



## Genetic analysis of leukosis incidence in United States Holstein and Jersey populations

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### ABSTRACT

Bovine leukosis (BL) is a retroviral disease caused by the bovine leukosis virus that affects only cattle. It is associated with decreased milk production and increased cull rates due to development of lymphosarcoma. The virus also affects the immune system. Infected cows display a weak response to some vaccinations. It is important to determine if the heritability of BL susceptibility is greater than zero, or if the environment is the only factor that can be used to reduce the transmission and incidence of the disease. Accordingly, the aim of this study was to estimate the heritability for BL incidence and the genetic merit of sires for leukosis resistance in Holstein and Jersey cattle. Continuous scores and binary milk ELISA results for 13,217 Holstein cows from 114 dairy herds across 16 states and 642 Jersey cows from 8 dairy herds were considered. Data were obtained from commercial testing records at Antel BioSystems (Lansing, MI). Out of the 13,859 animals tested, 38% were found to be infected with the disease. Linear and threshold animal models were used to analyze the continuous and binary data, respectively. Results from both models were similar in terms of estimated breeding values and variance components in their respective scales. Estimates of heritability obtained with the 2 approaches were approximately 8% for both breeds, indicating a considerable genetic component underlying BL disease incidence. The correlation between the estimated breeding values from the 2 models was larger than 0.90, and the lists of top 10% bulls selected from each model had about 80% overlap for both breeds. In summary, results indicate that a simple linear model using the continuous ELISA scores as the response variable was a reasonable approach for the genetic analysis of BL incidence in cattle. In addition, the levels of heritability found indicate that genetic selection could also be used to decrease susceptibility to bovine leukosis virus infection in Holstein and Jersey cattle.

Further research is necessary to investigate the genetic correlations of BL with other production and reproduction traits, and to search for potential genomic regions harboring major genes affecting BL susceptibility.

**Key words:** bovine leukosis, heritability, milk ELISA, threshold model

### INTRODUCTION

Bovine leukosis (BL) is a retroviral disease in cattle caused by the bovine leukosis virus (BLV). The disease causes a neoplastic condition of tissues that affects lymph nodes and lymphocytes, giving rise to clinical disease including bovine leukemia, lymphosarcoma, and malignant lymphoma. Bovine leukosis is a blood-borne disease, and the virus survives and transfers within lymphocytes (Ott et al., 2003); a small number of infected animals show clinical signs of the infection. The National Animal Health Monitoring System (NAHMS) reported that BLV was widely prevalent in US dairy herds and 89% of all operations had cattle seropositive for BLV (NAHMS, 1997). The report also indicated that 44% of dairy cattle in the United States were infected with BLV.

The virus can be transmitted in many different ways, including direct exposure to infected blood, saliva, semen, and milk. Kobayashi et al. (2010) studied 90 dairy farms in Japan and found that housing system, dehorning, and presence of horseflies were significantly associated with within-farm seroprevalence of BLV. However, infection rates are relatively low in utero and through ingestion of milk and colostrum from infected animals (Hopkins and DiGiacomo, 1997), although the virus may transfer from infected mothers to progeny during parturition (Nagy et al., 2007). The disease can also be spread by direct transfer of blood from one animal to another. Biting or sucking of insects may be a route of transmission, as well as several routine management practices and tools such as contaminated needles, dehorning, and ear taggers. Gouge dehorning, ear tagging, and branding can contaminate feed areas and other facilities with blood. Multiple use of the same

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needle during routine vaccinations, use of unsterilized needles, and failure to change gloves during pregnancy examination can also increase the number of BLV positive animals. In a self-contained naturally infected herd of 120 dairy cattle where reactors were not preferentially culled, the prevalence rate increased from 6.1 to 34.5% during 1976 to 1978 (Wilesmith et al., 1980). Bulls can also transmit the virus if semen contains blood or lymphocytes, and infection can occur also during natural copulation. Increasing animal density per pen increases the risk of infection (Kobayashi et al., 2010).

