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OLDENBURGER BREEDING & SPORT

7th International Workshop on
Linear Profiling in the Warmblood Horse
on 29-30 March 2023 in Grebin / Plön, Germany

Genetic and genomic correlation analyses of linear traits and their implications for targeted support of sport horse breeding

K.F. Stock [1], M. Wobbe [1], H. Alkhoder [1], I. Workel [2], A. Hahn [2], W. Schulze-Schleppinghoff [2]

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

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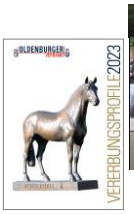
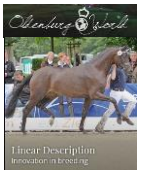
Outline

- background:
  indicator vs. target traits in sport horse breeding
- routine genetic evaluations for riding horses
  - data sources and trait definitions
  - complementary tools for breeders
- study approach
  - to close an information gap → sport
  - to gain further insight → genomics
- implications for breeding applications

Background





- routine data collection of the studbooks
  - detailed information on specifically defined traits by linear description
  - early and targeted breeding support by **genetic linear profiles**
- data from equestrian sport
  - information on the ultimate breeding goal traits
  - challenging data structure, trait definition, modeling
  - late availability of genetic proofs (breeding values) for competition performance

➢ suitability and value of linear conformation and performance traits as **indicator traits** in sport horse breeding

Study approach

- routine genetic evaluations → estimated breeding values (EBV) for a representative and variable sample of horses
  - EBV for linear conformation and performance traits from the genetic evaluation of the Oldenburg studbooks (OL, OS)
  - EBV for sport traits from the national genetic evaluation for riding horses in Germany (FN)
  - ➢ OL/OS mare population
- different definitions of sport traits
  - rank-based → individual ranking among all starters
  - level-based → highest level achieved (lifetime summary)
  - ➢ dressage (DR, DL) and show-jumping (JR, JL)

Routine genetic evaluations I

EBV for linear traits (LIN-EBV)

- OL+OS linear data 2012-2022
- 34,601 linear profiles of 31,953 horses
- 46 traits: conformation, special remarks, gaits, jumping

single- / multiple-trait repeatability linear animal models:

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

Routine genetic evaluations II

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

EBV for sport performance: dressage (D), show-jumping (J)

- sport data 1995-2022 (national /FN, international/FEI)
- 6.1m starts of 279k horses for D, 13.9m starts of 328k horses for J
- 2 traits per discipline: ranking (R) and highest level achieved (L)

single- / multiple-trait repeatability linear animal models:

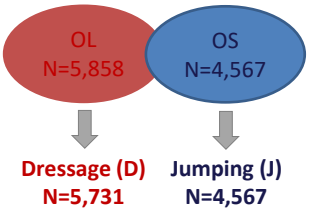
$y_{ijklop} = \mu + COMP_i + SEX_j \times AGE_k + RIDER_l + animal_o + pe_o + e_{ijklop}$ (DR, JR)

$y_{jmnop} = \mu + Sex_j + L\_AGE_m + L\_YEAR_n + animal_o + e_{jmnop}$ (DL, JL)

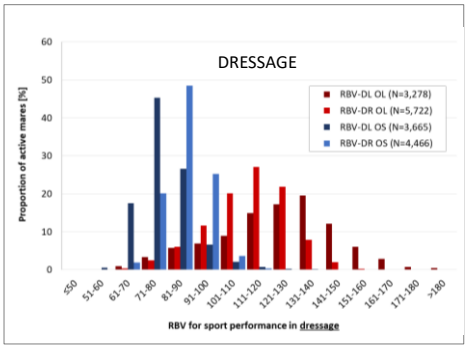
fixed effects: COMP = individual competition, SEX = stallions / gelding / mare, AGE (L_AGE) = competition age (age at achieving highest level) in years, RIDER = rider category or individual rider, L_YEAR = year of achieving highest level; random effects: animal = additive genetic effect, pe = permanent environmental effect of the animal

