



Department of Large Animal Sciences



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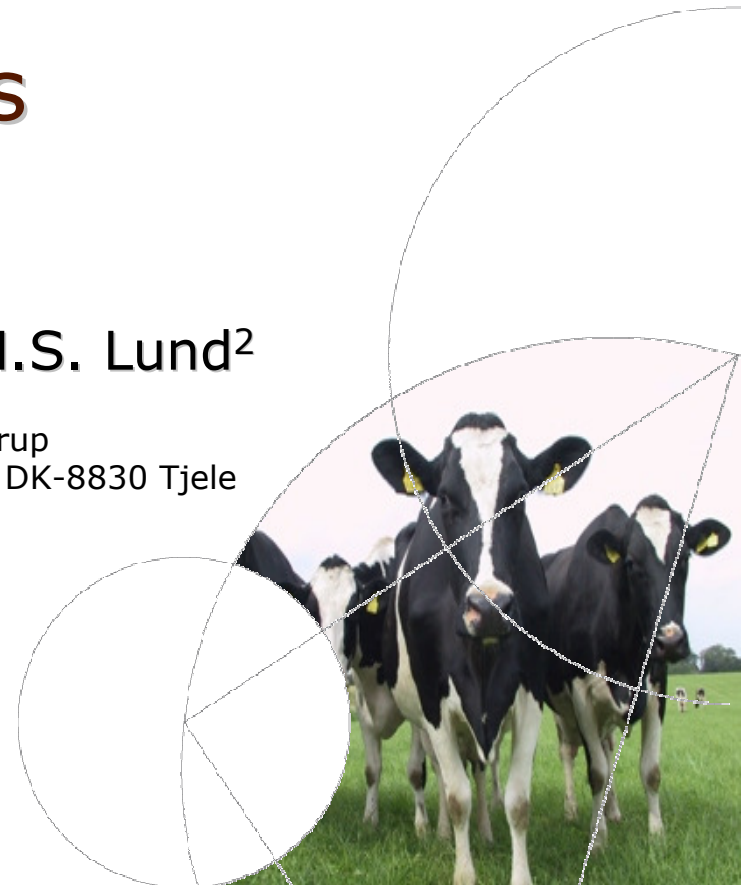
Genetic parameters for pathogen-specific mastitis in Danish Holstein Cattle

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Nordic udder health index

- Direct and indirect measures of udder health
 - Mastitis treatments
 - Lactation average somatic cell score
 - Fore udder attachment
 - Udder depth
- Improvement?
 - Adding pathogen information?
 - Bacteriological culturing of milk samples



Motivation

Pathogen information may prove beneficial in a breeding context because:

- Direct measure of an infection of the udder and the pathogen causing the infection
- Mastitis caused by different pathogens may be considered as different traits
- r_a between pathogen-specific mastitis and SCS may depend on causative pathogen
- Economic values of mastitis caused by different pathogens may differ



Objectives of study

- To estimate genetic variation and h^2 of pathogen-specific mastitis traits
- To estimate r_a among different pathogen-specific mastitis traits



Data I

Editing

- Minimize bias of pathogen data
- Reduce extreme category problems
- Removal of unreliable data

Final data set: 168,158 first lactations from 1529 herds



Data II

- Mastitis incidence, before editing in ():
 - Unspecific: 0.230
 - *Strep. dysgalactiae*: 0.152 (0.100)
 - *E. coli*: 0.140 (0.112)
 - CNS: 0.140 (0.119)
 - *Staph. aureus*: 0.155 (0.145)
 - *Strep. uberis*: 0.187 (0.160)
 - ~~Other: 0.144 (0.147)~~
 - ~~Culture negative: 0.236 (0.216)~~
- Mastitis with pathogen information: 0.72
- Frequency of culled animals: 0.172 (0.191 vs 0.166)



Threshold model

$$\lambda_{ijklm} = YM_i + AGE_j + b t_{ijklm} + hys_k + sire_l + e_{ijklm}$$

where

- λ_{ijklm} = liability to mastitis
- YM_i = "fixed" effect of yr×mo of calving
- AGE_j = "fixed" effect of calving age
- hys_k = random effect of herd×yr×season
- $sire_l$ = transmitting ability of sire
- b = "fixed" regression coefficient of λ on the length of period at risk
- t_{ijklm} = period at risk, defined as the number of d from 15 d before calving to the date of culling or to the end of the period at risk.
- All cows treated for mastitis were assigned a full period
- (Heringstad *et al.*, 2001)
- e_{ijklm} = residual $\sim$ iid $N(0,1)$

Full Bayesian approach via Gibbs sampling implemented in the DMU package (Madsen and Jensen, 2006)



Results I (h^2)

Mastitis trait	h^2	95% CI	ESS
Unspecific	0.114	[0.086;0.138]	1527
<i>Strep. dysgalactiae</i>	0.044	[0.017;0.064]	238
<i>E. coli</i>	0.050	[0.021;0.077]	256
CNS	0.052	[0.022;0.077]	312
<i>Staph. aureus</i>	0.039	[0.018;0.058]	277
<i>Strep. uberis</i>	0.079	[0.043;0.112]	356

