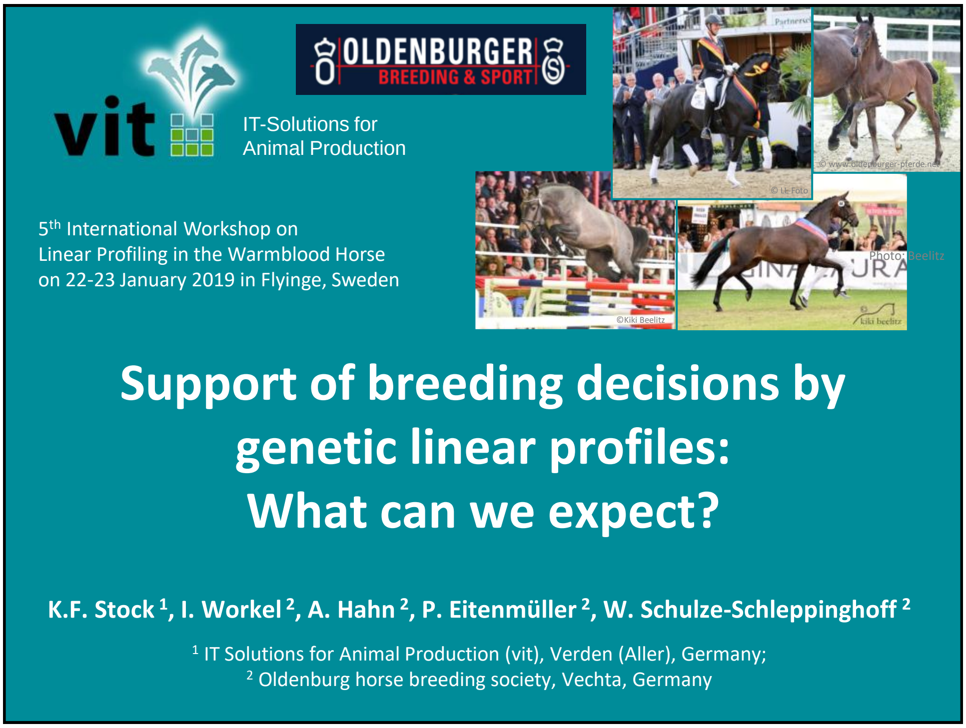


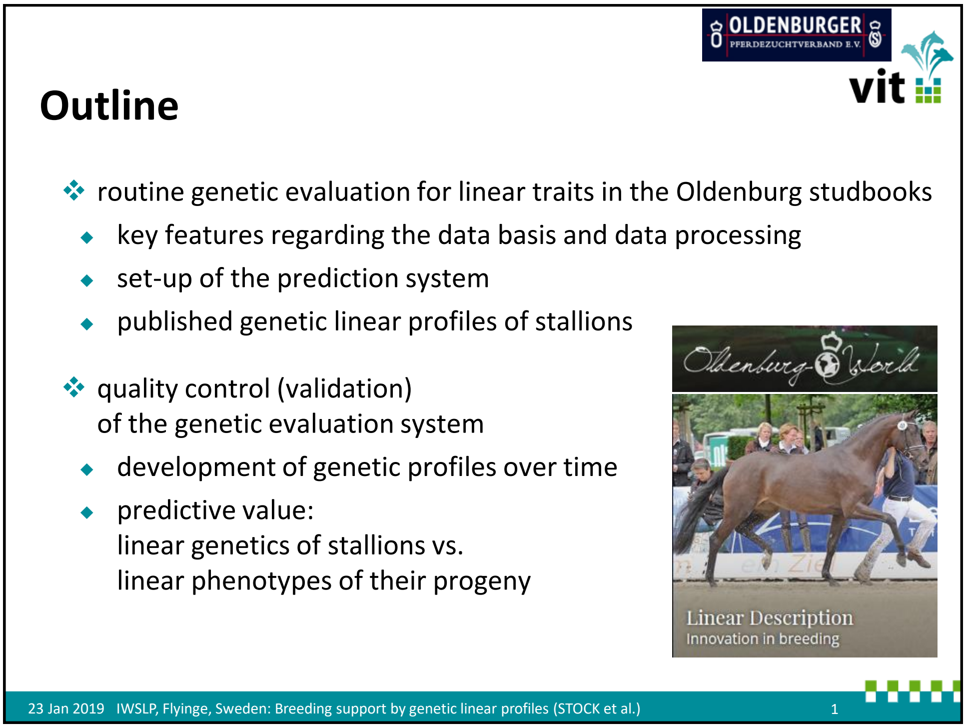
IT-Solutions for
Animal Production

5th International Workshop on
Linear Profiling in the Warmblood Horse
on 22-23 January 2019 in Flyinge, Sweden

Support of breeding decisions by genetic linear profiles: What can we expect?

