ABSTRACT: Animal health improvement is gaining interest internationally to increase profitability and instil consumer confidence. This study’s objective was to quantify contributions that genetic selection can make toward improving bovine animal health. After edits, data were available from 54,364 calves for BVDV, 5,589 animals for BoHV-1, and 5,530 animals for Fasciola hepatica. Variance components were estimated for all traits using animal linear models; a dam’s genetic and permanent environmental component was included in the analysis of BVDV. Direct heritability estimates for BVDV, BoHV-1, and F. hepatica across the different analyses performed (i.e., continuous versus categorical dependent variables, different age classes) were 0.16, 0.30 to 0.34 and 0.14, respectively. A maternal heritability (0.05) also existed for BVDV. Results show that heritable genetic variation in these three diseases exists; because data are routinely available for BVDV and F. hepatica, a national breeding program to improve resistance is possible.

Keywords: Animal health, Disease, Heritability

Introduction

By 2025, it is estimated that reproductive performance will be close to optimum in Irish dairy cattle, based on extrapolation of the genetic trend for reproductive performance from 2010 to 2013. Animal health is likely to be the largest hindering factor to realizing the full genetic potential of animals once optimal reproductive performance is achieved. Moreover, consumer concern is intensifying regarding animal health and welfare implications of modern-day farming systems. Although national eradication and control strategies are in place in many countries for several diseases, the potential contribution of genetic selection to improved animal health is often overlooked. Therefore, research on the potential impact of targeted breeding programs in improving the health of the national herd is necessary. To this end, genetic variation in Irish cattle for susceptibility to bovine tuberculosis and detailed reproductive traits (e.g., cystic ovaries) has been discussed elsewhere (Richardson et al., 2014; Carthy et al., 2014)). Additionally, genetic variation in disease susceptibility and animal health in cattle has been highlighted previously although heritability of animal health traits is generally low (<0.10; Berry et al., 2011)). Such determinations, however, remain useful and data relating to many disease traits are lacking or non-existent. Finally, estimates of heritability are often based on limited datasets or controlled environments (Snowder et al., 2005) which may not be reflective of the variance components under commercial conditions.

The objective of the present study was to estimate genetic parameters for bovine viral diarrhea virus (BVDV), bovine herpesvirus type 1 (BoHV-1) the causative agent of IBR, and Fasciola hepatica (F. hepatica) in commercial Irish dairy and beef cattle. Results from this study will be useful in determining the feasibility and utility of a national breeding program for improved animal health as a complementary approach to on-going national eradication and control strategies.

Materials and Methods

Bovine viral diarrhea virus (BVDV). BVDV enzyme-linked immunosorbent assay (ELISA) results were available for 2,049,065 calves, sampled by ear-biopsy, between 2 and 28 days of age and born during the years 2012 and 2013. Calves originated from 1,781,720 dams in 73,769 Irish dairy and beef herds. Persistent BVD infection was defined in the present study as whether or not calves consistently tested positive for BVDV. All calves initially positive for BVDV were re-tested and calves yielding a negative or inconclusive retetest were discarded from the analysis. Calves initially testing negative for BVDV were assumed negative. Only dams that remained within the same herd during the 300-day period prior to the birth of the calf were retained for analysis. This maximized the likelihood of equal exposure to BVDV among contemporaneous dams during the critical period of gestation. Calves were assigned to contemporary groups of herd-year-season of calving. Contemporary groups were defined within 1) first parity animals and 2) second parity and greater. The range in calving dates within contemporary group was restricted to <60 days. Only contemporary groups with at least five calving events of which at least one BVDV positive calf existed were retained. Animals with an unknown sire were discarded. Following all edits, BVD data were available on 54,364 calves from 52,928 dams in 4,353 contemporary groups from 3,411 herds.

Bovine herpesvirus type 1 (BoHV-1). Data originated from a seroprevalence study of BoHV-1 undertaken across 24 vaccinated and unvaccinated Irish dairy herds. Serological results for BoHV-1 were available from 8,742 animals from the 24 herds over the period October 2010 to February 2013. Animals were separated into calves (i.e., <1 year of age), maiden heifers (i.e., >1 year but had not calved at the time of sampling) and mature animals (i.e., natural mating bulls and females calved at least once at the time of sampling). Of the 8,742 animals, 92 were beef breed females were used to generate natural mating bulls within closed herds. Holstein, Friesian, or Jersey were the main breed proportion for 88% of the animals.

Due to legislative requirements, all BoHV-1 vaccines administered in the Republic of Ireland since
December 31st 2004 are gE deleted (Kaashoek et al. (1994)) DIVA (differentiating infected from vaccinated) vaccines (Simon, 2004). For diagnostic purposes, two complimentary ELISAs are available for use in vaccinated and unvaccinated herds i.e. IBR gB for use in unvaccinated herds and IBR gE for use in vaccinated herds (Van Oirschot et al. (1997); Lehmann et al. (2002)). As the vaccines are gE-deleted, a positive serological response identified by the IBR gE assay only identifies animals who have been exposed to wild-type BoHV-1. The three categories of animals included in the analysis were managed separately on farms and contemporary group in the present study, therefore, was defined as animal category by date of sampling. Only contemporary groups with at least one home-born animal positive for anti-BoHV-1 antibodies were retained. Animals with an unknown sire or not born in the herd where they were sampled were discarded. Parities greater than five were grouped together and stage of lactation was defined for cows as ≤60 days, 61-120 days, 121-180 days, 181-240 days, 241-305 days and >305 days.