Bovine leukosis reduces milk production, increases death losses, and has a negative effect on the dairy cattle industry in general; BLV infection is one of many pathogens that also affect reproduction (Thurmond and Hietala, 1997; Moen et al., 1998; Bartels et al., 2006). Bovine leukosis is a disease that has important effects on the international animal industry and sale of animal products (Vanleeuwen et al., 2010). The estimated economic effect of BLV infection was \$44 million in the United States in 1987 (Thurmond, 1987), but the true cost of BLV infection may be greater than current estimates due to losses in milk production (Brenner et al., 1989; Wu et al., 1989). Decreased productivity and profitability is associated with the subclinical BLV infection (Erskine et al., 2012), and positive BL herds have been significantly associated with high infectious disease incidence, reproductive inefficiency, low milk production, and higher culling rates (Emanuelson et al., 1992). A BLV-negative cow has a longer life span, produces a total of 3.5% more milk, and has, on average, 48 fewer days open per lactation than a BLV-positive cow (Brenner et al., 1989). Advantages of negative over positive BLV animals were estimated at 488 kg of milk, 15 kg of milk fat, and 16 kg of milk protein per lactation (Byrem et al., 2011). Using data from 20 western states with large populations of dairy cows and 46.3% BLV prevalence, Ott et al. (2003) indicated that cows in test-positive BLV herds produced 218 kg (3%) less milk per year than cows in test-negative BLV herds. Similar estimates were reported by Emanuelson et al. (1992) with data from 14,424 herds in Sweden, in which the decline in milk production associated with BLV infection was 2.5%. Even when BLV infection does not seem to affect the overall animal health, it still affects significantly the milk yield (Motton, 2002).

Some other studies used individual cow data to investigate the association between milk yield and BLV infection, and different results have been reported. The difference between test-negative and test-positive BLV herds was 3.5% per cow per year (Brenner et al., 1989); however, this percentage was 11% according to D'Angelino et al. (1998). Nationally it was estimated that BLV reduced milk production by 0.7% in 1995 and

led to a loss of \$285 million for producers. Moreover, such a loss in milk production cost consumers an additional \$240 million in that year, bringing the total economic loss due to BLV infection up to \$525 million, without including any veterinary expenses associated with BLV (Ott et al., 2003). In another study, Thurmond (1987) estimated the nonmilk economic losses at \$80 million. In Michigan, reduced milk production was associated with increased BLV prevalence, and BLV affected economic status in high-producing dairy herds (Erskine et al., 2012). High disease incidence in dairy herds increases the expenses associated with milk production, and, because BL affects the immune response to some vaccinations (Yamamoto et al., 1984; Erskine et al., 2011), this might be the reason behind an association between BLV infection and incidence of other diseases.

Furthermore, restriction of exports is one of the most important economic effects of BL disease. Animals or animal products infected with BLV cannot be accepted in many countries, and large monetary losses may occur to breeders by rejecting heifers, embryos, or semen produced from their animals.

Bovine leukosis virus is not known to cause disease or even to be transmissible to humans. However, higher attention and concern was brought after discovery of the human T cell leukemia virus type 1 (HTLV-1) and the significant effect of retroviruses as human pathogens (Poesz et al., 1980); HTLV-1 is considered to be the cause of adult T-cell leukemia (Acheson, 2007; Matsuoka and Jeang, 2007). The BLV and HTLV-1 genome sequences, as well as sequences of their proteins (amino acids), are similar enough to infer that both viruses have a common ancestor (Willems et al., 2000). In addition, some research has shown a potential link between consumption of BLV-contaminated dairy and beef and incidence of breast cancer worldwide (Rees, 2012).

Clinical signs of BL are rarely seen, and in most cases a clinical test is required to determine whether an animal is infected (Schwartz and Levy, 1994). Milk ELISA test is one of the methods used for that purpose; ELISA is an assay to detect the antibodies linked to BLV in milk or blood samples. The estimated sensitivity of milk ELISA is 98%, the specificity is 100% (Jacobsen et al., 1985; Monke et al., 1992). Results of the milk ELISA test are recorded on a continuous scale and then dichotomized using a threshold of 0.1; animals with milk ELISA score higher than that cutoff are considered infected.

Dairy studies published in 1997 and 2007 (NAHMS, 2007, 1997) reported similar percentages for the presence of antibodies against BLV, indicating ineffective progress in reducing the prevalence of the disease. However, taking into account that different testing methods

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