K.F. Stock [1], I. Workel [2], A. Hahn [2], P. Eitenmüller [2], W. Schulze-Schleppinghoff [2]

[1] IT Solutions for Animal Production (vit), Verden (Aller), Germany;
[2] Oldenburg horse breeding society, Vechta, Germany



Outline

- routine genetic evaluation for linear traits in the Oldenburg studbooks
  - key features regarding the data basis and data processing
  - set-up of the prediction system
  - published genetic linear profiles of stallions
- 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

Linear Description
Innovation in breeding

23 Jan 2019 IWSLP, Flyinge, Sweden: Breeding support by genetic linear profiles (STOCK et al.) 1

Linear data basis (2012 - 2018)

- Oldenburg linear scheme (OL, OS)
    - conformation and performance (movement, jumping)
    - 7-point numeric linear scale (-3 to +3),
      reduced scale (0 to +3) for defect traits / special remarks
    - foals, mares, stallions
      (registration, studbook inspection,
      mare performance test, preselection for licensing)

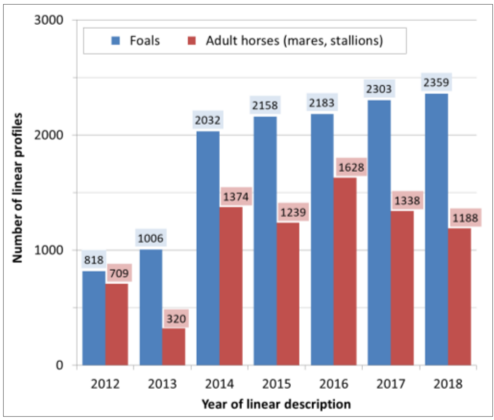
- extension of linear data collection (routine)
    - most/all events since 2015
    - in Germany and abroad

➢ **in total N=20,655 linear profiles of 19,651 horses**
(varying depth = numbers of traits depending on assessment type)

Distribution of linear data I

- in total 20,655 linear profiles
- 2:1 relation between age groups
    - about 13,000 foals (62%)
    - about 7,700 adult horses
      (6,200 mares, 1,550 stallions)

➢ **optimum use of linear data across age groups**



Distribution of linear data II

- in total 20,655 linear profiles
- wide range of traits
  - 'standard' descriptors (e.g. length of neck, suppleness in trot)
  - rare characteristics (e.g. broken toe axis FL/HL, tail tone)
- varying conditions of linear description
  - presentation in hand
  - free movement and free jumping
  - presentation under rider

➢ **optimum use of linear data across traits and assessment types**

Tab.: Information structure of the linear data

Trait category	**No. of linear traits: assessed (total) → included in GE**	**No. of assess-ments 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 parameters for linear traits (2016)

- plausible patterns of heritabilities (h^2)
  - relatively low average h^2 of 0.06 - 0.10 for WALK, CANTER, BEHAVIOR
  - higher averages (several traits with $h^2 > 0.2$) for CONFORMATION, TROT, JUMPING
- support of multiple trait approach for optimum use of linear data
  - mostly strong positive additive genetic correlations between analogous traits assessed in foals and adult horses

Quelle: St.Georg / ©Kiki Beelitz

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Genetic evaluation (since 2017)

- selected linear traits (overall and genetic variation, heritability > 10%)
- trait definition within age group and trait category, considering multiple assessments as repeated observations of the same trait
- benefit from the large amount of foal data through **joint analyses (foals – adult horses) in pairs of analogous linear traits**
  e.g. frame F – frame A, set of neck F – set of neck A

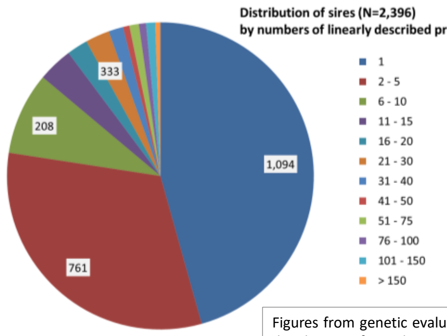
➢ prediction system (routine genetic evaluation):
single- and multi-trait repeatability linear animal models

foals:
$y_{ijkno} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_M_k + SEX_l + animal_o + e_{ijklop}$
adult horses (mares, stallions):
$y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_Y_m + PTYPE_n + animal_o + pe_o + e_{ijmnop}$

