MARTIN-LUTHER-UNIVERSITY HALLE-WITTENBERG
Institute of Agricultural and Nutritional Sciences, Group Animal Breeding

Relationships between estimated breeding values for claw health and production as well as functional traits in dairy cattle

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61st Annual Meeting of the European Association for Animal production, August 23rd – 27th, 2010
HERAKLION – CRETE ISLAND, GREECE, Session 09, Paper 02, Book of Abstracts p 67

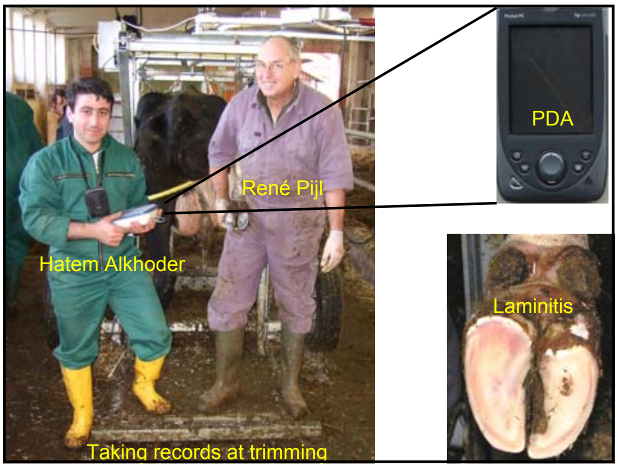
Introduction

- Claw diseases are a major issue in dairy cows
- Culling rate is over 12 % per year for claw disorder
- Costs per lameness are between 130 – 600 €
- The genetic improvement of claw health is possible
- Genetic correlations between milk yield and claw disorder were in the range of 0.06 to 0.34 (KÖNIG et al. 2005)
  ➔ antagonistic

The data base

- Records taken at hoof trimming (whole herd) by the professional hoof trimmer René Pijl during 2002 to 2010
- Diagnoses (Laminitis, Dermatitis digitalis, etc.)
  Plus:
  - Pedigree data from VIT, Verden
  - Data on milk yield, fertility, longevity from VIT
- Since the data contains new clients as well as old ones, different subsets of data can be extracted for different types of analysis

herds visited up to 17 times	166
claw trimming dates	929
cows up to 17 times treated	26.122
complete records	79.181



Incidence rates of disorders in four subsets of the data

Disorder		All data n=79,181 %	Heifers at first visit n=16,287 %	Disorder status per lactation n=40,033 %	Lifetime disorder status (If ≥ 4 observations per cow) n=8,106 %
Laminitis	LAM	36.47	39.78	47.38	76.47
Dermatitis Digitalis	DD	19.92	26.68	25.69	54.49
Dermatitis Interdigitalis	DID	11.74	7.94	17.00	43.02
White line disease	WLD	13.86	12.40	18.70	46.47
Sole ulcer	SU	7.01	5.03	9.96	26.89
Rotation	ROT	23.86	37.11	28.45	43.08
Tylom (Hyperplasia)	TYL	9.26	4.06	10.68	22.70
Thick hock	TH	2.89	2.68	4.04	10.76

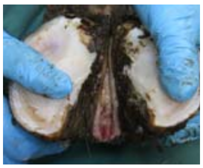
➔ This includes clinical as well as sub-clinical cases!

Rotation

Dermatitis Digitalis

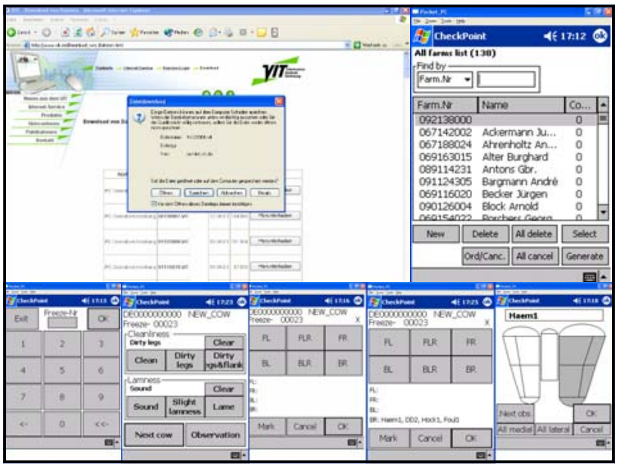
Laminitis

Dermatitis interdigitalis



White line disease

Sole ulcer



All farms list (130)

