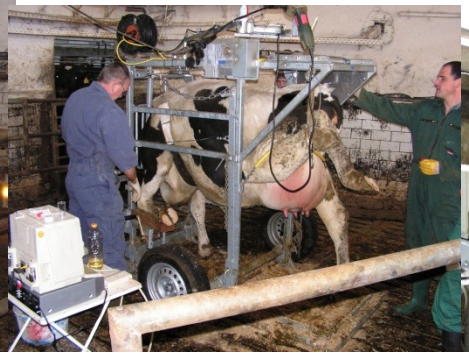
Martin-Luther-University Halle-Wittenberg
Institute of Agricultural and Nutritional Sciences (IANS)
Animal Breeding

Hoof health - index values and collecting data

Hermann H. Swalve

World Conference
World Holstein Friesian Federation
Puy du Fou, France
November 21/22, 2023

Overview

- Claw health / claw diseases
- Is it worthwhile to have genetic evaluations on claw (hoof) diseases?
- Problems encountered when working with claw health data
- Lessons learnt in own projects on claw/hoof diseases
- Survey on genetic evaluations in selected countries
- Conclusions

Claw diseases from a genetic perspective

- This is not only a question on the magnitude of the heritability
  - ➔ quantitative genetic-statistical model
  - ➔ many genes can contribute
  - ➔ but also a question of the magnitude of variation

- Quite clearly: environmental factors and genetic factors play a role

- Genetic selection has a sustainable, accumulative effect

- Within a given range, the magnitude of the heritability and the genetic variation can be enlarged by precision when collecting phenotypes

Selection response:

$\Delta G = i * h^2 * \sigma_P$

or

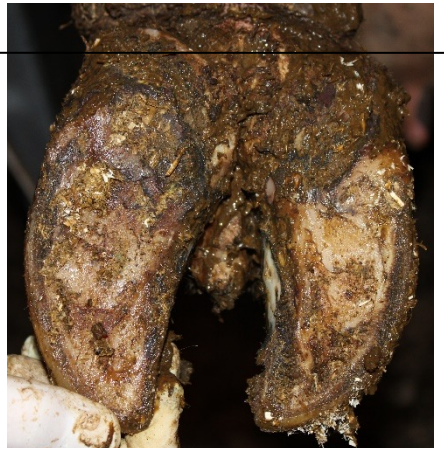
$\Delta G = i * r_{TI} * \sigma_A$

➔ Heritability and variation are important!

Problems encountered when working on claw health

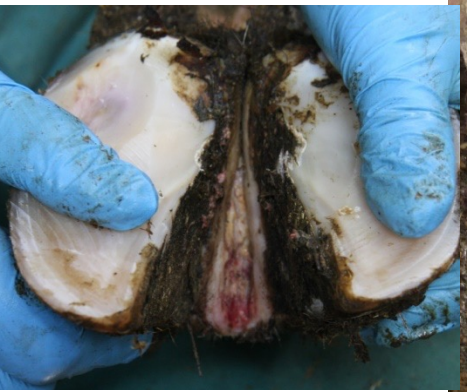
Topic / Problem	Remarks
Who collects data?	**Farmers, veterinarians, hoof trimmers, or a mixture of sources**
Definition of disease	(Even among vets quite often unclear!) **What is a clear expression of a specific disease?** **Also unclear: clinical / sub-clinical**
Definition of contemporary groups	**Entire herds are inspected vs. individual cows are treated**
Editing the data	**Some contemporary groups may be incomplete / missing / inaccurate / non-informative**

Some claw diseases



Interdigital Hyperplasia

Interdigital Dermatitis



Digital Dermatitis (Mortellaro‘s Disease)

Sole Hemorrhage (Laminitis)