Following all edits, 5,589 IBR records from 4,523 animals separated into 53 contemporary groups were analyzed. Of the 5,589 records, 2,581 were tested using BoHV-1gB and 3,230 using IBRgE; 236 animals had records for both gB and gE ELISAs.

F. hepatica (liver fluke).

All bovine livers in Irish slaughter plants are examined for F. hepatica damage at the point of slaughter by an Irish Department of Agriculture appointed veterinary inspector. These data are recorded on a centralised database. Data were available on 11,427 livers from animals slaughtered between November 2013 and January 2014 from a single abattoir. Only herds that had some evidence of F. hepatica infestation were retained; 9,404 records remained. Following the removal of animals with no known sire, 5,530 animals from 1,161 contemporary groups remained.

Analysis

Variance components for each trait were estimated separately using linear mixed models as follows:

BVD= Parity + Het + Rec + CG + a + dam + PE$_{\text{dam}}$ + e

IBR = CG + Parity + Stage + Het + Rec + a + PE$_{\text{animal}}$ + e

Fluke = CG + Sex + Age + Het + Rec + a + e

Where Parity=parity of the cow, Het = heterosis coefficient, Rec= recombination loss coefficient, CG=contemporary group (fixed effect in IBR and fluke model and random effect in BVD model), a = animal genetic effects, dam = dam genetic effect, PE$_{\text{dam}}$ = dam permanent environmental effect, e=residual, Stage=stage of lactation, PE$_{\text{animal}}$=animal permanent environmental effect, Sex = sex of animal, and Age = age of animal. Breed was accounted for by assigning founder animals to genetic groups; in all instances the pedigree of each animal was traced back to the founder population. The assumed distribution of the dependent variables was binary.

Results and Discussion

Bovine viral diarrhoea virus (BVDV). The prevalence of BVDV persistent infection in the study population was 8.87%. This however is not representative of the national prevalence as data edits were imposed to maximize the likelihood of exposure of dams to BVDV. The prevalence of BVDV within the dataset prior to edits was 0.63%. The direct heritability (standard error in parenthesis throughout) for susceptibility to BVDV was 0.16 (0.02); the maternal heritability for susceptibility to BVDV was 0.05 (0.02). Dam repeatability for BVDV was 0.48 (0.02). A negative genetic correlation -0.16 (0.32) existed between the direct and maternal genetic effects but it was not different from zero. No previous estimates of genetic parameters for susceptibility to BVDV persistent infection exists in the literature for cattle. The relatively low heritability of BVDV susceptibility reported in the present study is consistent with the low heritability estimates for susceptibility to bovine respiratory disease reported in other cattle populations (Heringstad et al. (2008); Snowden et al. (2005)) as well as most other diseases in cattle (Berry et al. (2011)).

The genetic standard deviation for the direct and maternal effects was 0.08 and 0.04 units, respectively, signifying considerable differences in animal genetic merit for BVDV resistance. Figure 1 illustrates a frequency distribution of the mean progeny prevalence of BVDV per sire for sires with at least 50 progeny in at least 10 different herds; some bulls had up to 26% of their progeny test positive for BVDV. The relationship between mean progeny BVDV prevalence per sire and sire estimated breeding value (EBV) for BVDV is in Figure 2 with the association between mean grand-progeny BVD prevalence and maternal grandsire EBV for BVDV in Figure 3; only animals with >50 progeny in >10 herds were plotted.

Bovine herpesvirus type 1 (BoHV-1). The incidence of gB and gE positive records in the database was 28.5% and 35.8%, respectively. Variance components and both heritability and repeatability estimates for BoHV-1 status are in Table 1. Heritability estimates for gE (0.03 to 0.06; the lower estimated was not different from zero) was lower than observed for gB (0.28 to 0.34). The repeatability estimates for both varied from 0.42 to 0.69. No heritability existed between the direct and maternal genetic effects but it was not different from zero. For BoHV-1 in cattle exists in the literature. The heritability estimates for both gE and gB are, nonetheless, either side of the heritability estimate reported in the present study for BVDV. The genetic standard deviation for the binary trait of BoHV-1 status was 0.07 and 0.15 units for gE and gB, respectively indicating considerable genetic variation present in these study herds. The genetic correlation between gE and gB varied from 0.01 to 0.06; the standard errors varied from 0.18 to 0.19;

F. hepatica (F. hepatica). The prevalence of liver-fluke in the 5,530 animals included in the analysis was 41%. The heritability of presence of liver-fluke was 0.15 (0.0629). The genetic standard deviation for the presence of
**F. hepatica** was 0.16 units. No previous estimates of genetic parameters for susceptibility to liver-fluke in cattle exist in the literature. Pan et al. 2004 reported a heritability of 0.084 to 0.124 (SE = 0.025 to 0.042) for susceptibility to *Neospora caninum* in Canadian Holstein cattle. Heritability estimates for gastrointestinal nematode burden, measured as eggs per gram of faeces or larvae per gram of faeces, ranged from 0.00 to 0.25 (SE = 0.02 to 0.05) in Dutch Holstein-Friesian cattle (Cooppieters et al. (2009)); the average was 0.09.

**Conclusions**

Considerable heritable genetic variation in susceptibility to the three diseases examined in the present study clearly exists. As BVDV status is available for all calves born in Ireland due to requirements of the national BVD eradication scheme and as liver-fluke data are now being routinely collected by the majority of Irish slaughter plants, national genetic evaluations for both diseases are possible. Inclusion of these traits in the national dairy and beef breeding goals may be a useful strategy in complementing on-going eradication and control measures for these diseases on Irish farms.

**Literature Cited**

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