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# Genetics of linear traits for specifying and enhancing breeding programs for sport horses

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## Background



- 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 (regular training of judges, fine-tuning regarding linear trait definitions, ...)
- breeding progress and success of studbooks depending on strong and competitive breeding programs
  - trait definitions (clear, objective)
  - routine data **collection** and **use**
    - ✓
    - ?!



For Romance I - Diamond Hit - Landadel

## Study approach

- increased importance of linear profiling in sport horse studbooks  
(worldwide inventory, *Stock et al. EAAP 2015*)
  - expected increase of genetic evaluations and genomic applications for linear traits
- relatively large number of linear conformation and performance traits
  - varying proximity to the breeding goal(s)
  - varying - presumptive - importance and practical relevance  
(for the studbook and the individual breeder)



- **monitoring of realized breeding strategies**  
using genetic proofs (i.e. estimated breeding values) for linear traits

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Genetics of linear traits in sport horse breeding programs (Stock et al.), 30 Aug 2017, Tallinn, Estonia

## Linear data basis (2012-2016)

- linear description in the Oldenburg studbooks (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 (now routine)
  - selected events only in the pilot phase, most/all events since 2015
  - in Germany and abroad
- **in total N=12,931 linear profiles of 12,631 horses**  
(varying depth = numbers of traits depending on assessment type)

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Genetics of linear traits in sport horse breeding programs (Stock et al.), 30 Aug 2017, Tallinn, Estonia

# Data collection → Genetic analyses (I)

- mobile data collection (tablet PC) making it possible to:
  - efficiently collect detailed linear data (active input of deviations only)
  - routinely work with refined trait definitions / comprehensive linear schema (basis of highly valued individual assessment reports, considerable potential for research)
  - directly use maximal information from routine assessments
- standardized detailed information on conformation, gaits, jumping, and behavior



# Data collection → Genetic analyses (II)

- mobile data collection (tablet PC)
- standardized detailed information on conformation, gaits, jumping, and behavior
- trait definition:
  - within age group (F foals, A adults)
  - within trait category (analogous traits across assessment types → presentations / assessments as repeated observations)
- selected linear traits (standard deviation, variance, kurtosis)
  - N=46 conformation traits
  - N=40 performance traits (foals: N=17)

Tab.: Recorded and genetically analyzed linear traits

Trait category	No. of traits	
	recorded	gen. anal.
Conformation	73	46
Walk (H, F, R)	6	5
Trot (H, F, R)	11	8
Canter (F, R)	10	9
Jumping (F)	16	13
Special remarks (H, F, R)	8	4
Behavior (H, F, R)	7	1

H = in hand, F = free, R = under rider



# Genetic analyses

- estimation of genetic parameters (REML / VCE6) and genetic evaluation (BLUP / PEST) using uni- and multivariate linear animal models

- foals:

$$Y_{ijkno} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE\_M}_k + \text{SEX}_l + \text{animal}_o + e_{ijklop}$$

- mares+stallions:

$$Y_{ijmnop} = \mu + SB_i + \text{EVENT-TEAM}_j + \text{AGE\_J}_m + \text{PTYPE}_n + \text{animal}_o + pe_o + e_{ijmnop}$$

- **plausible patterns of heritabilities ( $h^2$ ), support of multiple trait approach**
  - 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
  - mostly strong positive additive genetic correlations between analogous traits assessed in foals and adult horses

# Genetic evaluation for linear traits

- in total 1,812 sires with 1-289 linearly described offspring
  - F (foals): 931 sires with 1-217 offspring (F-OL: 651 / 1-217; F-OS: 419 / 1-69)
  - A (adults): 1,268 sires with 1-148 offspring
- definition of sire groups based on numbers and distribution of offspring
- breeding values
  - base definition: sires born  $\geq 1995$  and  $> 2$  linearly described adult horses (N=263)
  - standardization to  $100 \pm 20$  (genetic standard deviation)
- **relative breeding values (RBV) for linear traits**
  - distinct RBV for F and A
  - combined RBV with weights of 40% F + 60% A

# Sire groups

Note: OS as studbook exclusively for show jumping, OL as the original Oldenburg studbook with broader breeding goal (dressage, but also show jumping, ...)