White Line Defect

Sole Ulcer

Projects on claw diseases

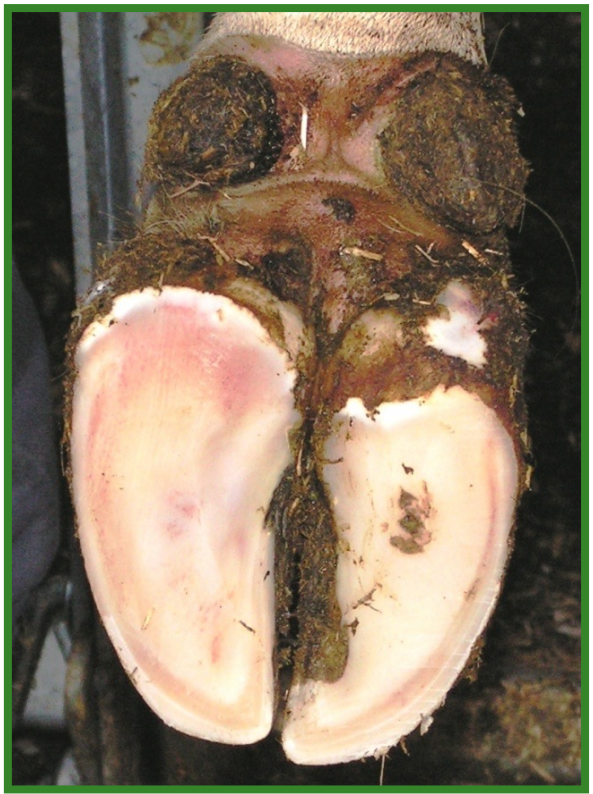
- can help to shed light on problems that exist in large field data sets like national databases
- only after diving deep into the subject conclusions for edits of large data sets can be drawn
- some examples from own work …

Study on sole hemorrhage (laminitis)

- Non-infectious
- Mostly caused by sudden feeding of easy soluble carbohydrates
- Toxins destroy micro-circulation of blood in limbs

Here:

- Scored as 1/0
- Even very mild cases scored = 1
  (large debates about the scoring …)



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A study based on records taken at time of hoof trimming reveals a strong association between the IQ motif-containing GTPase-activating protein 1 (*IQGAP1*) gene and sole hemorrhage in Holstein cattle

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Prevalences in sole hemorrhage study by cohort

- N = 1,962 cows
- 7 herds
- 2 – 5 visits/herd
- Some cohorts exhibt extreme frequencies
- First analysis: 1,174 cows

➔ Extreme cohorts left out

- 2nd analysis: Full data

Cohort	# of cows	Percentage of full data (%)	Prevalence in cohort
A_1	75	3.82	0.39
A_2	47	2.40	0.66
B_1	92	4.69	0.30
B_2	80	4.08	0.50
B_3	79	4.03	0.92
B_4	69	3.52	0.71
C_1	87	4.43	0.55
C_2	73	3.72	0.53
C_3	70	3.57	0.66
C_4	165	8.41	0.68
D_1	114	5.81	0.49
D_2	80	4.08	0.25
D_3	93	4.74	0.54
D_4	84	4.28	0.73
E_1	154	7.85	0.55
E_2	31	1.58	0.61
F_1	40	2.04	0.43
F_2	82	4.18	0.35
F_3	70	3.57	0.43
F_4	65	3.31	0.40
F_5	82	4.18	0.70
G_1	75	3.82	0.87
G_2	80	4.08	0.59
G_3	75	3.82	0.89

Sole hemorrhage / Laminitis: One QTL with large effect found

Result:

- (intronic) SNP within IQGAP1 = Ras GTPase-activating-like protein (BTA 21)
  - ➔ tolerance, not resistance
- IQGAP1 is responsible for neo-vascularization in studies on humans and mice

Probability / Genotype	Probability for status = 1	
	Full data	Initial data
P(y = 1| AA)	.506	.369
P(y = 1| AG)	.578	.519
P(y = 1| GG)	.615	.559
Difference P(GG) – P(AA)	10.9**	19.0***

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Digital Dermatitis (BDD / Mortellaro‘s disease)

Bovine Digital Dermatitis (BDD)

= Hairy heel warts

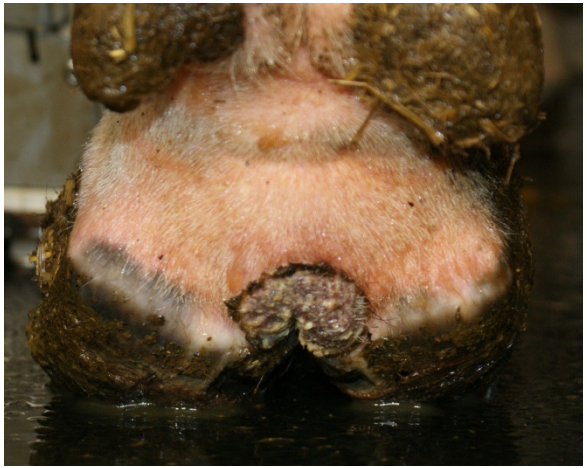
- Large abundance in many herds

- **Drastic difference in prevalence among herds**
- **“Sudden“ outbreaks of the disease may occur**
- **Infectious (Bacteria ➔Treponema)**