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)

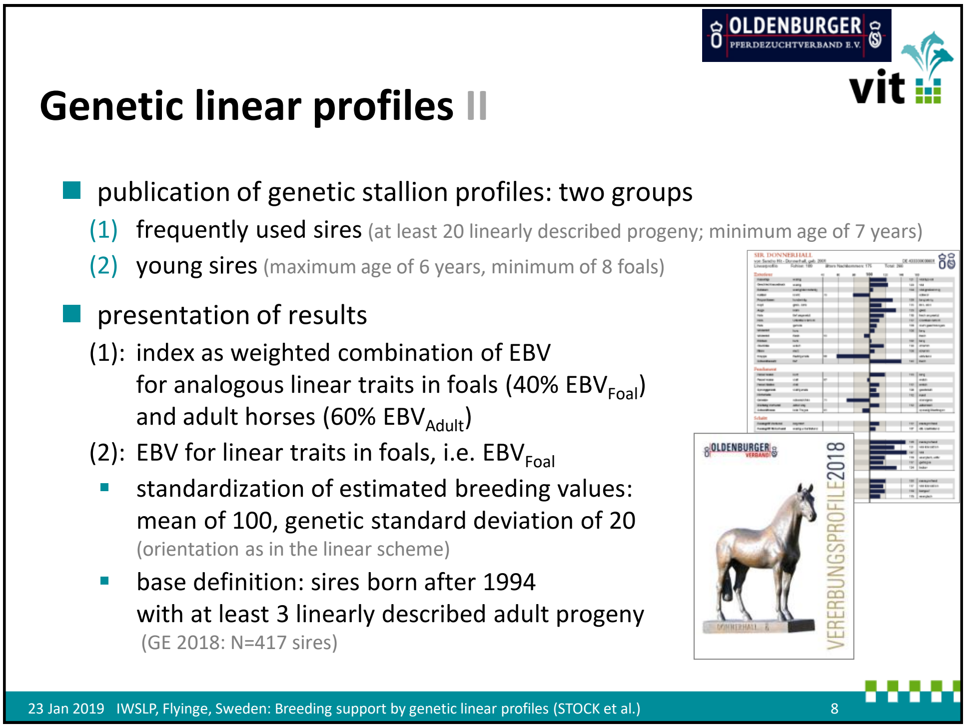
Genetic linear profiles I

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



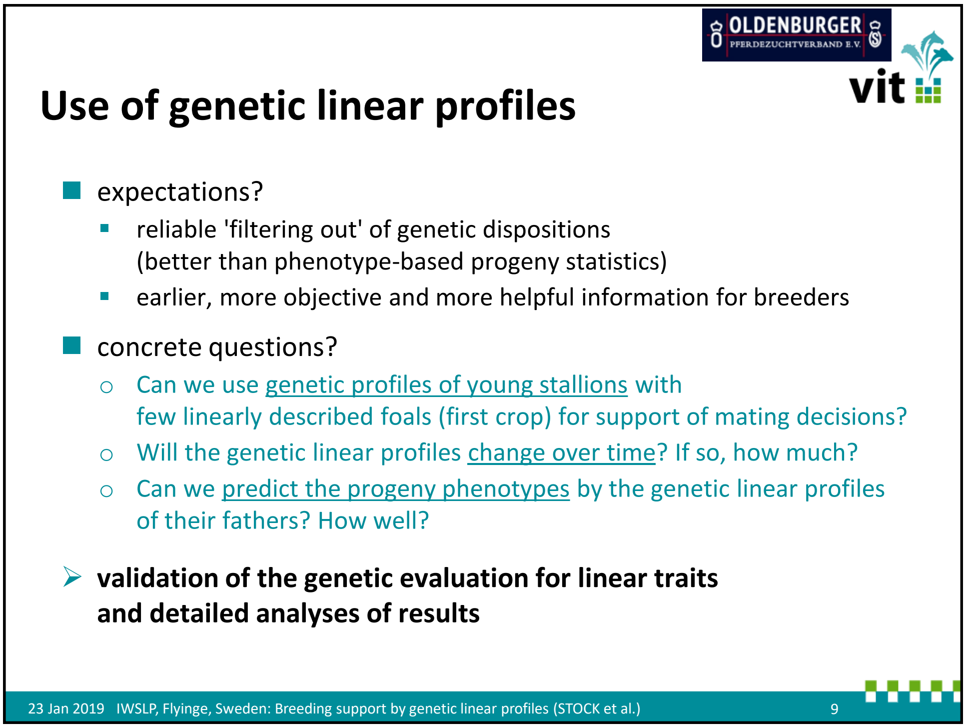
Age group	No. of sires	No. of linearly described progeny	
		mean	range
Foals	1,226	10.5	1 - 327
Adult horses	1,788	4.4	1 - 192
Foals and/or adult horses	2,396	8.2	1 - 444

