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Validation of breeding applications for sport horses based on linear profiling across age groups

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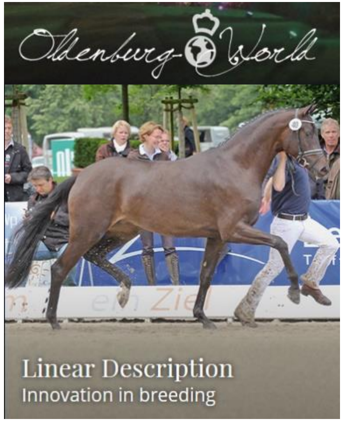
Background & motivation

- implementation of linear systems for riding horses
  - conformation and performance (gaits, jumping, behavior)
  - foals and/or adult horses (broodmares, stallions, young riding horses)
  - ➢ substantial improvement of phenotype data quality if accompanied by appropriate data quality management (training of judges, fine-tuning regarding linear trait definitions, ...)

Linear data basis in the Oldenburg studbooks (OL, OS)

- ✓ from 2012-2018 20,655 linear profiles of 19,651 horses
- ✓ conformation and performance (movement, jumping)
- ✓ same linear scheme and 7-point numeric linear scale (-3 to +3) for all horses, i.e. across age groups



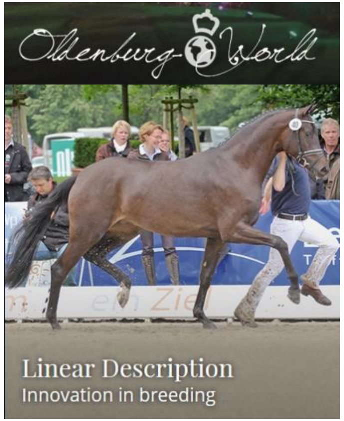
Background & motivation II

- implementation of linear systems for riding horses
- extension of <u>breeding applications based on linear profiling</u>
  - clearly distinct set of traits (descriptive)
  - potentially powerful tool for breeders

Routine genetic evaluation for linear traits in the Oldenburg studbooks (OL, OS)

✓ since 2017, annually in October / November

✓ conformation and performance (46 traits)



Background & motivation

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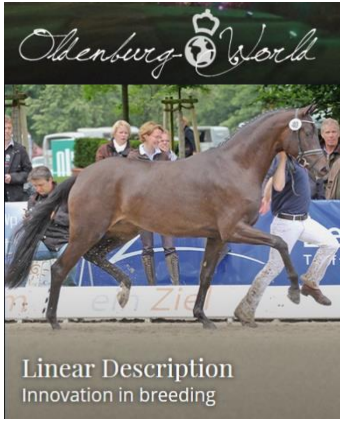
quality control (validation)
of the genetic evaluation system

- ➢ development of genetic profiles over time
- ➢ predictive value: linear genetics of stallions vs. linear phenotypes of their progeny

OLDENBURGER VERBAND

VERERBUNGSPROFILE2018



Oldenburg-World

Linear Description
Innovation in breeding

Genetic evaluation for linear traits

- data structure → prediction system
  - multiple trait approach (age groups)
  - repeated observations for performance-related linear traits

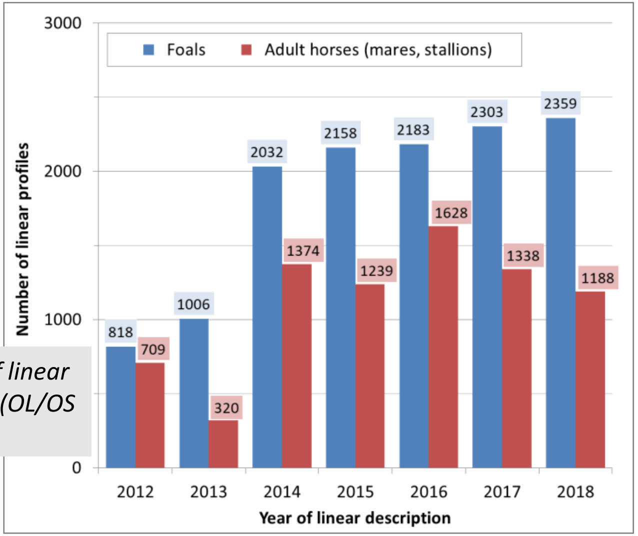


Fig.: Distribution of linear data by age group (OL/OS 2012-2018).

Tab.: Information structure of the linear data.