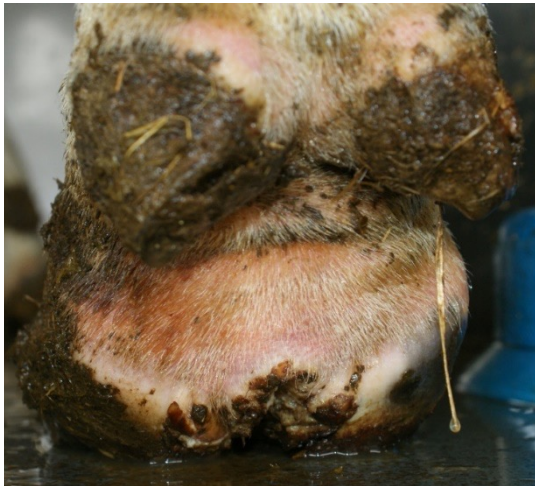
  ➔ Related diseases in humans (e.g. Lyme Disease)

Scoring of BDD using the M-scheme

M2. classic case



M2. Herd with footbath

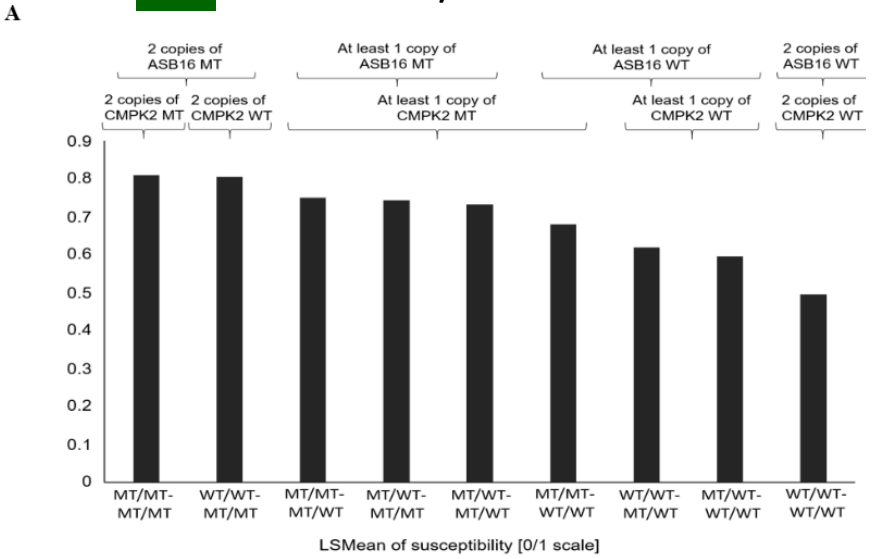


M4. “encapsulated“, hyperkeratosis

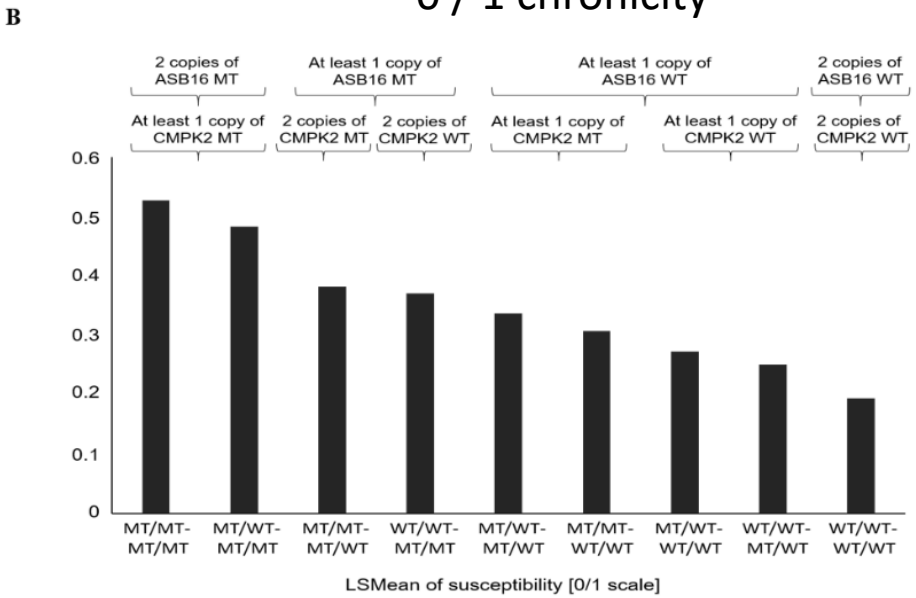
Scoring visit of Halle team in 1,200 cow dairy with robotic rotary parlour (56 Robots)

