

Influence of Genetic Factors on the Susceptibility of Cattle to Bovine Leukemia Virus Infection*

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Abstract—An epidemiological study of a dairy herd in Florida was undertaken to investigate the factors that influence infection with bovine leukemia virus (BLV). Using the glycoprotein antigen immunodiffusion test, 75.8–82.7% of the cows were found to have antibodies to BLV between 1975 and 1977. Prevalence of BLV antibodies increased until 5 yr of age after which it remained at a steady level. The data were examined by least squares analysis of variance to determine heritability of susceptibility to BLV infection. A heritability estimate of 0.48 ± 0.22 was determined, suggesting considerable genetic influence on susceptibility to BLV infection.

INTRODUCTION

BOVINE leukemia virus (BLV) has many morphological, biochemical and biophysical similarities with the other mammalian and avian leukemia viruses [1–10]. BLV particles have been identified repeatedly in cultures of lymphocytes from cattle with lymphosarcoma [1, 3–5, 11–13]. Transmission experiments have shown that BLV has oncogenic activity [14–16]. Sero-epidemiological studies have demonstrated a strong association between BLV infection and bovine lymphosarcoma [17–20] and have indicated that the predominant mode of transmission of BLV is horizontal [21, 22]. Electron microscopical studies detected BLV in 19 out of 20 fluorescent antibody-positive cattle but failed to demonstrate the virus in 12 antibody-negative animals [19]. As a result of these findings, it is widely accepted that BLV is causally related to bovine lymphosarcoma, a systemic malignancy also referred to as bovine leukemia and bovine leukosis [23].

Many epidemiological investigations have examined the influence of various factors on infection of cattle with bovine lymphosarcoma or BLV. Studies on clinical cases have suggested that the prevalence of bovine lymphosarcoma is related to age [24–29], breed [25, 29], type of production (dairy or beef) [25, 27], and herd size [26, 28, 29]. Serological studies have found that the prevalence of antibodies to BLV antigens is similarly related to age [18, 22, 30] and type of production [30, 31], but not herd size [30, 31]. In addition, familial aggregations of cases of bovine lymphosarcoma have been demonstrated [11, 32–38], suggesting the possibility that genetic factors might influence the susceptibility of cattle to the disease.

The present study was undertaken to investigate the factors that influence infection of dairy cattle with BLV and, in particular, to measure the extent to which susceptibility to BLV infection is inherited in the cow.

MATERIALS AND METHODS

Cattle

The cattle studied were those cows in the University of Florida Dairy Research Unit herd which were 18 months of age or older. The composition of the herd by breed was 56% Holstein, 31% Jersey, 7% Holstein

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crosses, 4% Guernsey and 2% Brown Swiss. The animals ranged in age from 18 months to 13 yr old. The cows were bled for serum collection as follows: 227 animals in October 1975, 225 in August 1976 and 219 in August 1977. Six cases of bovine lymphosarcoma had been confirmed histopathologically in the herd between September 1976 and June 1978. The breed and age of each animal were recorded at the time of bleeding. Furthermore, the sire of each cow was identified, all cattle in the herd having been sired by artificial insemination.

Serology

Each serum sample was tested for BLV antibodies using the agar gel immunodiffusion test with a glycoprotein antigen (Leukassay-B, Pitman-Moore Inc., Washington Crossing, New Jersey). Agar gel plates were prepared with 0.7% Noble agar (Difco Laboratories, Detroit, Michigan) in 0.15M borate buffer, pH 8.6, containing 7% sodium chloride. Fifteen millilitres of agar were dispensed into each 100 mm Petri dish. One central and 6 peripheral wells, each 7 mm in diameter and 3 mm apart, were cut in each quadrant of the Petri dish, allowing for 1 control pattern and 3 test patterns per dish. Each pattern of wells consisted of a central antigen well surrounded by 6 equidistant serum wells. For the control pattern, the serum wells were filled with negative, weak positive or strong positive control sera. For each test pattern, they were filled alternately with positive control serum and test sera. The plates were incubated for 48 hr in a humidified chamber at room temperature. Test sera were recorded as positive when precipitation lines of identity formed with positive control serum. Each positive reaction was interpreted to indicate past infection with BLV. This test was chosen for the present study because of its simplicity and because of its high relative sensitivity and relative specificity when compared with established tests for the serodiagnosis of BLV infection [39-41].

Data analysis

The dairy herd data were examined by least squares analysis of variance to determine the heritability of susceptibility to BLV infection in the cow. Statistical analysis was performed by use of Harvey's Least Squares Maximum Likelihood Mixed Model computer program [42], with the model:

$$y_{ijklm} = \mu + a_i + b_{ij} + c_{ijk} + F_l + e_{ijklm}$$

where y_{ijklm} represents the test result for BLV antibodies, μ the mean, a_i the breed of

the cow (fixed effect), b_{ij} the sire of the cow (random nested effect), c_{ijk} the cow herself (random nested effect), and F_l other fixed effects (linear, quadratic and cubic terms for age). The model, therefore, was a nested design (daughters nested within sires and sires nested within breeds) with cross-classified fixed effects. Heritability, as 4 times the paternal half-sib correlation, was estimated using the formula:

$$\text{Heritability} = \frac{4\sigma_s^2}{\sigma_c^2 + \sigma_s^2 + \sigma_e^2}$$

where σ_s^2 was the sire variance, σ_c^2 the variance among daughters within sires, and σ_e^2 the error variance representing the variability among observations within daughters within sires. Heritability is defined as the ratio of additive genetic variance to phenotypic variance [43]. It measures the fraction of the total phenotypic variance due to variation in breeding values of individuals, the breeding value of any individual being equal to the sum of the average effects of the genes it carries [44].