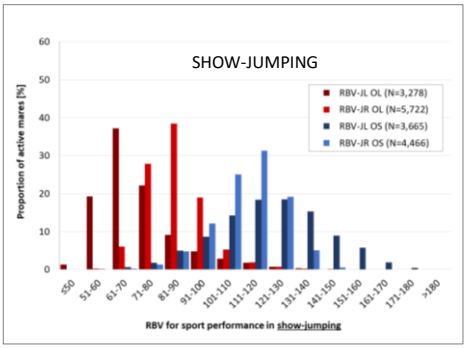
Study sample

- 'active mares' = mares with OL/OS-registered progeny in 2020-2022 plus registered active broodmares 2023
- results of routine genetic evaluations 2022
  - EBV for linear traits for 12,172 mares
  - EBV for sport traits for 10,298 mares



Dressage vs. show-jumping

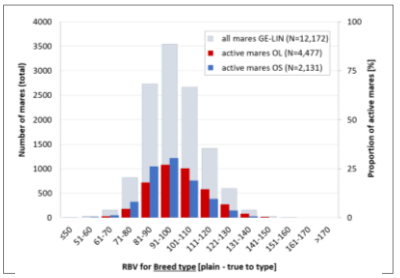


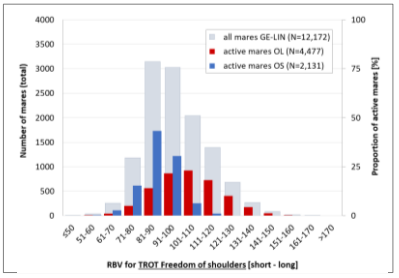


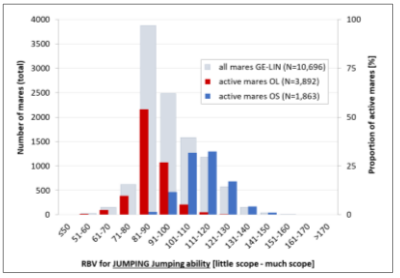
Sport trait (L level, R rank)		OL (N=5,731) N	EBV mean	std	range	OS (N=4,567) N	EBV mean	std	range
Dressage	DL	3,278	**123.7**	**22.7**	61 - 213	3,665	78.9	9.9	56 - 168
	DR	5,722	**112.6**	**15.3**	57 - 166	4,466	86.5	8.0	60 - 128
Show-jumping	JL	3,278	71.7	15.3	42 - 172	3,665	**120.9**	**20.6**	53 - 183
	JR	5,722	85.6	11.4	54 - 168	4,466	**111.5**	**13.1**	55 - 155

EBV distributions of linear traits

conformation
gaits jumping





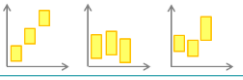


Methodology

- statistical analyses using SAS software
  - EBV for indicator traits (linear description):
    LIN – all 46 traits
  - EBV for target traits (sport performance):
    DL and DR for dressage, JL and JR for show-jumping
- EBV correlations
  - ➢ **Pearson correlation coefficients**
- analysis of variance
  - linear regression
  - class variable:
    LIN-EBV <90, 90-110, >110
  - ➢ **Least Square Means (LSM)**

strength and direction of the relationship between two variables

model prediction
('what may I expect for X if Y is ...')



