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OLDENBURGER BREEDING & SPORT

4th International Workshop on
Linear Profiling in the Warmblood Horse
on 14-15 March 2018 in Visselhövede, Germany

Genetic profiles in the Oldenburg studbooks

indicating the potential of refined linear data

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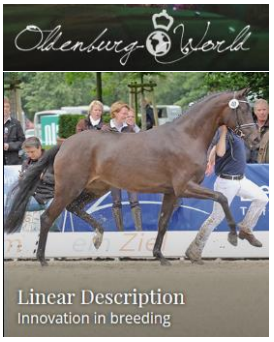
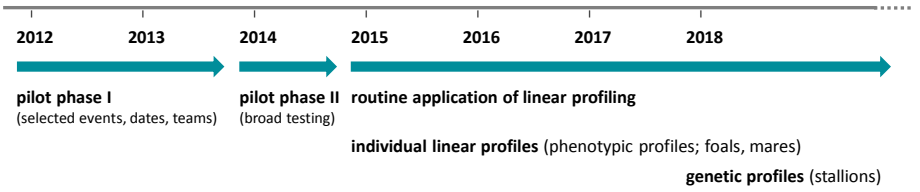
Outline

- development of linear profiling in the Oldenburg studbooks
  - routine data collection and use
  - data quality management
  - visibility for breeders
- analyses of linear data
  - from simple statistics to advanced and refined analyses
  - from individual phenotypic characterization to genetic and genomic profiles
- use of linear data in the breeding program: prospects and future role of linear data



Linear profiling in Oldenburg (OL, OS)



(A) development and implementation
- pilot studies related to research projects
  (extra staff for testing and optimizing the system, first data screening)
- application-oriented project work

→ **sound basis for broad implementation**

(B) routine and extension
- monitoring of linear data collection and data quality management
  - quality and coverage of the linear scheme (lacking traits?)
  - use of traits and scale, internal consistency of linear data, ...
    (unclear definitions? topics for training sessions and technical meetings)
- consolidation and improvement of applications

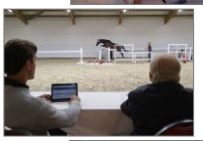
→ **smooth transition** to new routine applications (acceptance↑)
→ **improved services** for the studbooks and for individual breeders

Determinants of the development

- **close collaboration of science and practice**
  as key to fast progress and successful implementation
  - smooth transition from R&D to routine
  - transparency and exchange, flexibility of applications
    → acceptance and use
- **early use of linear data**
  as important driver of innovation
  - continued engagement for optimization of the whole system
    (data quality management)
  - high motivation of maximize information output
    (internal use → publication of consolidated information)

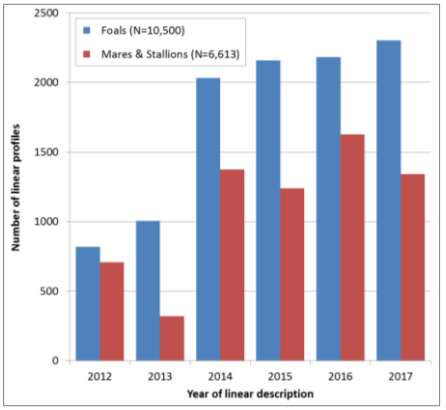
Linear data basis (2012 - 2017)

- Oldenburg linear scheme
  - same scheme in both 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=17,113 linear profiles of 16,451 horses**
  (varying depth = numbers of traits depending on assessment type)


Distribution of linear data

- in total 17,113 linear profiles of 16,451 horses
- linear profiles of foals
  - 5,538 fillies and 5,142 colts
  - mean age of 2.3 months
- linear profiles of adult horses
  - 5,318 mares (49% > 5years old, mean age of 7 years) including 1,985 linear profiles from mare performance tests (mean age 3.7 years)
  - 1,295 stallions (mean age 2.6 years)



Data collection → Genetic analyses

- 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 and 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 and jumping
  - ➢ behavior

Genetic analyses

- trait definition
  within age group and trait category
- 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

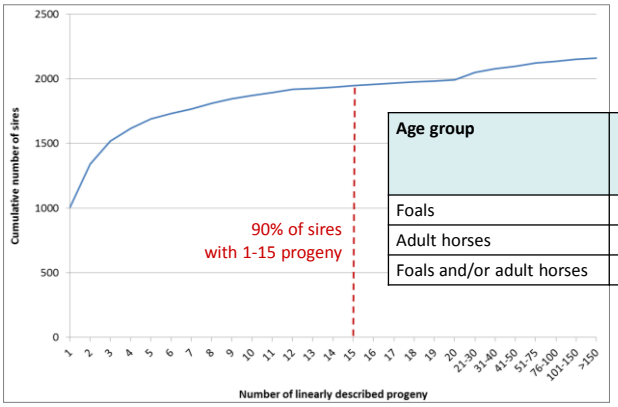
- estimation of genetic parameters and genetic evaluation using uni- and multivariate linear animal models
  - foals:
    $y_{ijkno} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_M_k + SEX_l + animal_o + e_{ijklop}$
  - mares+stallions:
    $y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_J_m + PTYPE_n + animal_o + pe_o + e_{ijmnop}$

Genetic parameters for linear traits

- plausible patterns of heritabilities (h^2) across age groups
  - 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
  - mostly strong positive additive genetic correlations between analogous traits assessed in foals and adult horses


Genetic profiles for linear traits (I)

- genetic evaluation (GE) based on all available linear data
  - foals and adult horses (mares, stallions)
  - multiple-trait linear animal model with repeated observations



Age group	No. of sires	No. of linearly described progeny	
		mean	range
Foals	1,976	9.7	1 - 289
Adult horses	1,610	4.1	1 - 175
Foals and/or adult horses	2,160	7.6	1 - 377

Figures from genetic evaluation 2017 with progeny numbers per sire (Tab.) and cumulative number of sires by number of linearly described progeny (Fig.)