Trait category	No. of linear traits: assessed (total) → included in GE	No. of assessments per event	
		foals	adults
Conformation	74 → 23	1	1
Walk (H, F, R)	6 → 2	1	1 - 2
Trot (H, F, R)	12 → 6	1	1 - 3
Canter (F, R)	10 → 4	(1)	2 - 3
Jumping (F) → (F, R)	16 → 10	0	1 (1 - 2)
Special remarks (H, F, R)	8 → 1	1	1 - 3
Behavior (H, F, R)	9 → 0	1	1 - 3

H = in hand, F = free, R = under rider; GE = genetic evaluation

Genetic evaluation for linear traits II

- data structure → prediction system
  - multiple trait approach (age groups)
  - repeated observations for performance-related linear traits
- single- and multi-trait repeatability linear animal models

foals: $y_{ijkno} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_M_k + SEX_l + animal_o + e_{ijklop}$

adult horses: $y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_Y_m + PTYPE_n + animal_o + pe_o + e_{ijmnop}$

fixed effects: SB = studbook (OL, OS), EVENT-TEAM = date, place, assessor, assistance, SEX = male / female, AGE_M (AGE_Y) = age in months (years), PTYPE = presentation type (assessment in hand, free, under rider)

- consideration of four ancestral generations
- prediction of breeding values using PEST software (Groeneveld et al. 1990)

Genetic linear profiles

- impact of linear data structure on information basis per sire
- more linearly described progeny = more reliable prediction

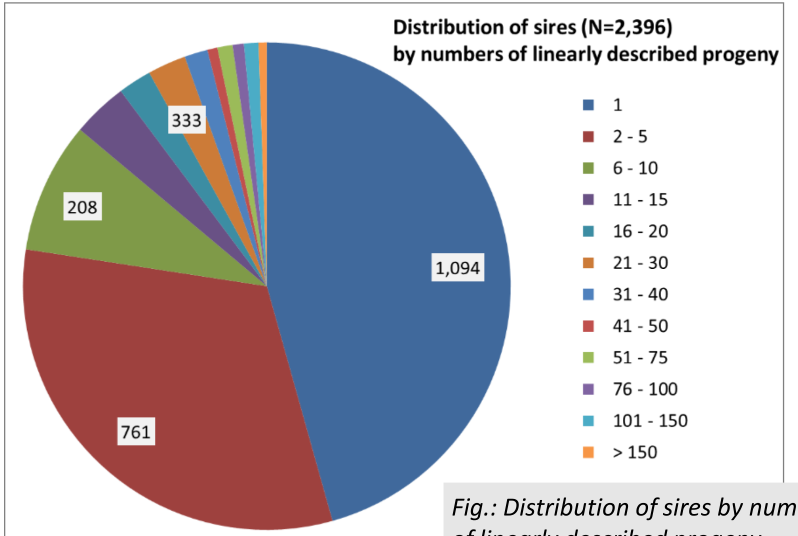


Fig.: Distribution of sires by numbers of linearly described progeny.

Information density in genetic evaluation (GE 2018):

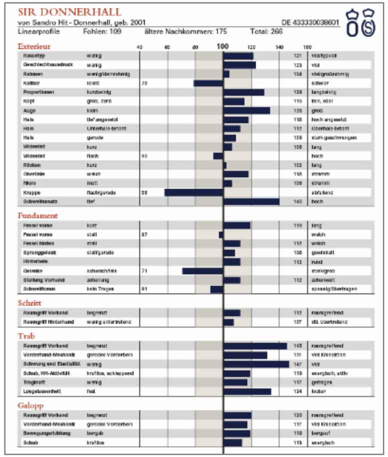
- ✓ 957 horses linearly described as foals and adults
- ✓ 366 sires (15 %) with ≥ 10 linearly described progeny

Tab.: Progeny numbers per sire in the genetic evaluation for linear traits (GE 2018).

Age group	No. of sires	No. of linearly described progeny	
		mean	range
Foals	1,226	10.5	1 - 327
Adult horses	1,788	4.4	1 - 192
Foals and/or adult horses	2,396	8.2	1 - 444

Genetic linear profiles II

- presentation of results
    - standardization of estimated breeding values (EBV): mean of 100, genetic standard deviation of 20
      (orientation as in the linear scheme)
    - base definition: sires born after 1994
      with at least 3 linearly described adult progeny
      (GE 2018: N=417 sires)