Figures from genetic evaluation for linear traits 2018 with progeny numbers per sire (Tab.) and distribution of sires by numbers of linearly described progeny (Fig.) , indicating large differences. Many sires have only few progeny, but 366 sires (15%) have at least 10 progeny with linear data.



Genetic linear profiles II

- publication of genetic stallion profiles: two groups
  - (1) frequently used sires (at least 20 linearly described progeny; minimum age of 7 years)
  - (2) young sires (maximum age of 6 years, minimum of 8 foals)
- presentation of results
  - (1): index as weighted combination of EBV for analogous linear traits in foals (40% EBV_{Foal}) and adult horses (60% EBV_{Adult})
  - (2): EBV for linear traits in foals, i.e. EBV_{Foal}
    - standardization of estimated breeding values: 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)



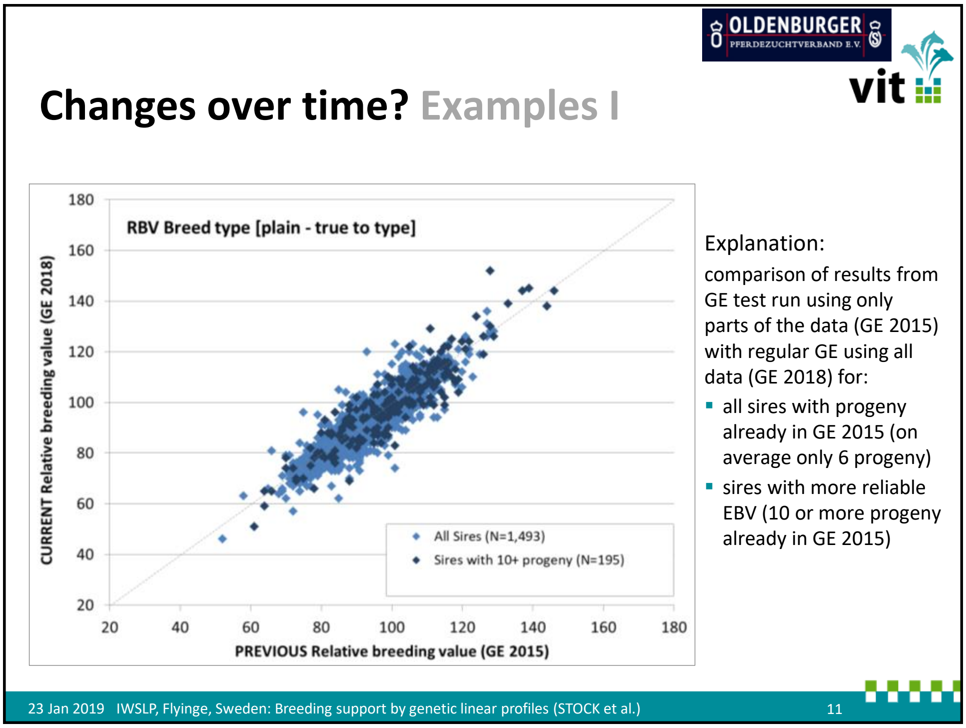
Use of genetic linear profiles

- expectations?
  - reliable 'filtering out' of genetic dispositions (better than phenotype-based progeny statistics)
  - earlier, more objective and more helpful information for breeders
- concrete questions?
  - ○ Can we use genetic profiles of young stallions with few linearly described foals (first crop) for support of mating decisions?
  - ○ Will the genetic linear profiles change over time? If so, how much?
  - ○ Can we predict the progeny phenotypes by the genetic linear profiles of their fathers? How well?

