ASSOCIATIONS OF *NEOSPORA CANINUM* SEROPOSITIVITY WITH ENVIRONMENT AND MANAGEMENT IN DANISH DAIRY HERDS

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Neospora caninum infections were described for the first time in Norwegian dogs[2], and later characterized[4] in 1988. *N. caninum* infection was detected for the first time in Denmark[1] in material from an aborted bovine fetus in 1994. The organism is found world wide and is highly associated with abortions in cattle. The life cycle is still not known completely, and knowledge about the route of transmission neither at the cow level nor at the herd level is still scarce. In Denmark, associations with cow level factors were studied[6], and the purpose of the present study, partly on the same herds, is to identify associations of environment and management factors with *Neospora caninum* seropositivity in dairy herds. Neospora infection is now considered one of the most important causes of bovine abortions in Denmark.

Materials and Methods

The study comprised all cows (n=1175) in 20 dairy herds that were originally selected as part of a case control study on bovine abortions. Case herds were identified among herds submitting abortion material to the Danish Veterinary Laboratory (DVL). They were herds having at least 2 abortions within the last week preceeding admission, or at least 3 abortions within the last month, or at least 6 abortions within the last 3 months. A control herd was sampled in the same veterinary practice as where the case herd belonged and should not have experienced any abortions within the last 3 months before admission to the project. Data concerning breed, herd size, production, reproduction, herd health, and purchase of cattle were collected from the National Central Cattle Data Base. Each farmer was personally interviewed by the second author with respect to production system, management, cow environment, and feeding plans. A total of 32 factors were chosen for the analyses. A cross sectional blod sampling of all 1175 cows in the herds were tested using iscom-ELISA and IFAT[3]. A positive sample was defined as having both OD-value > 0.2 on the ELISA and having

positive fluorescence in IFAT at a dilution ≥1:640. All other results were considered negative.

The data were characterized using traditional descriptive statistics for associations between case control status and over all and matched pairs seropositivity. Multivariate analyses for associations between herd probability for seropositivity and exposure to the 32 independent variables were performed using ordinary stepwise logistic regression and stepwise regression in SAS[7]. The software program EGRET[5] was used for logistic normal regression, betabinomial regression and logistic binomial regression for bivariate and multivariate analyses.

Results

There is a strong association between seropositivity and case control status of the herd (OR=4.7; p=0.000). Multivariate analyses using SAS stepwise logistic regression showed that feeding of cows with hay, whole seed silage, grass silage, molasses, grasseed straw and fresh cut green roughage, and storage of concentrates detached, and import of replacement cows from outside the farm were associated with neospora caninum seropositivity. This was partly confirmed using ordinary stepwise regression. Analyses using EGRET with and without accounting for random effects showed similar importance of fodder, spreading of slurry on pasture, import of replacement cows, and presence of cats in the herd.

Discussion

Biological inference from small data sets require the use of alternative analytical approaches in order to give convincing results. The results do not give a very clear pattern, except for the case control status, and purchase of replacement cows. Obviously there seem to be associations with the type of feed offered to the cows and neospora caninum seropositivity. It is unlikely that the association is due to the nutrients themselves, but they may be contaminated with animal faeces with infective stages of the causative agent, either due to the presence of dogs or cats as latent carriers, or due to contamination from e.g. birds, mice or rats. However, we have no precise information on the latter species. The results indicate the need for further studies on transmission routes other than the intrauterine that so far is believed to be the primary mechanism of spreading the disease.

References

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