RESULTS

The results of the least squares analysis of variance are summarized in Table 1. Prevalence of BLV antibodies was significantly influenced by sire (nested within breed), cow (nested within sire within breed) and age, but not by breed. Variance component estimates were: $\sigma_s^2 = 0.01691$, $\sigma_c^2 = 0.06627$, and $\sigma_e^2 = 0.05791$. Heritability thus was 0.48 (± 0.22 S.E.).

The prevalence of BLV antibodies in the dairy herd was 78.9% (179 of 227 seropositive) in 1975, 82.7% (186 of 225) in 1976 and 75.8% (166 of 219) in 1977. The regression of prevalence of BLV antibodies on age is shown in Fig. 1. The prevalence increased from 18 months to 5 yr of age and thereafter remained at a consistently high level of about 90%.

DISCUSSION

It was demonstrated over 30 yr ago that genetic factors influence the incidence of leukemia in mice [45, 46]. Later, it was found that susceptibility of mice to leukemogenesis by Gross virus was genetically determined [47, 48]. Many investigators have reported familial aggregations of cases of leukemia in man [49-56] and cattle [11, 32-38]. It was concluded that the aggregations of human cases probably resulted from a genetic predisposition to leukemia [55, 56]. The results of the bovine

Table 1. Least squares analysis of variance showing factors influencing prevalence of BLV antibodies in Florida dairy cows, 1975-1977

Source of variation	Degrees of freedom	Mean squares	F-ratio
Breed	4	0.379	1.20
Sire within breed	79	0.316	1.73*
Cow within sire within breed	265	0.183	3.15*
Age (linear)	1	1.174	20.28*
Age (quadratic)	1	0.589	10.17*
Age (cubic)	1	0.344	5.94†
Error	319	0.058	

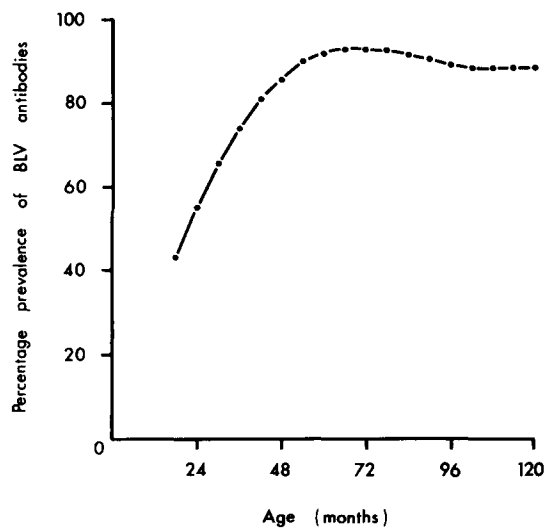
* $P < 0.01$.† $P < 0.025$.

Fig. 1. Regression of prevalence of BLV antibodies on age in a Florida dairy herd, 1975-1977.

studies were interpreted to suggest either genetic susceptibility to bovine lymphosarcoma or vertical transmission of an infectious agent [33-36]. Subsequent work indicated that BLV, the putative infectious agent of bovine lymphosarcoma, was transmitted horizontally in most instances [21, 22]. There are ample data, therefore, to warrant further investigation of genetic factors as host determinants of human and bovine leukemia.

This study used least squares analysis of variance procedures to examine for any influence of genetic factors on infection with BLV in a dairy herd. Heritability was estimated from the paternal half-sib correlation, a method that minimized non-genetic biases by consideration of only sire effects. As a result, the only possible non-genetic influence on the heritability estimate would have been transmission of infection via frozen semen from sire to dam to fetus. However,

recent studies have indicated no evidence of transmission of BLV from infected bulls to offspring sired by artificial insemination [57, 58]. The results, therefore, provide convincing evidence of genetic susceptibility to BLV infection and, consequently, to bovine lymphosarcoma. The heritability of 0.48 suggests that this trait is quite highly heritable. For comparison, the milk yield of cattle has a heritability value of about 0.25 [59].

The relatively large S.E. of 0.22 arises from the small sample size (671 observations on 349 cows by 84 sires) and the analysis of binary data (positive and negative test reactions being coded 1 and 0, respectively). Assuming the heritability estimate to be unbiased, the standard error suggests that there is about a two-third's chance that the true value of heritability falls between 0.26 and 0.70 (0.48 ± 0.22).

Only a small proportion of the cattle that develop detectable antibodies to BLV manifest clinical disease [20], demonstrating that BLV is only one of the determinants of bovine lymphosarcoma. The heritability study reported herein suggests that genetic factors may be another of the multiple determinants of the disease since they have been shown to influence infection of cattle with BLV. This study also examined other variables (breed and age) for their influence on BLV infection.

There was no significant difference ($P > 0.05$) in prevalence of BLV antibodies between the different breeds in the dairy herd. However, there was a well-defined relationship between prevalence of BLV antibodies and age. Prevalence progressively increased until 5 yr of age after which it remained at a steady level. Similar age trends have been demonstrated in other serological studies [18, 22, 30]. Although no cattle less than 18 months old were examined in this study, the

data did indicate that many animals became infected after calthood, supporting horizontal transmission as the major mode of spread of BLV.

The heritability study reported in this paper considered only 1 dairy herd and, therefore, needs to be repeated by examination of an appropriate sample of herds from a wider geographical area. Nevertheless, the initial

results indicate that the susceptibility of cattle to BLV infection is partially under genetic control, suggesting genetic selection as a possible method for control of bovine lymphosarcoma.

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