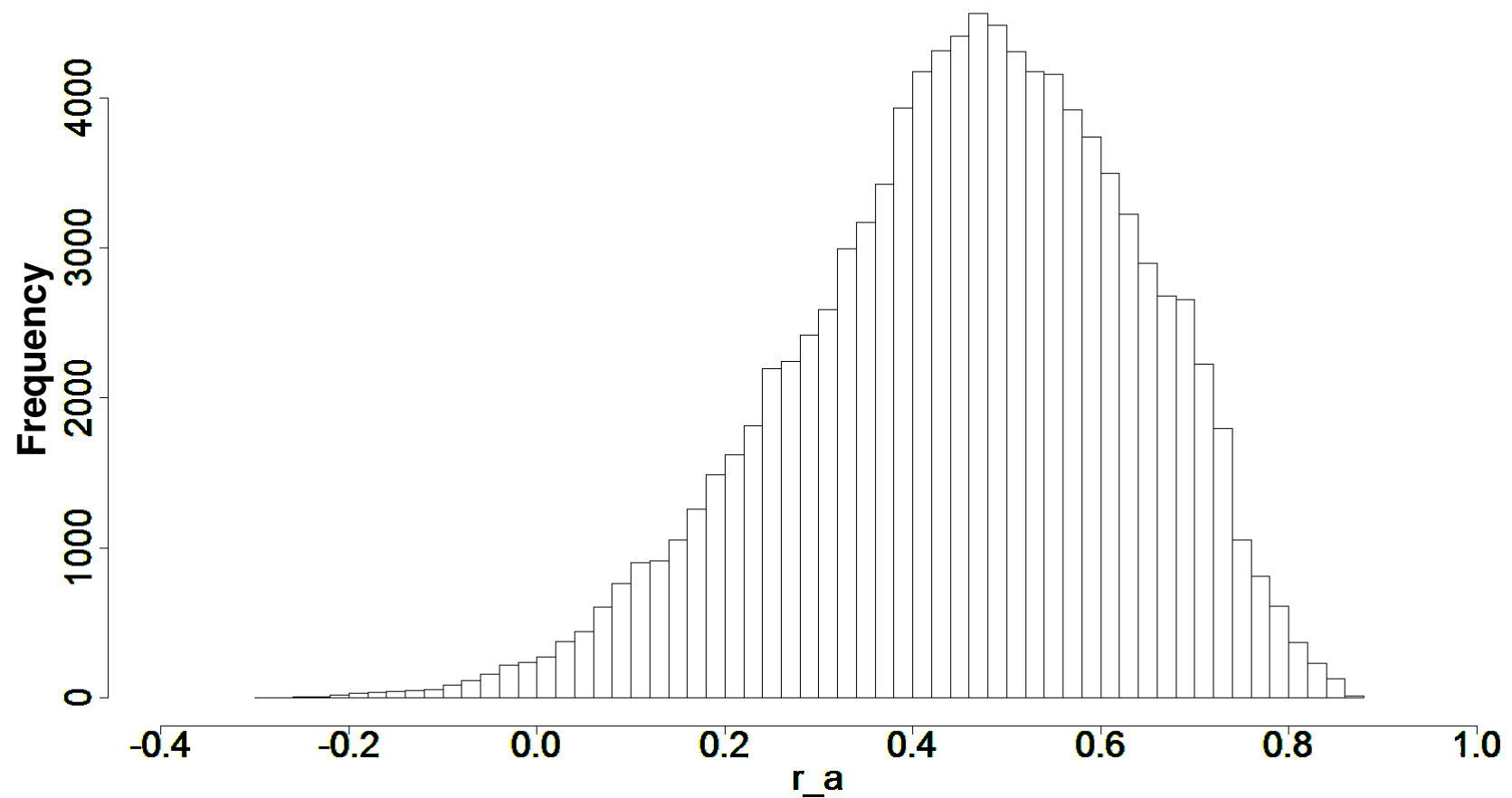


Results II (r_a)

	<i>E. coli</i>	CNS	<i>Staph. aureus</i>	<i>Strep. uberis</i>
<i>Strep. dysgalactiae</i>	0.637	0.640	0.714	0.768
<i>E. coli</i>		0.602	0.452	0.628
CNS			0.608	0.745
<i>Staph. aureus</i>				0.631



Posterior density of r_a



r_a between *E. coli* and *Staph. aureus*



Economic values

- Including pathogen information in the genetic evaluation of udder health may prove beneficial
 - especially as the cost of mastitis caused by different pathogens varies:
 - Contagious pathogen: €483/case
 - Environmental pathogens: €272/case

(Østergaard *et al.*, 2008)



Conclusion

- h^2 of unspecific mastitis consistent with other studies of similar populations
- Pathogen-specific h^2 of mastitis were low –in most cases consistent with other studies
- r_a in all cases different from unity → different pathogen-specific mastitis traits may be considered as different traits