Farm.Nr

Farm.Nr	Name	Co...
092138000		0
067142002	Ackermann Ju...	0
067188024	Ahrenholtz An...	0
069163015	Alter Burghard	0
089114231	Antons Gbr.	0
091124305	Bargmann André	0
069116020	Becker Jürgen	0
090126004	Block Arnold	0

Dirty legs

Sound

DE0000000000 NEW_COW
Freeze- 00023

BR: Haem1, DD2, Hock1, Foul1

Statistical models

$PR\ (Y_{hjklm} = 1) = \theta\ (\mu + CACL(LN)_{hk} + BB_j + LN_k + DIMCL(LN)_{lk} + PU_m)$ **

$PR\ (Y_{hjklm} = 1) = \theta\ (\mu + CACL(LN)_{hk} + BB_j + LN_k + DIMCL(LN)_{lk} + AN_m + PU_m)$ *

$Y_{hjklmn} = \mu + CACL(LN)_{hk} + BB_j + LN_k + DIMCL(LN)_{lk} + AN_m + PU_m + e_{hijklmn}$ *

Y_{hjklm}, Y_{hjklmn} = trait of claw disorder (1 = positive 0 = negative)

PR = probability, θ = link function (logit and probit), μ = overall mean

$CACL(LN)_{hk}$ = fixed effect of calving age h in classes (1,..., 4) nested within lactation number k

BB_j = fixed effect of herd-visit j (1,..., 918)

LN_k = fixed effect of lactation number k (k = 1, 2, …, ≥ 6)

$DIMCL(LN)_{lk}$ = fixed effect of days in milk l (l = 1, …, 8: with classes of 50 days) nested within lactation number k

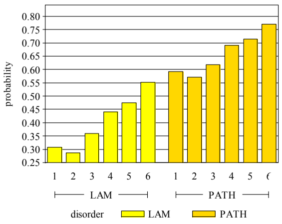
AN_m = random animal effect for animal m (additive genetic variance)

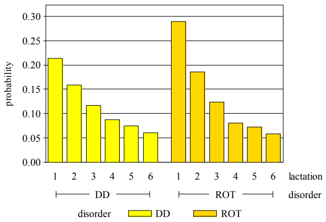
PU_m = random permanent environmental effect of animal m

e_{hjklmn} = random rest effect

* ASREML 2.0 ** proc glimmix SAS 9.1

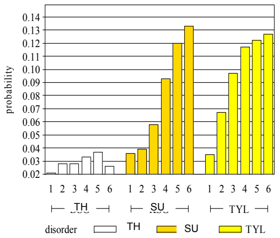
LSMEANS of incidence rate for parity (1)

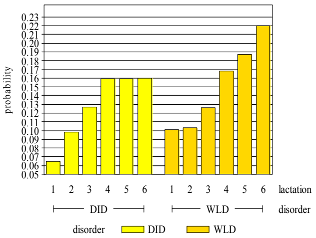




LAM = Laminitis
DD = Dermatitis Digitalis
DID = Dermatitis Interdigitalis
WLD = White Line Disease
SU = Sole ulcer
TH = Thick hocks
TYL = Tylom (Hyperplasia interdigitalis)
PATH = any disease of the above
ROT = Rotation

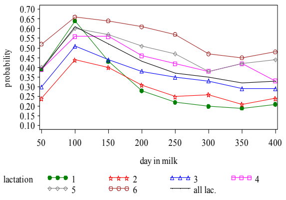
LSMEANS of incidence rate for parity (2)

