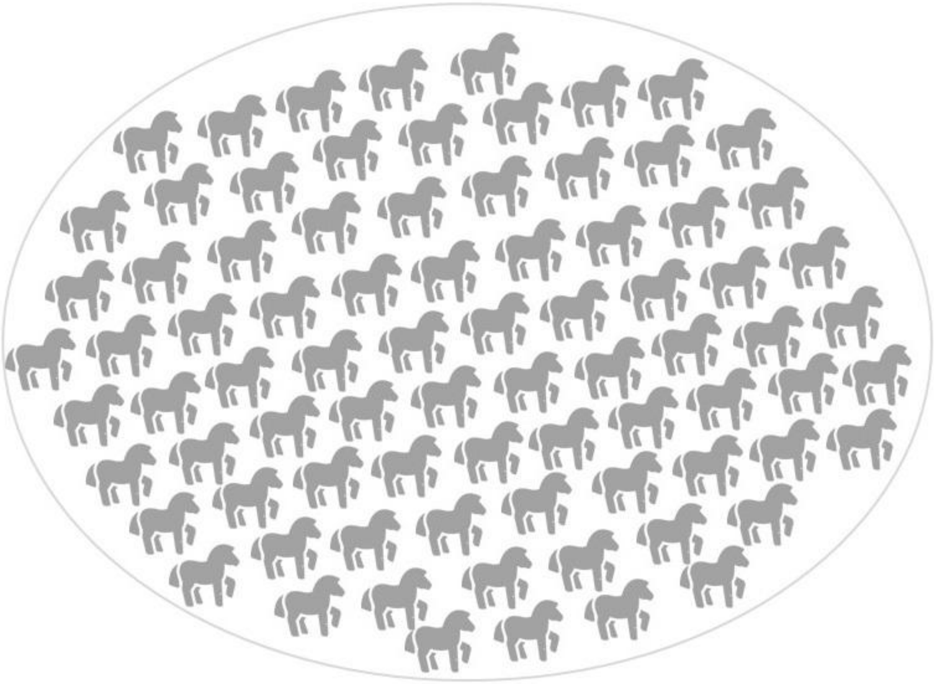
- ➢ genetic (dis-)similarity (e.g., also between full-sibs)
- ➢ better recognition of genetic differences and patterns
  = better conditions for identifying associations with distribution of phenotypic data

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

pheno SNP PED vit

```
horse        SNP1                SNP2                        SNP3
1:  acggttagctacaattatttaaacgggaggagggattttattaaccagatgtg    gcg
2:  acggttatctacaattatttaaacgggaggagggattttattaaccaaatgtg    tca
3:  acggttaactacaattatttaaatgggaggagggattttattaaccagatgtg    atg
4:  acggttaactacaattatttaaatgggaggagggattttattaaccaaatgtg    ata
5:  acggttatctacaattatttaaatgggaggagggattttattaaccaaatgtg    tta
6:  acggttatctacaattatttaaatgggaggagggattttattaaccaaatgtg    tta
```

Development concept



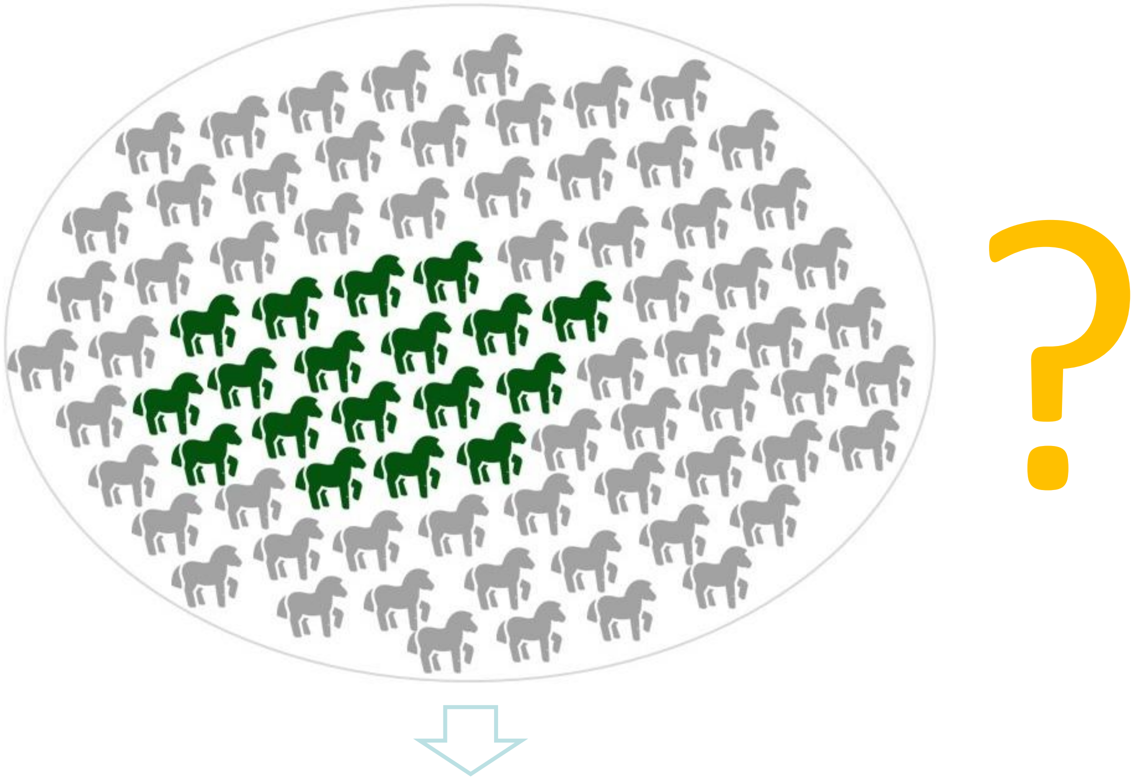
- ➢ routine linear description as phenotypic basis (target traits)

