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Contextual herd factors associated with cow culling risk in Québec dairy herds: A multilevel analysis

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ABSTRACT

Several health disorders, such as milk fever, displaced abomasum, and mastitis, as well as impaired reproductive performance, are known risk factors for the removal of affected cows from a dairy herd. While cow-level risk factors are well documented in the literature, herd-level associations have been less frequently investigated. The objective of this study was to investigate the effect of cow- and herd-level determinants on variations in culling risk in Québec dairy herds: whether herd influences a cow's culling risk. For this, we assessed the influence of herd membership on cow culling risk according to displaced abomasum, milk fever, and retained placenta.

A retrospective longitudinal study was conducted on data from dairy herds in the Province of Québec, Canada, by extracting health information events from the dairy herd health management software used by most Québec dairy producers and their veterinarians. Data were extracted for all lactations starting between January 1st and December 31st, 2010. Using multilevel logistic regression, we analysed a total of 10,529 cows from 201 herds that met the inclusion criteria. Milk fever and displaced abomasum were demonstrated to increase the cow culling risk. A minor general herd effect was found for the culling risk (i.e. an intra-class correlation of 1.0% and median odds ratio [MOR] of 1.20). The proportion of first lactation cows was responsible for this significant, but weak herd effect on individual cow culling risk, after taking into account the cow-level factors. On the other hand, the herd's average milk production was a protective factor. The planning and management of forthcoming replacement animals has to be taken into consideration when assessing cow culling risks and herd culling rates.

1. Introduction

Several health disorders, such as milk fever, displaced abomasum, and mastitis, as well as impaired reproductive performance, are known risk factors for the subsequent removal from a dairy herd of the affected animals (Gröhn et al., 1998; Rajala-Schultz and Gröhn, 1999; Beaudeau et al., 2000; De Vries et al., 2010). High culling rates can sometimes be viewed as a sign of management failure (Eicker and Fetrow, 2003) despite the lack of consensus on an acceptable culling rate, each herd having an optimal culling rate for its own management and dynamics (Rapnicki et al., 2003). Nevertheless, culling rates greater than 30% are common in American and Canadian dairy herds (Fetrow, 1987; Radke and Lloyd, 2000; Smith et al., 2000), despite improvements in cows' health and herd productivity (LeBlanc et al., 2006; Mee, 2007). While cow-level culling risk factors are well documented in the literature, herd-level associations have been less frequently investigated. But even without having this specific objective in mind, a significant herd effect on cow culling risk was reported by some studies (Beaudeau et al., 1995; Emanuelson and Oltenacu, 1998; Gröhn et al., 1998). The farmer's management style and attitude were shown to contribute significantly to the variation in farms' performance (Bigras-Poulin et al., 1985; Tarabla and Dodd, 1990). It is also recognized that group- or herd-level variables can affect or modify individual-level outcomes independently of the characteristics of the individuals (Diez Roux, 1998). Therefore we could hypothesize that several herd characteristics can modify the cow culling risk, such as suggested by Beaudeau et al. (2000): the availability of

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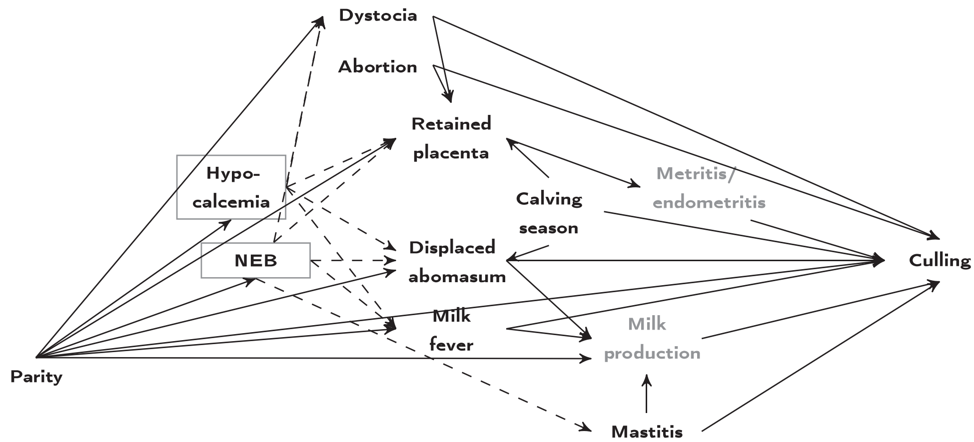

Fig. 1. Directed acyclic graph (DAG) for the effect of retained placenta, milk fever, and displaced abomasum on culling (grey: intermediate variables; boxes/dashed lines: unobserved [latent] variables; NEB: negative energy balance).

nulliparous heifers and milk quotas, the farmer's attitude towards risk and uncertainty, the milk and beef market, etc. Hence it would be interesting to integrate the population context into individual-level analyses to untangle the relationships between the variables at various levels (Guthrie and Sheppard, 2001), which has not yet been done in dairy cow culling research. Multilevel models achieve this goal by decomposing the variability across hierarchical levels (Stryhn and Christensen, 2014).