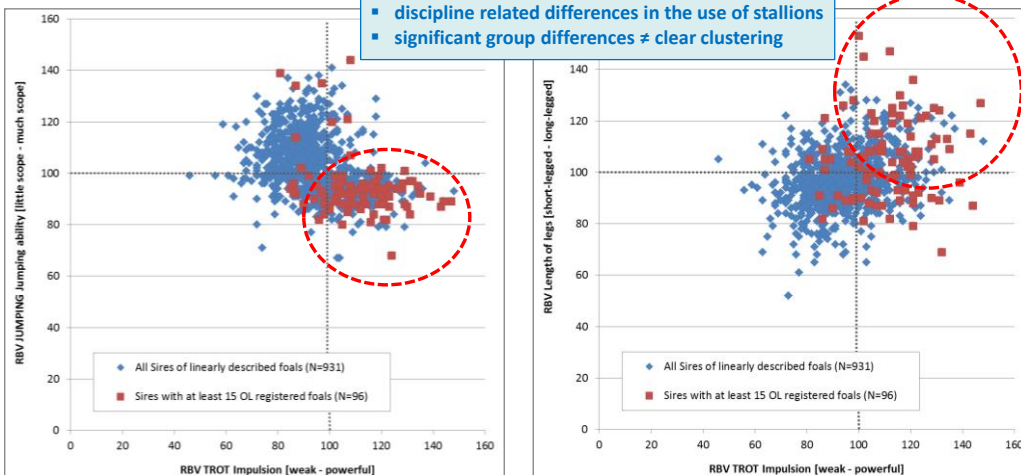


- ❖ **pOL** popular OL stallions:  
 ≥ 15 OL registered foals, N=96 of 931 sires (F)  
 (incl. 87 sires with 100% OL registration and only 9 sires with also OS registered foals)
- ❖ **DRE** dressage stallions:  
 ≥ 5 registered foals with 100% OL registration, N=178 of 314 sires (F N<sub>off</sub> ≥ 5)
- ❖ **JUMP** jumping stallions:  
 ≥ 5 OS registered foals, N=101 of 931 sires (F)
- ❖ **PERF** stallions with reasonable numbers of performance tested progeny:  
 ≥ 5 adult horses with linear data from free movement and/or presentation under rider, N=109 of 1,268 sires (A)  
 (data sources: mare performance test, stallion preselection for licensing)

# RBV distributions within sire groups



Note:  
 ▪ discipline related differences in the use of stallions  
 ▪ significant group differences ≠ clear clustering



# Analyses of RBV distributions

- combined RBV of sires for linear conformation and performance traits
- monitoring of realized breeding strategies by comparisons between groups of sires (significant differences? qualitative and quantitative view)
- analysis of variance (GLM procedure of SAS):

$$y_{ijk} = \mu + \text{SORIGIN}_i + \text{SGROUP}_j + e_{ijk} \quad \text{with}$$

$y_{ijk}$  = breeding value of the sire,

$\text{SORIGIN}_i$  = fixed effect of sire origin (DE life number Yes/No),

$\text{SGROUP}_j$  = fixed effect of sire group (qualifying for predefined sire group Yes/No)