EBV correlation patterns: LIN-CONF I

Linear trait	Active mares with EBVs + phenotypic data (own and/or 2+ progeny)				All active mares with EBVs			
	DL (N=980)	DR (N=958)	JL (N=912)	JR (N=880)	DL (N=2,519)	DR (N=4,561)	JL (N=2,519)	JR (N=4,561)
CONF **Breed type** [plain - true to type]	0.25	0.28	0.07	0.07	0.21	0.28	-0.11	-0.04
CONF **Gender expression** [weak - strong]	0.18	0.22	-0.01	0.02	0.19	0.28	-0.11	-0.04
CONF **Frame** [small-framed - large-framed]	0.21	0.17	0.18	0.08	0.18	0.18	-0.05	-0.02
CONF **Caliber** [light - heavy]	-0.01	-0.03	0.04	0.03	-0.06	-0.13	0.08	0.05
CONF **Length of legs** [short-legged - long-legged]	0.18	0.14	0.11	0.04	0.22	0.26	-0.11	-0.07
CONF **Head shape** [coarse - fine]	0.09	0.15	-0.03	-0.03	0.16	0.25	-0.12	-0.06
CONF **Eye size** [small - large]	0.02	0.05	-0.11	-0.07	0.11	0.08	-0.12	-0.03
CONF **Set of neck** [low - high]	0.15	0.18	-0.01	0.01	0.23	0.24	-0.19	-0.15
CONF **Muscling area of neck** [ewe-necked - top line dominated neck]	0.17	0.17	-0.03	-0.03	0.25	0.20	-0.21	-0.18
CONF **Shape of neck** [straight - arched]	0.23	0.21	<0.01	0.03	0.27	0.26	-0.19	-0.14
CONF **Length of withers** [short - long]	0.05	0.05	-0.05	-0.08	0.21	0.17	-0.28	-0.26
CONF **Height of withers** [flat - high]	-0.21	-0.20	-0.11	-0.07	-0.19	-0.21	0.14	0.09
CONF **Length of back** [short - long]	-0.10	-0.10	0.05	0.11	-0.20	-0.19	0.17	0.10
CONF **Line (strength) of back** [dipped (weak) - roached]	0.22	0.20	<0.01	-0.08	0.33	0.32	-0.28	-0.22
CONF **Line (strength) of loins** [dipped (weak) - roached]	0.08	0.01	<0.01	-0.04	0.07	0.06	-0.03	0.02
CONF **Angle (inclination) of croup** [flat (level) - sloping]	-0.08	0.02	0.05	0.03	-0.01	0.04	<0.01	-0.01
CONF Set of tail [low - high]	-0.09	-0.17	0.03	0.01	-0.31	-0.32	0.32	0.25

- overall minor role of linear conformation aspects
- some associations for D, but no strong indicator of sport performance

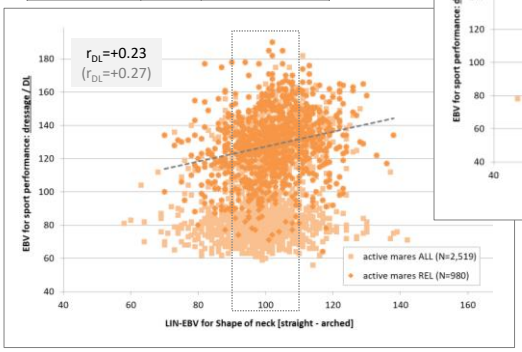
EBV correlation patterns: LIN-CONF II

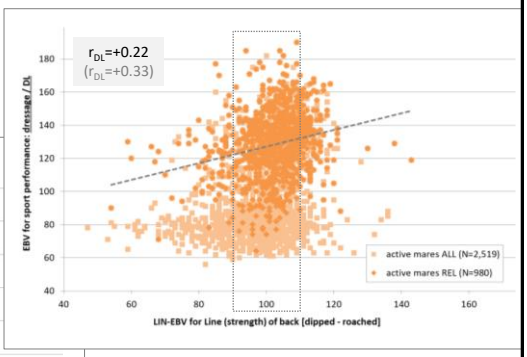
Linear trait	Active mares with EBVs + phenotypic data (own and/or 2+ progeny)				All active mares with EBVs			
	DL (N=980)	DR (N=958)	JL (N=912)	JR (N=880)	DL (N=2,519)	DR (N=4,561)	JL (N=2,519)	JR (N=4,561)
CONF **Length of forelimb pastern** [short - long]	0.18	0.14	0.05	0.03	0.24	0.22	-0.21	-0.17
CONF **Stance of forelimb pastern** [upright - sloping (weak)]	-0.03	0.01	<0.01	0.03	-0.10	-0.08	0.04	0.02
CONF **Stance of hind limb pastern** [upright - weak]	-0.06	-0.03	-0.10	-0.05	0.01	-0.03	-0.08	-0.04
CONF **Hock angulation** [straight - angulated]	0.13	0.08	0.12	0.08	-0.03	-0.05	0.11	0.07
CONF **Size of joints** [small - big]	-0.01	-0.02	0.19	0.19	-0.15	-0.13	0.20	0.12
CONF **Toe stance of forelegs** [toe-in - toe-out]	-0.03	-0.07	0.05	0.11	-0.08	-0.05	0.11	0.09
SPECIAL REMARK **Tail tone** [un-toned - over-toned]	-0.11	-0.05	0.14	0.06	-0.26	-0.18	0.29	0.22