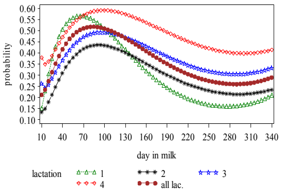


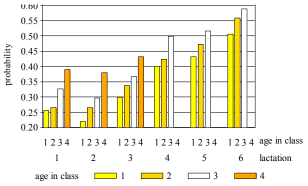


LAM = Laminitis
DD = Dermatitis Digitalis
DID = Dermatitis Interdigitalis
WLD = White Line Disease
SU = Sole ulcer
TH = Thick hocks
TYL = Tylom (Hyperplasia interdigitalis)
PATH = any disease of the above
ROT = Rotation

Laminitis: LSMEANS of incidence rate for stage of lactation and age at calving







Incidence rates for disorders in the respective “best“ and “worst“ herds

Herd	LAM	DD	DID	WLD	SU	Observations N	Visits N	Ave. milk yield (kg)
A	21.74^{b}	16.29	15.97	11.45	7.35	637	11	8684
B	59.27^{w}	15.83	16.41	13.51	10.18	375	6	8971
C	41.02	0.20^{b}	6.80	10.72	9.63	424	9	9056
D	37.23	37.48^{w}	23.29	15.98	12.51	666	9	8515
E	37.14	2.52	2.26^{b}	11.31	6.86	602	9	9156
F	41.96	17.93	34.24^{w}	10.76	9.90	718	11	8657
G	36.63	15.07	22.32	6.09^{b}	8.37	571	11	8425
H	41.81	21.54	15.63	23.19^{w}	7.23	995	10	8840
I	35.86	3.76	11.59	12.65	3.35^{b}	664	11	8704
J	47.83	23.73	24.67	14.44	17.23^{w}	498	7	8627

b = “best“ herd
w = “worst“ herd

Estimates of heritabilities and proportion of permanent environmental effect in three subsets of the data

	Heritability estimates					Ratio of permanent environ. effect			
	All parities			Parity1	Par. ≥ 2	All parities			Par. ≥ 2
	Linear	Logit	Probit	Logit	Logit	Linear	Logit	Probit	Logit
LAM	0.13	0.17	0.20	0.19	0.16	0.14	0.13	0.13	0.15
DD	0.06	0.09	0.09	0.07	0.10	0.11	0.11	0.11	0.10
DID	0.08	0.19	0.20	0.17	0.19	0.05	0.06	0.04	0.06
WLD	0.06	0.12	0.12	0.10	0.12	0.11	0.12	0.10	0.13
SU	0.05	0.14	0.13	0.22	0.12	0.09	0.11	0.08	0.14
ROT	0.18	0.21	0.23	0.27	0.21	0.27	0.19	0.19	0.19
TYL	0.15	0.30	0.30	0.32	0.30	0.29	0.23	0.21	0.22
TH	0.04	0.12	0.10	0.08	0.11	0.19	0.23	0.15	0.23
SE	0.006-0.008	0.010-0.028	0.011-0.023	0.011-0.051	0.016-0.035	0.005-0.008	0.010-0.028	0.011-0.023	0.015-0.035

Estimates of heritabilities; genetic correlations (below diagonal)

	LAM	DD	DID	WLD	SU	ROT	TYL	TH
LAM	**0.133** *(0.009)*							
DD	-0.05 *(0.061)*	**0.057** *(0.006)*						
DID	0.22 *(0.051)*	0.34 *(0.063)*	**0.075** *(0.006)*					
WLD	0.33 *(0.057)*	-0.12 *(0.072)*	0.12 *(0.065)*	**0.062** *(0.006)*				
SU	0.48 *(0.055)*	0.01 *(0.078)*	0.20 *(0.068)*	0.16 *(0.073)*	**0.052** *(0.006)*			
ROT	-0.22 *(0.059)*	0.09 *(0.071)*	-0.20 *(0.068)*	-0.25 *(0.048)*	-0.19 *(0.068)*	**0.143** *(0.026)*		
TYL	0.29 *(0.067)*	0.04 *(0.083)*	0.47 *(0.069)*	-0.05 *(0.065)*	0.27 *(0.077)*	-0.22 *(0.058)*	**0.167** *(0.019)*	
TH	0.39 *(0.11)*	-0.05 *(0.13)*	-0.14 *(0.12)*	0.20 *(0.11)*	0.34 *(0.13)*	-0.07 *(0.10)*	0.32 *(0.11)*	**0.075** *(0.007)*