Functional mutations on BTA 11 (CMPK2) and BTA 19 (ASB16)

0 / 1 affected



0 / 1 chronicity



Functional Variants Associated With *CMPK2* and in *ASB16* Influence Bovine Digital Dermatitis

*Diana Oelschlaegel[1], Monika Wensch-Dorendorf[1], Grit Kopke[1], Roswitha Jungnickel[1], Benno Waurich[1], Frank Rosner[1], Dörte Döpfer[2], Bertram Brenig[3] and Hermann H. Swalve[1]**

frontiers | Frontiers in Genetics

ORIGINAL RESEARCH
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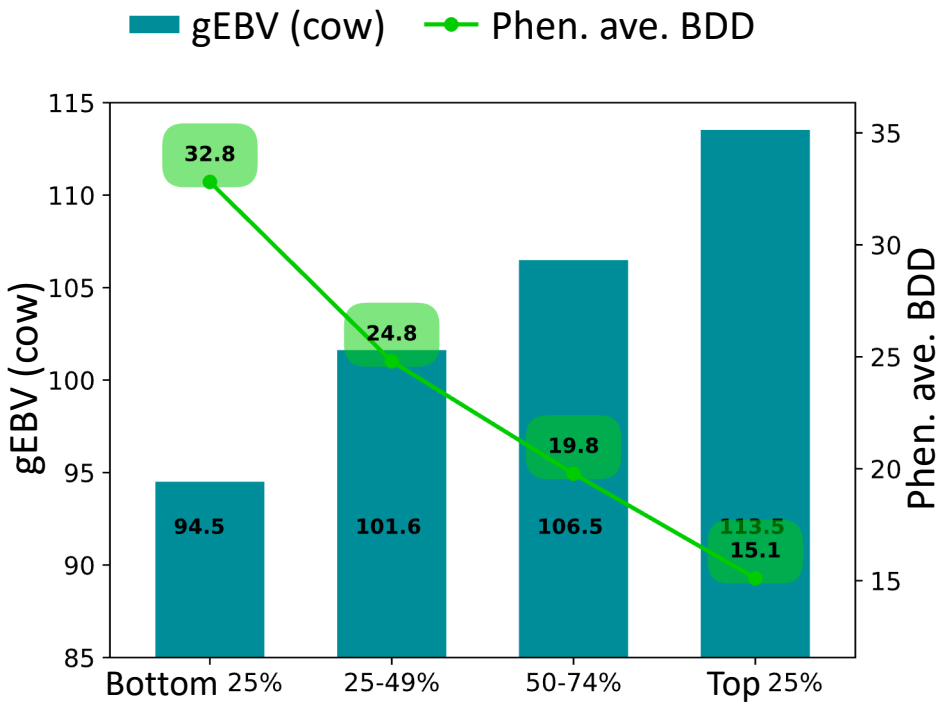
Validation of genomic breeding values for BDD

