Genetic Susceptibility to *Neospora caninum* Infection in Holstein Cattle in Ontario

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ABSTRACT

Neospora caninum has been reported to be an important cause of endemic fetal loss and occasional abortion epidemics in cattle around the world. This study examined 12,016 sera collected from 9723 Holstein cows on 125 herds across Ontario in 1998, 1999, and 2000. An enzyme-linked immunosorbent assay was used to examine the sera for antibodies to *N. caninum*. The overall prevalence of *N. caninum* antibodies in the cattle was 11.2% and the prevalence in individual herds varied from 0 to 70.4%. Among 3109 daughter-dam pairs, 619 positive dams had 252 positive daughters, giving a detected vertical transmission rate of 40.7%. In contrast, there were only 6.7% positive daughters from negative dams (167 of 2490). Pedigree edits left 8031 cows with 1463 sires for estimation of heritability. Five genetic models (sire model, animal model, sire-dam model, a sire-maternal grandsire model, and a maternal effects model) with fixed effects of bleeding year-month, age of the animals, and herd were fitted to the data. The estimated heritability of susceptibility to *N. caninum* ranged between 0.084 and 0.124. The sire-maternal grandsire model and the maternal effects model provided better fit than the other models because the maternal genetic variance was much greater than the direct genetic variance. To reduce the incidence of *N. caninum* infection, more emphasis should be placed on management practices than on genetic selection. (**Key words:** *Neospora caninum*, genetic susceptibility, dairy cattle)

Abbreviation key: AIC = Akaike information criterion, AM = animal model, AMM = animal maternal effects model, MSE = mean square error, SDM = sire-dam model, SGM = sire-maternal grandsire model, SM = sire model, S/P = sample-to-positive.

INTRODUCTION

Neospora caninum is a protozoan parasite that was first identified in dogs (Dubey et al., 1988) and has subsequently been found to be an important cause of endemic fetal loss, and occasional abortion epidemics, in dairy cattle (Anderson et al., 1991). In Australia, Boulton et al. (1995) examined 729 aborted bovine fetuses and reported that 152 were associated with *N. caninum*, i.e., an attributable fraction of 21%. In Californian dairy cattle, Anderson et al. (1995) attributed 42.5% of examined aborted fetuses (113 of 266) to *N. caninum* and concluded that this parasite was the major cause of abortion. Currently, *N. caninum* is the single most common infectious cause of abortion diagnosed in Ontario cattle, as 15% of all bovine abortion submissions to the Animal Health Laboratory, University of Guelph, are associated with this parasite (McEwen et al., 2001).

Not all cattle that are seropositive for *N. caninum* have an abortion. However, the risk of abortion for seropositive cows has been shown to be twice that for seronegative cows on a dairy herd in central California (Paré et al., 1997). Similarly, Atkinson et al. (2000) showed that the abortion rate was 26% (18 of 68) for *N. caninum*-seropositive cows but only 3% (3 of 117) for seronegative cows on a commercial dairy herd in Australia. In general, it appears that *N. caninum*-seropositive cattle are 3 to 4 times more likely to abort than seronegative animals (Paré et al., 1997; Moen et al., 1998; Corbellini et al., 2002).

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Abortion in cattle attributable to fetal infection with *N. caninum* is now recognized in many countries (Dubey and Lindsay, 1996) and generally occurs between 3 and 7 mo of gestation. Aside from the economic cost of failed reproduction, *N. caninum* infection can also cause indirect economic losses as a result of premature culling and diminished milk production. For example, seropositive cows in their first lactation on a 2000-head farm in California had a greater risk of being culled (1.6 times) and produced less milk (2.5 lb/d per cow) than seronegative cows (Thurmond and Hietala, 1996, 1997). Thus, *N. caninum* may have a significant impact on the profitability of dairy cattle.