- publication of genetic stallion profiles: two groups

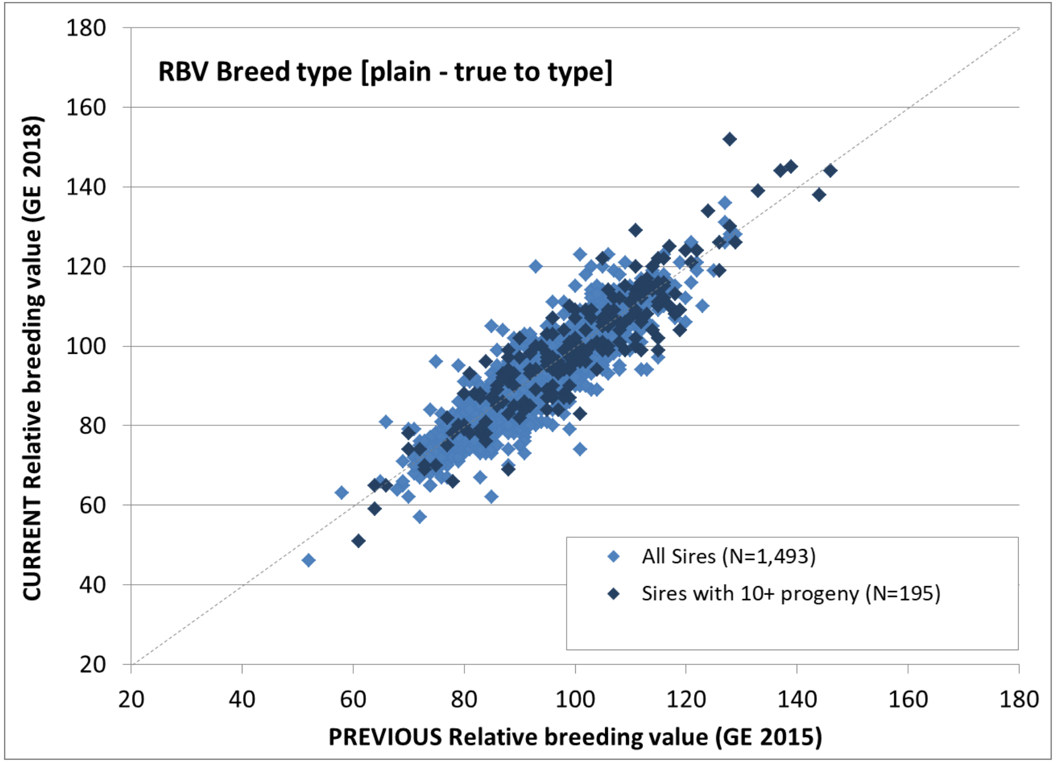
(1) frequently used sires → index (40% EBV_{Foal}, 60% EBV_{Adult})

(2) young sires → EBV_{Foal}

Validation and detailed analyses

- GE test run with truncated data
    - resembling GE 2015, i.e. considering linear data from 2012-2015
    - reduced data basis of N=9,656 linear profiles
      (foals: N=6,014, adult horses: N=3,642)
- comparison of GE test run results ('early prediction' / GE 2015)
  with regular GE results (full data 2012-2018 / GE 2018)
- approved protocol for EBV trend validation: Interbull method III
- analysis of results by sire groups:
  all sires, frequently used sires, young sires

Changes over time? Examples I



Explanation:

comparison of results from GE test run with truncated data (GE 2015) with regular GE run using all data (GE 2018) for:

- all sires with progeny already in GE 2015 (on average only 6 progeny)
- sires with more reliable EBV (10 or more progeny already in GE 2015)