➢ **validation of the genetic evaluation for linear traits and detailed analyses of results**

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)
- zooming into the results for:
  - all sires
  - frequently used sires
  - young sires

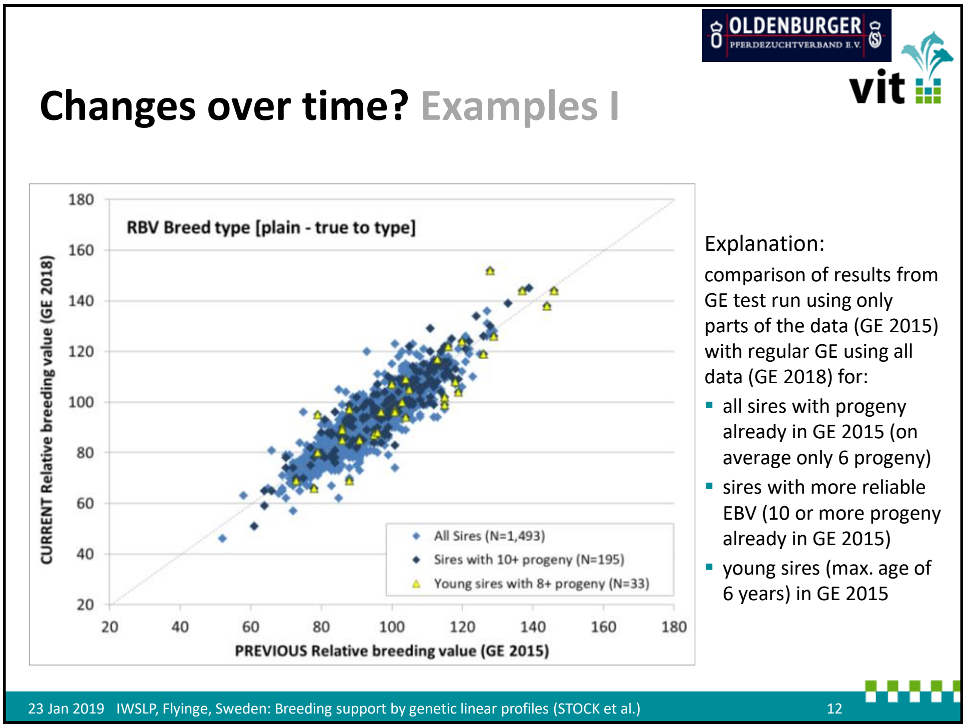


Changes over time? Examples I

Explanation:

comparison of results from GE test run using only parts of the data (GE 2015) with regular GE 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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- young sires (max. age of 6 years) in GE 2015

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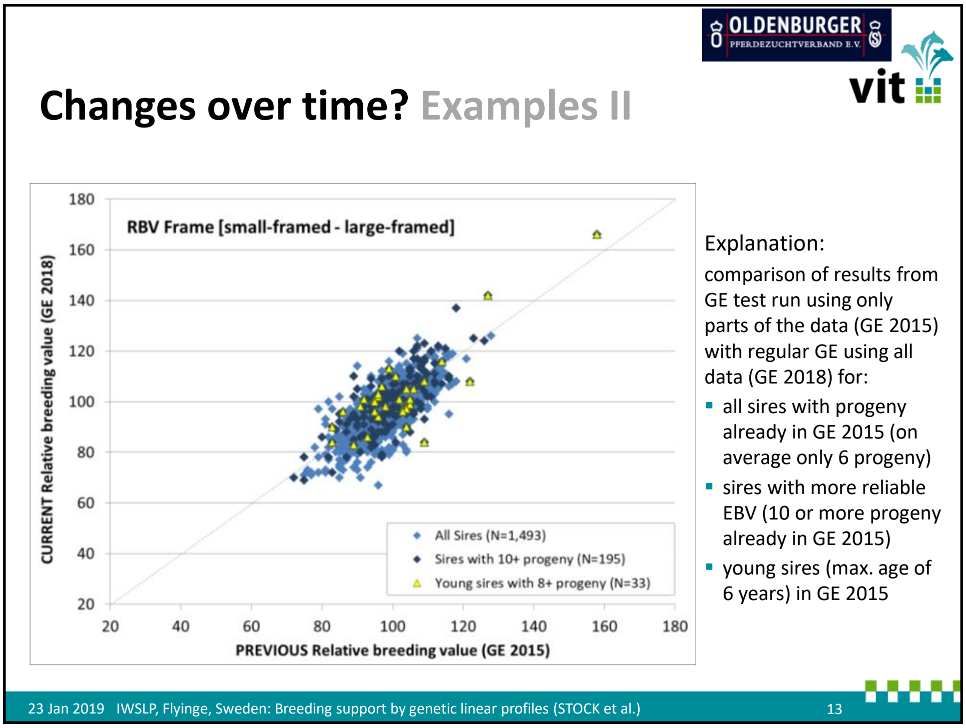

Changes over time? Examples II

Explanation:

comparison of results from GE test run using only parts of the data (GE 2015) with regular GE 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)
- young sires (max. age of 6 years) in GE 2015

