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Genetic evaluation for bovine tuberculosis resistance in dairy cattle

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ABSTRACT

Genetic evaluations for resistance to bovine tuberculosis (bTB) were calculated based on British national data including individual animal tuberculin skin test results, postmortem examination (presence of bTB lesions and bacteriological culture for *Mycobacterium bovis*), animal movement and location information, production history, and pedigree records. Holstein cows with identified sires in herds with bTB breakdowns (new herd incidents) occurring between the years 2000 and 2014 were considered. In the first instance, cows with a positive reaction to the skin test and a positive postmortem examination were defined as infected. Values of 0 and 1 were assigned to healthy and infected animal records, respectively. Data were analyzed with mixed models. Linear and logit function heritability estimates were 0.092 and 0.172, respectively. In subsequent analyses, breakdowns were split into 2-mo intervals to better model time of exposure and infection in the contemporary group. Intervals with at least one infected individual were retained and multiple intervals within the same breakdown were included. Healthy animal records were assigned values of 0, and infected records a value of 1 in the interval of infection and values reflecting a diminishing probability of infection in the preceding intervals. Heritability and repeatability estimates were 0.115 and 0.699, respectively. Reliabilities and across time stability of the genetic evaluation were improved with the interval model. Subsequently, 2 more definitions of "infected" were analyzed with the interval model: (1) all positive skin test reactors regardless of postmortem examination, and (2) all positive skin test reactors plus nonreactors with positive postmortem examination. Estimated heritability was 0.085 and 0.089, respectively; corresponding repeatability estimates were 0.701 and 0.697. Genetic evaluation reliabilities and across time stability did not change. Correlations of genetic evaluations for bTB with other traits in the current breeding goal were mostly not different from zero. Correlation with the UK Profitable Lifetime Index was moderate, significant, and favorable. Results demonstrated the feasibility of a national genetic evaluation for bTB resistance. Selection for enhanced resistance will have a positive effect on profitability and no antagonistic effects on current breeding goal traits. Official genetic evaluations are now based on the interval model and the last bTB trait definition.

Key words: genetic evaluation, bovine tuberculosis resistance

INTRODUCTION

Bovine tuberculosis (**bTB**) is a chronic bacterial disease of cattle caused by *Mycobacterium bovis* infection primarily involving the respiratory tract. The disease affects animal health and welfare, causing substantial financial strain to the dairy cattle sector worldwide through involuntary culling, animal movement restrictions, and the cost of control and eradication programs (Allen et al., 2010). Furthermore, bTB is considered a zoonotic disease with considerable public health implications in countries where it is not subject to mandatory eradication programs.

In Great Britain, the majority of bTB cases are recorded in south western England and Wales. A bTB control and eradication program has been in place in these areas since 1950 consisting of primarily routine and targeted surveillance of cattle herds, culling of positive animals, and movement restrictions on infected herds. Surveillance is based on the administration of the single intradermal comparative cervical tuberculin test (skin test) involving 2 separate injections of sterile purified mixtures of *Mycobacterium avium* and *M. bovis* antigens (tuberculins) in the deep layer of the skin of the neck, followed by examination of the skin for localized allergic reactions after 72 h (de la Rua-Domenech et al., 2006). When reaction to the *M. bovis*

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tuberculin injection is deemed to be less than or equal to that to the *M. avium* tuberculin injection, then the skin test is considered negative (nonreactor). A positive skin test result (known as a reactor) is declared when the reaction to *M. bovis* tuberculin exceeds that to *M. avium* tuberculin by more than 4 mm, according to the standard international interpretation (de la Rua-Domenech et al., 2006). In all other cases, the test is considered inconclusive and repeated 60 d later. If one or more animals in a herd react positively to the skin test, then a new bTB incident, also known as breakdown, is declared, prompting animal movement restrictions, suspension of the official bTB free (**OTF**) status of the herd, and systematic testing of all animals in the herd at 60-d intervals. Animals with a positive or 2 consecutive inconclusive skin tests are compulsorily slaughtered and examined at the abattoir for visible lesions of bTB in their organs. Tissue samples from a representative number of infected animals from each herd are submitted to the laboratory to isolate *M. bovis* in bacteriological culture. A positive postmortem examination result (presence of lesions, positive *M. bovis* culture, or both) signals a downgrading of the herd's OTF status from "suspended" to "withdrawn." The breakdown remains open and skin testing continues in the herd until 1 or 2 (depending on the postmortem results and location of the herd) consecutive negative tests at minimum intervals of 60 d are obtained on all remaining animals.

Implementation of bTB control and eradication programs incurs significant costs to taxpayers on an annual basis. During 2010–2011, these costs amounted to £152 million in Great Britain and £23 million in Northern Ireland (Abernethy et al., 2013). However, despite the investment and good control efforts, the incidence and prevalence of bTB cases in Great Britain constantly increased between the mid-1980s and 2012, although they have leveled off in more recent years. Even so, just over 4,800 new breakdowns were declared in cattle herds and more than 36,000 animals had to be slaughtered for bTB control purposes in 2015 (DEFRA, 2016). This has been partly attributed to a reservoir of endemic *M. bovis* infection in wildlife, especially badgers, in large parts of England and Wales. All these facts hinder progress toward achieving the DEFRA's goal for Great Britain to be OTF by the year 2038.

The presence of genetic variation among individual animals in their immunological response to *M. bovis* exposure was documented by Pollock and Neill (2002). This genetic variation was subsequently quantified and moderate heritability estimates were reported in cattle (Bermingham et al., 2009; Brotherstone et al., 2010; Tsairidou et al., 2014). The amount of genetic variation and the level of estimated heritability render resistance to bTB amenable to improvement via genetic selection. Breeding for enhanced bTB resistance could complement existing control and eradication programs. However, relevant tools have not been widely available as no formal genetic evaluation systems have been put in place.

The objective of the present study was to assess the feasibility of a national genetic evaluation for bTB resistance in dairy cattle based on British population data. We combined data from various sources and developed automated data handling procedures suitable for a routine commercial process. We investigated different models and trait definitions.

MATERIALS AND METHODS

Data

Population surveillance data were made available from the Animal and Plant Health Agency (**APHA**) of the Department for Environment, Food and Rural Affairs (**DEFRA**). Data consisted of tuberculin skin test and postmortem examination records of dairy and beef cattle from Great Britain (predominantly England and Wales), spanning the period 1957–2014, although more than 90% of the recorded data were after 2000. Skin tests had been applied to individual animals every 2 mo within a given breakdown (defined as the period of disease surveillance in a herd prompted by the first detection of an infected animal and ending with the lifting of herd movement restrictions). Animals were classified as nonreactors, inconclusive reactors, and reactors as described by de la Rua-Domenech et al. (2006).

Negative skin test results for individual animals (nonreactors) were not being systematically recorded in the APHA database before 2011. Therefore, the British Cattle Movement Service (**BCMS**) database was used to identify contemporaries of reactors and inconclusive reactors in the APHA database that were present in the same herd during each breakdown. All contemporaries found in the BCMS database that were not included in the APHA data were considered to be nonreactors. The combined APHA-BCMS data were merged with milk recording data to derive information about the date of calving and parity number of the animals. A final match with the national pedigree data set (including data from the official Herdbooks) maintained by the Edinburgh Genetic Evaluation Services on behalf of the Agriculture and Horticulture Development Board (Dairy), retrieved the identification of the sire of each cow. Figure 1 illustrates the combination of data from