Estimates of heritabilities; genetic correlations (below diagonal) in comparison with correlations between EBV for sires with more than four daughters and an accuracy ≥ 80 % (above diagonal)

	LAM	DD	DID	WLD	SU	ROT	TYL	TH
LAM	**0.133** *(0.009)*	0.10 63‡	0.35* 112‡	0.20* 89‡	0.60* 56‡	-0.30* 139‡	0.02 100‡	0.06 37‡
DD	-0.05 *(0.061)*	**0.057** *(0.006)*	0.38* 61‡	-0.11 61‡	0.29* 45‡	-0.17 63‡	0.36* 60‡	0.27 32‡
DID	0.22 *(0.051)*	0.34 *(0.063)*	**0.075** *(0.006)*	0.22 87‡	0.28* 56‡	-0.19* 102‡	0.41* 88‡	-0.01 34‡
WLD	0.33 *(0.057)*	-0.12 *(0,072)*	0.12 *(0.065)*	**0.062** *(0.006)*	0.11 55‡	-0.14 87‡	-0.07 79‡	-0.08 34‡
SU	0.48 *(0.055)*	0.01 *(0.078)*	0.20 *(0.068)*	0.16 *(0.073)*	**0.052** *(0.006)*	-0.29* 56‡	0.12 52‡	0.23 28‡
ROT	-0.22 *(0.059)*	0.09 *(0.071)*	-0.20 *(0.068)*	-0.25 *(0.048)*	-0.19 *(0.068)*	**0.143** *(0.026)*	-0.30* 94‡	0.23 37‡
TYL	0.29 *(0.067)*	0.04 *(0.083)*	0.47 *(0.069)*	-0.05 *(0.065)*	0.27 *(0.077)*	-0.22 *(0.058)*	**0.167** *(0.019)*	0.26 37‡
TH	0.39 *(0.11)*	-0.05 *(0.13)*	-0.14 *(0.12)*	0.20 *(0.11)*	0.34 *(0.13)*	-0.07 *(0.10)*	0.32 *(0.11)*	**0.075** *(0.007)*

‡ = number of sires   * = significant

Number of sons within quartiles of high / low EBV for claw disease for five sires of sons

(Ns = number of sons per sire-of-sons, No = number of observations, Ne = number of grand dghts)

trait	quartile	S Ns=12 Ne=322 No=1058	A Ns=17 Ne=615 No=1058	P Ns=15 Ne=628 No=2201	B Ns=28 Ne=1193 No=4431	L Ns=14 Ne=871 No=3177
LAM	High	7*	11*	12*	16*	2
	Low	3	4	2	7	11*
DD	High	2	5	14*	3	13*
	Low	7*	10*	1	23*	.
DID	High	4	6	12*	11	5
	Low	7*	8*	2	11	7
WLD	High	6	4	4	7	2
	Low	4	9*	11*	12	10*
SU	High	9*	8*	15*	17*	1
	Low	2	6	.	9	12*

High = High resistance / low incidence

Low = Low resistance / high incidence *indicates the quartile of the sire

Genetic correlations between official EBV for feet & leg traits and own EBV for resistance to claw disorder for two subsets of sires

(Gr. 1 accuracy ≥ 70% and Gr. 2 accuracy ≥ 85%)