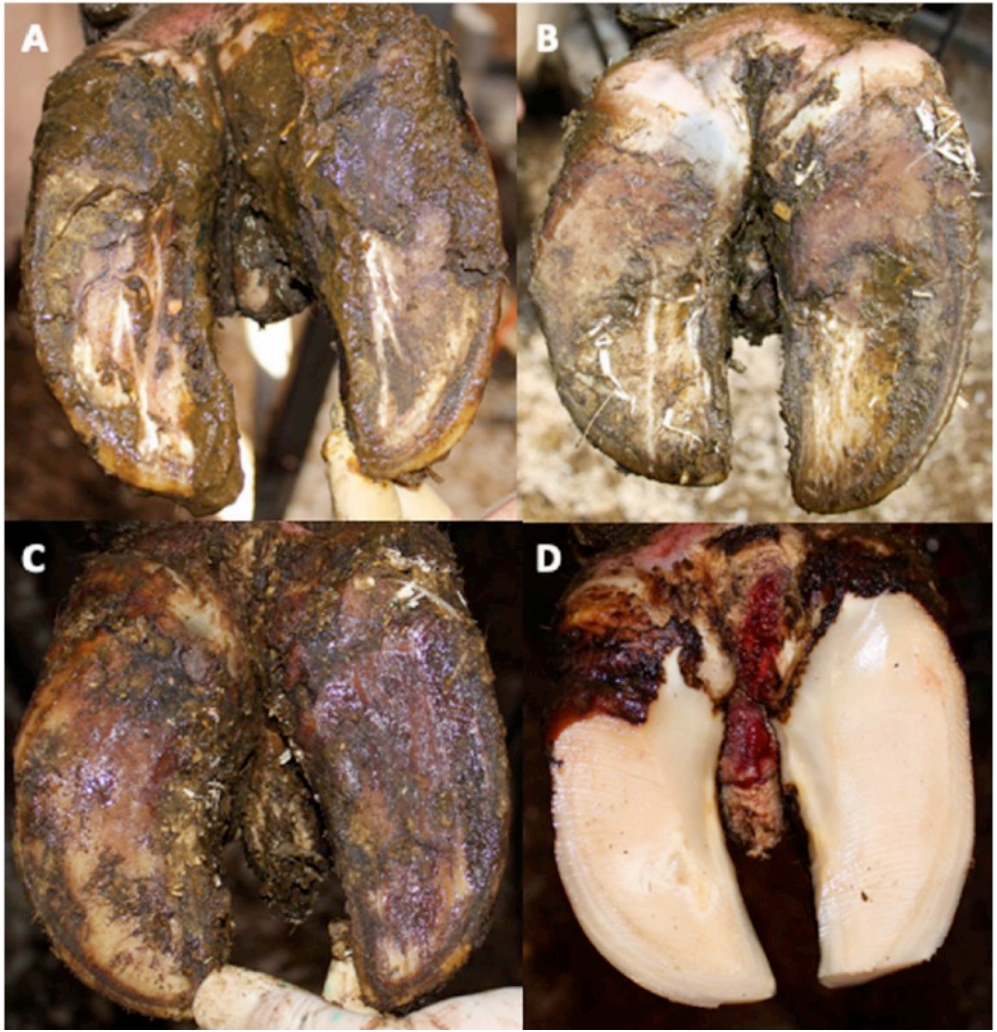
gEBV class of sire (1 = niedrig 5 = hoch)	gEBV	Parity 1 (n = 31,304)	2 (n = 23,286)	3 (n = 14,801)
1	< 85	0.21^{a}	0.20^{a}	0.17^{a}
2	86 – 95	0.20^{a}	0.18^{a}	0.15^{ab}
3	96 – 105	0.17^{b}	0.16^{b}	0.13^{bc}
4	106 – 115	0.15^{c}	0.15^{b}	0.13^{bc}
5	> 115	0.13^{c}	0.13^{b}	0.10^{c}

Validation of own gEBV for BDD from reference sample of n = 5,040 M-stage scored cows in an independent sample of classical hoof trimmer data.
Shown are LSMEANS for prevalence for daughters by class of sire‘s gEBV



Validation of official gEBV for cows in independent sample of 39,133 cows (VIT data)
(Genotyping and gEBV as calves / Phenotypes 2 years later)

Interdigital Hyperplasia / Tyloma



When did the cows exhibit IH?

- This table: Results from pilot study; only cows trimmed regularly from parity 1 onwards
- **Only cows that developed tyloma**
- Shown: Parity of first observation

Parity	≥ 1 Tyloma		2 Tyloma	
	N	%	N	%
01	78	56.9	39	44.3
02	33	24.1	22	25.0
03	15	11.0	13	14.8
04	8	5.8	9	10.2
05	2	1.5	4	4.6
06	1	0.7	1	1.1
Total	137	100.0	88	100.0

➔ Data from 1st parity only is always incomplete!

