vit IT-Solutions for Animal Production

3rd International Workshop
on Linear Profiling in the Warmblood Horse
on February 24-25, 2017, in Gomadingen / Germany

Breeding applications for linear traits – implications of linear data analyses in Oldenburg and beyond

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, Germany;
[2] Oldenburg horse breeding society, Vechta, Germany

Outline

- linear profiling in the Oldenburg studbooks
  - data collection and routine processing of linear data
  - individual linear profiles
  - simple statistics and refined analyses
- data quality management focus of research and development (science to practice): optimization of recording and use of linear data
  - trait definitions and comparative analyses
  - genetic parameters for linear conformation and performance traits
- use of linear data in the breeding program: prospects and future role of linear data

Linear profiling in Oldenburg

close collaboration of science and practice as key to success

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

  → sound basis for broad implementation of the new system
- 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

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)
  - foals, mares, stallions
- extension of linear data collection
  - selected events only in the pilot phase,
    most/all events since 2015
    - foal registration
    - studbook inspection
    - mare performance test
    - preselection for licensing of stallions
  - in Germany and abroad
- **in total N=12,931 linear profiles of 12,631 horses**
  (different depth = numbers of traits depending on assessment type)

Linear data basis: distribution

Year	Age group	Type of event	OL	OS	Total	
2012	foals	registration	670	148	818	pilot phase (selected events / dates)
	mares	SBI, MPT (+SBI)	414	28*	442	
	stallions	preselection	136	131	267	
2013	foals	registration	788	218	1,006	
	mares	SBI, MPT (+SBI)	250	56*	306	
	stallions	preselection	14	0	14	
2014	foals	registration	1,563	473	2,036	broad testing
	mares	SBI, MPT (+SBI)	1,083	46*	1,129	
	stallions	preselection	169	78	247	
2015	foals	registration	1,599	559	2,158	routine application
	mares	SBI, MPT (+SBI)	929	50*	979	
	stallions	preselection	135	128	263	
2016	foals	registration	1,559	608	2,167	
	mares	SBI, MPT (+SBI)	1,009	44*	1,053	
	stallions	preselection	35	11	46	
Total	**foals**	**registration**	**6,179**	**2,006**	**8,185**	
	mares	**SBI, MPT (+SBI)**	**3,685**	**224***	**3,909**	
	stallions	**preselection**	**489**	**348**	**837**	

SBI = studbook inspection, MPT = mare performance test; * OL/OS distinction only for central MPT in Vechta

Linear traits (I)

- spectrum of traits according to the Oldenburg linear scheme 2016
  - conformation and correctness (N=80 traits)
  - movement in hand (N=19 traits)
  - free movement (N=34 traits) and free jumping (N=16 traits)
  - presentation under rider (without jumping) / in lungeing (N=41 traits)

➢ mobile data collection (tablet PC) making it possible to:
  - ➢ efficiently collect detailed linear data (active input of deviations only)
  - ➢ directly use maximal information from routine assessments

Tab.: Depth of linear profiles in dependence on the assessment conditions

Age group	Type of event	Conf	MovH	MovF/FJ	MovR	Total
Foals	registration	80	-	29	-	**109**
Mares +Stallions	studbook inspection (SBI)	80	19	-	-	**99**
	mare performance test (MPT)	(80)	(19)	34+16	41	**190**
	preselection for licensing	80	19	34+16	41	**190**

Conf = conformation, MovH (MovF, MovR) = movement in hand (free, under rider), FJ = free jumping

Linear traits (II)

- complexity of linear data structure implying:
  - considerable potential for research
  - highly valued individual assessment reports
- important for data processing and analyses:
  - 'defect traits' in each of the four trait groups (expected variation?)
  - analogous traits across presentation types (optimal modelling?)
- trait definitions within:
  - a.1) age group (foals vs. mares+stallions)
  - a.2) age group and studbook (OL, OS)
  - b.1) within evaluation type (e.g. impulsion in trot under rider)
  - b.2) within trait category (presentations / assessments as repeated observations)

