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Herd-level prevalence of selected endemic infectious diseases of dairy cows in Great Britain

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ABSTRACT

To implement appropriate and effective disease control programs at the national level, up-to-date and unbiased information on disease frequency is needed. The aim of this study was to estimate the prevalence of selected endemic infectious diseases in the population of dairy herds in Great Britain. Bulk milk tank (BMT) samples from 225 randomly selected dairy farms, stratified by region and herd size, were tested for antibodies against bovine viral diarrhea virus (BVDV), bovine herpesvirus type 1, *Mycobacterium avium* ssp. *paratuberculosis*, *Leptospira* Hardjo, *Salmonella* spp., *Coxiella burnetii*, *Fasciola hepatica*, *Neospora caninum*, and *Ostertagia ostertagi*. Furthermore, the presence of BVDV, *C. burnetii*, and *Chlamydia*-like organisms was determined by PCR. The apparent herd prevalence was estimated as a weighted proportion of positive herds. The true prevalence was calculated when a test was used with known test characteristics for the cut-off value used. Among unvaccinated herds, the true prevalence of BMT antibodies against BVDV was estimated at 66% [95% confidence interval (CI): 56–77%], *M. avium* ssp. *paratuberculosis* 68% (95% CI: 59–77%), bovine herpesvirus type 1 62% (95% CI: 52–73%), *Leptospira* Hardjo 47% (95% CI: 34–60%), and *Salmonella* spp. 48% (95% CI: 39–56%). The apparent prevalence of BMT antibodies against *C. burnetii* was 80% (95% CI: 75–85%), *F. hepatica* 55% (95% CI: 48–62%), *N. caninum* 46% (95% CI: 38–54%), and *O. ostertagi* 95% (95% CI: 91–98%). The BVDV, *C. burnetii*, and *Chlamydia*-like antigens were detected in 5 (95% CI: 2–9%), 29 (95% CI: 21–36%), and 31% (95% CI: 24–38%) of herds, respectively. Our results show that dairy cows across GB are frequently exposed to the studied pathogens, which are endemic at high levels with some geographical variations. These prevalence estimates provide a much-needed basis to assess whether nationwide control programs for the studied pathogens are justified by their potential economic, environmental, and public health implications. Should surveillance and control programs be initiated, the estimates presented here are a baseline against which progress can be assessed.

Key words: prevalence, endemic infectious disease, dairy cow, bulk milk, ELISA

INTRODUCTION

Several infectious diseases of dairy cows such as bovine viral diarrhea virus (**BVDV**), Johne's disease caused by *Mycobacterium avium* ssp. *paratuberculosis* (**MAP**), infectious bovine rhinotracheitis, and liver fluke are generally regarded as being widespread and endemic in the United Kingdom (Carslake et al., 2011; Sekiya et al., 2013). These diseases are known to have a significant effect on dairy production due to their effects on fertility (Fray et al., 2000; Lanyon et al., 2014; Walz et al., 2015), milk production (Tiwari et al., 2007; McAloon et al., 2016), and, subsequently, culling (Murphy et al., 2006; Smith et al., 2010).

In Great Britain (**GB**) in 2005, the total costs of dairy and beef cattle endemic infectious diseases (disease, control, and prevention) were estimated to be as high as £10 million ($12.4 million) for Johne's disease and £61.1 million ($75.7 million) per annum for BVDV (Bennett and Ijpelaar, 2005). However, due to a lack of reliable prevalence data at national level, these figures are likely to underestimate the true situation. With the exception of bovine tuberculosis in GB and BVDV in Scotland, controlling such diseases is voluntary for GB farmers. However, the need to control endemic infectious disease can be overlooked by farmers, as it can be difficult to associate their presence with visible losses. This is often because clinical signs associated with

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such diseases on a given animal in an infected herd are absent, mild, or nonspecific, leading to a general acceptance of their occurrence on dairy farms in endemic areas (Carslake et al., 2011; Statham, 2011). In such cases, from the farmers' perspective, there is often very little, if any, financial incentive to control the disease (Stott et al., 2005). Nevertheless, examples from European countries suggest that the control or elimination of some of these pathogens [e.g., bovine herpesvirus type 1 (**BHV-1**) in Scandinavian countries and Austria, BVDV in Sweden] can be achieved and would be beneficial (Ackermann and Engels, 2006; Lindberg et al., 2006).