Trait	Gr.	LAM	DD	DID	WLD	SU	ROT	TYL	TH
Locomotion	1	0.28*	0.13	0.17*	0.11	0.30*	-0.09	0.24*	0.08
	2	0.43*	0.23	0.02	-0.11	0.42*	-0.17	0.16	0.05
Feet & Legs (Final Score)	1	0.21*	0.01	0.12	0.11	0.29*	-0.08	0.29*	0.12
	2	0.25*	-0.08	-0.03	-0.13	0.30*	-0.14	0.20	0.15
Rear-legs-rear-view	1	0.17*	-0.11	0.02	0.05	0.22	-0.03	0.14*	0.04
	2	0.18*	-0.25	0.09	-0.04	0.27	-0.13	0.15	0.14
Rear-legs-side-view	1	-0.01	0.01	0.01	0.13	-0.13	-0.07	-0.24*	-0.10
	2	-0.12	0.01	0.14	0.10	-0.31	-0.13	-0.06	-0.04
Foot angle	1	-0.02	0.14	-0.04	-0.18*	0.03	0.04	0.29*	0.06
	2	-0.12	0.16	-0.27*	-0.34*	-0.07	0.20*	0.16	-0.02
Hock quality	1	0.14	0.00	0.07	0.26*	0.19*	-0.17*	0.11	0.09
	2	0.11	-0.06	0.11	0.06	0.17	-0.34*	0.12	0.23
Number of sires	1	253	146	189	163	130	231	208	101
	2	111	39	65	54	32	96	76	28

König and Swalve (2006); model calculation: Selection for conformation is not enough!

* = significant

Genetic correlations between official EBV for trait complexes and own EBV for resistance to claw disorders (accuracy ≥ 0.85)

	LAM	DD	DID	WLD	SU	ROT	TYL	TH
Conformation	0.22*	-0.18	0.07	-0.07	0.26	-0.16	0.00	0.14
Total Merit	0.37*	0.11	0.15	-0.09	-0.11	-0.28*	-0.07	0.24
Dairy production	0.09	0.22	-0.00	-0.16	-0.10	-0.13	-0.03	0.09
Longevity	0.51*	0.06	0.27*	0.15	-0.03	-0.30*	-0.09	0.27
Fertility	0.34*	-0.14	0.07	0.03	-0.08	-0.17	-0.13	0.17
Udder health	0.18	-0.20	0.15	0.02	-0.36	-0.16	-0.05	0.02
Number of sires	111	39	65	54	32	96	76	28

* = significant

Strategies to estimate the relationship between milk production traits and claw disorders

S1* Correlations between own sire EBV for claw disorders with national EBV for production traits

S2* Own sire EBV for production from RRM and own sire EBV for claw disorders; 1st lactations only

S3* Direct estimation of genetic correlations between claw disorders and 305-d production; 1st lactations only

S4* Direct estimation of genetic correlations between claw disorders and milk at time of trimming; first three lactations

S5** Estimation of the regression of claw disorders status on 305-d milk yield

* ASREML 2.0

** proc glimmix SAS 9.1

Model for EBV for production traits

$$y_{ijkl}= HTD_i + \Sigma\ c_{jm}.f_{jm} + \Sigma\ b_{kn}.a_{kn} + \Sigma\ b_{kn}.p_{kn} + e_{ijkl}$$

y_{ijkl} = milk production trait on test day n in th or animal k

HTD_i = fixed effect of Herd-Test-Day

f_{jm} = regression coefficien of calving year- 1,..,472)

c_{jm} = m-th

a_{kn} and p_{kn} 1,..,17295)

b_{kn} der 2) of

e_{ijlkl} = 56987)

S2

- Random Regression Animal Model
- Legendre Polynomials (order 2)

Multivariate sire model for lactation milk yield and disorders - 1^{st} lactations only

PR (Y_{ijkm} =1) = θ (μ +$CACL_i$ + BB_j + $DIMCL_k$ + S_m)
M_{ijklmn} = μ + $CACL_i$ + BET_j + $CICL_k$ + YS_l + S_m + e_{ijklmn}

Y_{ijkm} = trait of claw disorder (1 = positive 0 = negative)
PR = probability, θ = link function (logit an
$CACL_i$ = fixed effect of calving age
BB_j = fixed effect of he
$DIMCL_l$ = fixed
M_{ijklmn} = tra
BET_j = fixe
Ys_l = fixed
$CICL_k$ = fixed e … classes
S_m = random … (1,…,425)
e_{ijklmn} = random r … (1,…,10486)