- overall minor role of linear conformation aspects
- some associations for D, but no strong indicator of sport performance

EBV correlation patterns: LIN-CONF III

LIN-EBV Shape of neck	Sport EBV: DL	
	LSM	confidence limits
<90	120.09	116.21 - 123.97
90-110	128.09	126.61 - 129.57
>110	133.51	130.80 - 136.23





LIN-EBV Line (strength) of back	Sport EBV: DL	
	LSM	confidence limits
<90	119.54	114.97 - 124.11
90-110	128.42	127.03 - 129.81
>110	133.38	129.91 - 136.85

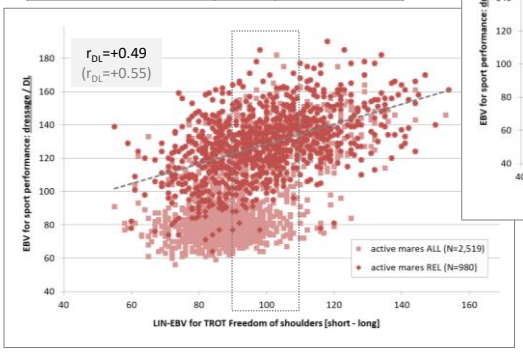
EBV correlation patterns: LIN-GAITS I

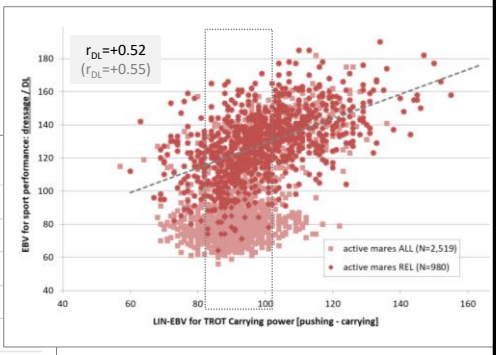
Linear trait	Active mares with EBVs + phenotypic data (own and/or 2+ progeny)				All active mares with EBVs			
	DL (N=980)	DR (N=958)	JL (N=912)	JR (N=880)	DL (N=2,519)	DR (N=4,561)	JL (N=2,519)	JR (N=4,561)
WALK **Freedom of shoulders** [short - long]	0.31	0.45	-0.07	-0.07	0.52	0.55	-0.50	-0.34
WALK **Reach of hind limbs (overstepping)** [inactive (short) - active (long)]	0.35	0.48	-0.10	-0.09	0.58	0.61	-0.57	-0.40
TROT **Freedom of shoulders** [short - long]	0.49	0.46	0.12	0.04	0.55	0.61	-0.34	-0.23
TROT **Mechanics of front limbs** [straight forelimb - much knee action]	0.35	0.31	0.23	0.24	0.17	0.31	0.05	0.08
TROT **Impulsion** [weak - powerful]	0.44	0.43	0.16	0.05	0.49	0.54	-0.28	-0.20
TROT **Thrust (hind limb activity)** [inactive, sluggish - active, energetic]	0.45	0.42	0.13	0.12	0.43	0.50	-0.24	-0.16
TROT **Carrying power** [pushing - carrying]	0.52	0.50	0.11	0.04	0.55	0.59	-0.35	-0.24
TROT **Suppleness** [tense - supple]	0.22	0.22	0.29	0.20	0.04	0.17	0.13	0.14
CANTER **Freedom of shoulders** [short - long]	0.33	0.30	-0.06	-0.01	0.40	0.45	-0.27	-0.20
CANTER **Mechanics of front limbs** [straight forelimb - much knee action]	0.28	0.25	0.01	0.07	0.27	0.32	-0.13	-0.07
CANTER **Direction of movement** [downhill - uphill]	0.52	0.52	0.03	0.05	0.56	0.60	-0.38	-0.24
CANTER **Thrust (hind limb activity)** [inactive, sluggish - active, energetic]	0.40	0.36	0.12	0.13	0.30	0.34	-0.12	-0.07