⬜ horse with linear description

Source (horse pictogram): https://icons8.com

Genomic evaluation IAFH

Development concept



prediction algorithm

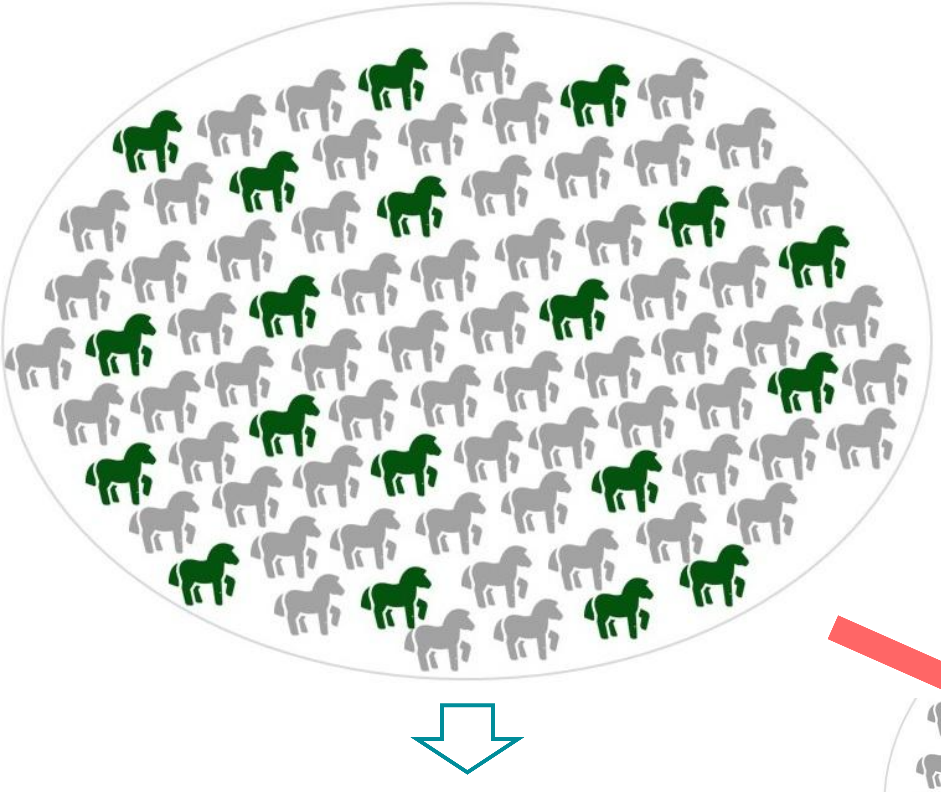
⬜ horse with linear description

🟩 SNP genotyped horse with linear description

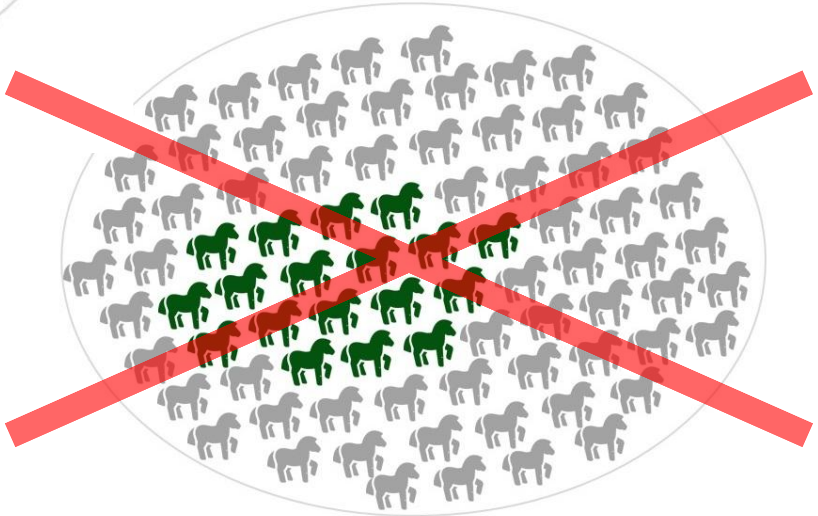
- ✓ routine linear description as phenotypic basis (target traits)
- ➢ careful checking of options for the joint reference population
  (= start of genome-wide SNP-genotyping)