Most research indicates that vertical transmission is the primary route by which cattle become infected with *N. caninum*. Thus, in seroepidemiological studies on 2 dairies in the San Joaquin Valley, California, 81% of seropositive cows (93 of 115) and 5% of seronegative cows (8 of 170) had congenitally infected calves (Paré et al., 1996). Similarly, Davison et al. (1999) in the United Kingdom concluded that the efficiency of vertical transmission was 95.2% (118 seropositive calves out of 124 offspring from seropositive dams). Finally, research on the rate of vertical transmission of *N. caninum* for 23 dairy herds in Québec indicated that while the prevalence of seropositive animals in herds varied from 4.3 to 61.8% (average = 21.9%), the overall rate of vertical transmission was 44.4%, varying from 0 to 85.7% within herds (Bergeron et al., 2000).

The high rate of vertical transmission of *N. caninum* has led to the recommendation to cull infected animals as the primary strategy to reduce their number in a herd. However, for herds with a high prevalence, culling all infected animals within a short period of time is not a practical way to eliminate *N. caninum* from a herd. Thus, to enable the dairy industry to develop optimal management strategies for limiting or reducing the impact of *N. caninum* infections, a large study was undertaken on dairy farms in Ontario. Serum samples were collected from Holstein cattle across the province, and an ELISA was used to determine the *N. caninum* antibody status of each sample. The objectives of this study were to use the resultant data to determine the prevalence of *N. caninum* in Ontario cattle, to estimate the efficiency of vertical transmission of the parasite, and to investigate the scope for genetic strategies to reduce the prevalence of *N. caninum* infections by estimating heritability under several genetic models.

MATERIALS AND METHODS

Collection and Analysis of Sera

Blood samples were collected from Ontario dairy herds in 1998, 1999, and 2000. Herds that were bled

in 1998 (n = 56) belonged to the Ontario Sentinel Herd Project (Cramer et al., 2002) and were intentionally selected for a study on udder health. These herds were considered representative of Ontario Holstein herds. Herds that were bled in 1999 (n = 86) were selected for a case-control study; 28 herds had had at least one abortion in the previous year that was diagnosed as due to *N. caninum* on the basis of fetal histopathology; 30 herds had had at least one abortion in the previous year that was diagnosed as not due to *N. caninum* on the basis of fetal histopathology; and 28 herds were selected on the basis of having a herd *N. caninum* seroprevalence that was less than 7%. Herds bled in 2000 (n = 50) were selected from the pool of herds previously sampled on the basis of a *N. caninum* seroprevalence that was $\geq 10\%$ in 1998 or 1999. Blood samples were collected only from lactating cows in the herds visited in 1998. However, for the herds visited in 1999 and 2000, samples were collected from adult cows and heifers greater than 6 mo of age. The 1998 and 1999 data were used to identify seropositive cows and existing daughters. The 2000 data were collected primarily to identify more daughters of the seropositive cows previously identified in 1998 and 1999. Thus, if seropositive dams were culled prior to the herd visit in 2000, information about their daughters would still have been used. Previous work with the same *N. caninum* serology data as used in this study has indicated that among all the herds, as a whole, the risk of cattle being culled was not associated with their *N. caninum* serostatus (Cramer et al., 2002; Hobson, 2003). Sera were prepared from all blood samples within 24 h of collection and stored at -70°C prior to analysis.

All sera were assayed for antibodies to *N. caninum* using a kinetic-ELISA at the California Animal Health & Food Safety Laboratory System, University of California, Davis (Paré et al., 1995). A sample-to-positive (S/P) control $V_{\max}$ (average maximum slope of the optical density over time) ratio of ≥ 0.45 was used to maximize the percentage correct classification of *N. caninum*-infection status, with an estimated sensitivity of 88.6% and specificity of 96.5%. Thus, for most analyses the cows were considered seropositive when the ELISA S/P ratios were ≥ 0.45 and seronegative when the S/P ratios were < 0.45 . For seroconversion analyses, S/P ratios in the range ≥ 0.45 to < 0.70 were defined as moderately positive, while values ≥ 0.70 were defined as strongly positive. At the S/P ratio ≥ 0.70 , the sensitivity and specificity of the antibody ELISA are 79 and 100%, respectively (Paré et al., 1995).