➔ Most cows acquire the condition by parity 4

➔ Results for parities > 1 are incomplete due to cows leaving herd

Missense variant in ROR2 gene on BTA08 (SNP rs377953295)
Effect on interdigital hyperplasia (Type A: one side / Type B: both sides)

Our approach

- Found herd with ≈ 50 % prevalence
- Case-control study
- SNP on BTA08

TABLE 3 | Statistical evaluation of SNP rs377953295 (exon 1) as causative variant for type A and type B interdigital hyperplasia (IH).

	Type A IH[a]			Type B IH[b]		
	T_T	A_T	A_A	T_T	A_T	A_A
IHF[c]	21	4	0	35	6	0
IHA[d]	38	24	7	24	22	7
Total	59	28	7	59	28	7
F-statistic	7.16			16.94		
P-values (χ^2, FET[e])	0.0279, 0.0026			0.0002, < 0.0001		

a) In type A IH: IHF, no IH; IHA, at least one IH at one hind leg.
b) In type B IH: IHF, no IH or only one IH; IHA, IH at both hind legs.
c) IHF: Interdigital hyperplasia free.
d) IHA: Interdigital hyperplasia affected.
e) FET: Fisher's exact test.

Interdigital Hyperplasia in Holstein Cattle Is Associated With a Missense Mutation in the Signal Peptide Region of the Tyrosine-Protein Kinase Transmembrane Receptor Gene

Xuying Zhang[1], Hermann H. Swalve[2], René Pijl[3], Frank Rosner[2], Monika Wensch-Dorendorf[2] and Bertram Brenig[1]

frontiers in Genetics
ORIGINAL RESEARCH
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Lessons learnt from „small“projects

- **Sole Hemorrhage study:**
  non-informative cohorts may affect estimation of SNP-effects

- **BDD study:**
  high precision of M-stage scoring enables gEBV from small reference sample with good results in validation study and high estimates for h^2 (0.33)

- **Interdigital Hyperplasia study:**
  Very difficult trait; avoid to restrict data to 1st parity; the “masked“ heritability is indeed large!

- Genomic selection for improved hoof health in general works amazingly well!

The survey questions

1. Traditional genetic evaluation for hoof health – yes/no
2. Genomic evaluation for hoof health – yes/no
3. Reliabilities for a ‘typical‘ gEBV (young bull w/out daughters) ?
4. Which traits are evaluated?
5. Genetic parameters?
6. Specific supervision programs implemented for producers/vets/ hoof trimmers?
7. Which traits are published?
8. How many records in database as of 2023?
9. Hoof health included in TMI? Weight?

The survey – countries asked to complete the survey and responses

- Countries to which the survey was sent:
  AUS, CAN, DFS, DEU, ESP, FRA, ITA, NLD, NZL, GBR, USA

- Countries responding: All

The survey: More details

	AUS /NZL	CAN	DFS	DEU	ESP	FRA	GBR	ITA	NLD	USA
Traditional genetic evaluation?	**no**	**no** (One-step genomic)	**no**	**yes**	**yes**	**in 2023**	**yes** lameness advantage plus DD	**no, Indirect** (Conf. traits)	**yes**	**no**
Genomic evaluation	**no**	**yes** MT-ssGBLUP	**yes** MT-ssGBLUP	**yes**	**yes**	**yes,** in 2023 ssGBLUP	**yes** lameness advantage plus DD	**no, indirect**	**yes**	**no, but plans**
Traits evaluated (details next slide)	-	**8 traits**	**7 x 3 traits**	**6 traits**	**15** (now) **(6)** (in 2011)	**7**	**2 (5)** Lame, DD, loc, F&L, bone q.	**15** (ICAR atlas, simplified)	**6 x 3**	**5 – 6** (mobility)
Traits published	-	**all,** plus hoof health index	**all,** plus Claw health index	Claw health index plus DD	Claw health index	**all,** plus inf./n. inf. plus index	**2**	Cuurently: Feet&Legs index	**6** plus Claw health index	
Hoof health in TMI	-	Incl. in durability / 2.7 %	**5 %**	20 % in health index; TMI 3.6 %	Claw health Index in ICO 3%	planned	**6%**	Data collection, Work in progress	**8 %**	