Tab.: Overview of distinct linear traits

Trait category	No. of traits
Conformation	73
Walk (H, F, R)	6
Trot (H, F, R)	11
Canter (F, R)	10
Jumping (F)	16
Special remarks (H, F, R)	8
Behavior (H, F, R)	7

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

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

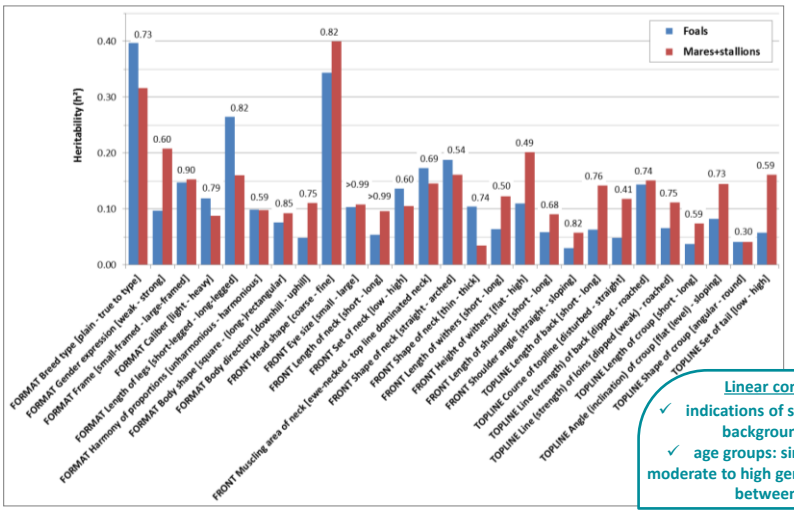
H = in hand, F = free, R = under rider

- 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:

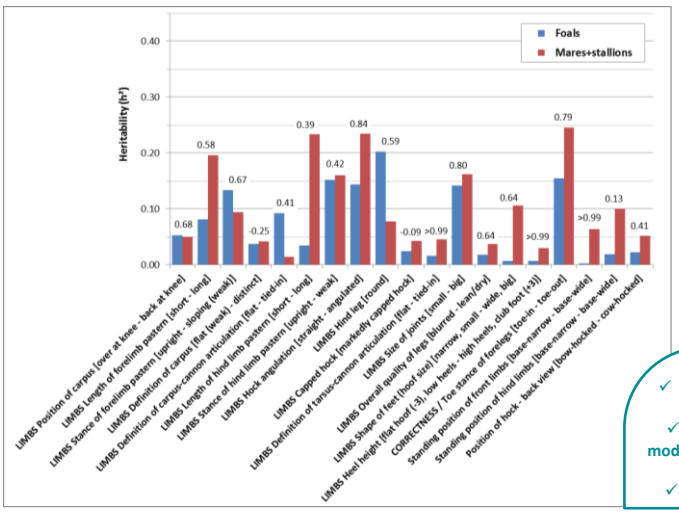
    $y_{ijmnop} = \mu + SB_i + EVENT\text{-}TEAM_j + AGE\_J_m + PTYPE_n + animal_o + pe_o + e_{ijmnop}$

Genetic parameters: body conformation



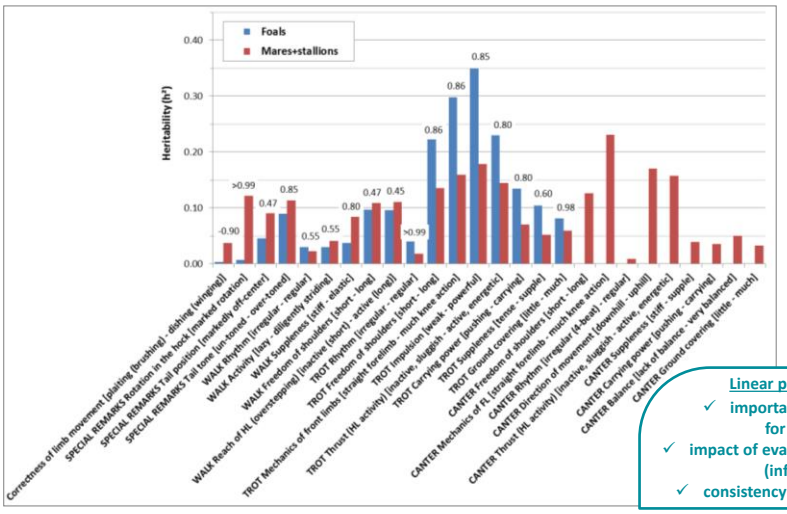
Linear conformation traits:
- ✓ indications of significant genetic background for many traits
- ✓ age groups: similar h² patterns, moderate to high genetic correlations between analogous traits

