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Implications of genetic correlations between linear gait and jumping traits in the sport horse

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Session 30
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Outline

- routine linear profiling and genetic evaluation for linear traits in the sport horse
  - advances and challenges for horse breeding
  - data structure, traits and modelling in the Oldenburg studbooks
- patterns of genetic correlations between linear traits
  - within trait (analogous traits across age groups)
  - across traits within trait group
- implications for breeding applications

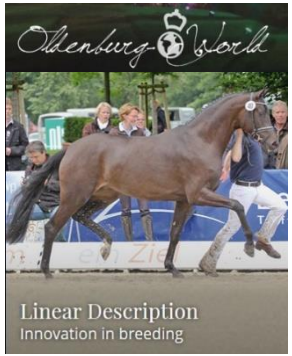
Background & motivation

- routine implementation of linear description in the sport horse implying access to highly valuable phenotypic data
  - clear and refined trait definitions
  - conformation and performance (gaits, jumping, behavior)
  - foals and/or adult horses (broodmares, stallions, young riding horses)
- breeding applications based on linear data
  - shared breeding goals → different systems, but similar sets of traits
  - potentially powerful tool for breeders

➢ How to make optimal use of the data?

Study basis I

- linear data collected by the Oldenburg studbooks (OL, OS)
  - since 2012
  - conformation and performance
    (135 linear trait aspects incl. special remarks)
  - same linear scheme and 7-point scale (-3 to +3)
    for all horses, i.e. across age groups



- until end of 2019:
  in total N=24,276 linear profiles of 22,891 horses

Study basis II

- linear data collected by the Oldenburg studbooks (OL, OS)
- routine genetic evaluation for linear traits
  - since 2017, annually in October / November
  - conformation and performance (46 traits)
  - trait definition within age group (foals, adult horses)
    → joint analyses of analogous traits

single- and multiple-trait repeatability linear animal models:

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

$y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_Y_m + PTYPE_n + animal_o + pe_o + e_{ijmnop}$ (adults)

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); random effects: animal = additive genetic effect, pe = permanent environmental effect of the animal

Data structure & modelling

- linear profiles compiled with 2:1 relation between age groups
  - about 15,100 foals (62%)
  - about 9,100 adult horses (7,264 mares, 1,880 stallions)
- distinct conditions of assessment
  - in hand
  - loose (free movement, free jumping)
  - under rider

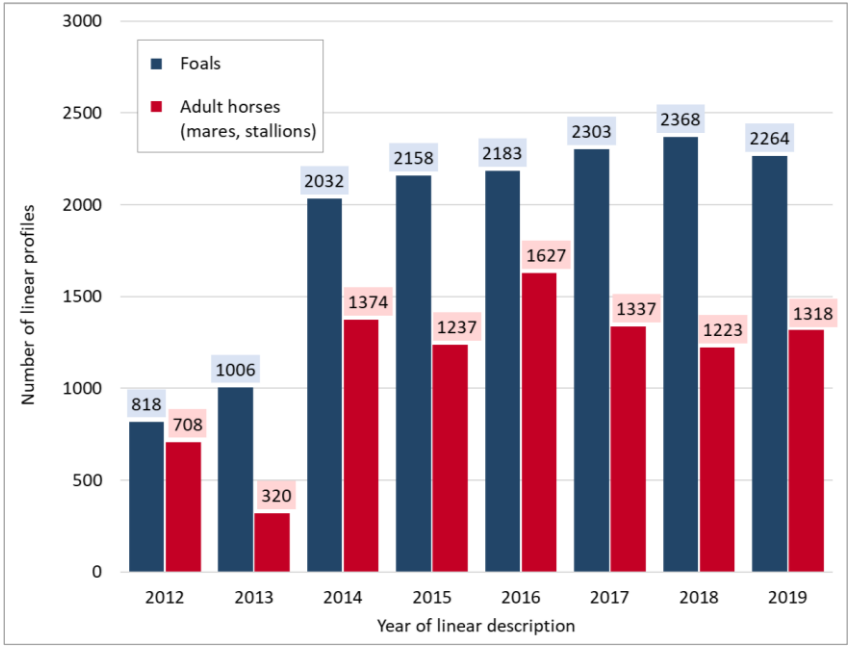
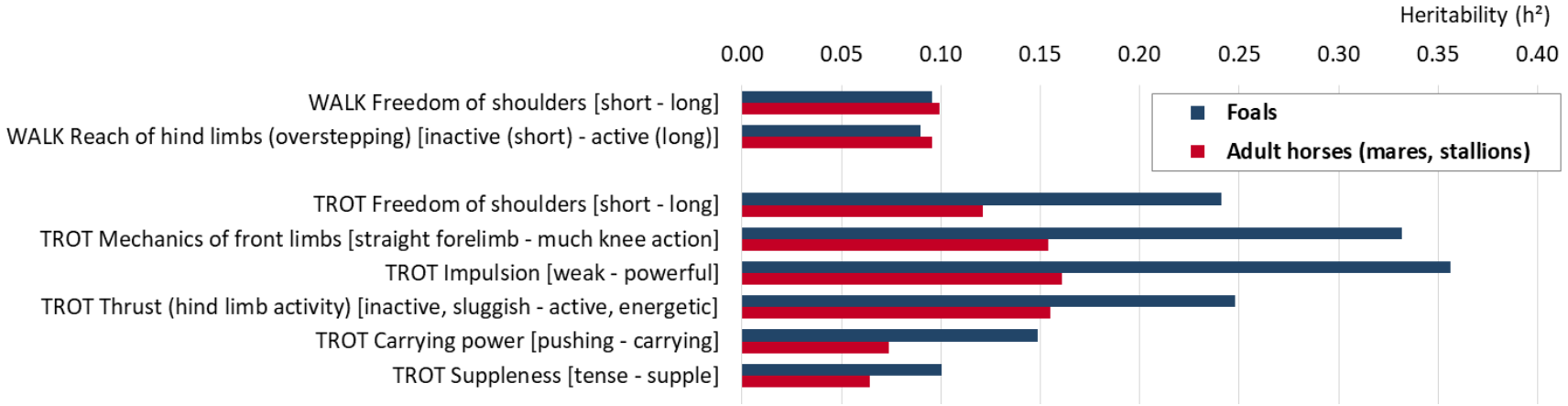