Genetic profiles for linear traits (II)

- genetic evaluation (GE) based on all available linear data
  - foals and adult horses (mares, stallions)
  - multiple-trait linear animal model with repeated observations
- presentation of results
  - weighted combination of EBV for analogous linear traits:
    Index = 0.6 EBV_{Adult} + 0.4 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 2017: N=345 sires)
  - publication of genetic stallion profiles
    - frequently used sires (at least 20 linearly described progeny)
    - young sires (first crop of foals, minimum 8 foals)

Genetic evaluation: frequently used sires

Trait	Mean	Std	Min	Max
WALK Freedom of shoulders [short - long]	101.47	18.02	57	159
WALK Reach of hind limbs (overstepping) [inactive (short) - active (long)]	101.61	17.53	55	151
TROT Freedom of shoulders [short - long]	106.26	18.75	55	148
TROT Mechanics of front limbs [straight forelimb - much knee action]	106.72	18.81	72	150
TROT Impulsion [weak - powerful]	107.96	17.77	72	164
TROT Thrust (hind limb activity) [inactive, sluggish - active, energetic]	108.61	19.33	62	159
TROT Carrying power [pushing - carrying]	106.80	20.13	70	155
TROT Suppleness [tense - supple]	104.18	15.28	69	151
CANTER Freedom of shoulders [short - long]	102.23	13.48	67	134
CANTER Mechanics of front limbs [straight forelimb - much knee action]	102.20	14.60	63	136
CANTER Direction of movement [downhill - uphill]	103.49	13.68	74	133
CANTER Thrust (hind limb activity) [inactive, sluggish - active, energetic]	103.98	15.32	74	145
JUMPING Rhythm [not fluent - fluent]	98.55	11.90	65	132
JUMPING Take-off power [weak - powerful]	99.81	12.74	72	134
JUMPING Reflexes [slow, inflexible - quick, flexible]	99.28	12.58	79	173
JUMPING Attention [inattentive - attentive]	99.28	13.15	72	171
JUMPING Overview [little - much]	99.02	9.82	74	137
JUMPING Jumping ability [little scope - much scope]	99.01	16.91	71	148
JUMPING Foreleg angulation [straight - angulated]	98.04	12.89	67	150
JUMPING Foreleg angulation [uneven]	99.18	10.47	66	138
JUMPING Back technique (bascule) [hollow back - rounded back]	98.51	12.81	72	149
JUMPING Hind leg technique (haunches) [tight - open]	98.18	8.77	80	129

Year of birth	No. of sires
1980-1990	4
1991-1995	16
1996-2000	20
2001-2005	33
2006-2010	46
2011-2013	18
Total	**137**

Results from genetic evaluation 2017 for frequently used sires with sire distribution by year of birth (above) and information on distribution of indices for linear traits in these sires (left)

Genetic profiles & phenotypes of progeny

Trait	Index:	<80	80-90	91-109	110-119	>119
WALK Freedom of shoulders [short - long]	N	12	29	55	24	17
	mLF	-0.04	0.00	0.15	0.23	0.33
	mLA	-0.12	-0.06	0.04	0.17	0.26
WALK Reach of hind limbs (overstepping) [inactive (short) - active (long)]	N	14	26	54	29	14
	mLF	0.10	0.02	0.19	0.32	0.36
	mLA	-0.12	0.02	0.12	0.20	0.44
TROT Freedom of shoulders [short - long]	N	11	18	42	32	34
	mLF	-0.20	-0.03	0.16	0.31	0.49
	mLA	-0.13	-0.04	0.06	0.20	0.29
TROT Mechanics of front limbs [straight forelimb - much knee action]	N	13	16	53	16	39
	mLF	-0.15	0.27	0.27	0.48	0.64
	mLA	-0.03	0.16	0.19	0.26	0.57
TROT Impulsion [weak - powerful]	N	7	19	48	29	34
	mLF	0.15	0.19	0.43	0.63	0.86
	mLA	0.01	0.03	0.21	0.38	0.51
TROT Thrust (hind limb activity) [inactive, sluggish - active, energetic]	N	7	19	47	26	38
	mLF	0.19	0.25	0.37	0.52	0.74
	mLA	0.08	0.11	0.29	0.43	0.61
TROT Carrying power [pushing - carrying]	N	8	24	48	23	34
	mLF	-0.38	-0.19	-0.10	0.06	0.19
	mLA	-0.20	-0.19	-0.09	0.03	0.13
TROT Suppleness [tense - supple]	N	7	12	74	23	21
	mLF	-0.15	0.00	0.06	0.11	0.20
	mLA	-0.11	-0.16	-0.01	0.14	0.08

Results from genetic evaluation 2017 for frequently used sires with number of sires (N) and mean linear values in their progeny (foals, mLF; adult horses, mLA) by classes of indices for linear traits

Conclusions & Perspectives

- successful routine implementation of linear profiling as important step towards more sustainable competitive breeding
  - substantial gain in information on conformation and performance
  - increased transparency
  - feasible tool for collection of high quality phenotypic data required to benefit from more targeted breeding applications
- ➢ to be accompanied by continuous data quality management for optimum use of linear description
- high value of refined linear phenotypes
  - specific individual characterization (linear profiles of presented horses)
  - improved genetic characterization (genetic stallion profiles)
  - appropriate basis of future genomic applications (genomic profiles)

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Thank you!

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  as important step towards more sustainable competitive breeding
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