Source (horse pictogram): https://icons8.com

Development concept



prediction algorithm

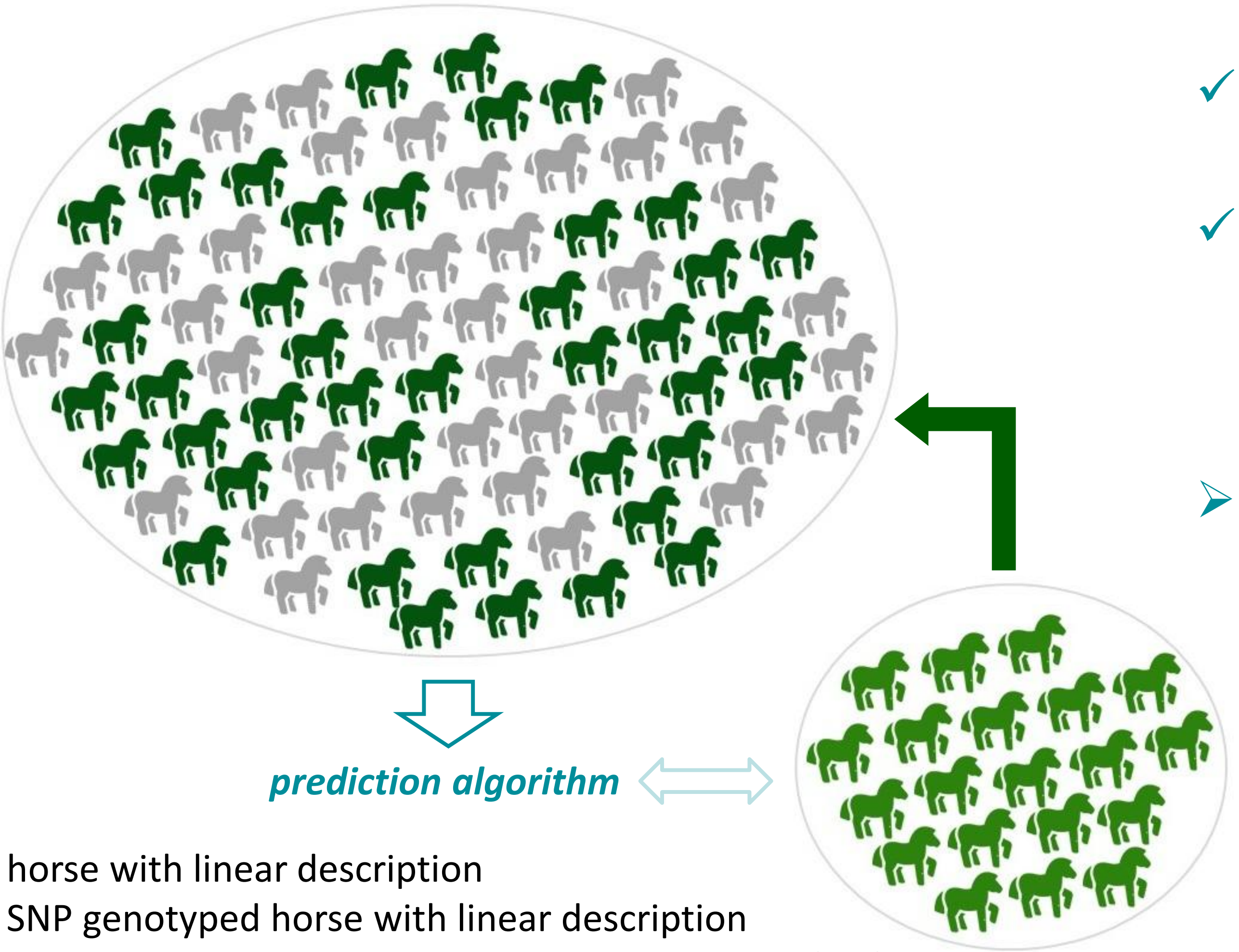


⬜ horse with linear description
🟩 SNP genotyped horse with linear description

- ✓ 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

Source (horse pictogram): https://icons8.com

Development concept IV



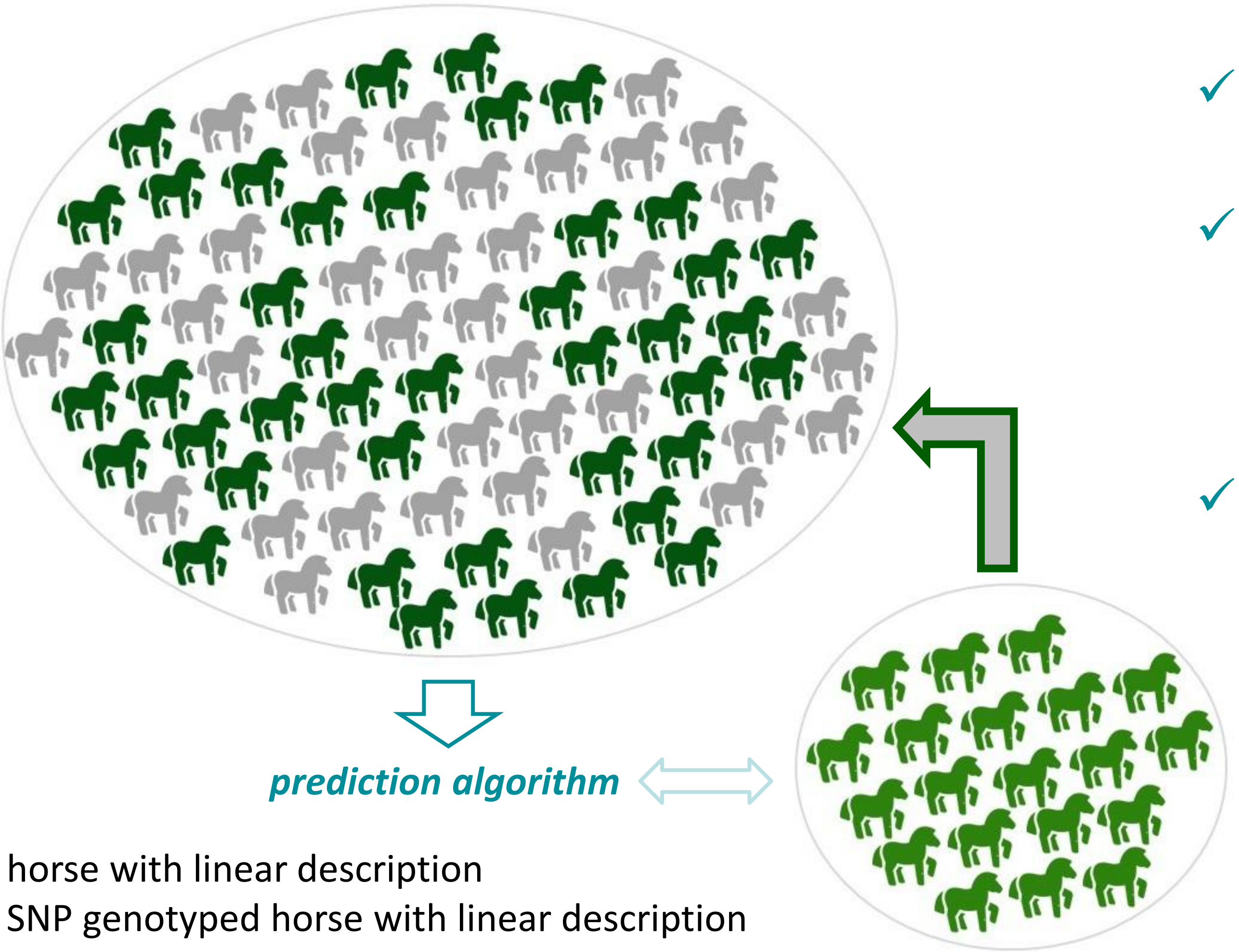
⬜ horse with linear description
🟩 SNP genotyped horse with linear description
🟩 SNP genotyped horse with no linear description (yet)

- ✓ 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)

€ ?