- relevant role of linear gait aspects for sport performance D
- indication of stronger association of hind limb than front limb related traits

EBV correlation patterns: LIN-GAITS II

LIN-EBV TROT Freedom of shoulders	Sport EBV: DL	
	LSM	confidence limits
<90	116.56	114.45 - 118.66
90-110	129.22	127.57 - 130.87
>110	140.55	138.29 - 142.82

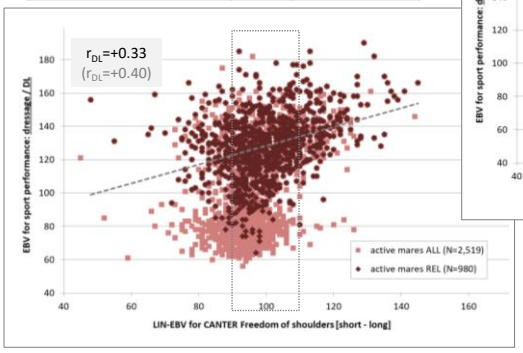


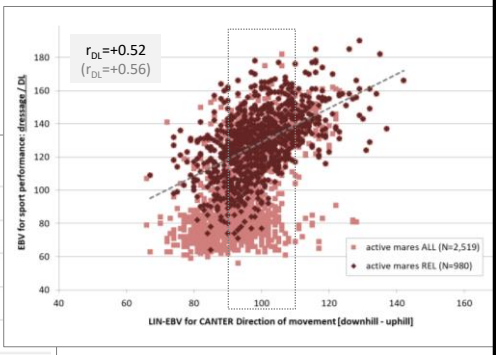


LIN-EBV TROT Carrying power	Sport EBV: DL	
	LSM	confidence limits
<90	114.77	112.53 - 117.00
90-110	129.28	127.82 - 130.75
>110	143.52	140.97 - 146.08

EBV correlation patterns: LIN-GAITS III

LIN-EBV CANTER Freedom of shoulders	Sport EBV: DL	
	LSM	confidence limits
<90	126.29	123.53 - 129.05
90-110	125.26	123.81 - 126.72
>110	143.81	140.85 - 146.77





LIN-EBV CANTER Direction of movement	Sport EBV: DL	
	LSM	confidence limits
<90	117.86	115.12 - 120.59
90-110	127.83	126.46 - 129.20
>110	147.51	144.17 - 150.85