Genetic parameters: limb conformation



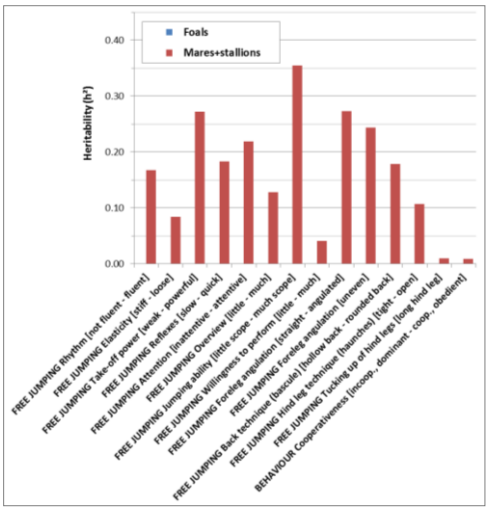
Linear conformation traits:
- ✓ indications of significant genetic background for many traits
- ✓ age groups: similar h² patterns, moderate to high genetic correlations between analogous traits
- ✓ challenging: limb conformation

Genetic parameters: movement



Linear performance traits:
- ✓ important role of genetics for movement / gaits
- ✓ impact of evaluation conditions (information density)
- ✓ consistency across age groups

Genetic parameters: jumping



Linear performance traits:
- ✓ important role of genetics for movement / gaits
- ✓ very important role of genetics for jumping and jumping characteristics
- ✓ impact of evaluation conditions (information density)
- ✓ consistency across age groups

Genetic parameters: details & summary

Trait group	Foals	Mares+stallions	Foals - Mares+stallions
	h^2 mean (range)	h^2 mean (range)	r_g mean (range)
Conformation (all traits)	0.098 (0.002 - 0.397)	0.123 (0.014 - 0.400)	0.640 (-0.245 to >0.999)
except limbs	**0.117** (0.030 - 0.397)	**0.137** (0.034 - 0.400)	**0.700** (0.303 to >0.999)
only limbs	0.070 (0.002 - 0.202)	0.105 (0.014 - 0.245)	0.561 (-0.245 to >0.999)
Walk	0.058 (0.030 - 0.097)	0.073 (0.023 - 0.110)	0.562 (0.446 to 0.801)
Trot	**0.182** (0.040 - 0.349)	**0.102** (0.018 - 0.179)	**0.844** (0.605 to >0.999)
Canter		0.095 (0.009 - 0.231)	
Jumping		**0.174** (0.010 - 0.354)	
Special remarks, behavior	0.036 (0.003 - 0.089)	**0.091** (0.037 - 0.121)	0.354 (-0.904 to >0.999)

Trait selection (std ≥0.3) within age group: F N_{conf}=28 h^2=0.135 (0.016 - 0.397), M+S N_{conf}=43 h^2=0.127 (0.014-0.400)

- **plausible pattern of heritabilities across trait groups**
- **clear indications of suitability of routinely collected linear data for genetic analyses**
- **high value of detailed linear profiles for breeding (regardless of age)**

Breeding values for linear traits

- prototypes of genetic evaluation
  - OL/OS studbooks
    - linear profiles of N=12,631 horses (2012-2016)
    - foals and adults (mares, stallions) → uni- / bivariate EBV
  - Swedish Warmblood studbook (SWB)
    - linear profiles of N=3,410 horses (2013-2016)
    - 3-year-olds → univariate EBV
- correlations between estimated breeding values (EBV) ≈ genetic correlations between linear traits
  - influenced by similarity / comparability of traits
  - influenced by genetic parameters and EBV reliabilities

