

High genetic correlation between antibody response and faecal shedding enables breeding for resistance against paratuberculosis

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Introduction

Paratuberculosis is an infectious disease of cattle caused by *Mycobacterium avium* subsp. *paratuberculosis* (Map). The heritability of antibody responses against Map has been estimated at 0.03 to 0.20. Selection of breeding stock based on antibody response is attractive only if it results in offspring with a higher resistance to infection, resulting in reduced shedding of Map rather than in offspring being unable to mount an antibody response given infection. Therefore, our aim was to estimate the genetic relation between antibody response and faecal shedding.

Materials and methods

Dataset PA1: 517,672 individual milk samples of 109,213 cows with $\geq 75\%$ Holstein-Friesian genes from 5,938 dairy herds tested by ELISA between 2007-2010. Data were selected from herd-year combinations with ≥ 2 positive ELISA results and ≥ 20 cows sampled. ELISA sample-to-positive (S/P) results were transformed to $\ln[(\frac{S}{P})+50]$.

Dataset PA2: 78,604 individual faecal samples of 52,348 cows with $\geq 75\%$ Holstein-Friesian genes from 435 dairy herds tested between 1996-2015 by either modified Löwenstein-Jensen culture method, ESP-TREK culture system or qPCR assay. Data were selected from herd-year combinations with ≥ 1 positive faecal sample, ≥ 20 cattle tested and $\geq 80\%$ of adult cattle tested. Results were expressed as positive or negative.



Analyses: Heritabilities (h^2) and genetic solutions for sires were estimated with sire-maternal grandsire models (linear model for PA1; logistic model for PA2) with random permanent environment effect and fixed effects herd*year, parity, birthyear and stage of lactation. In addition, for PA1 a covariable for milk production was included in the model, and for PA2 a fixed effect for test method.

Sire solutions were used to estimate MACE correlations (with correction for reliability) between PA1 and PA2. Sires with at least 15 daughters on 10 herds per trait were included in the evaluation, resulting in 446 sires for PA1 and 272 sires for PA2.

Results

	PA1	PA2
h^2 (se)	0.052 (0.003)	0.368 (0.040)
Genetic correlation between PA1 and PA2:	0.66	

Discussion

This study confirms previous heritability estimates. Moreover, the high genetic correlation between traits for antibody response and faecal shedding indicates that selection based on antibody response is likely to result in offspring with a higher resistance to infection resulting in lower faecal shedding.

Conclusion

Our results indicate that breeding for resistance to paratuberculosis by selection on antibody response is feasible.

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