The objective of this study was to investigate the effect of herd-level determinants on variations in cow culling risk in Québec dairy herds, i.e. to examine whether, over and above cow factors, herd influences a cow's culling risk. To this end, we assessed and used the effect of retained placenta (RP), milk fever (MF), and displaced abomasum (DA) on culling.

2. Materials and methods

2.1. Dataset

A retrospective longitudinal study was conducted using data from dairy herds in the Province of Québec, Canada, by extracting health information events from *DSA Laitier* (DSAHR Inc., Saint-Hyacinthe, QC, Canada), the dairy herd health management software used by more than half of Québec producers and their veterinarians. We had access to a purposive sample of all lactations taking place between January 1st, 2001 and December 31st, 2010 (249,536 cows from 3735 herds), keeping herds that had a minimum of three consecutive years of data with *DSA Laitier* and for which at least one culling was recorded over this period. From this dataset, we extracted the data for all lactations starting between January 1st and December 31st, 2010. If a cow had more than two lactations starting in 2010, only the first was kept. Production data were obtained from the sole Québec dairy herd improvement (DHI) service provider (Valacta, Sainte-Anne-de-Bellevue, QC, Canada). The health and production data were matched based on herd- and cow-level identification. If that was not successful, further matching within herd was tried, based on birth date, calving dates, and health and production history. Only herds for which at least 95% of the lactations from the health dataset could be matched with data from the production dataset were kept (42,809 cows from 714 herds). Herds with fewer than 30 animals, for which more than 30% of the DHI monthly tests were missing, and with a 2010 lactational incidence that was less than 3% for RP, and 1% for either MF or DA, were removed to avoid herds with gross under-reporting. Cows with a calving interval, or the interval between the last calving and the end of data, longer than 580 days were censored at their last calving date. If this censoring resulted in their first calving date, the observation was dropped.

The primary outcome, culling, was defined as a cow's being removed from the herd, i.e. due to death, sold to another herd, or sent for slaughter. A directed acyclic graph (DAG, Fig. 1) was used to identify a minimal set of measured confounders for each disease studied (RP, MF, DA) (Greenland et al., 1999; Shrier and Platt, 2008), with the help of DAGitty software (Textor et al., 2011). Its construction was based on empirical knowledge from the findings of previous studies and on the authors' educated knowledge. This resulted in a single common DAG for the three diseases, with the following confounders considered: clinical mastitis, parity (continuous), calving season (January to July and August to December), dystocia, and abortion.

Six variables describing herd characteristics were included as contextual variables based on Haine et al. (submitted for publication): herd size, proportion of primiparous cows, average age at first calving, average milk production, milk fever incidence, and pregnancy rate.

2.2. Data analysis

The data were analysed using a two-level logistic regression model with cows (first level) nested within herds (second level). The independent influence of cow factors and herd factors on the herd variance of culling was assessed using different models. We first estimated an 'empty' model (Model 1) with no variables entered and which only included a random intercept. We then adjusted the random intercept by adding cow-level factors in Model 2. Herd-level predictors (Model 3) were added to Model 2 to determine whether the cow-level differences were explained by herd characteristics (Merlo et al., 2005). The random inter-herd variability was estimated by the herd-level variance, the intra-cluster correlation coefficient (ICC), and the median odds ratio (MOR). The ICC was calculated based on the latent response formulation as follows:

$$\frac{\sigma_z^2}{\sigma_z^2 + (\pi^2/3}) \times 100 \quad (1)$$

where σ_z^2 is the herd variance (Goldstein et al., 2002; Snijders and Bosker, 2012). The ICC indicates the fraction of the total outcome variability that is attributable to the herd level and provides a measure of the within-herd homogeneity. A lower ICC indicates a lower likelihood of cows' sharing herd experiences. However, the ICC can