- <u>across-studbook correlation study</u> based on sire EBV for linear traits

Genetic correlation study

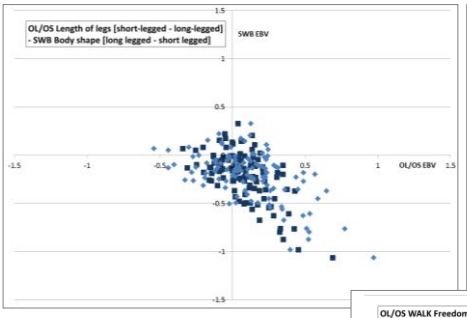
- cross distributions and 'raw' correlations (Pearson, Spearman) without correction for EBV accuracies → influenced by:
  - wide range of heritabilities ($h^2 < 0.05$ to $h^2 > 0.70$)
  - few stallions with higher reliabilities in both genetic evaluations

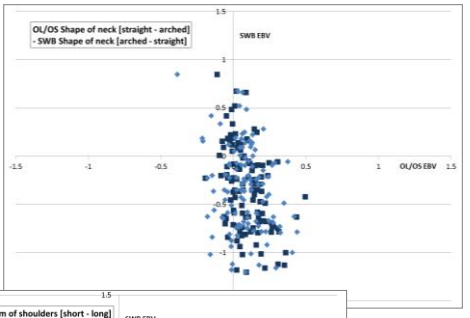
Sire group characteristics	Progeny group	No. of linearly described progeny per sire within studbook	
		OL/OS (N_{sires}=1,812)	SWB (N_{sires}=485)
All stallions: linearly described progeny in OL/OS or SWB	foals	8.8 (max. 217) / N_{sires}=931	-
	≥2.5-year-olds	3.4 (max. 148) / N_{sires}=1,268	7.0 (max. 106)
Stallion sample (N=207): linearly described progeny in OL/OS and SWB	foals	18.2 (max. 174) / N_{sires}=87	-
	≥2.5-year-olds	11.9 (max. 101) / N_{sires}=119	4.4 (max. 46)

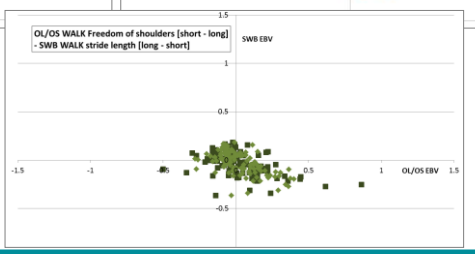
h^2 / n	0.05	0.10	0.15	0.20	0.25	0.30	0.40	0.50	0.60
5	0.06	0.11	0.16	0.21	0.25	0.29	0.36	0.42	0.47
10	0.11	0.20	0.28	0.34	0.40	0.45	0.53	0.59	0.64
15	0.16	0.28	0.37	0.44	0.50	0.55	0.63	0.68	0.73
20	0.20	0.34	0.44	0.51	0.57	0.62	0.69	0.74	0.78
25	0.24	0.39	0.49	0.57	0.63	0.67	0.74	0.78	0.82
30	0.28	0.43	0.54	0.61	0.67	0.71	0.77	0.81	0.84
35	0.31	0.47	0.58	0.65	0.70	0.74	0.80	0.83	0.86
40	0.34	0.51	0.61	0.68	0.73	0.76	0.82	0.85	0.88

Approximation of EBV reliabilities, based on heritability (h^2) and the number of informative progeny (n):
$r^2 = n / (n + k)$ with $k = (4 - h^2) / h^2$