Source (horse pictogram): https://icons8.com

Development concept v



prediction algorithm

- ⬜ 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)

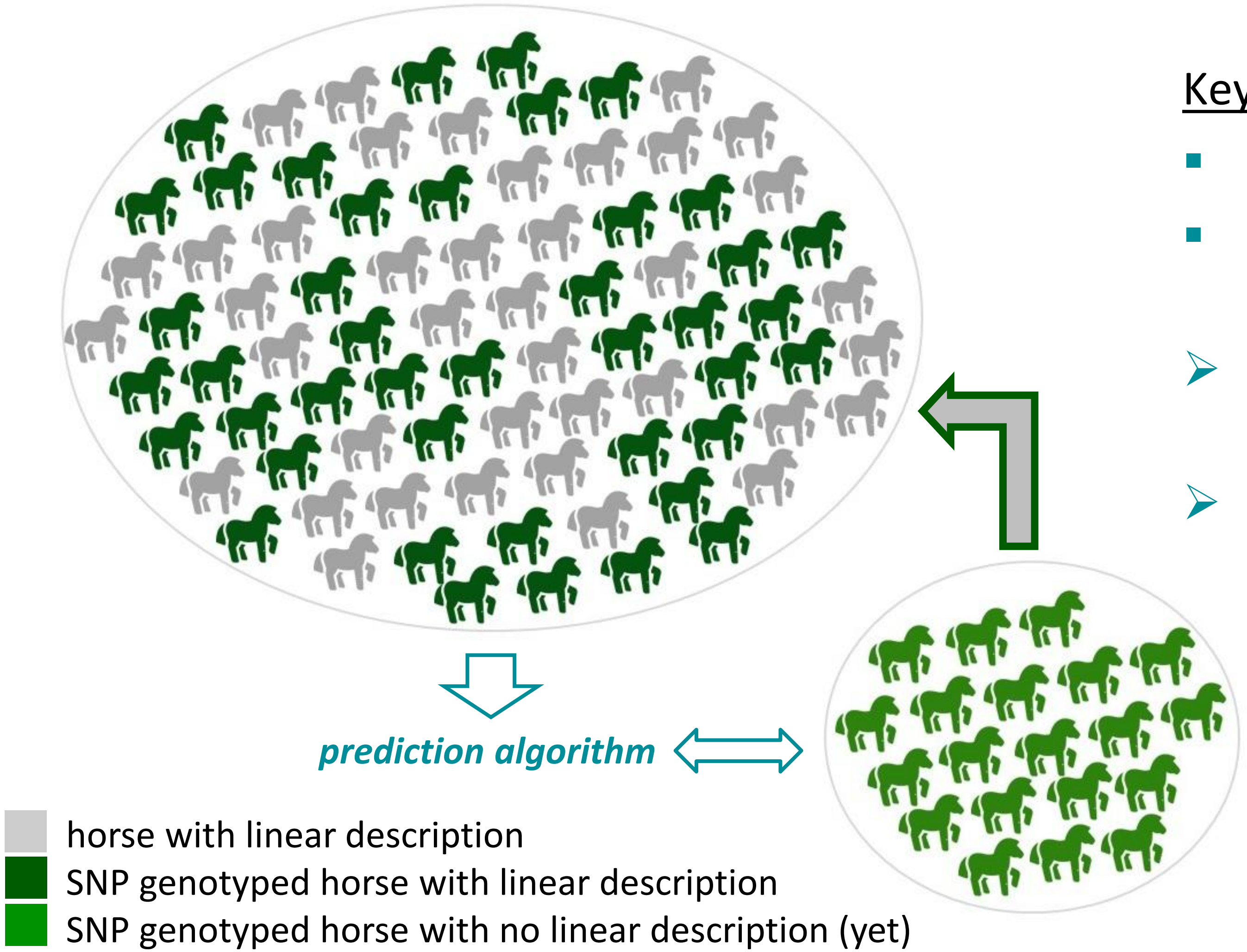
✓ careful checking of options for the joint reference population
(= start of genome-wide SNP-genotyping)
→ diverse, avoiding high level of pre-selection

✓ ensuring continued maintenance and growth (increasing number of reference animals
= horses with phenotype and SNP genotype)
→ routine SNP genotyping with 80K for parentage control (since 2021)

Source (horse pictogram): https://icons8.com

Genomic evaluation IAFH

Development concept → new routine


prediction algorithm

⬜ horse with linear description
■ SNP genotyped horse with linear description
🟩 SNP genotyped horse with no linear description (yet)

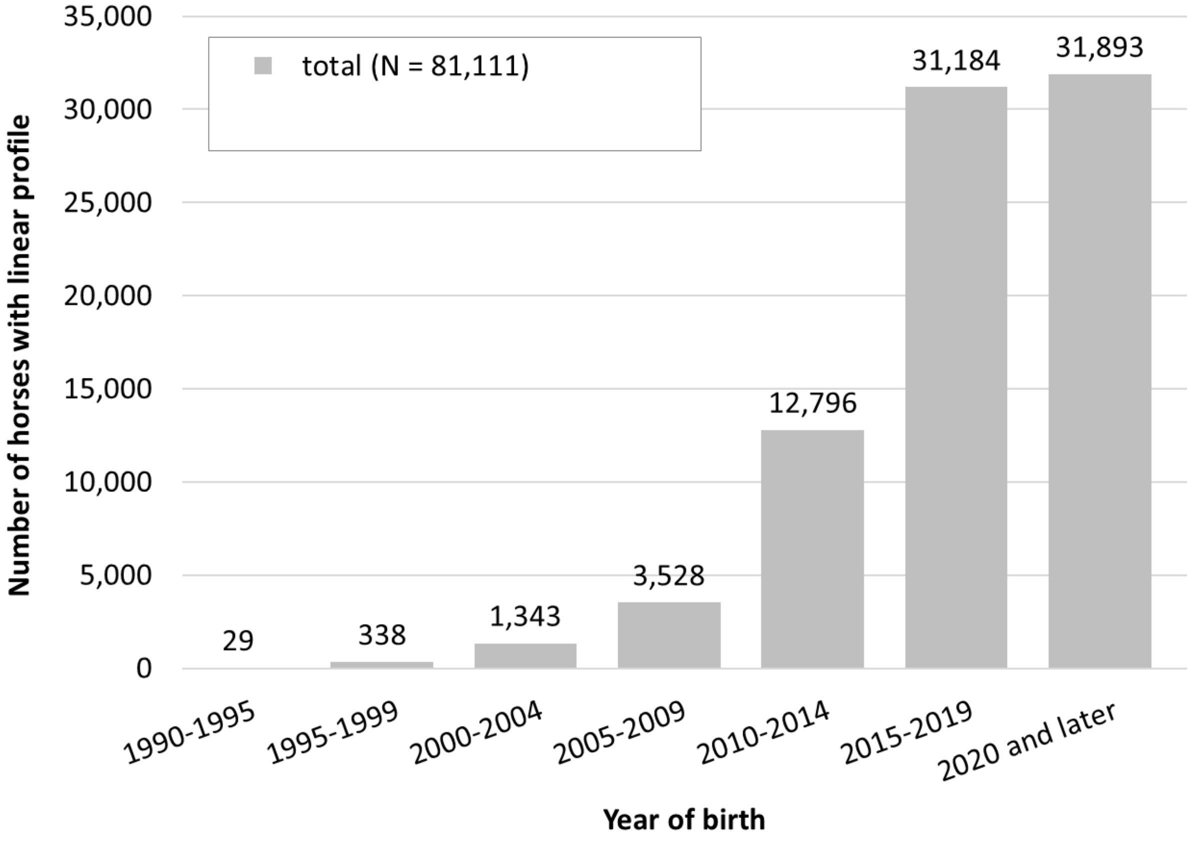
Source (horse pictogram): https://icons8.com