Fig. 1: Distribution of the 24,276 linear profiles compiled by the Oldenburg studbooks in 2012-2019 by year and age group

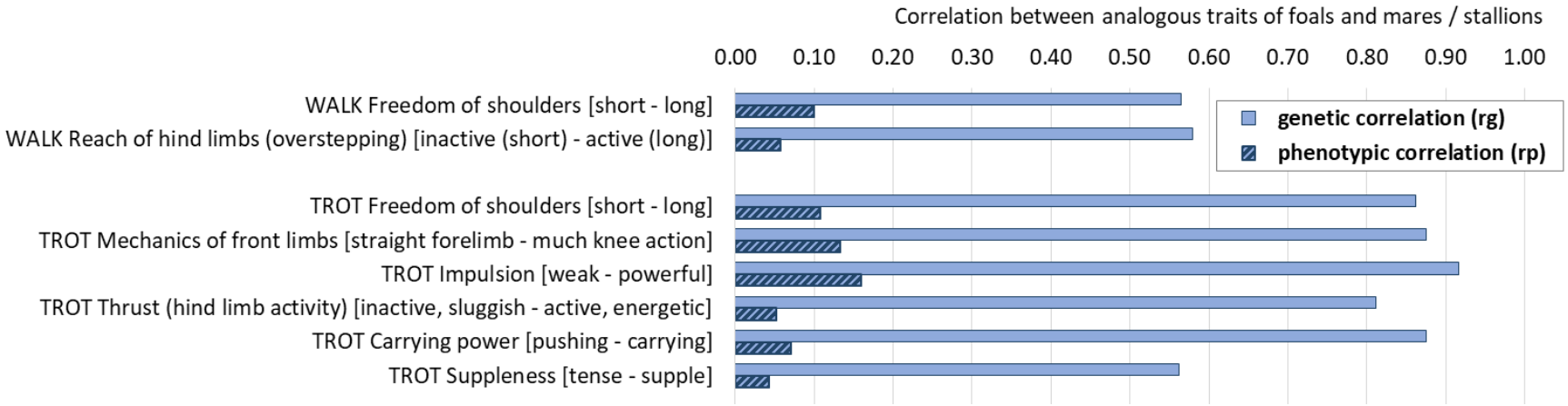
Data structure & modelling II

- results of multivariate estimation of genetic parameters indicating
  - similar patterns of heritabilities (linear aspects with higher / lower h^2)



Data structure & modelling III

- results of multivariate estimation of genetic parameters indicating
  - similar patterns of heritabilities (linear aspects with higher / lower h^2)
  - genetic similarity across age groups (favorably high additive genetic correlations between analogous traits in foals and adult horses)



Data structure & modelling IV

- results of multivariate estimation of genetic parameters indicating
  - similar patterns of heritabilities (linear aspects with higher / lower h^2)
  - genetic similarity across age groups (favorably high additive genetic correlations between analogous traits in foals and adult horses)
  - genetic similarity across presentation types (favorably high additive genetic correlations between traits assessed in adult horses under different conditions)

➢ multiple-trait repeatability linear animal model (pairs of analogous linear traits) ✓

➢ **options for further improvement?**

Correlation study

- results of the routine genetic evaluation for linear traits (GE2019): breeding values (BV) of sires with linearly described progeny
  - N=2,629 sires with 1 - 469 progeny (average 8.7, std. 27.1)
  - 75% of these sires with progeny in both age groups
  - direct use of BV, no deregression
- focus on linear traits with distinct grouping
  - BV for walk (N=2), trot (N=6), canter (N=4), jumping (N=10)
  - indices and individual BV for adult horse traits (A) and foal traits (F)