A total of 12,016 serum samples were analyzed. Cows with repeated samples included 811 sampled in 1998 and 1999, 1141 sampled in 1999 and 2000, and 413 sampled in 1998 and 2000. These repeated records were

Figure 1. Density distribution of *Neospora caninum* antibody ELISA S/P (sample-to-positive) ratios before logarithmic transformation.

used to compute the conversion rates between seropositive and seronegative status. Further analyses included only the record with the highest S/P ratio for cows with multiple records, leaving 9723 samples. These unique serum samples collected over the 3 yr included 3109 daughter-dam pairs; these were used to estimate the efficiency of vertical transmission. The analysis of heritability included 8031 cows and heifers whose sire, dam, and maternal grandsire were traceable in the pedigree file provided by the Canadian Dairy Network, Guelph, Ontario.

The raw ELISA S/P ratios were distributed with a long tail on the right (Figure 1). A logarithmic transformation by the formula $\ln(Y) + 4.5$ yielded transformed data whose distribution was much closer to normal (Figure 2).

Definitions of Prevalence, Vertical Transmission, and Seroconversion

The prevalence of seropositive animals (S/P ratio ≥ 0.45) in herds was defined as the number of seropositive animals divided by the total number of animals tested within that herd in a given year. The horizontal transmission rate was defined as the proportion of seropositive daughters born to seronegative dams. The efficiency of vertical transmission was estimated as the proportion of seropositive daughters born to seroposi-

tive dams. For calculation of both transmission parameters, the serostatus of the dam in each dam-daughter pair was defined on the basis of serological data that were obtained for the dam prior to the birth of the daughter; the dam was defined as *N. caninum* seropositive if it tested positive on one or more occasions; the dam was defined as *N. caninum* seronegative if all serum samples tested negative. Similarly, a daughter was defined as *N. caninum* seropositive if one or more serum samples collected from the animal tested positive.

A cow was considered to have seroconverted if the animal was seropositive in one year but seronegative in the previous year, or vice versa. The seropositive conversion rate was calculated by dividing the number of seropositive animals in a given year that converted from seronegative in the previous year by the total number of seronegative animals in the previous year. The seronegative conversion rate was obtained by dividing the number of seronegative animals in a given year that converted from seropositive in the previous year by the total number of seropositive animals in the previous year. A paired *t*-test was used to analyze the seroconversion data.

Genetic Models

The following models were used to estimate the heritability of susceptibility to *N. caninum* infection.

Figure 2. Density distribution of *Neospora caninum* antibody ELISA S/P (sample-to-positive) ratios after logarithmic transformation.

Sire model (SM): $y = X_s\beta_s + b_h c + Z_s s + e$ [1]

Animal model (AM): $y = X\beta + Z_a a + e$ [2]

Sire-maternal grandsire model (SGM):
 $y = X\beta + Z_s s + Z_g g + e$ [3]

Sire-dam model (SDM):
 $y = X\beta + Z_s s + Z_m m + e$ [4]

Animal maternal effect model (AMM):
 $y = X\beta + Z_a a + Z_m m + e$ [5]

g = vector of maternal grandsire effects;
 m = vector of maternal genetic effects; and
 e = vector of random residual effects.

The matrices X_s , X , Z_a , Z_s , Z_m , and Z_g are known incidence matrices that relate observations to their respective fixed and random effects. The variances and covariances for the random effects were $V(s) = A\sigma_s^2$, $V(g) = A\sigma_g^2$, $V(a) = A\sigma_a^2$, $V(m) = A\sigma_m^2$, $Cov(a, m) = A\sigma_{am}$, and $V(e) = I\sigma_e^2$, where A is the numerator relationship matrix between animals and I is the identity matrix. The variance components and computation of heritability in different models is shown in Table 1. The direct, maternal, and total heritability in the animal maternal effect model (AMM) were defined as $h_d^2 = \sigma_a^2/\sigma_p^2$, $h_m^2 = \sigma_m^2/\sigma_p^2$ and $h_T^2 = (\sigma_a^2 + 1.5\sigma_{am} + 0.5\sigma_m^2)/\sigma_p^2$, respectively, where $\sigma_p^2 = \sigma_a^2 + \sigma_{am} + \sigma_m^2 + \sigma_e^2$ (Willham, 1972).