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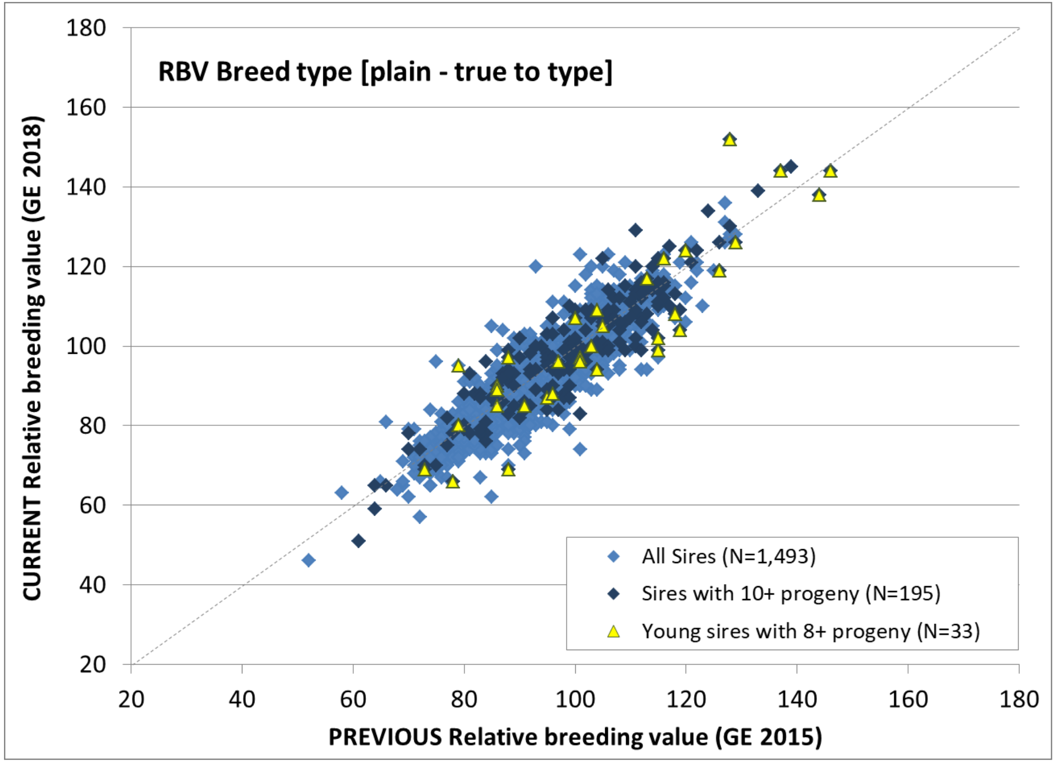

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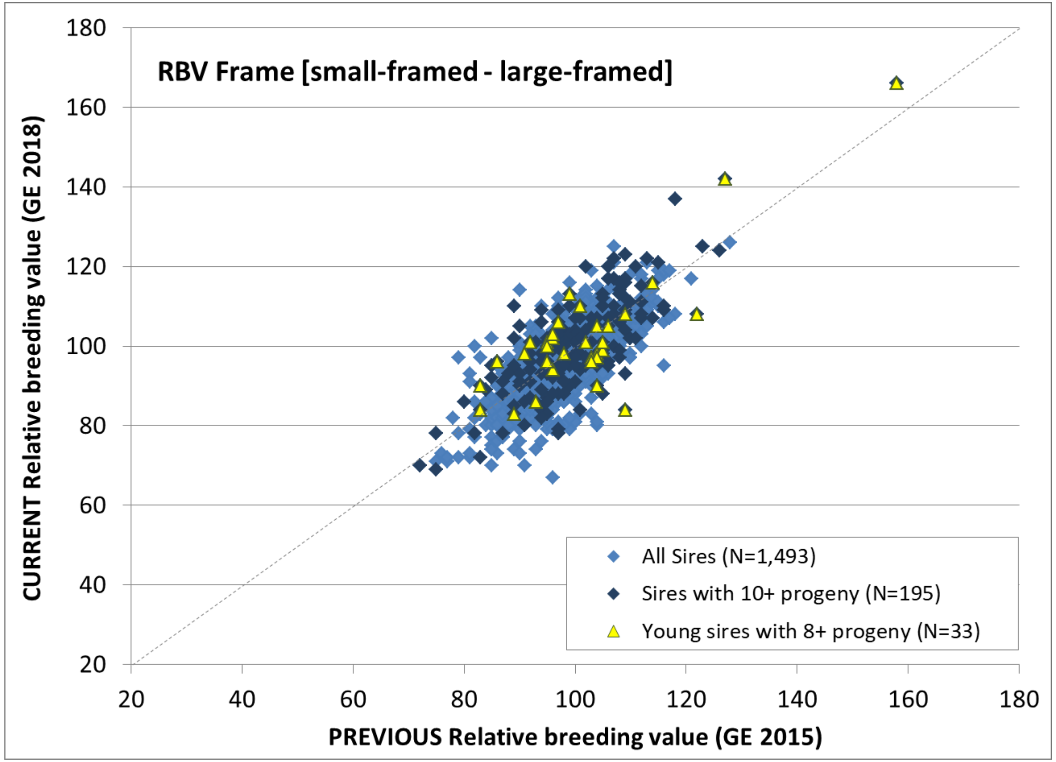
Changes over time? Examples II