➢ Pearson correlation coefficients (SAS software) ≈ genetic correlations

BV correlations: Gaits

TROT	TROT01	TROT02	TROT03	TROT04	TROT05	TROT06
TROT01	A: 0.121 F: 0.241	0.63	0.77	0.67	0.64	0.33
TROT02	0.63	A: 0.154 F: 0.332	0.52	0.56	0.48	0.41
TROT03	0.76	0.54	A: 0.161 F: 0.356	0.63	0.56	0.42
TROT04	0.67	0.53	0.64	A: 0.155 F: 0.248	0.81	0.13
TROT05	0.66	0.47	0.58	0.81	A: 0.074 F: 0.149	0.10
TROT06	0.46	0.48	0.57	0.24	0.24	A: 0.064 F: 0.101

TROT01 Freedom of shoulders [short - long], **TROT02** Mechanics of front limbs [straight forelimb - much knee action], **TROT03** Impulsion [weak - powerful], **TROT04** Thrust (hind limb activity) [inactive, sluggish - active, energetic], **TROT05** Carrying power [pushing - carrying], **TROT06** Suppleness [tense - supple]

WALK	WALK01	WALK02
WALK01	A: 0.099 F: 0.096	0.91
WALK02	0.92	A: 0.096 F: 0.090

WALK01 Freedom of shoulders [short - long], **WALK02** Reach of hind limbs (overstepping) [inactive (short) - active (long)]

CANTER	CANT01	CANT02	CANT03	CANT04
CANT01	A: 0.161	0.67	0.58	0.50
CANT02		A: 0.266	0.65	0.58
CANT03			A: 0.199	0.65
CANT04				A: 0.181

CANT01 Freedom of shoulders [short - long], **CANT02** Mechanics of front limbs [straight forelimb - much knee action], **CANT03** Direction of movement [downhill - uphill], **CANT04** Thrust (hind limb activity) [inactive, sluggish - active, energetic]

Tab. 1-3: Pearson correlation coefficients between breeding values (BV) of sires for linear gait traits defined within age group, considering all 2,629 sires with linearly described progeny in GE2019, with figures for adult horse traits (A) above the diagonal and figures for foal traits (F) below diagonal. Heritabilities of respective linear traits are shown on the diagonal.

BV correlations: Jumping

JUMPING	JUMP01	JUMP02	JUMP03	JUMP04	JUMP05	JUMP06	JUMP07	JUMP08	JUMP09	JUMP10
JUMP01	A: 0.086	0.58	0.42	0.57	0.71	0.60	0.57	0.04	0.51	0.50
JUMP02		A: 0.206	0.58	0.71	0.60	0.83	0.57	0.16	0.52	0.45
JUMP03			A: 0.236	0.67	0.40	0.52	0.63	0.12	0.49	0.42
JUMP04				A: 0.218	0.64	0.74	0.62	0.10	0.60	0.47
JUMP05					A: 0.131	0.67	0.51	0.07	0.48	0.37
JUMP06						A: 0.381	0.56	0.19	0.55	0.52
JUMP07							A: 0.283	-0.17	0.54	0.44
JUMP08								A: 0.195	0.20	0.09
JUMP09									A: 0.202	0.39
JUMP10										A: 0.113

JUMP01 Rhythm [not fluent - fluent], **JUMP02** Take-off power [weak - powerful], **JUMP03** Reflexes [slow - quick], **JUMP04** Attention [inattentive - attentive], **JUMP05** Overview [little - much], **JUMP06** Jumping ability [little scope - much scope], **JUMP07** Foreleg angulation [straight - angulated], **JUMP08** Foreleg angulation [uneven], **JUMP09** Back technique (bascule) [hollow back - rounded back], **JUMP10** Hind leg technique (haunches) [tight (under the body) - long hind leg]

Tab. 4: Pearson correlation coefficients between breeding values (BV) of sires for linear jumping traits defined for the age group of adult horses (A), considering all 2,629 sires with linearly described progeny in GE2019, with correlation figures above the diagonal and heritabilities of respective linear traits shown on the diagonal.

Summary & Conclusion

- detailed linear scheme as valuable tool for refined phenotyping: individual characterization of the horse and its genetics (proof of concept)
  - no indications of 'redundancies' (unclear / overlapping traits definitions)
  - plausible correlation patterns within groups of linear traits
- significant genetic correlations between linear traits implying possible strengthening of the prediction system (routine GE)
- ➢ larger multiple-trait setting as possible next step to optimize the use of data from detailed linear description in future breeding applications for sport horses

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Further information on
linear profiling and related activities:

Equine Phenotypes

- detailed linear scheme as valuable tool for refined phenotyping
- larger multiple-trait setting as possible next step to optimize the use of data from detailed linear description in future breeding applications for sport horses

Thank you !