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USABILITY OF BACTERIOLOGICAL MILK SAMPLES FOR GENETIC IMPROVEMENT OF UDDER HEALTH IN AUSTRIAN CATTLE

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Mastitis – Hot Topic

- **Complex trait:** different causative pathogens
- Selection for mastitis resistance: **Udder health index** in AT
- “New“ phenotypes - use of **pathogen-specific mastitis** based on data from bacteriological milk samples
- **Challenge**: availability of data

ADDA „Advancement of Dairying in Austria“ Project 2014-2017

… research along the dairy chain

- **Bacteriological milk analyses:** Harmonization in bacteriological data generation + integration in central cattle data base (RDV)

- **Pilot data**: collected over a period of 1 yr. (01.10.2015 – 30.09.2016)
  - 6,892 quarter milk samples analyzed in external laboratory
  - 203 farms in Austria
  - ~1,400 lactating cows with (suspected) udder health problems

Picture: K-Project ADDA – Advancement of Dairying in Austria/cattlecompetence.at

Bacteriological milk analyses

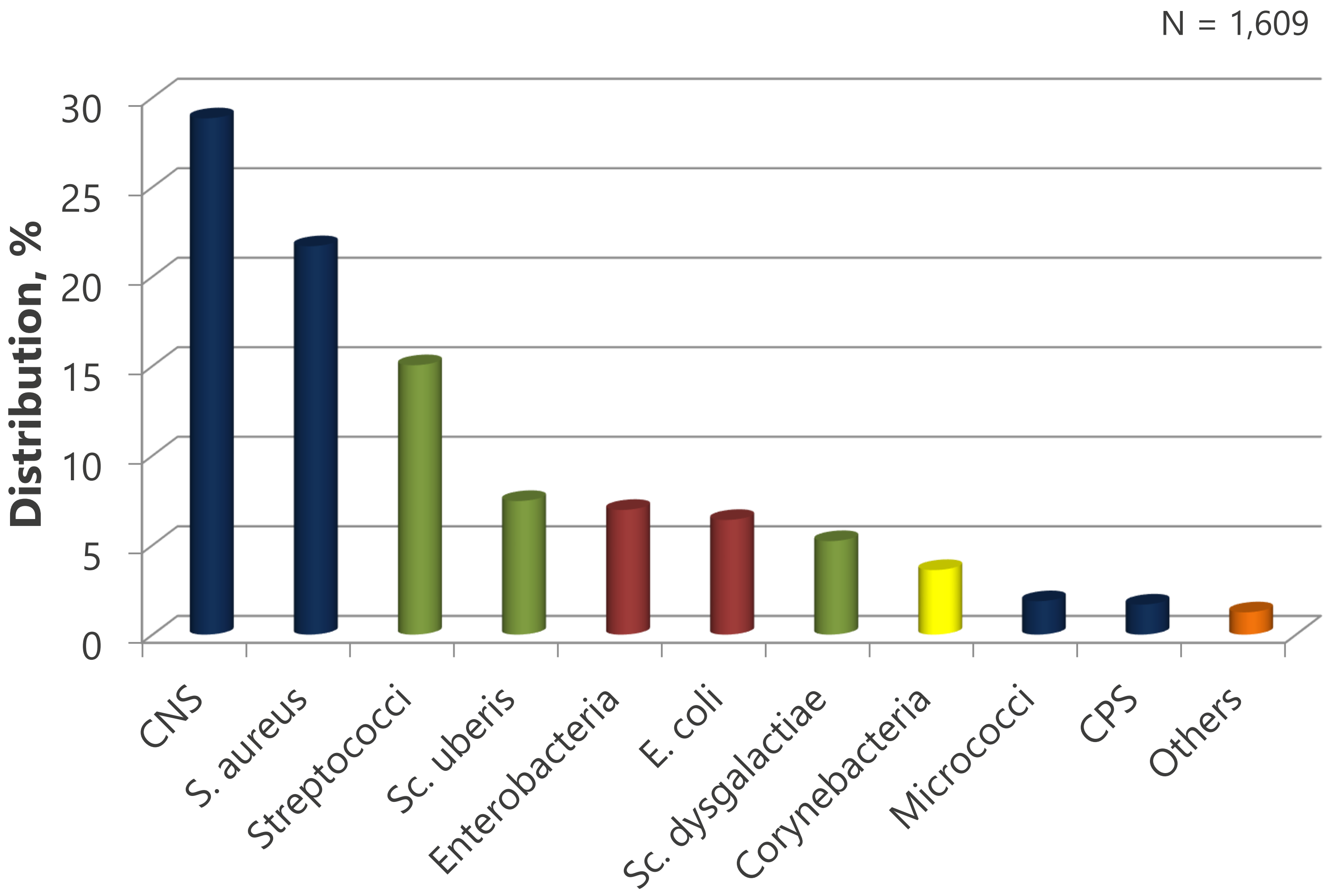

Figure 1: Distribution of pathogens in culture-positive milk samples.

Objective – Genetic Evaluation

Estimation of **heritabilities** for and **genetic correlations** between traits of **bacterial infection** and routinely recorded other direct and indirect udder health traits

.... in Austrian Fleckvieh cows

(dual purpose Simmental)

Data, data, data, ...

- **Laboratory data**: farm, cow and laboratory ID, date of sampling, pathogen denotation at quarter level, quarter location

- **Udder Health data:** veterinarian diagnoses (acute and chronic mastitis), test-day SCC, culling due to udder health problems

Traits, Definitions and Models

Traits of bacterial infection		Further udder health traits	
BACI	bact. infection	**AcM**	acute mastitis
GRAM+	gram-positive bact. infection	**ChM**	chronic mastitis
GRAM-	gram-negative bact. infection	**CULL**	culling due to udder health problems