<u>Key figures from current routine (IAFH LIN-GE 2025)</u>

- 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

IAFH LIN-GE 2025

Data basis: phenotypes



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

- N= 81,111 horses with linear description
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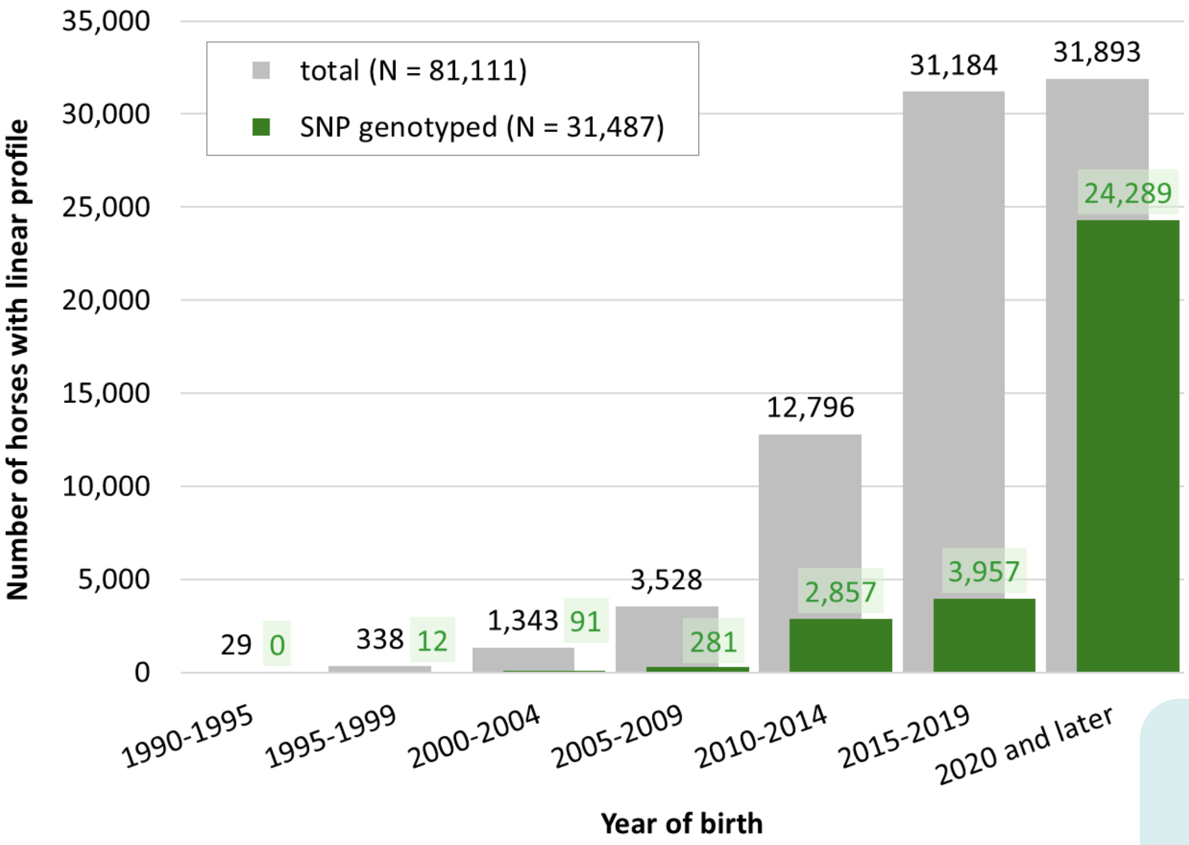
- ➢ more than 31,000 horses with linear description and 80K SNP genotypic data
- ➢ across-studbook genomic evaluation system with in total more than 400,000 horses

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

IAFH LIN-GE 2025

Data basis: phenotypes + SNP genotypes + pedigree



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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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		foals	adult horses *
conformation		28	28
movement	special remarks	1	1
	walk	4	4
	trot	7	7
	canter	-	7
jumping		-	12
total		40	59

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)

IAFH LIN-GE 2025

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
- <u>single step genomic evaluation</u>
  - 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

<u>foals:</u>

$y_{ijklop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_M_k + SEX_l + a_o + e_{ijklop}$

<u>adult horses:</u>

$y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_J_m + PTYPE_n + a_o + pe_o + e_{ijmnop}$

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)

Meilenstein der Pferdezucht
Genomische Zuchtwerte
jetzt verfügbar

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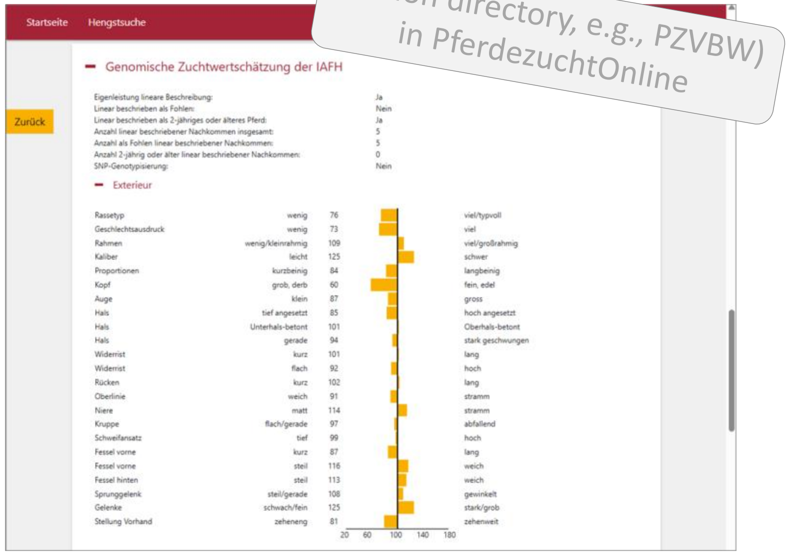
Trait group		Published gEBV total index (F+A)
conformation		28
movement	special remarks	1
	walk	4
	trot	7
	canter	7
jumping		12
total		59