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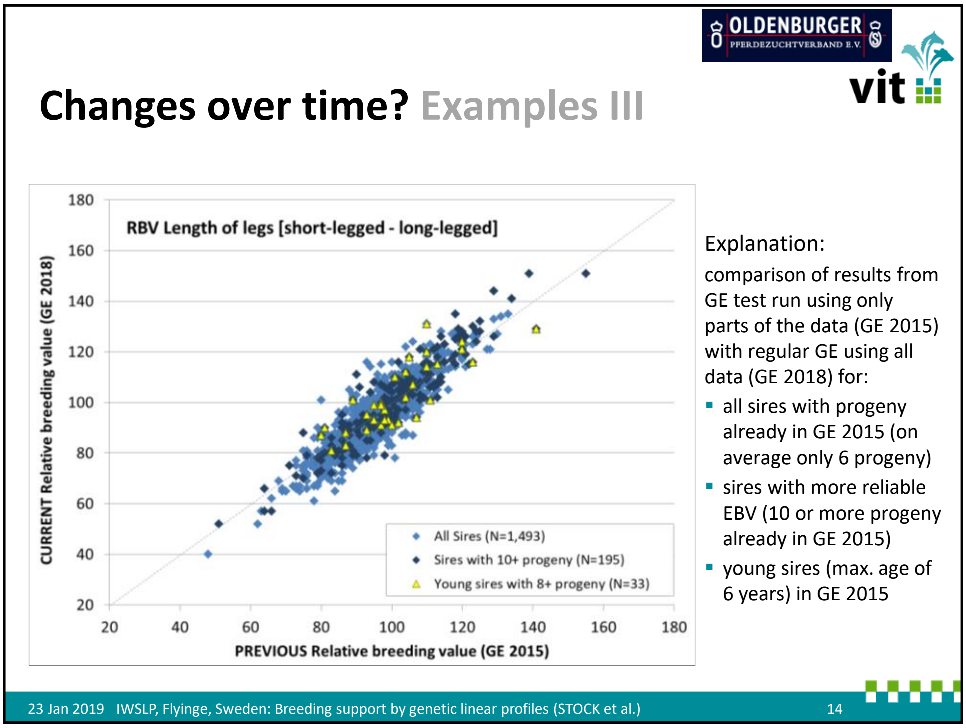
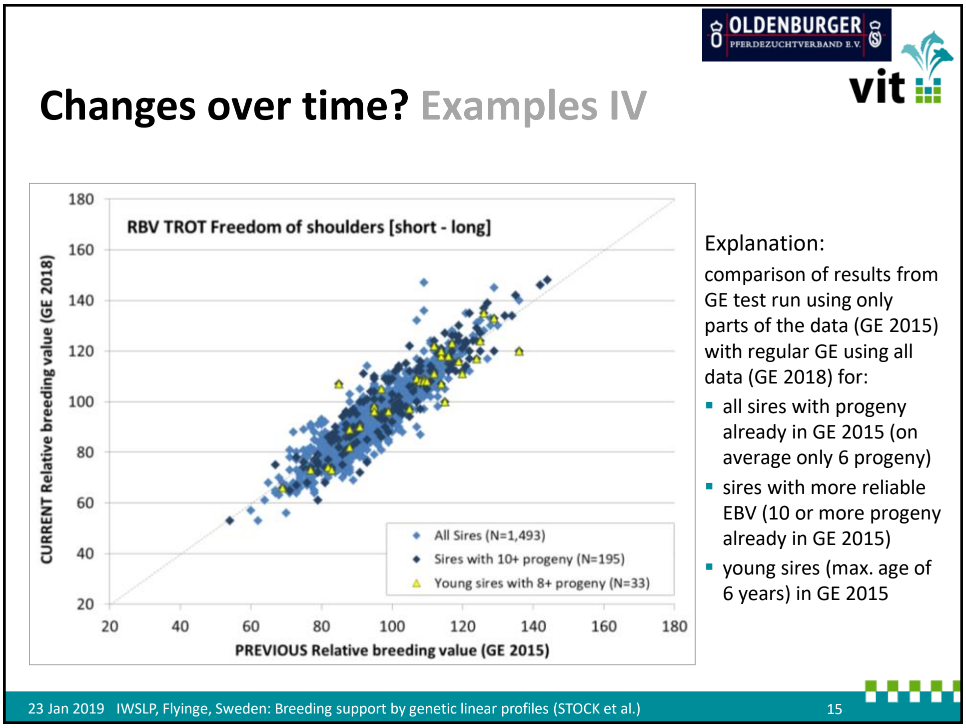