		SCS (continuous)	average somatic cell score (5-305d)

- **Binary 0 or 1**
- **Multivariate linear animal model**

Results I

Trait	Frequency	Heritability (SE)
BACI	7.2 %	0.01 (<0.01)
GRAM+	6.2 %	0.01 (<0.01)
GRAM-	1.3 %	0.01 (<0.01)
AcM	13.0 %	0.04 (0.01)
ChM	2.4 %	0.03 (0.01)
CULL	2.9 %	0.02 (<0.01)
SCS, mean	2.1	0.20 (0.03)

→ Heritabilities lower than for diagnoses traits

Results II – Genetic Correlations

	GRAM+	AcM	ChM	CULL	SCS
GRAM+	-	0.52	0.83	0.95	0.91
GRAM-	- 0.20	0.48	-0.56	-0.24	0.00
BACI	-	0.62	0.75	0.96	0.88

Results II – Genetic Correlations

	GRAM+	**AcM**	**ChM**	**CULL**	**SCS**
GRAM+	-	0.52	0.83	0.95	0.91
GRAM-	**- 0.20**	0.48	-0.56	-0.24	0.00
BACI	-	0.62	0.75	0.96	0.88

→ Mastitis caused by **different pathogens** may be seen as **partly different traits**

Results II – Genetic Correlations

	GRAM+	AcM	ChM	CULL	SCS
GRAM+	-	**0.52**	**0.83**	**0.95**	**0.91**
GRAM-	- 0.20	0.48	-0.56	-0.24	0.00
BACI	-	**0.62**	**0.75**	**0.96**	**0.88**

→ Genetic correlations to unspecific mastitis medium to high, **partly different traits**

→ **Gram-positive bacteria** associated with acute, chronic as well as subclinical mastitis (both genetic and phenotypic level)

Results II – Genetic Correlations

	GRAM+	AcM	ChM	CULL	SCS
GRAM+	-	0.52	0.83	0.95	0.91
GRAM-	- 0.20	**0.48**	**-0.56**	**-0.24**	**0.00**
BACI	-	0.62	0.75	0.96	0.88

→ **Gram-negative bacteria** often associated with acute mastitis (both genetic and phenotypic level)

Results III – Genetic Correlations

	ChM	CULL	SCS
AcM	**- 0.02**	0.54	0.50
ChM	-	0.82	0.65
CULL	-	-	0.73

- **different traits**

Results III – Genetic Correlations

	ChM	CULL	SCS
AcM	- 0.02	0.54	0.50
ChM	–	0.82	0.65
CULL	–	–	0.73

- **medium to high**
- **partly different traits**

Conclusion

Bacteriological milk samples

- Heritabilities of traits of bacterial infection are low
- Useful for breeding as additional information and/or auxiliary traits
- further research with a larger data set should be carried out to confirm these results

→improved recording possible

Thank you!