All 5 models were fitted using ASREML (Gilmour et al., 2001). The SAS GLM, VARCOMP, and MIXED procedures (SAS, 1990) were also used in the analysis of the variation of susceptibility to *N. caninum* infection. The categorical analysis of serological status (i.e., seropositive or seronegative as defined with the ELISA S/P threshold of ≥ 0.45) with the sire model was fitted by ASREML using a probit link function (the cumulative normal distribution function) with the residual vari-

where

y = vector of the transformed ELISA antibody data, or the categorical infection status (sire model only);

β = vector of fixed effects of bleeding year-month, age (yr), and herd;

β_s = vector of fixed effects of bleeding year-month and age (yr);

b_h = regression coefficients of y on the herd seroprevalence;

c = vector of herd seroprevalence over the 3 yr;

s = vector of sire effects;

a = vector of direct additive genetic effects;

Table 1. The variance components and calculation of heritability with different models.¹

Model	Variance component	Heritability
Sire model	σ_s^2, σ_e^2	$4\sigma_s^2/(\sigma_s^2 + \sigma_e^2)$
Animal model	σ_a^2, σ_e^2	$\sigma_a^2/(\sigma_a^2 + \sigma_e^2)$
Sire-maternal grandsire model	$\sigma_s^2, \sigma_g^2, \sigma_e^2$	$4\sigma_s^2/(\sigma_s^2 + \sigma_g^2 + \sigma_e^2)$
Sire-dam model	$\sigma_s^2, \sigma_m^2, \sigma_e^2$	$4\sigma_s^2/(\sigma_s^2 + \sigma_m^2 + \sigma_e^2)$
Animal maternal effect model	$\sigma_a^2, \sigma_{am}, \sigma_m^2, \sigma_e^2$	$(\sigma_a^2 + 1.5\sigma_{am} + 0.5\sigma_m^2)/(\sigma_a^2 + \sigma_{am} + \sigma_m^2 + \sigma_e^2)$

¹ σ_s^2 = Sire genetic variance, σ_g^2 = maternal grandsire genetic variance, σ_a^2 = direct additive genetic variance, σ_m^2 = maternal genetic variance, σ_{am} = genetic covariance between direct and maternal effects, and σ_e^2 = residual variance.

ance set to 1. All remaining analyses of variance components used the log transformed ELISA S/P ratio directly.

The fit of the models to the complete data set was compared by mean squared error (MSE) and Akaike information criterion (AIC, Akaike, 1973). The MSE using the complete data set was computed as

$$MSE_c = \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2$$

where y_i = observed value, $\hat{y}_i$ = predicted value by a given model, and n = total number of observations in the data set (8031). The AIC was obtained by $n \times \ln(SSR/n) + 2 \times (p + 1)$, where SSR is the sum of squares of residuals, and p is the number of parameters in the model.

The models were also validated by randomly splitting the data into 2 parts (e.g., Varona et al., 1999): a retained part, consisting of 70% of the records, for parameter estimation, and a deleted part, consisting of the remaining 30% of the records, for measuring predictive ability. Random effects for all animals were kept in the analysis of the retained records to obtain the solutions needed to predict the deleted records. The predictive ability of the 5 models was compared by

$$MSE_d = \frac{1}{N_d} \sum_{i=1}^{N_d} (y_i - \hat{y}_i^*)^2$$

where y_i = observed value of a deleted record, $\hat{y}_i^*$ = predicted value of a deleted record using the solutions for a given model from the retained records, and N_d = number of deleted records.

RESULTS AND DISCUSSION

Seroprevalence Estimation

The overall prevalence of antibody to *N. caninum* in the 125 selected Holstein herds was 11.2%. The average herd seroprevalences were estimated at 10.8, 11.3, and 13.5% in 1998, 1999, and 2000, respectively (Table 2). The average herd seroprevalence in 2000 was higher than in the previous 2 yr because only herds with a *N. caninum* seroprevalence of 10% or greater in 1998 or 1999 were revisited in 2000.