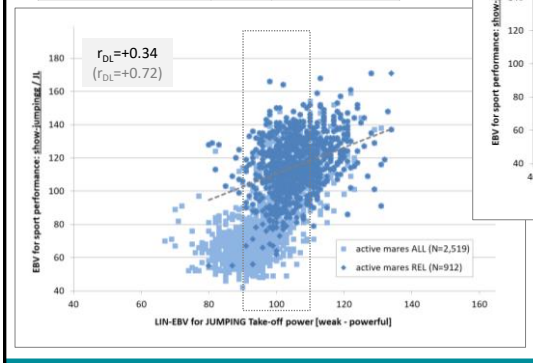
EBV correlation patterns: LIN-JUMP I

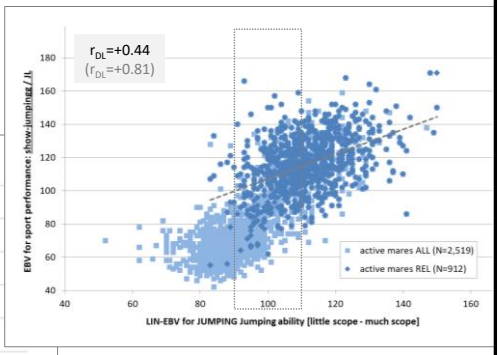
Linear trait	Active mares with EBVs + phenotypic data (own and/or 2+ progeny)				All active mares with EBVs			
	DL (N=980)	DR (N=958)	JL (N=912)	JR (N=880)	DL (N=2,519)	DR (N=4,561)	JL (N=2,519)	JR (N=4,561)
JUMPING **Rhythm** [not fluent - fluent]	-0.15	-0.03	0.21	0.17	-0.44	-0.25	0.48	0.42
JUMPING **Take-off power** [weak - powerful]	-0.29	-0.28	0.34	0.27	-0.65	-0.56	0.72	0.62
JUMPING **Reflexes** [slow, inflexible - quick, flexible]	-0.32	-0.30	0.19	0.17	-0.57	-0.52	0.59	0.50
JUMPING **Attention** [inattentive - attentive]	-0.24	-0.24	0.34	0.30	-0.66	-0.56	0.72	0.63
JUMPING **Overview** [little - much]	-0.24	-0.23	0.33	0.26	-0.59	-0.45	0.65	0.54
JUMPING **Jumping ability** [little scope - much scope]	-0.40	-0.37	0.44	0.34	-0.75	-0.64	0.81	0.68
JUMPING **Foreleg angulation** [straight - angulated]	-0.32	-0.21	0.12	0.15	-0.59	-0.49	0.59	0.49
JUMPING **Uneven forelegs** [markedly uneven]	-0.24	-0.23	0.03	0.05	-0.24	-0.22	0.19	0.17
JUMPING **Back technique (bascule)** [hollow back - rounded back]	-0.26	-0.22	0.18	0.07	-0.56	-0.45	0.58	0.49
JUMPING **Hind leg technique (haunches)** [tight (under the body) - long hind leg]	-0.37	-0.29	-0.03	0.02	-0.52	-0.47	0.41	0.31

- relevant role of linear jumping aspects for sport performance J
- indication of closer associations of traits relating to strength and quickness than technique

EBV correlation patterns: LIN-JUMP II

LIN-EBV JUMPING Take-off power	Sport EBV: DL	
	LSM	confidence limits
<90	114.48	109.52 - 119.43
90-110	112.40	111.10 - 113.69
>110	123.71	121.52 - 125.91





LIN-EBV JUMPING Jumping ability	Sport EBV: DL	
	LSM	confidence limits
<90	111.00	106.06 - 115.94
90-110	110.05	108.52 - 111.57
>110	121.33	119.75 - 122.92

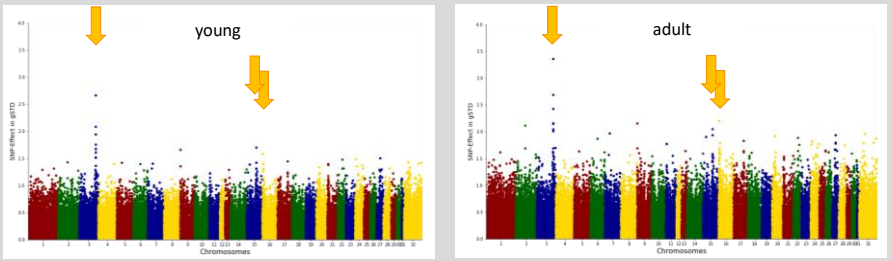
More detailed analyses via genomics

- information on genetic markers distributed over the whole genome ('genetic fingerprint')
  - ➢ high-resolution picture of genetic (dis-)similarities
  - ➢ details on the genetic background of traits and their relationships
  - → **improved understanding of equine movement characteristics**
- prototype single-step genomic evaluation (IAFH)
  - in total > 47,000 horses with 70K+ SNP genotypes
    (routine SNP genotyping for parentage control since 2021
    → continuously growing reference population for linear traits)
  - about 5,000 OL/OS 'reference' horses with
    - linear phenotypes (foals, adult horses) and
    - genome-wide SNP genotypic data
  - ➢ **genomic breeding values (gEBV), SNP effect estimates and 'TOP-SNPs'** (100 SNPs with largest effect estimates)