Publication of genomic breeding values II

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

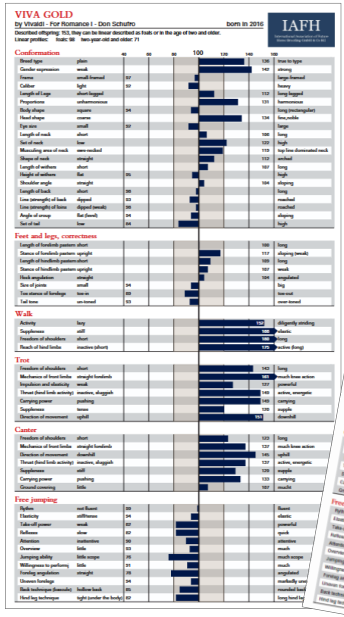


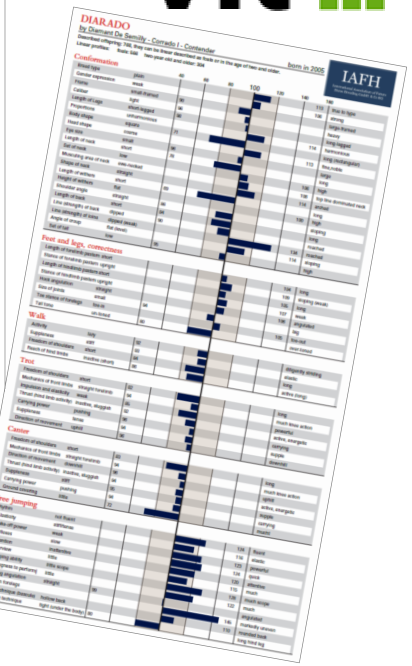
Genomische Zuchtwertschätzung der IAFH

Eigenleistung lineare Beschreibung: Ja
Linear beschrieben als Fohlen: Nein
Linear beschrieben als 2-jähriges oder älteres Pferd: Ja
Anzahl linear beschriebener Nachkommen insgesamt: 5
Anzahl als Fohlen linear beschriebener Nachkommen: 5
Anzahl 2-jährig oder älter linear beschriebener Nachkommen: 0
SNP-Genotypisierung: Nein

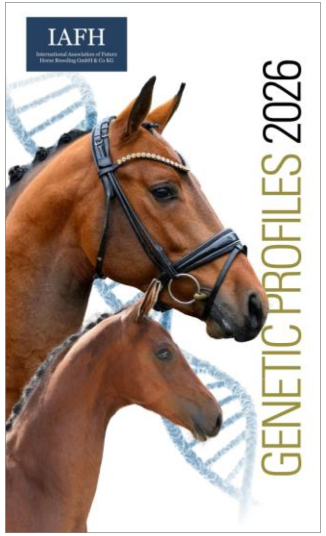
Exterieur

Rassetyp	wenig	76	viel/typvoll
Geschlechtsausdruck	wenig	73	viel
Rahmen	wenig/kleinrahmig	109	viel/großrahmig
Kaliber	leicht	125	schwer
Proportionen	kurzbeinig	84	langbeinig
Kopf	grob, derb	60	fein, edel
Auge	klein	87	gross
Hals	tief angesetzt	85	hoch angesetzt
Hals	Unterhals-betont	101	Oberhals-betont
Hals	gerade	94	stark geschwungen
Widerrist	kurz	101	lang
Widerrist	flach	92	hoch
Rücken	kurz	102	lang
Oberlinie	weich	91	stramm
Niere	matt	114	stramm
Kruppe	flach/gerade	97	abfallend
Schweifansatz	tief	99	hoch
Fessel vorne	kurz	87	lang
Fessel vorne	steil	116	weich
Fessel hinten	steil	113	weich
Sprunggelenk	steil/gerade	108	gewinkelt
Gelenke	schwach/fein	125	stark/grob
Stellung Vorhand	zeheneng	81	zehenweit



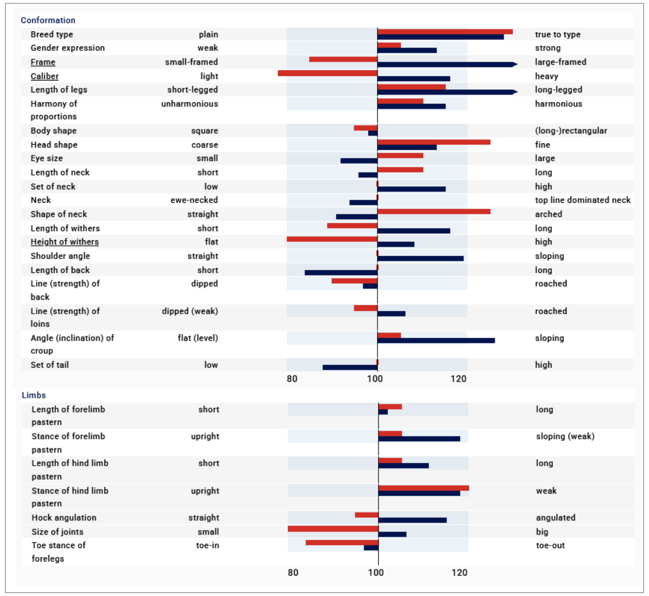


- publication of results
  - stallion directories of individual studbooks
  - IAFH genetic profiles (675 stallions)