→ distinct sets of analyses for pOL, DRE, JUMP, PERF,

$e_{ijk}$  = random residual

## Results:

### Differences between sire groups? (I)

Linear trait	pOL		DRE		JUMP		PERF	
	R <sup>2</sup>	P	R <sup>2</sup>	P	R <sup>2</sup>	P	R <sup>2</sup>	P
Breed type [plain - true to type]	0.081	<0.001	0.074	<0.001	0.021	0.988	0.049	<0.001
Gender expression [weak - strong]	0.098	<0.001	0.111	<0.001	0.043	0.009	0.031	<0.001
Frame [small-framed - large-framed]	0.028	<0.001	0.019	0.038	0.002	0.268	0.029	<0.001
Caliber [light - heavy]	0.006	0.023	0.020	0.022	0.001	0.461	0.009	0.007
Length of legs [short-legged - long-legged]	0.051	<0.001	0.128	<0.001	0.006	0.015	0.053	<0.001
Head shape [coarse - fine]	0.070	<0.001	0.045	0.002	0.033	0.840	0.024	<0.001
Eye size [small - large]	0.065	0.451	0.094	0.890	0.065	0.546	0.030	0.780
Set of neck [low - high]	0.016	0.104	0.040	0.012	0.015	0.193	0.012	<0.001
Muscling area of neck [ewe-necked - top line dominated neck]	0.046	<0.001	0.103	<0.001	0.054	<0.001	0.029	0.003
Shape of neck [straight - arched]	0.068	<0.001	0.161	<0.001	0.052	<0.001	0.029	<0.001
Length of withers [short - long]	0.005	0.204	0.018	0.025	0.009	0.014	<0.001	0.900
Height of withers [flat - high]	0.053	0.062	0.094	0.372	0.050	0.922	0.025	0.001
Length of back [short - long]	0.016	0.008	0.069	<0.001	0.019	0.002	0.016	0.003
Line (strength) of back [dipped - roached]	0.027	<0.001	0.049	<0.001	0.012	0.013	0.011	<0.001
Line (strength) of loins [dipped (weak) - roached]	0.002	0.479	0.012	0.344	0.005	0.060	0.001	0.570
Angle (inclination) of croup [flat (level) - sloping]	0.013	0.877	0.012	0.955	0.013	0.756	0.005	0.295
Set of tail [low - high]	0.033	<0.001	0.141	<0.011	0.016	0.003	0.024	<0.001
Length of forelimb pastern [short - long]	0.035	<0.001	0.158	<0.001	0.016	0.001	0.023	<0.001
Stance of forelimb pastern [upright - sloping (weak)]	0.011	0.027	0.034	0.025	0.007	0.427	0.013	0.155
Stance of hind limb pastern [upright - weak]	0.021	<0.001	0.035	0.005	0.007	0.381	0.023	<0.001
Hock angulation [straight - angulated]	0.002	0.330	0.022	0.034	0.003	0.189	0.015	0.002
Hind leg [round]	0.024	<0.001	0.048	<0.001	0.017	0.008	0.007	0.052
Size of joints [small - big]	0.006	0.037	0.036	0.001	0.008	0.016	<0.001	0.704
Toe stance of forelegs [toe-in - toe-out]	0.026	0.043	0.076	<0.001	0.035	<0.001	0.021	0.003
Tail tone [un-toned - over-toned]	0.001	0.437	0.020	0.040	0.004	0.092	<0.001	0.626

RBV for conformation:  
significant differences,  
but mostly minor

R<sup>2</sup> = coefficient of determination (R<sup>2</sup> ≥ 0.1 marked in bold), P = error probability (level of significance: P < 0.05)