Picture: K-Project ADDA – Advancement of Dairying in Austria/cattlecompetence.at

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Results II – Genetic Correlations

	GRAM+$_{SE}$	AcM $_{SE}$	ChM $_{SE}$	CULL $_{SE}$	SCS $_{SE}$
GRAM+	-	$0.52_{0.13}$	$0.83_{0.11}$	$0.95_{0.08}$	$0.91_{0.07}$
GRAM-	$-0.20_{0.27}$	$0.48_{0.19}$	$-0.56_{0.21}$	$-0.24_{0.27}$	$0.00_{0.22}$
BACI	-	$0.62_{0.16}$	$0.75_{0.14}$	$0.96_{0.07}$	$0.88_{0.11}$

Results III – Genetic Correlations

	ChM	CULL	SCS
AcM	$-0.02_{0.20}$	$0.54_{0.15}$	$0.50_{0.12}$
ChM	-	$0.82_{0.12}$	$0.65_{0.12}$
CULL	-	-	$0.73_{0.12}$

- **different traits**

Pilot data set

Table. Culture results from quarter milk samples submitted to diagnostic laboratories during the project ADDA (ADvancement of Dairying in Austria) from October 2015 to September 2016 in Austrian dairy farms (quarter level).

	Positive samples, (n = 1.533)	All samples, (n = 6.892)
Gram-positive bacteria		
Coagulase negative Staphylococci, %	30.4	7.2
Staphylococcus aureus, %	22.1	5.2
Streptococcus spp. (other than dysgal./ uberis), %	13.1	3.1
Streptococcus uberis, %	7.0	1.7
Streptococcus dysgalactiae, %	5.0	1.2
Corynebacteria spp., %	3.7	0.9
Enterococcus spp., %	2.4	0.6
Gram-negative bacteria		
Enterobacter spp., %	7.1	1.7
Escherichia coli, %	6.3	1.5
Others, %*	2.9	0.7

*includes gram-positive bacteria and non-bacterial pathogens (e.g. yeast, prototheca).

Model and Data Set

Multivariate linear animal model

- Fixed effects: foreign-gene proportion, year*month of calving,
  parity-age at calving, lab*year, type of recording*year

- Random effects: herd*year, animal (genetic effect), permanent
  environmental effect

Table 1. Number of records, cows, sires and herds of data sets for analyses.

Trait	Records	Cows	Sires	Herds
Gram+, Gram-, BACI	6,900	4,605	721	182
AcM	13,473	5.989	854	232
ChM	13,193	5,926	848	231
CULL	13,438	5,978	853	231
SCS_305	10,393	5,984	833	237

Data Editing

- Foreign gene proportion of < 50 % (cow)
- Cows from all parities
- Age at first calving 18 to 47 month (cow)
- Calving interval < 800d
- Only farms actively collecting milk samples
- . . .

Pedigree

- 5 generations

Final Data Set

Lactations	Cows	Herds	Pedigree
16,251	6,822	239	28,733

Traits, Definitions and Models

- **Binary 0 or 1**
- **Continuous - SCS**
- **Multivariate analyses were carried out for the trait combinations**

  1) **BACI, AcM, ChM, CULL and SCS_305, and**
  2) **GRAM+, GRAM-, AcM, ChM, CULL and SCS_305**

software package vce6

- *Heritability Transformation → following formula of Dempster and Lerner (1950)*

Trait definition

Trait	Details
Gram+, Gram-, BACI[1]	[1] Cows with at least one record on bacterial infection (BACI) between October 1, 2015 and September 30, 2016.
AcM, ChM, CULL[2]	[2]Cows with at least one record on acute (AcM) or chronic (ChM) mastitis, or culling due to udder health problems (CULL), calving between January 1, 2013 and March 31, 2017.
SCS_305[3]	[3]Mean SCS from 5 to 305 d after calving (SCS_305) recorded at test-days between January 1, 2015 and March 31, 2017.

Further results

Table. Heritability estimates after transformation from observable to underlying scale. Transformed threshold heritability estimates.

trait	h^2	SE
5-variate		
BACI	0.04	0.02
AcM	0.09	0.02
ChM	0.18	0.06
CULL	0.12	0.03
6-variate		
GRAM+	0.05	0.02
GRAM-	0.13	0.06
AcM	0.09	0.02
ChM	0.16	0.05
CULL	0.12	0.03