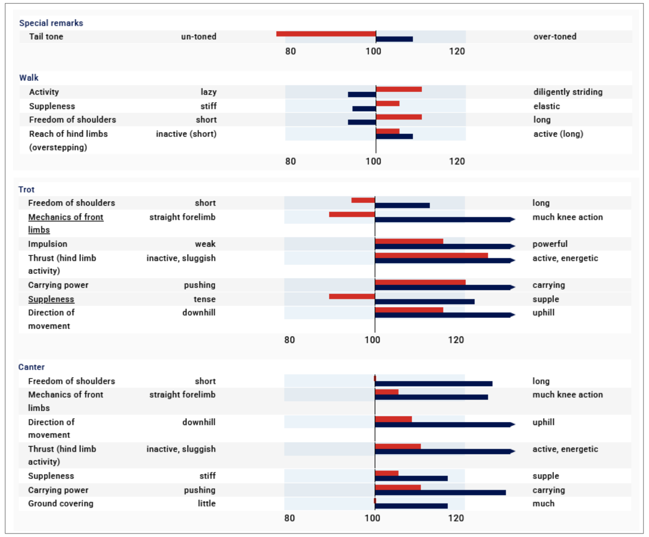


IAFH LIN-GE 2025

Publication of genomic breeding values



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

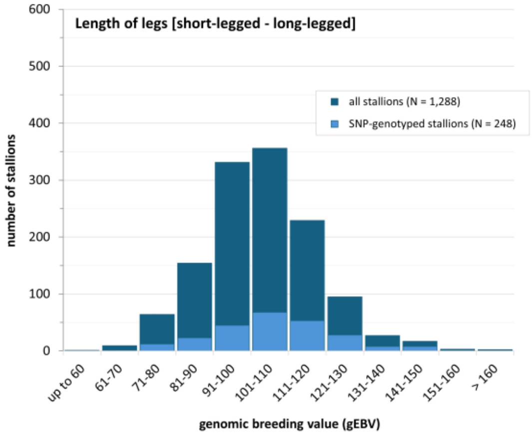


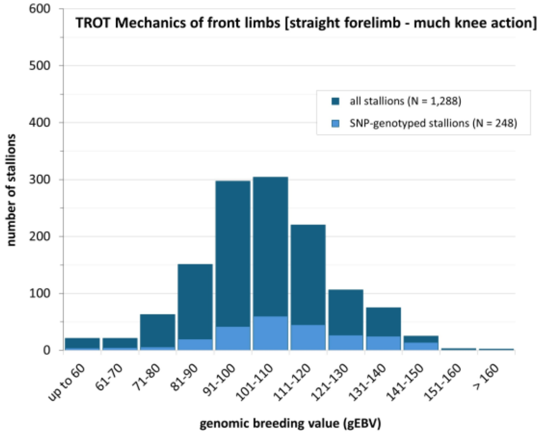
- publication of results
  - stallion directories of individual studbooks
  - IAFH genetic profiles (675 stallions)
  - mating program in the individual online account of studbook members: 1,288 stallions and own mare(s)
  - ➢ digital support of mating planning

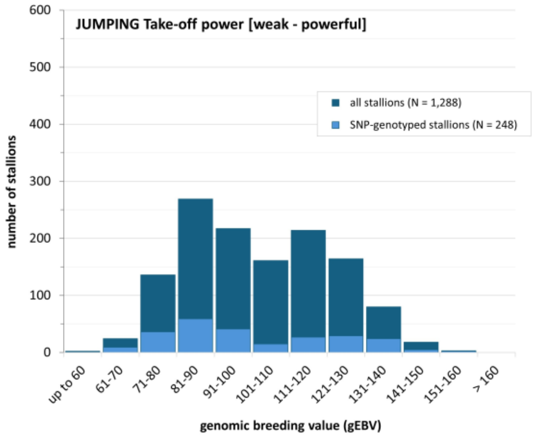
publication criteria (mating program) based on own linear profile (LIN) and number of linearly described progeny (pLIN):
stallions (N = 1,288) – at least 8 pLIN or LIN and at least 5 pLIN; mares (N = 34,805) – at least 3 pLIN or LIN(F) and at least 1 pLIN or LIN(A)

Performance of the genomic evaluation system

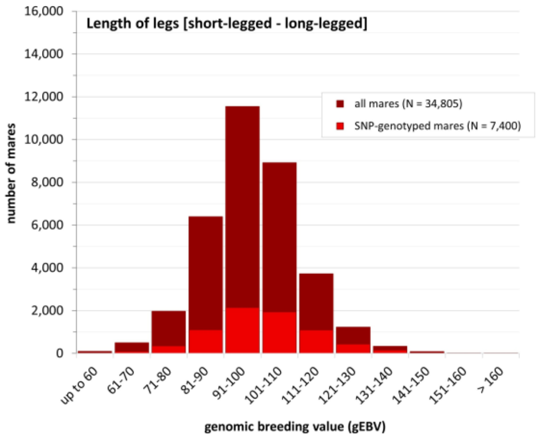
(1) distributions of genomic breeding values (gEBV) → gEBV distribution patterns

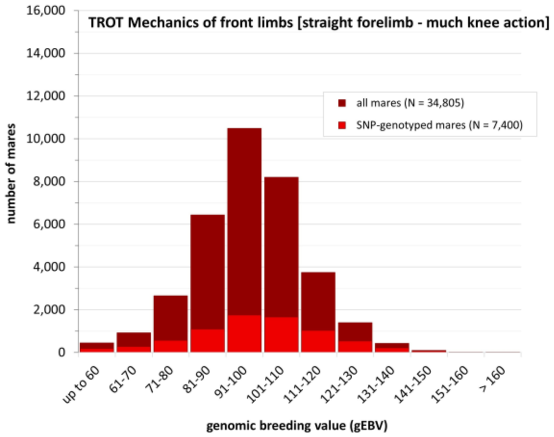


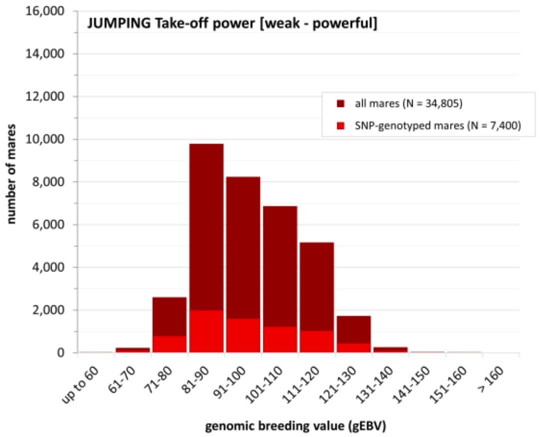




stallions
(N = 1,288)