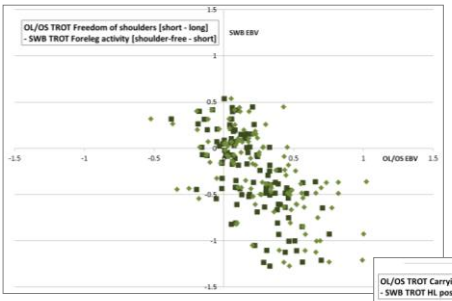
EBV correlations: conformation, walk

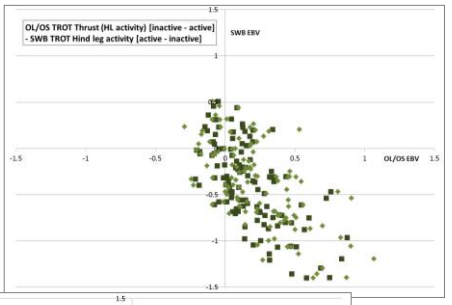


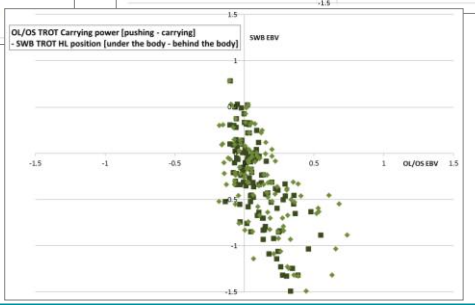




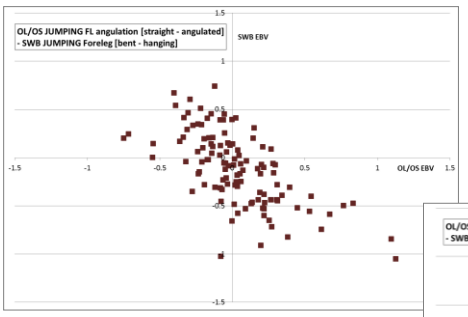
EBV correlations: trot

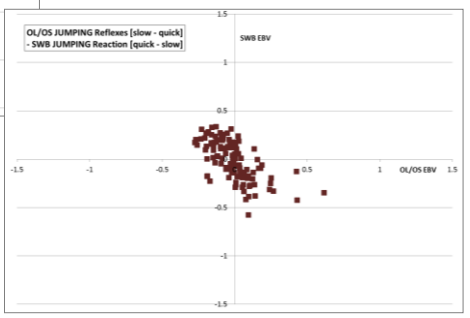






EBV correlations: jumping





Conclusions

- plausible patterns of results of genetic analyses
  - genetic parameters for linear trait groups (within and across age groups)
  - genetic correlations among linear traits within and across studbooks
    - positive impact of objectivity and clearness of trait definition → 'easy' and 'not so easy' linear traits
    - reflection of similarity of assessment and stability of linear traits
- benefits of routine breeding work using detailed linear profiles
  - characterization of individual horses
  - progeny statistics and genetic evaluation
- strong support of reasonable comparability of important linear traits across studbooks

Perspectives

- results of the comparisons of EBV for linear traits across studbooks as valuable supplements of data quality management
  - improved identification of more challenging linear traits → increased awareness as basis of improved education and training, targeted data checking
  - increased opportunities for studying the effects 'real life' data structures
- strengthening of initiatives for improved phenotyping as a whole
  - high value of early and comprehensive linear profiling (incl. foals)
  - increased motivation for continued activity in dialogue across studbooks (meetings / workshops for exchange of experiences, joint training of judges, ...)
  - promising starting point for future across-studbook collaboration in R&D and routine: linear traits as target traits in genomic applications

vit IT-Solutions for Animal Production

OLDENBURGER PFERDEZUCHTVERBAND E.V.

SWB

SLU Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Contact information
(vit, Genetic evaluation division / R&D):
PD Dr. habil. Kathrin F. Stock
E-mail: friederike.katharina.stock@vit.de
Phone: +49-4231-955 623 (Fax: -9623)
Mobile: +49-176-60931357
Info: http://www.equinephenotypes.org

Thank you!


Photo: Beelitz

promising starting point for future across-studbook collaboration
in R&D and routine: linear traits as target traits in genomic applications