## Results:

# Differences between sire groups? (II)



Linear trait	pOL		DRE		JUMP		PERF	
	R <sup>2</sup>	P	R <sup>2</sup>	P	R <sup>2</sup>	P	R <sup>2</sup>	P
WALK Freedom of shoulders [short - long]	0.088	<0.001	<b>0.254</b>	<0.001	0.090	<0.001	0.048	<0.001
WALK Reach of HL (overstepping) [inactive (short) - active (long)]	0.076	<0.001	<b>0.292</b>	<0.001	0.085	<0.001	0.034	<0.001
TROT Freedom of shoulders [short - long]	<b>0.161</b>	<0.001	<b>0.406</b>	<0.001	0.042	<0.001	0.090	<0.001
TROT Mechanics of front limbs [straight FL - much knee action]	0.082	<0.001	<b>0.120</b>	<0.001	0.004	0.283	0.072	<0.001
TROT Impulsion [weak - powerful]	<b>0.152</b>	<0.001	<b>0.322</b>	<0.001	0.026	<0.001	<b>0.104</b>	<0.001
TROT Thrust (HL activity) [inactive, sluggish - active, energetic]	<b>0.130</b>	<0.001	<b>0.332</b>	<0.001	0.039	<0.001	<b>0.133</b>	<0.001
TROT Carrying power [pushing - carrying]	<b>0.123</b>	<0.001	<b>0.306</b>	<0.001	0.040	<0.001	<b>0.102</b>	<0.001
TROT Suppleness [tense - supple]	0.094	<0.001	<b>0.109</b>	0.019	0.073	0.468	0.053	<0.001
CANTER Freedom of shoulders [short - long]	0.057	<0.001	<b>0.142</b>	<0.001	0.015	<0.001	0.041	<0.001
CANTER Mechanics of FL [straight forelimb - much knee action]	0.045	<0.001	<b>0.128</b>	<0.001	0.014	<0.001	0.045	<0.001
CANTER Direction of movement [downhill - uphill]	0.106	<0.001	<b>0.327</b>	<0.001	0.043	<0.001	0.108	<0.001
CANTER Thrust (HL activity) [inactive, sluggish - active, energetic]	0.054	<0.001	<b>0.129</b>	<0.001	0.027	0.103	0.065	<0.001
JUMPING Rhythm [not fluent - fluent]	0.041	<0.001	<b>0.310</b>	<0.001	0.079	<0.001	0.017	0.002
JUMPING Take-off power [weak - powerful]	0.040	<0.001	<b>0.382</b>	<0.001	0.082	<0.001	0.010	<0.001
JUMPING Reflexes [slow, inflexible - quick, flexible]	0.027	<0.001	<b>0.283</b>	<0.001	0.061	<0.001	0.011	<0.001
JUMPING Attention [inattentive - attentive]	0.025	<0.001	<b>0.395</b>	<0.001	0.078	<0.001	0.011	0.175
JUMPING Overview [little - much]	0.053	<0.001	<b>0.344</b>	<0.001	<b>0.114</b>	<0.001	0.027	0.001
JUMPING Jumping ability [little scope - much scope]	0.061	<0.001	<b>0.645</b>	<0.001	<b>0.150</b>	<0.001	0.009	<0.001
JUMPING Foreleg angulation [straight - angulated]	0.043	<0.001	<b>0.305</b>	<0.001	0.075	<0.001	0.013	0.005
JUMPING Foreleg angulation [uneven]	0.008	0.029	0.038	0.011	0.003	0.462	0.007	0.005
JUMPING Back technique (bascule) [hollow back - rounded back]	0.033	<0.001	<b>0.263</b>	<0.001	0.058	<0.001	0.002	0.103
JUMPING Hind leg technique (haunches) [tight - open]	0.054	<0.001	<b>0.370</b>	<0.001	0.060	<0.001	0.024	<0.001

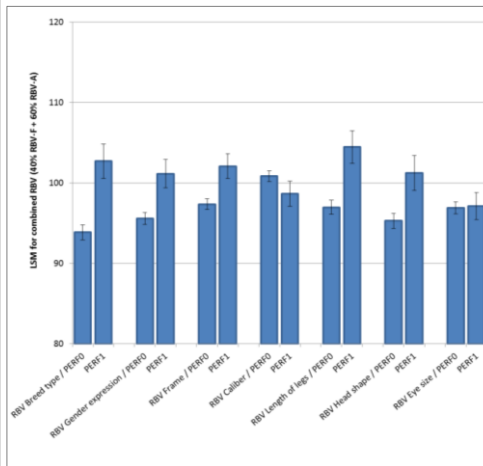
**RBV for gaits:**  
significant differences, several of clear and consistent relevance

**RBV for jumping:**  
significant differences, several of obvious distinctive relevance

R<sup>2</sup> = coefficient of determination (R<sup>2</sup> ≥ 0.1 marked in bold), P = error probability (level of significance: P < 0.05)

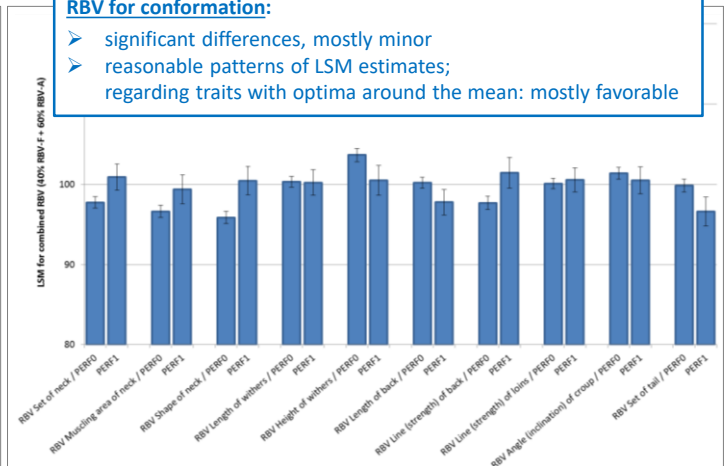
## Results:

# Least Square Means / Conformation (I)



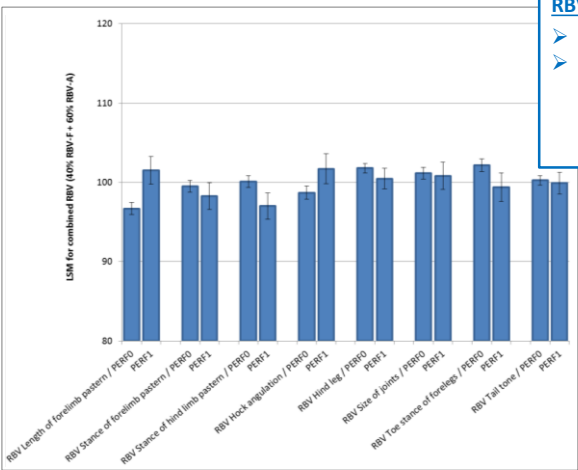
**RBV for conformation:**

- significant differences, mostly minor
- reasonable patterns of LSM estimates; regarding traits with optima around the mean: mostly favorable



Results:

# Least Square Means / Conformation (II)

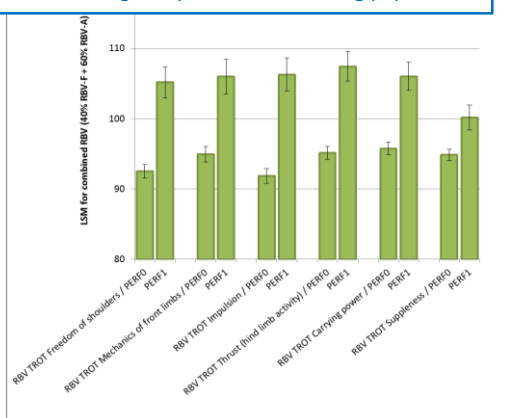
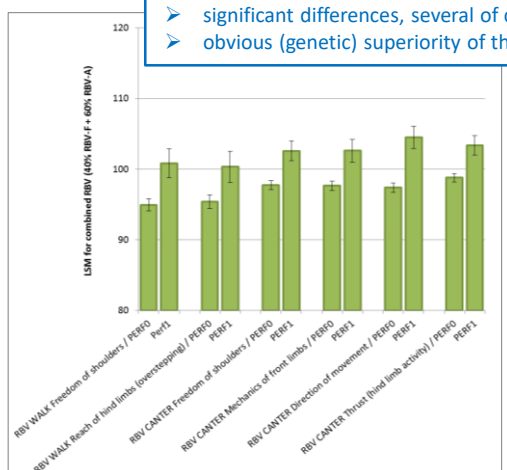


**RBV for conformation:**

- significant differences, mostly minor
- reasonable patterns of LSM estimates; regarding traits with optima around the mean: mostly favorable, some indications of possible benefits from systematic use of the refined information on conformation

Results:

# Least Square Means / Gaits



**RBV for gaits:**

- significant differences, several of clear and consistent relevance
- obvious (genetic) superiority of the sires with larger impact on the breeding population



# Summary of results & Conclusions



- grouping of sires based on numbers and distribution of progeny as feasible approach to monitoring realized breeding strategies
- consistency of results across sire groups
  - differences between disciplines (primary breeding goal)
  - relative importance of traits and trait groups
- favorable ranking of most discriminative traits
  - important characteristics of gaits (trot >> walk, canter)
  - overall minor role of conformation aspects

# Perspectives



- routine applications based on detailed linear profiles as important step towards optimal use of routine assessments
  - comprehensive linear profiles as standardized detailed output (highly valued increase of transparency, improved service for individual breeders)
  - substantially improved information basis for selection decisions (linear profile / phenotype → genetic profile → genomic profile)

**Note:**

visible benefit of high-quality data as best way to motivate effective and efficient data quality management (long-term investment into successful future breeding programs, incl. move from genetic to genomic evaluations)

- availability of **genetic and future genomic proofs for linear traits implying opportunities for more targeted breeding progress** (without unfavorable side effects) in the breeding programs for sport horses



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# Thank you!



- availability of **genetic and future genomic proofs for linear traits** implying **opportunities for more targeted breeding progress** (without unfavorable side effects) in the breeding programs for sport horses