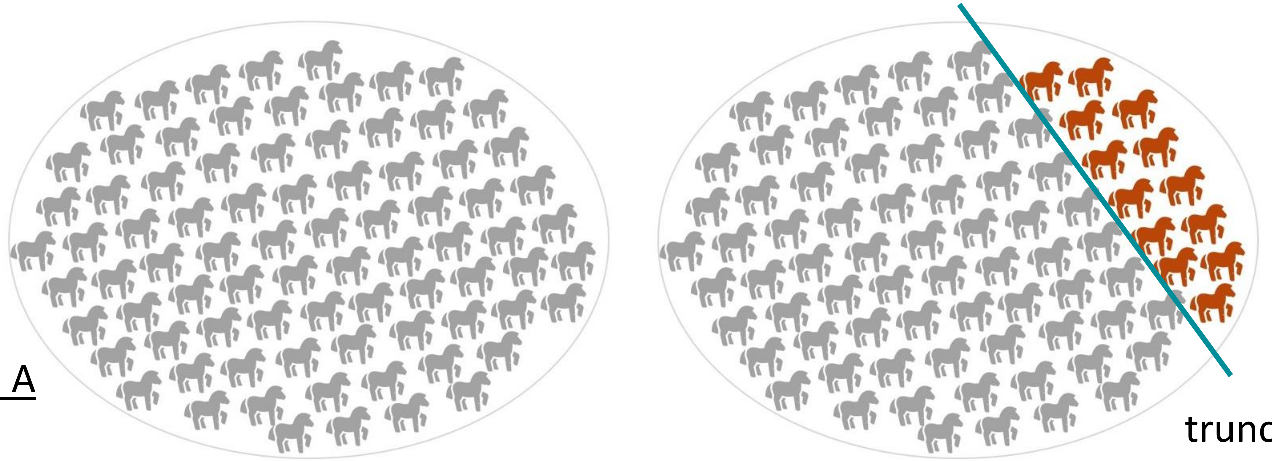
mares
(N = 34,805)

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

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?



test run A
all data

LIN 2012-2024

test run B
truncated data

LIN 2012-2020

horses with linear description
⬜ considered for genomic evaluation
🟧 not considered for genomic evaluation (validation animals)

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

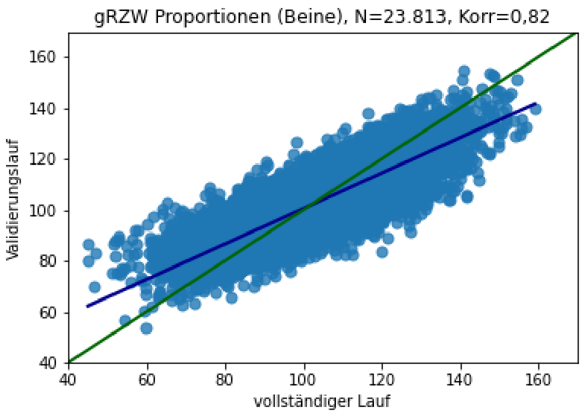
'forward validation' similar to the routinely used Interbull method (dairy cattle)

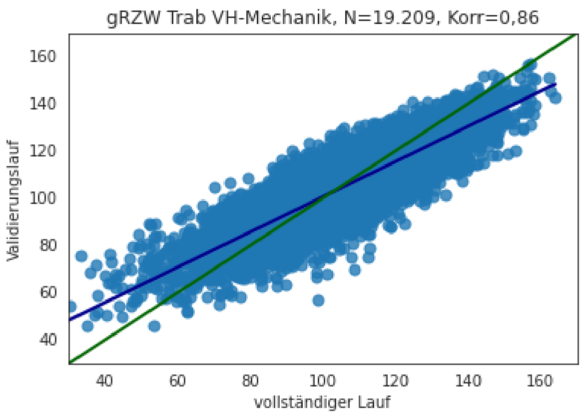
Genomic evaluation IAFH

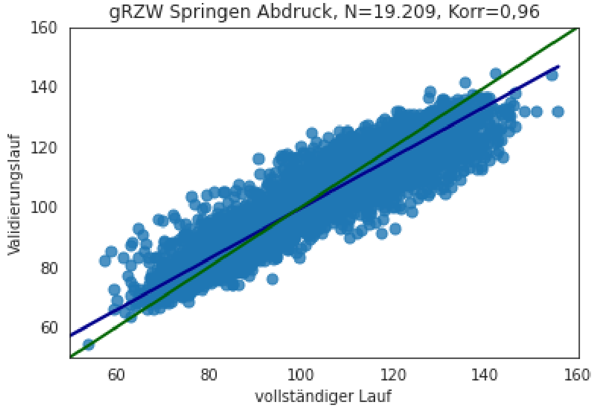
Performance of the genomic evaluation system III

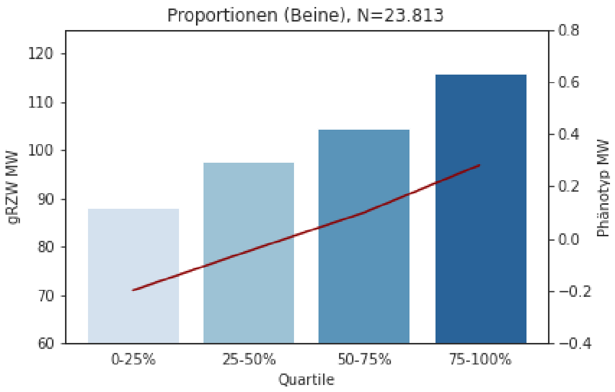
(1) distributions of genomic breeding values (gEBV) → gEBV distribution patterns

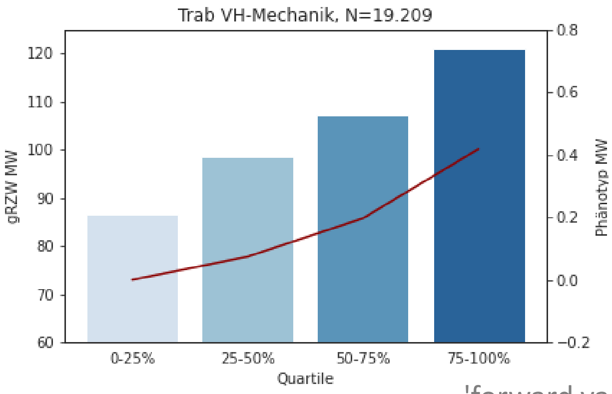
(2) validation → gEBV stability? gEBV as predictors of future phenotypes?











- ✓ moderate to high gEBV correlations (truncated vs. all data): Pearson correlation coefficients (r) of $r_{conformation}$ = 0.83, $r_{movement}$ = 0.88 (movement), and $r_{jumping}$ = 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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- information gain through the new joint genomic evaluation of the IAFH: 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

DSP

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