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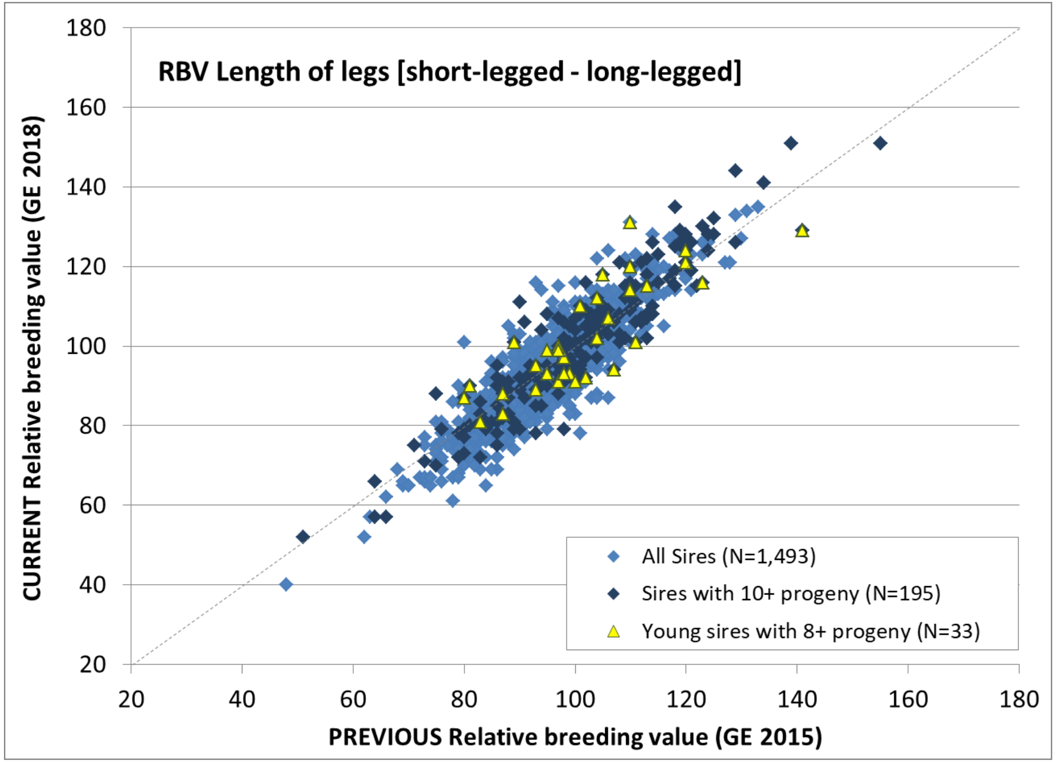
Changes over time? Examples III



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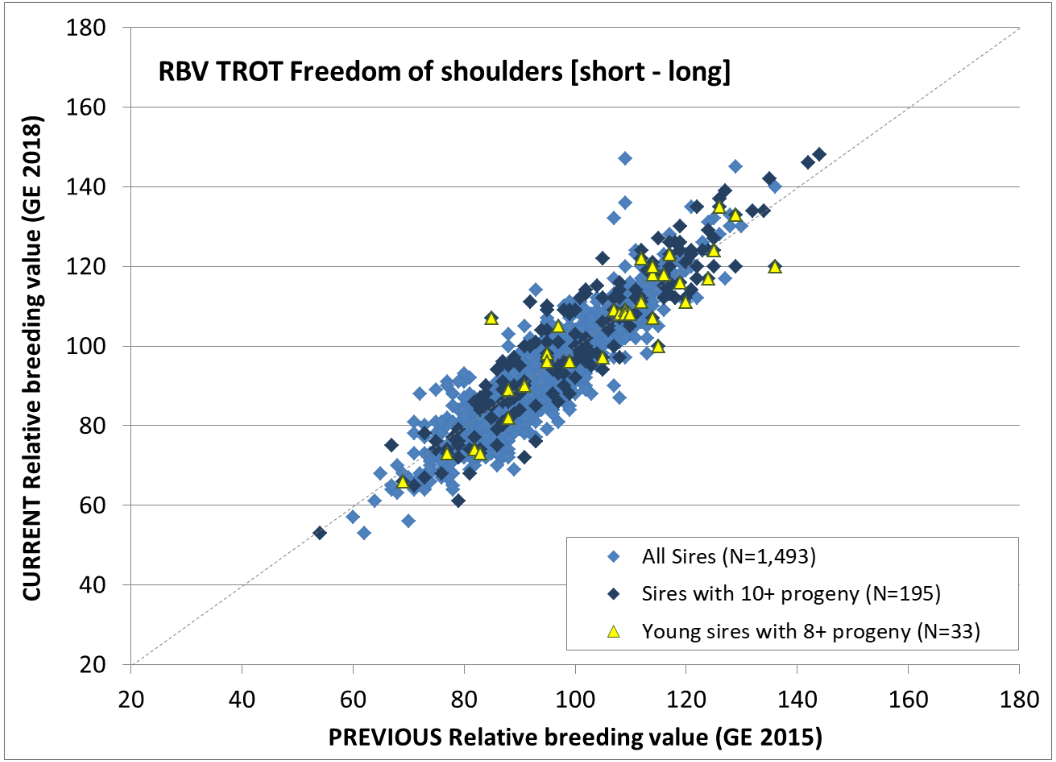
Changes over time? Examples IV



