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Genetic analysis of cases of subclinical mastitis

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Agent specific analysis in udder health

Research project
of State Research Institute for Agriculture in Thuringia
in cooperation with University of Halle

- Here to be presented: One representative farm
  - 400 cows in good milking hygiene and housing
- Bacteriological cultures at the laboratory of the animal health service of Bad Langensalza, Thuringia
  - 6885 milk samples from 1999 till 2001
- Animal-data from the farm management computer
- Milk yield and pedigree from milk control agency

Data

number of milk samples	6885
number of tested cows	786
mean sample rate per cow	8,8
variation of the sample rate per cow	1 - 30
sample structure	quarterly samples from entire herd; plus dry and fresh milking cows

28,7 % samples bacteriological positive

Mastitis agents: Frequencies

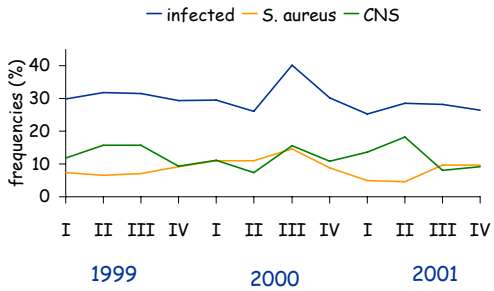
	% of all samples (n=6885)	% of infected (n=1973)
CNS (coagulase negative Staphylococci)	11,8	41,1
S. aureus	8,6	29,9
EPS (esculin positive Streptococci)	3,2	11,3
Str. uberis	1,7	6,1
Str. dysgalactiae	1,5	5,2
E. coli	1,2	4,1
Others (f. e. *Str. agalactiae, Corynebacterium bovis, yeast or* coliforms)	0,7	2,4

Infection rate

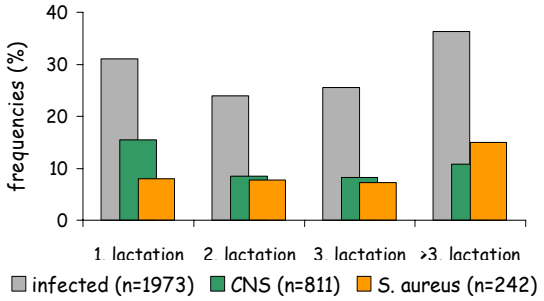
frequencies (%)	1999	2000	2001
infected	30,74 a	29,02 ab	26,54 b
CNS	13,36 a	9,76 b	12,92 a
S. aureus	7,50 a	10,96 b	6,53 a

$p \leq 0,05$

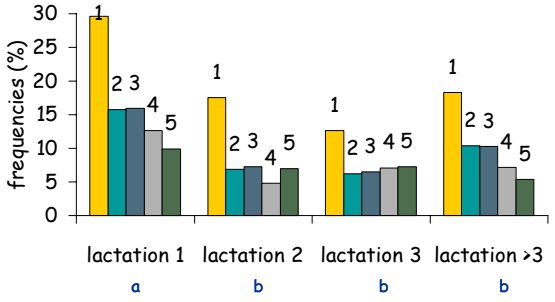
Infection rate



Infection rate by parity

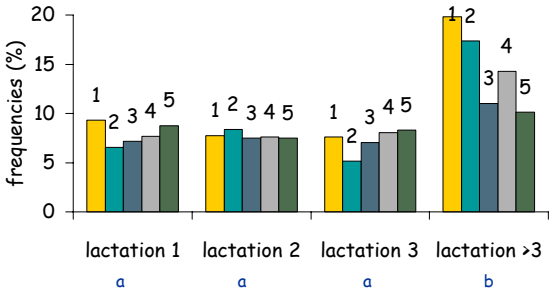


CNS-Infection rate by parity and stage of lactation (DIM <14, ≥14, ≥77, ≥140, ≥231)