The survey: More details for some countries

	CAN	DFS	DEU	ESP	NLD	FRA	ITA	GBR
Specific supervision when recording ?	Hoof trimmers / DairyComp data	yes, data also in management recording programs	yes, regionally organized / ICAR standard / Training programs	yes, organized with hoof trimming companies	yes, DigiKlauw software	no, but trained hoof trimmers only	yes, with hoof trimmers; customized software	-
No. of records in database	> 700,000 records from ≈ 240,000 cows	First lactation: > 3 Mill. records > 1.7 Mill cows Plus later lactations	2.3 Mill. events / 973,000 lact. / 555,000 cows	1.5 Mill events / 500,000 cows	Around 2.7 Mill. records per disease	522,180 phenotypes / 292,718 cows	10,097 phenot., 7,807 cows and heifers (update nov. 2023)	1.1 Mill. for DD
Individual diseases	DD, HHE, SH, DID, IH, TOE, SU, WLD	SU, SH, HHE, DD/DID, IH, DS/WLD, CS	DD, SU, IH, PHL, WLD, LAM(SH)	Originally: SU, DD, WLD, CDW, PHL, IH Plus additional 9 new traits	SH, DD, DID, SU, IH, WLD	SH(2), DD, SU, IH, WLD, HHE	D, DD, F, HHE, SH, EMO, L, UC, WLD, IH, plus 5 other foot traits using ICAR atlas	

The survey: Heritabilities estimated / used in genetic evaluation

	DFS			NLD			CAN	ESP	FRA	DEU
	Parity			Parity						
	1	2	3+	1	2	3+				
Sole hemorrhage	.02	.02	.02	.05	.05	.05	.03	-	.04/.03	.03
Digital Dermatitis	.05	.05	.04	.11	.12	.10	.09	.06	.08	.12
Interdig. Dermat.	-	-	-	.05	.08	.07	.04	-	-	-
Sole ulcer	.04	.05	.05	.03	.05	.07	.05	.06	.06	.11
Interdig. Hyperpl.	.05	.07	.08	.03	.07	.11	.06	.13	.10	.11
White Line Defect	.01	.02	.02	.05	.05	.07	.04	.02	.05	.06
Cork Screw	.01	.01	<.01	-	-	-	-	-	-	-
Heel Horn Erosion	-	-	-	-	-	-	.05	-	.04	-
Toe Ulcer	-	-	-	-	-	-	.05	-	-	-
Interdig. Phlegm.	-	-	-	-	-	-	-	.01	-	.09
Conc. Dorsal Wall	-	-	-	-	-	-	-	.02	-	-

(GBR: h^2 DD = 0.012)

The survey: Things to discuss, uncertainties, shortcomings

- **What is ‘a record‘?**
  - A recording of a a single disease event? What is a single event?
  - A record per lactation? Which lactations are included?
  - Is a healthy cow in a herd that recorded ‘events‘ equal to a record disease=no?
  - Ideally: All records for genetic evaluation origin from hoof trimming of entire herd
    ➔ information as in milk recording schemes ➔ all cows present at day x
    ➔ may be healthy, or affected by a disease
  - But: Treating a cow for a disease individually apart from regular trimming also is valuable information

- **How does the trait ‘lameness‘ compare to record individual diseases? – is it less valuable?**
- **How to calculate an effective contribution to a total merit index? (Simple % weights may not be the answer)**
- **Plus: uncertainties about definitions of individual diseases**

The survey: Conclusions

- A number of countries have made large efforts to establish genetic/genomic evaluations (CDN, DFS, DEU, ESP, NLD)
- A further group of countries is well underway with implementing more sophisticated systems (FRA, USA, ITA, GBR)
- Countries without genetic evaluation for hoof health
  - No interest in the topic?
  - Difficulties in establishing recording programs?
  - Hoof diseases not too important in individual countries?
- Plus: Only a selected number of countries was addressed – more countries could be included …

Final remarks

- **Three reasons for investing time and money in work on claw health:**
  - ✓ **Welfare of the cows**
  - ✓ **Economic benefits for farmers**
  - ✓ **(Infectious diseases only): A cow that did not get sick will be one cow less spreading the disease**
    ➔ large indirect effects
    (Hulst, de Jong, Bijma – Genetics – 2021)

- **Precision of recording is everything!**
  Phenotype is king! (Mike Coffey)

- **Even small reference samples may work well!**