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Theatre presentation 10

Genetic parameters for pathogen

specific clinical mastitis in Norwegian Red cows

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Genetic parameters for pathogen specific clinical mastitis in Norwegian Red cows

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Outline

- Short background

- Objectives

- Material and methods

- Results

- Conclusion

Background

- Inflammation of the mammary gland

- Mild to severe, subclinical to clinical

- Caused by several different pathogens

- Genetic evaluation of Norwegian Red is based on records of veterinary treatments of clinical mastitis

- Since year 2000, pathogen data fram mastitis-laboratories recorded in the Norwegian Dairy Herd Recording System.

- Only recordings, not used in genetic analyses so far in Norway.

Objectives

- Estimate heritabilites of and genetic correlations among the three most common pathogens with respect to clinical mastitis (CM) in Norwegian Red cows

- Can mastitis caused by different pathogens be considered to be different traits?

- Examine whether ranking of bulls differ between the various pathogen specific mastitis traits

Data

- First lactation cows, calving from January 2000 through December 2008

- Sired by Norwegian Red AI-bulls

- 20-36 months of age at calving

- Lactation was defined as 30 days before calving to 300 days-in-milk, culling or next calving

- Only milk samples associated with a CM-record (+/- 7 days) was considered

- Only herds with at least one milk sample that could be associated with CM was included.

Data

- The three most frequent CM-pathogens

  - *Staphylococcus aureus*

  - *Escherichia coli*

  - *Streptococcus dysgalactiae*

- Unspecific mastis was defined as a CM health record with

  - no milk sample analyzed

  - Milk sample analyzed but no pathogens found

  - Milk sample anlyzed and pathogen other than the above was found

Data

- 234,088 first lactation cows

- 1,565 sires, with a total of 3,156 bulls in the pedigree file

- Four binary (0/1) traits
  - Unspecific CM   14.5 %
  - *E.coli* CM   0.4 %
  - *Str.dysgalactiae* CM   0.6 %
  - *S.aureus* CM   1.9 %

- Overall CM frequency = 16.9 %
- only 6.8 % of all CM-cases in 2009 had a corresponding bacterial milk sample

Model

- Multivariate threshold sire model

$$\lambda = X\beta + Z_h h + Z_s s + e$$

λ - unobserved liabilities

β - systematic effects

       - age at first calving (17 classes – 20-36 months)

       - month-year of calving (108 classes)

h - random herd-5-year effects (7720 levels)

s - random sire effect

e - residual effects

- RJMC procedure in DMU -> Gibbs sampling with 500 000 iterations + 5000 burn in.

ze# Results

Table 1. Posterior means (SD) for sire (σ^2_s) and herd (σ^2_{h5y}) variances, and the corresponding heritabilitiy[1] (h^2) with the 95% highest posterior density (HPD) intervals for four clinical mastitis traits.

Mastitis traits	σ^2_s	σ^2_{h5y}	h^{2*}	HPD interval
Unspecific CM	0.017 (0.002)	0.123 (0.004)	**0.06** (0.006)	0.05 - 0.07
E.coli	0.008 (0.003)	0.095 (0.019)	**0.03** (0.010)	0.02 - 0.05
S.aureus	0.010 (0.002)	0.130 (0.008)	**0.04** (0.008)	0.02 - 0.05
Str.dysgalactiae	0.006 (0.002)	0.142 (0.013)	**0.02** (0.007)	0.01 - 0.03

$$* \ h^2 = \frac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_h^2 + \sigma_e^2}$$

Results

Table 2. Posterior means (SD) for genetic correlations between four mastitis traits, and their 95 % highest posterior density interval in brackets.

	Unspecific CM	E.coli	S.aureus
E.coli	**0.79** (0.09)		
	[0.60 - 0.94]		
S.aureus	**0.85** (0.07)	**0.80** (0.10)	
	[0.72 - 0.96]	[0.60 - 0.95]	
Str.dysgalactiae	**0.87** (0.07)	**0.75** (0.14)	**0.82** (0.10)
	[0.73 - 0.96]	[0.47 - 0.94]	[0.61 - 0.96]

Results

Table 3. Spearman rank correlations of the sire posterior mean for unspecific clinical mastitis, *Staphylococcus aureus*-mastitis, *Streptococcus dysgalactiae*-mastitis and *Escherichia coli*-mastitis.

	Unspecific clinical mastitis	*E.coli*	*S.aureus*
E.coli	0.95		
S.aureus	0.95	0.95	
Str.Dysgalactiae	0.98	0.97	0.96

Results

Table 4. The ten highest ranking bulls for unspecific clinical mastitis, and their rank for three pathogen specific mastitis traits.

	Rank based on sire posterior means for		
Unspecific clinical mastitis	*E.coli*	*S.aureus*	*Str.dysgalactiae*
1	*5*	15	*5*
2	*6*	*5*	*1*
3	15	14	*2*
4	14	32	14
5	*1*	*3*	*3*
6	*2*	*7*	*10*
7	*3*	*2*	15
8	*9*	*10*	13
9	*7*	12	*9*
10	21	*1*	*4*

Conclusions

- Heritabilities ranged from 0.02 to 0.04 for pathogen specific mastitis

- Genetic correlations among the CM traits was positive and strong, but lower than 1

- Some minor re-ranking of sires was observed.

- Indicates that these pathogen specific mastitis traits can be considered to be different traits, and that pathogen data may provide additional info regarding breeding values of bulls.

- However, pathogen info is too sparse at this point to be used in routine genetic evaluation.

- Farmers and veterinarians should be encouraged to collect more milk samples from mastitis cows for pathogen analysis.

Thank you for the attention