When control programs are implemented, it is important that they are accompanied by continuous monitoring of herd status to assess the effectiveness of the program and progress toward goals; this can be achieved through serological testing at the herd level (Lindberg and Alenius, 1999; Houe et al., 2006). Testing of bulk milk samples is a particularly cost-effective strategy and has become part of surveillance and disease-control programs for several endemic infectious diseases of dairy cattle (Booth et al., 2013; Sekiya et al., 2013).

The application of a suitable disease control or elimination program at national or regional level and the monitoring of the progress of that program should be based on knowledge of the baseline frequency and distribution of the disease in the population (Ackermann and Engels, 2006; Humphry et al., 2012; Sayers et al., 2015). Such estimates can allow informed decisions on the justification of a program at the national level and provide a baseline against which the effect of the control program can be assessed. With the exception of BVDV in Scotland, for which a survey of Scottish dairy farms has recently been carried out to inform the Scottish BVDV elimination program (Humphry et al., 2012), presently, in GB, there is a lack of reliable and up-to-date estimates of the prevalence of endemic diseases in the national dairy herd. This is because, for the majority of endemic diseases, no active disease surveillance is in place. Several private and public routine recording systems exist; however, at the national level, the information they provide is likely to be biased (Velasova et al., 2015).

In addition to these ongoing recording systems, one-off surveys are often carried out (Davison et al., 2005; Salimi-Bejestani et al., 2005; Woodbine et al., 2009b); although useful, their results should be interpreted with caution because of issues such as nonprobabilistic selection of studied farms (Paton et al., 1998; Woodbine et al., 2009b; Williams and Winden, 2014) and failure to adjust prevalence estimates for the study design (Paton et al., 1998) or for test performance (Davison et al., 2005; Woodbine et al., 2009a; Williams and Winden, 2014). Furthermore, one-off studies are only useful for a limited period of time, as the prevalence can change as a result of the implementation of control measures and changes in the dairy industry, the more apparent of which are increased herd size, genetic selection, and application of new technological innovations (Barkema et al., 2015). It is therefore reasonable to assume that the few available estimated prevalence figures could no longer be accurate. Accordingly, the aim of our study was to generate new information on the prevalence and distribution of selected important infectious diseases of dairy cows at the national level to provide a basis for a future monitoring of disease trends over time and for the implementation of suitable and effective disease control or elimination programs at the national level.

MATERIALS AND METHODS

Study Population and Sampling Design

A nationwide, cross-sectional study of commercial dairy herds was conducted in GB from April 2014 to March 2015. The study population was selected by means of stratified random sampling from a sample frame comprising 10,491 dairy farms, representing approximately 95% of the total population of all dairy farms in GB, held by the dairy industry (AHDB Dairy, division of the Agricultural and Horticultural Development Board). The registered farms were stratified by 6 regions (north England, Midlands, southeast England, southwest England, Scotland, and Wales) and then within each region by herd size (small: <50 cows; medium: 50–149 cows; large: ≥150 cows), creating 18 strata. The herd size was based on the total number of lactating and dry cows. An equal number of farms within each stratum was selected using simple random sampling. The total number (n) of farms to study was calculated using ProMesa software v.1.62 (http://www.promesa.co.nz/) according to the formula:

$$n = \frac{\sum_{i=1}^{e}\left[\frac{(n_i)^2 \times p_i \times (1-p_i)}{w_i}\right]}{N^2 \times \frac{AE^2}{Z^2} + \sum_{i=1}^{e}\left[n_i \times p_i \times (1-p_e)\right]},$$

$$w_i = \frac{n_i \times \sqrt{p_i \times (1-p_i)}}{\sum_{i=1}^{e}\left[n_i \times \sqrt{p_i \times (1-p_i)}\right]},$$

where e is the number of strata, n_i is the number of farms in stratum i (i.e., large farms in Scotland), p_i is the expected prevalence in stratum i (50% was used as