Session 15: Dairy genetics free communications

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Genetics of Tuberculosis in Irish Dairy Cattle

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Abstract

There is a lack of information on genetic parameters for tuberculosis (TB) susceptibility in dairy cattle. *Mycobacterium bovis* is the primary agent of tuberculosis in cattle.The objective of this study was to quantify the genetic variation present among Irish Holstein - Friesian dairy cattle in their susceptibility to *M. bovis* infection. A total of 15,182 cow and 8,104 heifer single intradermal comparative tuberculin test (a test for *M. bovis*-purified protein derivative [PPD] responsiveness) records from November 1, 2002, to October 31, 2005 were available for inclusion in the analysis. Data on abattoir TB carcass lesions (confirmed *M. bovis* infection) were also available for inclusion in the analysis. Linear animal models, and sire and animal threshold models were used to estimate the variance components for susceptibility to *M. bovis*-PPD responsiveness and confirmed *M. bovis* infection. Heritability estimates from the threshold sire models were biased upwards. The threshold

animal model produced heritability estimates of 0.14 in cows and 0.12 in heifers for susceptibility to *M. bovis*-PPD responsiveness, and 0.18 in cows for confirmed *M. bovis* infection susceptibility. Therefore, exploitable genetic variation exists among Irish dairy cows for susceptibility to *M. bovis* infection. A favourable genetic correlation close to unity was observed between susceptibility to confirmed *M. bovis* infection and *M. bovis*-PPD responsiveness, indicating that direct selection for resistance to *M. bovis*-PPD responsiveness will indirectly reduce susceptibility to confirmed *M. bovis* infection.

Keywords. *Mycobacterium bovis*, tuberculosis, genetics, heritability

Introduction

Mycobacterium bovis is the principal agent of bovine tuberculosis (bTB), which is an ongoing problem for the Irish cattle industry. A bTB eradication policy was introduced in Ireland in 1954. Progress was rapid during the initial stages of the programme, leading to a considerable reduction in the incidence of the disease by the mid-1960s. However, since then progress has stalled (More and Good, 2006), indicating a need to investigate alternative strategies. One such approach would be genetic selection for increased resistance to bTB. However, this requires genetic variation for resistance to infection with *M. bovis*. The objective of this study therefore, was to quantify the genetic variation present among Irish Holstein-Friesian dairy cattle for susceptibility to infection with *M. bovis*, as measured by the single intradermal comparative tuberculin test (SICTT; a test for *M. bovis* exposure and presumed infection).

Materials and Methods

Post - mortem examination of every animal at slaughter for tuberculous lesions is an integral part of the ongoing bTB eradication scheme in Ireland. *M. bovis* infection is confirmed through histopathology or culture. Susceptibility to confirmed *M. bovis* infection in this study was dichotomized as lesioned (an animal with a confirmed tuberculous lesion following the SICTT) or non - lesioned (a non - reactor with no subsequently confirmed *M. bovis* infection). Individual

animal *M. bovis* infection status in Ireland however is primarily based on the SICTT, which involves injecting *M. bovis*-purified protein derivative (PPD) into the neck of each animal, and comparing the reaction induced to that produced by *Mycobacterium avium*-PPD (a measure of sensitisation to environmental mycobacteria). Susceptibility to *M. bovis*-PPD responsiveness in this study was dichotomized as standard reactors (animals with a *M. bovis*-PPD reaction 4 mm or greater than the *M. avium*-PPD reaction) and non reactors (animals with a *M. bovis*-PPD reaction equal to the *M. avium*-PPD reaction).

A total of 73,483 herd summary and 1,345,036 animal SICTT results from 12,544 positive herd - tests (herd tests with at least 1 *M. bovis* standard reactor) in 5,164 herds, as well as 21,024 positive abattoir animal lesion records from 1 November 2000 to 31 October 2005, were obtained from the Irish Department of Agriculture Fishers is and Food Animal Health Computer System and Factory Lesion Database, respectively. Pedigree information was obtained from the Irish Cattle Breeding Federation database.

In Irish production systems cows and heifers are generally segregated, hence likely to experience different *M. bovis* infection pressures. Multiparous cows and nulliparous heifers were therefore treated as two distinct contemporary groups. An attempt was made to include only animals that had a high likelihood of being exposed to *M. bovis*, by dividing the data into episodes using herd SICTT summary records. A *M. bovis*-PPD responsiveness (confirmed *M. bovis* infection) episode was defined as a herd restriction initiated by 2 or more standard reactors (a confirmed lesion) within the contemporary group, with at least one of the animals being home bred (not implemented, as resulted in excessive loss of lesion records). Each episode was terminated by two consecutive clear herd tests. Only Holstein-Friesian animals were retained. Animals with no known sire, that calved outside the normal age for a given parity, that had inconclusive SICTT results, or that moved into the herd within 6 weeks of the SICTT (as it takes 3-6 weeks to develop a positive reaction to the test post infection) were discarded. Only episodes with at least one standard reactor (case of confirmed *M. bovis* infection) and 10 or more animals were retained. Datasets following all edits consisted of

15,182 cow and 8,104 heifer *M. bovis*-PPD responsiveness records, and 13,791 confirmed *M. bovis* infection cow records (there were insufficient data for analysis of confirmed *M. bovis* infection in heifers). Pedigree information of each animal was traced back four generations. Linear animal models, and sire and animal threshold models in the statistical package ASREML were used to estimate the variance components for susceptibility to *M. bovis* - purified protein derivative (**PPD**) responsiveness and confirmed *M. bovis* infection. The fixed effects of herd-episode, year of herd-test, month of herd-test, year of herd-test × month of test interaction were added to all models. The fixed effect of month of calving was also added to the *M. bovis*-PPD responsiveness and confirmed *M. bovis* infection cow models and Holstein - Friesian breed fraction was added to the *M. bovis*-PPD responsiveness heifer model.

Results and Discussion

The appropriateness of the heritability estimates from the threshold models were determined by their comparability with the binary transformed liability estimates. Heritability estimates from the sire threshold models were biased upwards, which most likely resulted from the absence of a dam effect in these models. Heritability estimates from the animal threshold moles most resembled the binary transformed estimates. The heritability estimates (standard errors in parentheses) estimated using the animal threshold model were 0.14 (0.028) in cows and 0.12 (0.039) in heifers for susceptibility to *M. bovis*-PPD responsiveness, and 0.18 (0.041) in cows for confirmed *M. bovis* infection susceptibility. Therefore, exploitable genetic variation exists among Irish dairy cattle for susceptibility to *M. bovis* infection. Sire rankings from the animal linear and threshold models were similar; indicating that either model could be used for the analysis of susceptibility to *M. bovis*-PPD responsiveness. A very strong genetic correlation of 0.99 (0.002) was observed between susceptibility to confirmed *M. bovis* infection and *M. bovis*-PPD responsiveness, indicating that direct selection for resistance to *M. bovis*-PPD responsiveness will indirectly reduce susceptibility to confirmed *M. bovis* infection.

Conclusions

This study clearly shows that exploitable genetic variation exists for *M. bovis*-PPD responsiveness. Furthermore, the almost unity genetic correlation between susceptibility to confirmed *M. bovis* infection and *M. bovis*-PPD responsiveness indicates that SICTT data from the national bTB eradication programme can be used to routinely estimate breeding values for susceptibility to *M. bovis* infection. Sire rankings from the linear and threshold animal models were similar, indicating that both models are suitable for the genetic evaluation of susceptibility to *M. bovis*-PPD responsiveness in the national dairy herd. However, limitations on existing computing resources would favor the use of linear animal models.

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References

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