Changes over time? Examples III

Explanation:

comparison of results from GE test run using only parts of the data (GE 2015) with regular GE 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)
- young sires (max. age of 6 years) in GE 2015



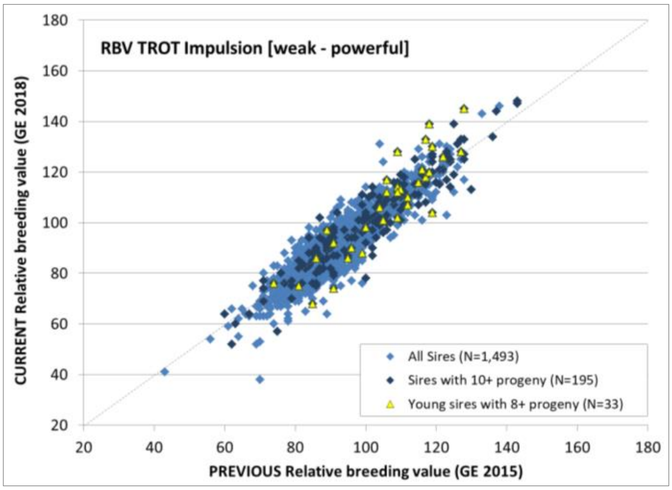
Changes over time? Examples IV

Explanation:

comparison of results from GE test run using only parts of the data (GE 2015) with regular GE 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)
- young sires (max. age of 6 years) in GE 2015

Changes over time? Examples V



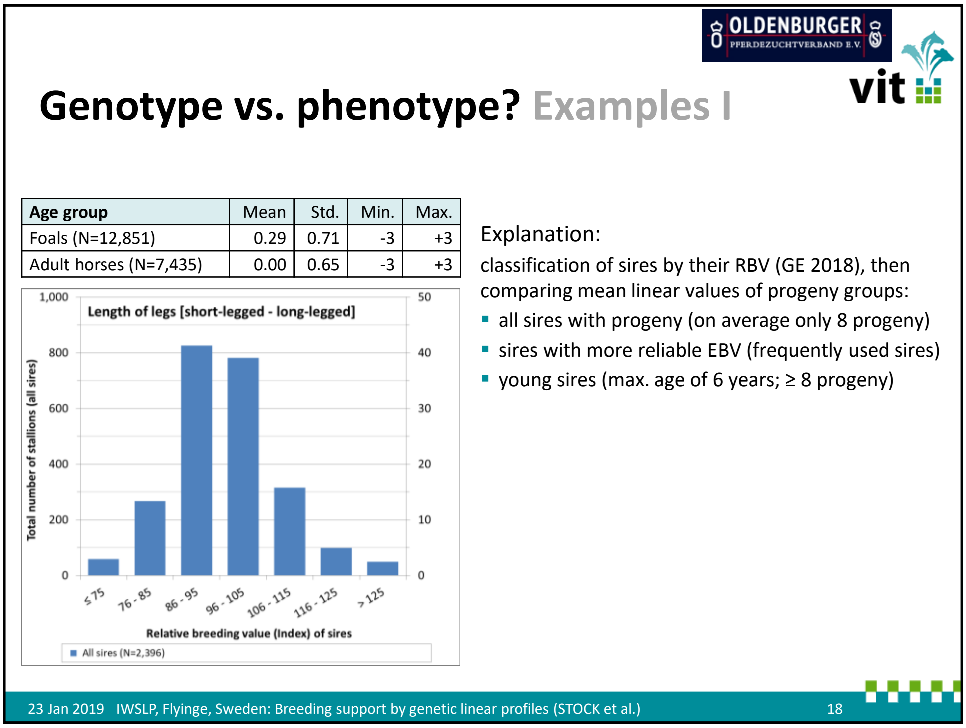
Explanation:

comparison of results from GE test run using only parts of the data (GE 2015) with regular GE 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)
- young sires (max. age of 6 years) in GE 2015

Changes over time? Yes – plausible!