Serological Conversion

On the basis of the ELISA S/P threshold of ≥ 0.45 , the seropositive conversion rate was 3.98% of 778 cows between 1998 and 1999, 5.08% of 886 cows between 1999 and 2000, and 7.71% of 350 cows between 1998 and 2000 (Table 3). The seropositive conversion is examined in more detail in Tables 4 to 6. There were 27 animals (of 778) that converted from seronegative in 1998 to moderately seropositive in 1999, and 4 animals (of 778) that converted from seronegative in 1998 to strongly seropositive in 1999. Table 5 shows that there were 31 animals (of 886) that converted from seronegative in 1999 to moderately positive in 2000, and 14 animals (of 886) that converted from seronegative in

Table 2. *Neospora caninum* seroprevalence in the selected Holstein herds (125) across Ontario in the years 1998, 1999, and 2000.¹

	1998	1999	2000
Herds (no.)	56	86	50
Seroprevalence (%)	10.8	11.3	13.5
Variation (%)	0-66.7	0-70.4	0-64.2
Total animals (no.)	3334	4487	4195

¹Overall herd average over the 3 yr was 11.2%.

Table 3. Seroconversion rate between seropositive and seronegative cows using an ELISA S/P (sample-to-positive) threshold of ≥ 0.45 when the animals had repeated records in the years 1998, 1999, and 2000.

Period	1998–1999 ¹	1999–2000 ¹	1998–2000 ¹
Seropositive conversion (%) —→+ — +	3.98 (778) ²	5.08 (886) ²	7.71 (350) ²
Seronegative conversion (%) —→+ + —	42.42 (33) ³	28.24 (255) ³	65.43 (81) ³
Total samples (no.)	811	1141	431

¹There was a significant difference for the ELISA S/P ratio of animals between the 2 yr tested by a paired *t*-test ($P < 0.001$).

²The number in parentheses denotes the number of seronegative animals in the first year.

³The number in parentheses denotes the number of seropositive animals in the first year.

1999 to strongly positive in 2000. Finally, Table 6 indicates that there were 25 animals (of 350) that converted from seronegative in 1998 to moderately positive in 2000, and only 2 animals (of 350) that converted from seronegative in 1998 to strongly positive in 2000.

Using the ELISA S/P threshold of ≥ 0.45 , the seronegative conversion rate was 42% of 33 cows between 1998 and 1999, 28.2% of 255 cows between 1999 and 2000, and 65% of 81 cows between 1998 and 2000 (Table 3). Paired *t*-tests indicated that the changes for these animals were all significant ($P < 0.001$). The seronegative conversion rates between 1998 and 1999 and between 1998 and 2000 were remarkably high. However, about 78% of the conversion for these 2 periods was from moderately positive to seronegative. Detailed information on seronegative conversion is given in Tables 4, 5, and 6.

In summary, there was a general tendency over time for seropositive cattle to undergo seronegative conversion, rather than vice versa, which is consistent with data from Canadian cow-calf herds (Waldner et al., 2001).

Vertical Transmission of *N. caninum* Infection

Among the collected ELISA data, 3109 daughter-dam pairs from 117 herds (1 to 151 dam-daughter pairs per

herd) were available to estimate the efficiency of vertical transmission of *N. caninum*. The seroprevalence of *N. caninum* for the 3109 daughters was 13.5%. Among the 3109 daughter-dam pairs, 619 seropositive dams had 252 seropositive daughters, which resulted in an overall detected vertical transmission rate of 40.7%. In contrast, there were only 167 seropositive daughters from 2490 seronegative dams, which gave a detected horizontal transmission rate of 6.7% (Table 7). Interestingly, the estimate for the rate of vertical transmission increased to only 45% when the ELISA S/P threshold was raised from ≥ 0.45 to ≥ 0.70 (Table 7).