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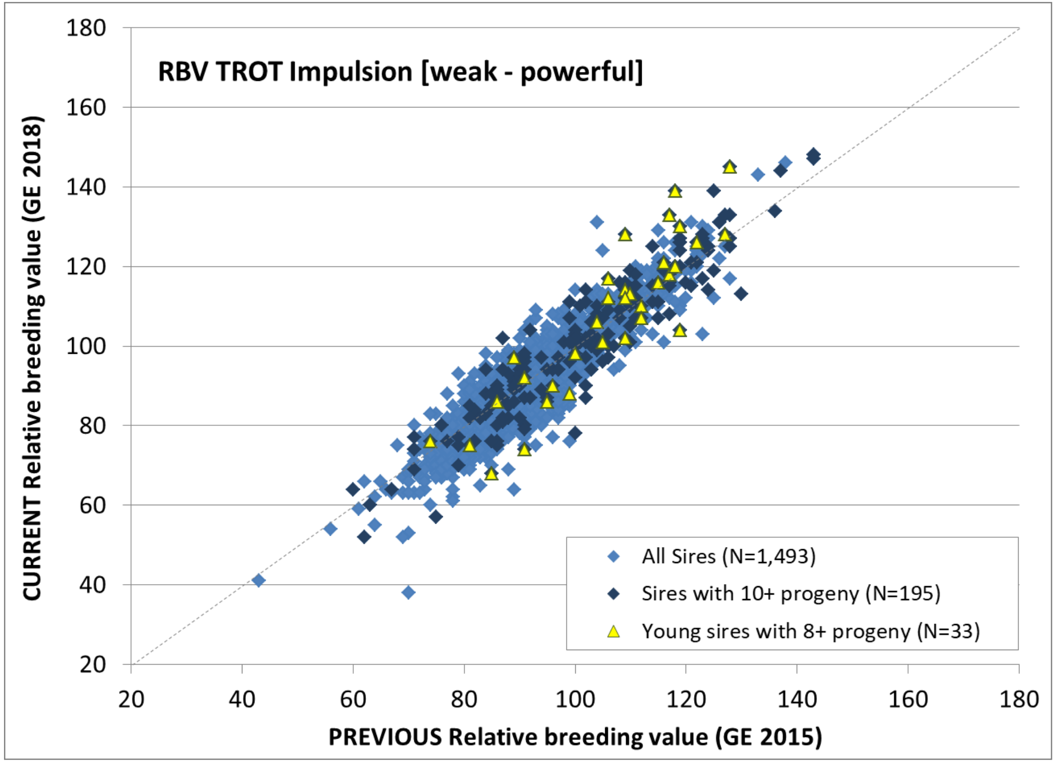
Changes over time? Examples V



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  (on average only 6 progeny)
- sires with more reliable EBV
  (10 or more progeny already in GE 2015)
- young sires (max. age of 6 years) in GE 2015

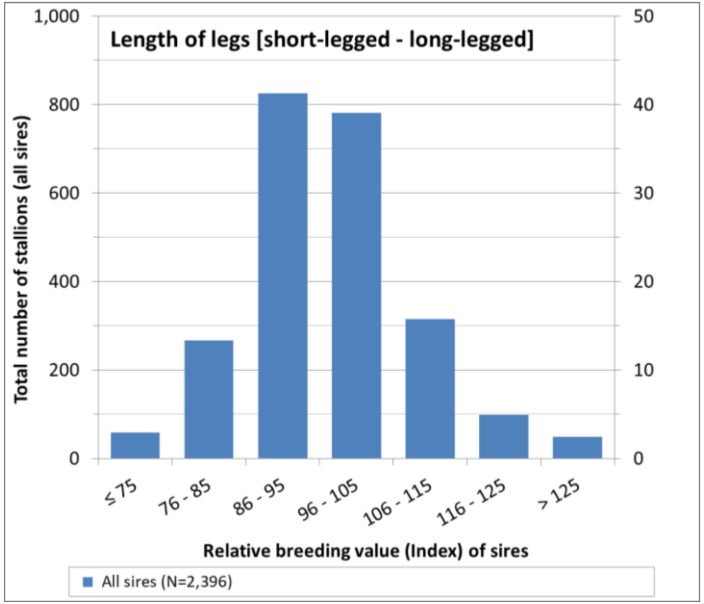
Changes over time? Yes – plausible!