- 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



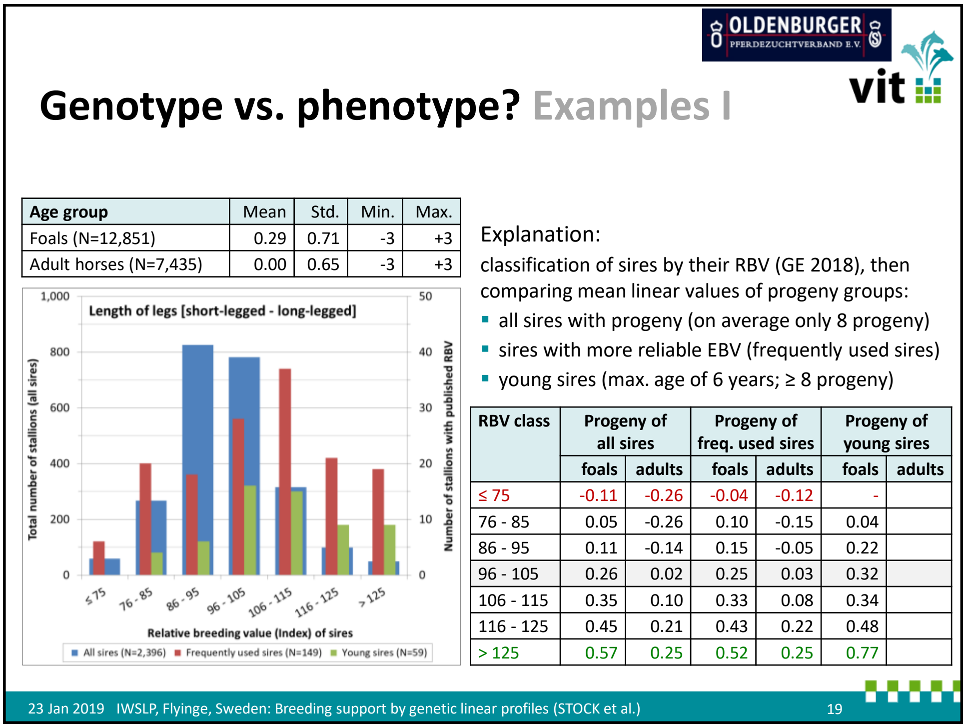
Genotype vs. phenotype? Examples I

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), 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)



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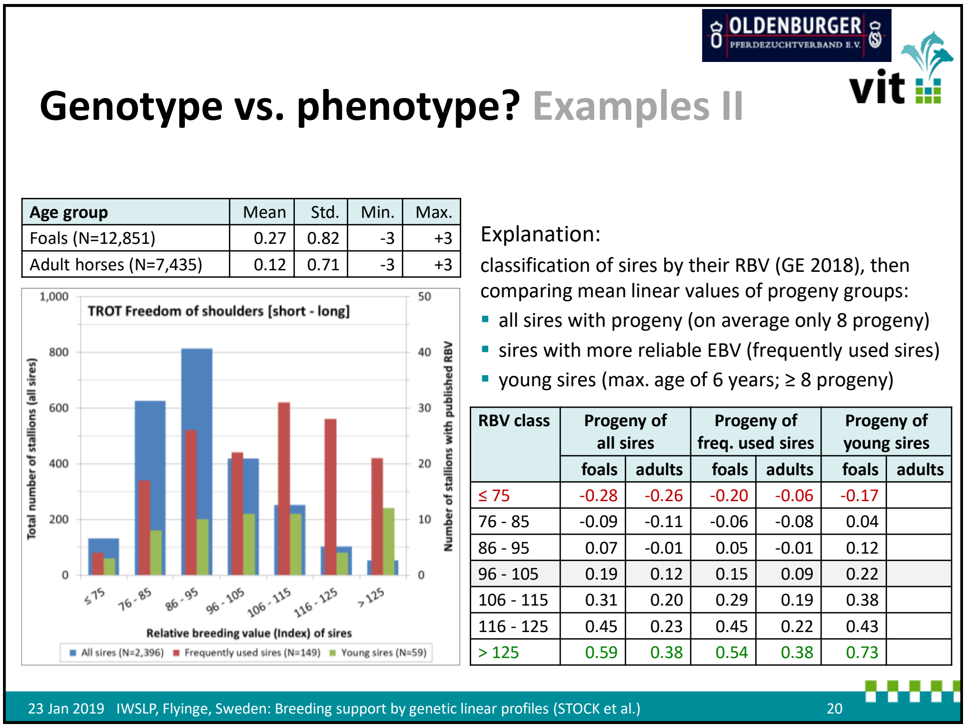
- young sires (max. age of 6 years; ≥ 8 progeny)

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	



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

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)

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	

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
- distribution patters (all sire groups)
  - 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; all sire groups)
  - 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, advanced use of linear data implies improved prediction.

- ➢ 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

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Thank you!

- ➢ 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

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