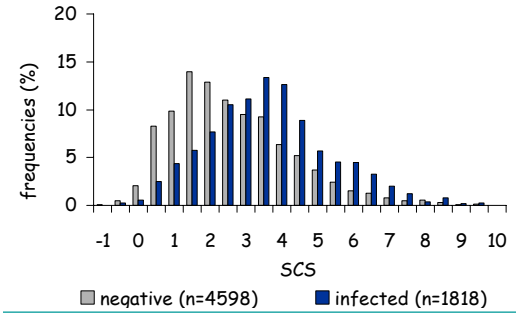
p ≤ 0,05

S. aureus-Infection rate by parity and stage of lactation (DIM <14, ≥14, ≥77, ≥140, ≥231)



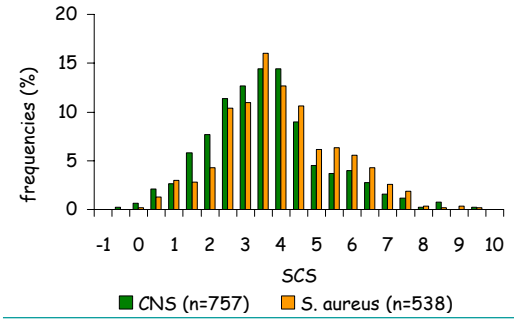
p ≤ 0,05

Distribution of SCS* for negative and positive samples (all infections)



*nearest test day following bacteriological culture

Distribution of SCS* for positive samples: CNS and S. aureus



*nearest test day following bacteriological culture

LS-Means for SCS*

bacteriological culture	LS-Means SCS*	s. e.	
negative	3,30	0,052	a
CNS	3,73	0,069	b
S. aureus	3,84	0,074	b

SAS-PROC MIXED; Model:

Covariables	Milk yield, DIM, DIM²
Fixed effects	lactation, season.year
Random effect	Animal

*nearest test day following bacteriological culture

Treshold-animal-model

$$Pr\ (y_{ijklmn} = 1) = \Theta\ (\mu + parity_i + slac_j + season_k + year_l + animal_m + env_n + e_{ijklmn})$$

Pr	Probability for occurrence
Θ	probit link function
y_{ijklmn}	trait in milk sample (= 1 for infected, CNS, *S. aureus*)
$parity_i$	fixed effect number of parity (i= 1, 2, 3, >3)
$slac_j$	fixed effect stage of lactation (j= 1-5)
$season_k$	fixed effect of the season (k= spring, summer, autumn, winter)
$year_l$	fixed effect of the year (l= 1999, 2000, 2001)
$animal_m$	random effect of the animal (m= 1, 2, 3, …)
env_n	permanent environment (n= 1, 2, 3, …)
e_{ijklmn}	residual effect

estimated with ASREML

Heritabilities

	h^2	s. e.
Occurrence of agents in milk samples	0,051	0,029
Occurrence of CNS	0,066	0,038
Occurrence of *S. aureus*	0,030	0,034

estimated with ASREML

Two-trait-model

ASREML, bivariate, linear (SCS) – non-linear (infection)

			Variance components		
	h^2	s. e.	animal	perm. env.	residual
infected	0,059	0,032	0,068	0,177	0,914
SCS at TD	0,054	0,036	0,188	1,076	2,198
Correlation			0,689	0,754	0,094
CNS	0,092	0,048	0,097	0,228	0,726
SCS at TD	0,042	0,034	0,145	1,143	2,193
Correlation			0,822	0,427	0,059
S. aureus	0,068	0,052	0,074	0,389	0,626
SCS at TD	0,062	0,037	0,217	1,078	2,196
Correlation			0,684	0,566	0,051

Conclusion

- improper generalisation for mastitis agents
  - *S. aureus* vs. CNS
- *S. aureus* and CNS are clearly contrasting over time or within and across parities
- bacteriological cultures of milk samples indicate the infection
  - especially CNS as subclinical disease
- Heritabilities for subclinical cases
  - Single trait analysis around 5 %
  - Bivariate analyses including SCS between 6-9 %