IB trend test: passed (conformation, performance; EBV_{Foal}, EBV_{Adult};)

- overall stability of the system, no obvious systematic change (indication of bias)
- similarity of predictions (<u>all sire groups</u>)
  - RBV correlations mostly ≥ 0.85, consistent patterns across traits
  - increase of information on linear traits, i.e. progeny phenotypes
    → increase of reliability of RBV for linear traits
    → potential of larger deviations from the mean of 100
- individual sires with substantial changes of RBV (<u>all sire groups</u>)
  - 'new' information on progeny
  - main reason: many more linearly described progeny

Genotype vs. phenotype? Examples I

Age group	Mean	Std.	Min.	Max.
Foals (N=12,851)	0.29	0.71	-3	+3
Adult horses (N=7,435)	0.00	0.65	-3	+3



Explanation:

classification of sires by their RBV (GE 2018)

Genotype vs. phenotype? Examples I

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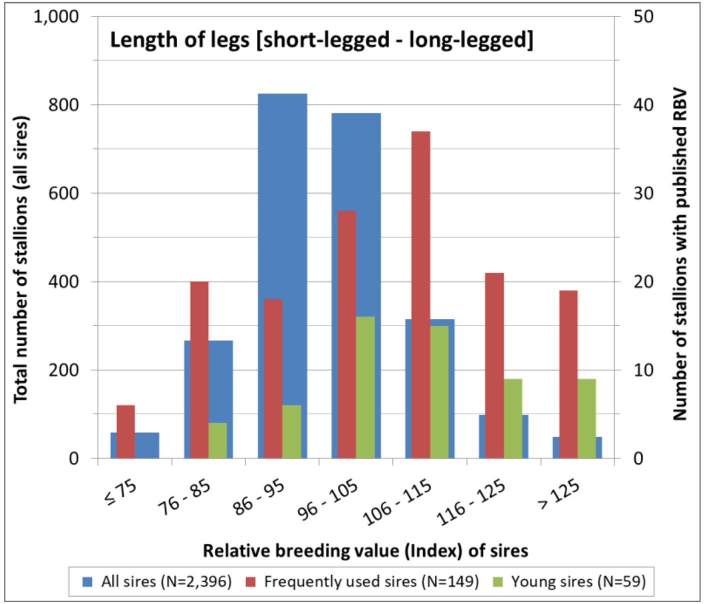


RBV class	Progeny of all sires		Progeny of freq. used sires		Progeny of young sires	
	foals	adults	foals	adults	foals	adults
≤ 75	-0.11	-0.26	-0.04	-0.12	-	
76 - 85	0.05	-0.26	0.10	-0.15	0.04	
86 - 95	0.11	-0.14	0.15	-0.05	0.22	
96 - 105	0.26	0.02	0.25	0.03	0.32	
106 - 115	0.35	0.10	0.33	0.08	0.34	
116 - 125	0.45	0.21	0.43	0.22	0.48	
> 125	0.57	0.25	0.52	0.25	0.77	

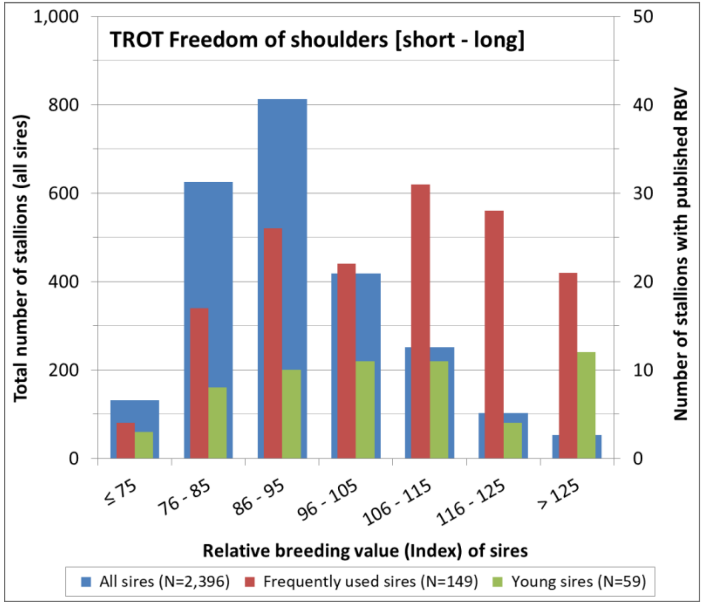
Explanation:

classification of sires by their RBV (GE 2018), then comparing mean linear values of progeny groups:

- all sires with progeny (on average only 8 progeny)
- sires with more reliable EBV (frequently used sires)
- young sires (max. age of 6 years; ≥ 8 progeny)

Genotype vs. phenotype? Examples II

Age group	Mean	Std.	Min.	Max.
Foals (N=12,851)	0.27	0.82	-3	+3
Adult horses (N=7,435)	0.12	0.71	-3	+3



RBV class	Progeny of all sires		Progeny of freq. used sires		Progeny of young sires	
	foals	adults	foals	adults	foals	adults
≤ 75	-0.28	-0.26	-0.20	-0.06	-0.17	
76 - 85	-0.09	-0.11	-0.06	-0.08	0.04	
86 - 95	0.07	-0.01	0.05	-0.01	0.12	
96 - 105	0.19	0.12	0.15	0.09	0.22	
106 - 115	0.31	0.20	0.29	0.19	0.38	
116 - 125	0.45	0.23	0.45	0.22	0.43	
> 125	0.59	0.38	0.54	0.38	0.73	

Explanation:

classification of sires by their RBV (GE 2018), then comparing mean linear values of progeny groups:

- all sires with progeny (on average only 8 progeny)
- sires with more reliable EBV (frequently used sires)
- young sires (max. age of 6 years; ≥ 8 progeny)

Genotype vs. phenotype? Consistent!

- structure of sire groups to be considered
  - age → possible representation with progeny in both age groups
  - restrictions (no. of progeny) → pre-selected sample

Genotype vs. phenotype? Consistent! II

- structure of sire groups to be considered
- distribution patters (<u>all sire groups</u>)
  - good discrimination between sires (RBV / genetic linear profiles)
  - good discrimination between progeny groups (phenotypic linear profiles)
  - consistency implying favorable predictive value
- individual progeny with substantial departure from group mean (= expectation; <u>all sire groups</u>)
  - mating partner (linear profile of the dam)?
  - phenotype = genotype + non-genetic factors + X
  - high reliability (RBV) ≠ 100% predictability (phenotype)

Conclusions

- positive answers to concrete questions of breeders
  - Can we use genetic profiles of young stallions with few linearly described foals (first crop) for support of mating decisions? **YES – they are valuable early indicators.**
  - Will the genetic linear profiles change over time? If so, how much?
    YES – changes are possible and expected, can be substantial.
    more progeny with linear data → RV reliability ↑ → changes ↓
  - Can we predict the progeny phenotypes by the genetic linear profiles of their fathers? How well?
    YES – prediction is possible, advanced use of linear data implies continuous improvement.

- support of expectations regarding linear profiling
  - reliable 'filtering out' of genetic dispositions
    (better than phenotype-based progeny statistics)
  - earlier, more objective and more helpful information for breeders

Prospects

- international engagement for strengthening of linear profiling
  - increase (supplement to or replacement of valuating scoring)
  - improvement (data quality management)
  - reasonable harmonization (comparability across studbooks)

- ➢ new and improved phenotypes as suitable targets for new and improved breeding applications
- ➢ collaborative approaches to capture the full potential using genetic and genomic tools

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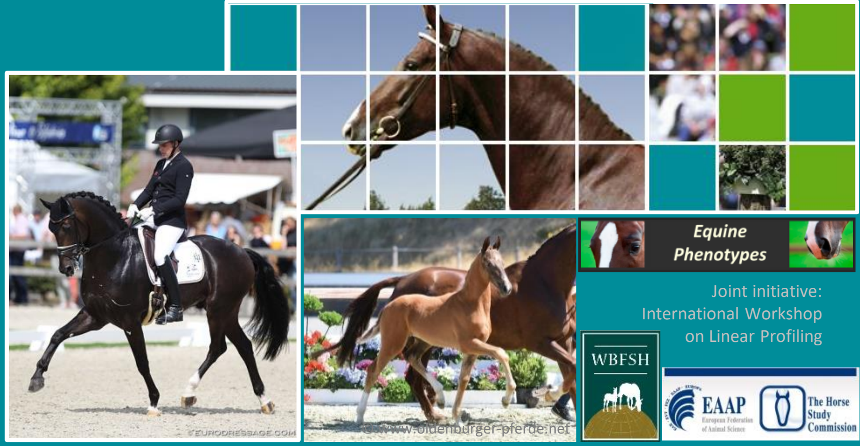

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- collaborative approaches to capture the full potential using genetic and genomic tools

Thank you !