Genomic results I

➢ **support of the 'trait pairs' approach YOUNG - ADULT for genetic evaluation**

- analogous linear traits in young and adult horses
  - polygenic, mostly minor variance proportion explained by the TOP-SNPs
  - similar SNP effect patterns of trait pairs
  - gEBV correlations ≈ SNP effect correlations
  - substantial overlap of the TOP-SNPs: 40-70 of 100

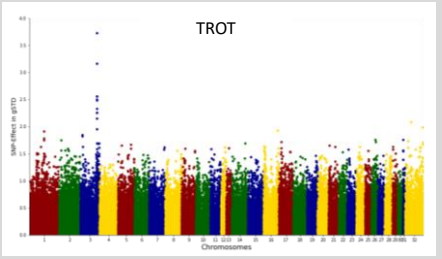


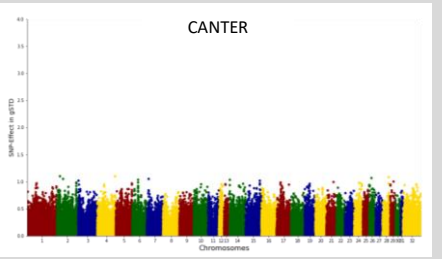
Distribution of standardized SNP effect estimates from single-step genomic evaluation for linear traits along the equine chromosomes: **TROT Thrust (hind limb activity)** [inactive, sluggish - active, energetic] in foals (left) and adult horses (right)

Genomic results II

- no indications (yet) for reasonable amounts of shared genetic basis of distinct movement aspects across gaits

- similar aspects of different gaits
  - visible impact of size and strength of the information basis
  - mostly dissimilar SNP effect patterns
  - gEBV correlations > SNP effect correlations
  - minor overlap of the TOP-SNPs: <20 of 100





Distribution of standardized SNP effect estimates from single-step genomic evaluation for linear traits along the equine chromosomes: **TROT Carrying power** [pushing - carrying] (left) and **CANTER Direction of movement** [downhill - uphill] (right)

Summary of results & Conclusions I

- <u>linear conformation traits</u> (conformation, special remarks)
  - mostly absent or significant, but low EBV correlations in the order of -0.2 < r < +0.2
  - some functionally plausible indications of relevance, mainly for dressage performance
    conformation of neck (shape, muscling) and back (strength)

- functionality, balanced and responsible breeding as main drivers for detailed linear description of conformation
- valuable tool for monitoring

Summary of results & Conclusions II

- linear performance traits (gaits, jumping)
  - mostly significant correlations (P < 0.001) within discipline
  - EBV correlations of r > 0.5 for both disciplines, with results patterns indicating favorable focuses when using linear traits as indicators
    - dressage: hind limb > front limb related traits
      reach of hind limbs in WALK, carrying power (besides freedom of shoulders) in TROT, direction of movement in CANTER
    - show-jumping: strength, quickness > technique
  - genomics hinting towards limited genetic similarity of apparently 'similar' characteristics of different gaits

- suitability of linear performance traits as indicators for performance in sport
- complementary genomic analyses helping to improve our understanding and breeding consideration of equine movement characteristics

IT-Solutions for Animal Production

Thank you!

Take home messages

- high value of detailed linear phenotypes for current and future breeding applications for sport horses
- genetic linear profiles as rightly appreciated tool for breeders
  - early and specific information on the inheritance of stallions
  - targeted support of mating decisions (wide range of traits)
- linear traits as appropriate targets for genomic tools

Contact information (vit, Genetic evaluation division / Scientific coordination):
PD Dr. habil. Kathrin F. Stock E-mail: friederike.katharina.stock@vit.de
Phone: +49 - 4231 - 955 623, Fax: +49 - 4231 - 955 9623), Mobile: +49 - 176 - 60 931 357

http://www.equinephenotypes.org