The vertical transmission rate obtained in this study was considerably lower than the estimates of 81 (Paré et al., 1996), 94 (Waldner et al., 2001), and 95.2% (Davison et al., 1999) obtained from work in California, Alberta (Canada), and the United Kingdom, respectively. However, it was similar to an overall herd estimate of 44% reported for Québec (Bergeron et al., 2000) and 39 to 43% for a herd in the USA (Dyer et al., 2000). The discrepancy between these 2 sets of studies is probably due to the fact that the blood samples in the latter reports, as described here, were all collected from animals over 6 mo of age. In contrast, Paré et al. (1996), Waldner et al. (2001), and Davison et al. (1999) used precolostral blood samples. Thus, because of the man-

Table 4. Conversion of serological status among the 3 ELISA S/P (sample-to-positive) categories when the cows had repeated records in the years 1998 and 1999.¹

1998	1999			Total
	–	+	++	
–	747	27	4	778
+	11	4	5	20
++	3	0	10	13
Total	761	31	19	811

¹Categories were classified in terms of the ELISA S/P ratio. Category: – (seronegative) = S/P ratio < 0.45 , + (moderately seropositive) = S/P ratio ≥ 0.45 and < 0.70 , and ++ (strongly seropositive) = S/P ratio ≥ 0.70 .

Table 5. Conversion of serological status among the 3 ELISA S/P (sample-to-positive) categories when the cows had repeated records in the years 1999 and 2000.¹

1999	2000			Total
	–	+	++	
–	841	31	14	886
+	58	25	24	107
++	14	26	108	148
Total	913	82	146	1141

¹Categories were classified in terms of the ELISA S/P ratio. Category: – (seronegative) = S/P ratio < 0.45 , + (moderately seropositive) = S/P ratio ≥ 0.45 and < 0.70 , and ++ (strongly seropositive) = S/P ratio ≥ 0.70 .

Table 6. Conversion of serological status among the 3 ELISA S/P (sample-to-positive) categories when the cows had repeated records in the years of 1998 and 2000.¹

1998	2000			Total
	–	+	++	
–	323	25	2	350
+	40	9	6	55
++	13	2	11	26
Total	376	36	19	431

¹Categories were classified in terms of the ELISA S/P ratio. Category: – (seronegative) = S/P ratio <0.45, + (moderately seropositive) = S/P ratio ≥0.45 and <0.70, and ++ (strongly seropositive) = S/P ratio ≥0.70.

ner in which samples were collected in the work described here, seronegative conversion of daughters could account for the relatively low detected rate of vertical transmission. Because it is generally assumed that cattle remain permanently infected with *N. caninum*, these data suggest that some of the animals defined as seronegative were in fact false negatives. However, at present, it is not possible to identify such animals antemortem. If antemortem diagnostic tests are developed that allow identification of these animals, it would be important to include them in future genetic analyses, as they probably represent a population of animals with a superior ability to control *N. caninum* infection.

Estimation of the Variance Components

Heritability of susceptibility to *N. caninum* was estimated first using a simple sire model because this model permitted analysis of infection status either as a categorical variable or as a continuous variable. The sire variance from the categorical analysis was 0.023 ± 0.012 on the probit scale, with residual variance fixed at 1, and heritability was 0.090 ± 0.047 . When the log transformed ELISA data were used, the estimated heritability by the same sire model was 0.115 ± 0.036 (Table

Table 7. The *Neospora caninum* serological status of 3109 dams and their daughters >6 mo of age using 2 ELISA S/P (sample-to-positive) cut-off points.

Cut-off	Dam	Daughter		Total
		Seronegative	Seropositive	
≥0.45	Seronegative	2323	167	2490
	Seropositive	367	252	619
	Total	2690	419	3109
≥0.70	Seronegative	2694	108	2802
	Seropositive	169	138	307
	Total	2863	246	3109

8). Expression of serological status in just 2 categories (infected or not infected) appeared to capture most, but not all, of the genetic information in the ELISA S/P ratios. Subsequent analyses were all based on the log-transformed ELISA S/P ratios.

The estimated (co)variances, the heritability of susceptibility to *N. caninum*, and the model selection criteria (MSE_c, MSE_d, and AIC) for 5 genetic models are shown in Table 8. The estimated heritabilities by SM, AM, SGM, SDM, and AMM were 0.115, 0.084, 0.124, 0.103, and 0.301, respectively. The total heritability estimated with the animal maternal effect model was considerably higher than with the other 4 models, because the estimated maternal variance was remarkably higher than the animal direct genetic variance. The large proportion of the maternal variance by the animal maternal effect model confirms that maternal environment plays an important role in the transmission of *N. caninum*. However, it is possible that the effect of *N. caninum* infection in a dam would be confounded with the estimates of the direct genetic and maternal genetic effects because *N. caninum* infection in a dam might affect the dam's performance. If that was the case, this would bias the estimates of both effects. However, on many farms it does not appear that *N. caninum* has a significant impact on production (Cramer et al., 2002; Hobson et al., 2002).