S3

- Multivariate sire model
  - Threshold model for disorders
  - Linear model for production
- lactation milk yield
- 1^{st} lactations only

Bivariate animal model for milk yield at trimming and disorders - First three lactations

PR (Y_{hjklm} =1) = θ (μ +$CACL(LN)_{hk}$ + BB_j + LN_k+ $DIMCL(LN)_{lk}$ + AN_m + PU_m)

$M_{hijklmn}$ = BTi + Σ $c_{jm}.f_{jm}$ + LN_k + $CACL(LN)_{hk}$ + $CICL(LN)_{lk}$ + AN … + $e_{hijklmn}$

The model for claw disorder is the same as the first

M_{hijklm} = test day production … cells)
LN_k = fixed effect
BT_i = fix
f_{jm}
… k
c_{jm} … lactation curve
$CICL(LN)_{lk}$ … (1,..., 5) nested within
AN_m = … animal m (1,…, 29384)
PU_m = ra … manent environmental effect of animal m (1,…,7267)
$e_{hijklmn}$ = random residual effect (1,…, 24123)

S4

- Bivariate animal model
  - Threshold model for disorders
  - Linear model for production
- Test day production at time of trimming
- First three lactations

Regression models with and without nesting of stage-of-lactation-effect – GLIMMIX analysis

PR (y_{hjklm} =1) = θ (μ +$CACL(LN)_{hk}$ + BB_j + LN_k+ $DIMCL(LN)_{lk}$ + b1M + b2M^2 + PU_m)

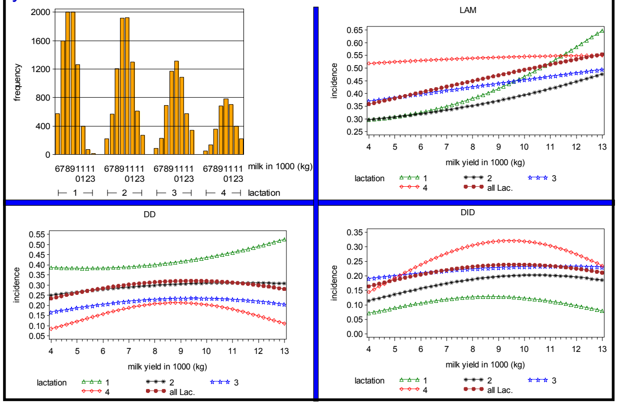
PR (y_{hjklm} =1) = θ (μ +$CACL(LN)_{hk}$ + BB_j + LN_k+ $DIMCL(LN)_{lk}$ + b1$M(LN)_k$ + b2$M^2(LN)_k$ + PU_m)

Y_{hjklm} = trait of claw disorder (1 = positive 0 = negative)
PR = probability, θ = link function (logit and pro … ean
$CACL(LN)_{hk}$ = fixed effect of calving age h in … lactation number k
BB_j = fixed effect of her
LN_k = fixed eff
$DIMCL(LN)_{lk}$ =
PU_m = ra … mal m (1,…,8991)
M = mi …)
b1, b2 = line … coefficient of claw disorder on milk

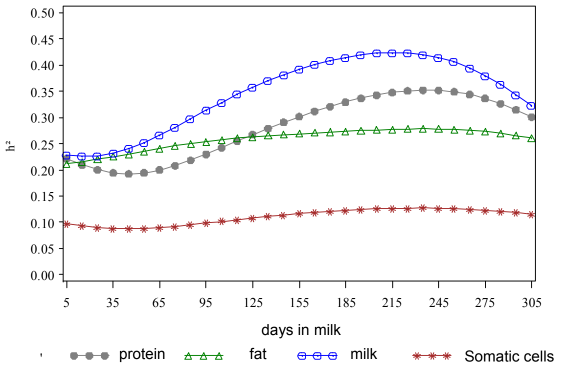
S5

- Two separate regression models
  - focus on regressions and fixed effects
  - cow effect added as random effect
  - cow effect includes genetic and p.e.
  - cow effect accounts for repetitions
- All lactations

Phenotypic relationships between LAM, DD and DID and milk yield – S5 - GLIMMIX



Estimates of heritabilities for milk production trait using the RRM in the first lactations – S2 (production part)



Genetic correlation between claw disorders and production traits for 1st lactation only

(for the correlation between EBV, there are 52 sires ≥ 30 daughters in the first lactation and ≥ 30 daughters in the other lactations)

Here: High EBV for disorders ➔ more disorders!

		LAM	DD	DID	WLD	SU
With national EBV - **S1**	milk	0.29*	-0.09	0.21	0.16	0.06
	protein	0.17	-0.14	0.21	0.19	0.08
	fat	0.10	-0.16	0.16	0.15	-0.06
	protein %	- 0.33*	-0.06	-0.08	0.00	0.02
	fat %	-0.22	-0.03	-0.09	-0.04	-0.08
	scs	0.10	-0.12	0.21	0.22	0.19
With our EBV - **S2**	milk	0.21	-0.11	0.12	0.03	0.07
	protein	0.11	-0.18	0.12	0.05	0.08
	fat	0.09	-0.24	0.12	0.16	0.02
	protein %	-0.26	-0.13	-0.02	0.05	0.01
	fat %	-0.16	-0.08	-0.03	0.10	-0.04
	scs	0.08	-0.14	0.16	0.17	0.10
r_g **S 3**	milk	0.35	0.07	0.19	0.28	0.20
	protein	0.28	0.07	0.21	0.26	0.34
	fat	0.25	-0.32	0.03	0.10	0.48

* = significant

🟩 Genetic correlations from multvariate analyses for 1st lactation
SE are between 0.10 and 0.15

Genetic correlation between claw disorders and production traits for first three lactations – production at time of trimming

(for the correlation between EBV, there are 52 sires ≥ 30 daughters in the first lactation and ≥ 30 daughters in the other lactations)

Here: High EBV for disorders ➔ more disorders!

		LAM	DD	DID	WLD	SU
With VIT EBV – **S1**	milk	0.12	-0.17	0.04	-0.09	-0.01
	protein	-0.02	-0.30	-0.03	-0.06	-0.08
	fat	-0.15	-0.22	-0.05	-0.21	-0.25
	protein %	-0.26	-0.14	-0.10	0.09	-0.09
	fat %	-0.22	0.00	-0.05	-0.06	-0.15
	scs	0.00	-0.03	0.23	0.20	-0.15
r_g **S4**	milk	0.21	-0.04	0.03	0.17	0.06
	protein	0.15	-0.12	-0.02	0.18	0.02
	fat	0.06	-0.13	-0.07	0.15	0.12
	scs	0.08	-0.02	0.20	0.07	-0.25

* = significant

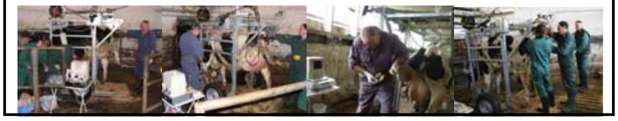
🟩 Genetic correlations from bivariate analyses in the first three lac.
SE are between 0.07 and 0.13

Conclusions (1)

- Recording data at time of hoof trimming is very important to provide a database for genetic improvement of hoof health
- Incidence of claw diseases is high (sub-clinical cases included)
- Laminitis is of utmost importance
- Claw diseases partly have a genetic background; this can nicely be demonstrated when comparing sire families
- the estimated heritabilities for claw disorders in this study show that a substantial genetic variation exists; genetic improvements are possible!

Conclusions (2)

- genetic correlations with milk yield were marginal
- genetic improvement of hoof health will not have negative effects on milk yield
- moderate correlations between conformation scores and claw disorders may help somewhat
- but if we wish to fight claw diseases genetically, we have to do recording of the diseases (see SWE + NL)
- genetic improvement of hoof health is ***absolutely essential***



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Thank you for your attention!