Collectively, the results suggest that the maternal permanent effect is a major factor influencing the high vertical transmission rate of *N. caninum*, since the heritability of direct genetic effects estimated by all models was small (8 to 12.4%). As a result, management practices (prevention, culling of infected cows, etc.) should be more effective for controlling *N. caninum* infection than genetic selection.

Finally, the fit of the 5 models was compared based on 3 different criteria in Table 8. A model with a smaller MSE_c, MSE_d, or AIC was considered a better fit for the data. The models ranked consistently with the 3 different criteria. The fit of the sire-dam model was slightly better than that of the animal-maternal-effect model, but the differences were small. Both of these models were clearly superior to the remaining 3, especially for the 2 criteria measured on all the data (MSE_c and AIC). Accounting for maternal variation when modeling *N. caninum* infection status was essential.

CONCLUSIONS

The overall mean seroprevalence of *N. caninum* in the selected Ontario Holstein herds was 11.2%, with a median of 7.1%, and varied from 0 to 70.4% in different herds over the 3 yr of the study. The apparent efficiency of vertical transmission of *N. caninum* in the selected

Table 8. Estimates of (co)variance components and heritability (SE in parentheses) of susceptibility to *Neospora caninum* and model selection criteria (MSE_c, MSE_d, and AIC)¹ by a sire model (SM), an animal model (AM), a sire-maternal grandsire model (SGM), a sire-dam model (SDM), and an animal maternal effect model (AMM), with the transformed ELISA data.

Parameters	SM	AM	SGM	SDM	AMM
σ^2_s	0.0073 (0.0023)		0.0079 (0.0039)	0.0068 (0.0031)	
σ^2_g			0.0021 (0.0019)		
σ^2_a		0.0219 (0.0080)			0.0251 (0.0094)
σ^2_m				0.1020 (0.0017)	0.0689 (0.0019)
σ^2_{am}					0.0142 (0.0032)
σ^2_e	0.2473 (0.0040)	0.2375 (0.0050)	0.2439 (0.0036)	0.1543 (0.0072)	0.1601 (0.0058)
σ^2_p	0.2546 (0.0652)	0.2594 (0.0672)	0.2539 (0.0636)	0.2631 (0.0702)	0.2683 (0.0705)
h^2_d					0.094 (0.044)
h^2_m					0.257 (0.089)
h^2_T	0.115 (0.036)	0.084 (0.042)	0.124 (0.032)	0.103 (0.025)	0.301 (0.061)
MSE _c	0.2429	0.2307	0.2259	0.1051	0.1085
AIC	-11,354	-11,768	-11,935	-18,077	-17,823
MSE _d	0.2404	0.2316	0.2286	0.2186	0.2198

¹MSE_c = Mean square error with complete data set, MSE_d = mean square error with partially deleted (30%) data set, AIC = Akaike information criterion (Akaike, 1973).

herds was 40.7%. The *N. caninum* seropositive conversion rate of cows over 6 mo of age for the 2-yr period of the study was between 3.98 and 7.71%, whereas the *N. caninum* seronegative conversion rate was between 28.24 and 65.43%. The estimated heritability of susceptibility to *N. caninum* using 5 models was between 0.084 and 0.301 with logarithmic-transformed ELISA data, and the estimated heritability using a sire model and the binary serological status (seropositive and seronegative) was 0.090. Direct and maternal heritabilities estimated by maternal effects mode were 0.094 and 0.257, respectively. The sire-dam model and the animal maternal effect model fit the data better than other models. Maternal effect accounted for a greater variation in susceptibility to *N. caninum* than direct genetic effect, suggesting that management practices are more important than genetic selection in reducing the incidence of this parasite.

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