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Prevalence and risk factors for Bovine Herpesvirus Type 1 (BoHV-1) infection in Irish beef herds: results from the National Beef Welfare Scheme 2023

Jonas Brock[1,2*], Maria Guelbenzu-Gonzalo[1], Jose Maria Lozano[3], Elizabeth A. Lane[4], Michael Gunn[1], Sean Brady[1], Hans-Hermann Thulke[2] and David A. Graham[5]

Abstract

Infectious bovine rhinotracheitis (IBR), caused by bovine herpesvirus-1 (BoHV-1), is a highly contagious disease with significant economic impacts on the cattle industry. It can also lead to respiratory distress, reproductive losses and compromised animal welfare, and thus represents a key target for control. This study aimed to assess the prevalence and identify risk factors associated with BoHV-1 infection in Irish beef herds. Conducted under the National Beef Welfare Scheme (NBWS), the study involved testing 10,659 beef breeding herds, representing approximately 20% of the national beef herd population. A total of 189,404 animals were tested. Using a 'snapshot' testing strategy herd-level BoHV-1 status was determined based on the presence of antibodies to the gE glycoprotein in up to 20 randomly selected animals, preferably over 9 months of age to exclude maternally derived antibodies. Vaccination histories were not available for participating herds. Results indicated an animal-level apparent prevalence of 11.4% and a herd-level apparent prevalence based on positive snapshots of 48.8% (defined as herds with ≥ 1 positive animal). Larger herds and high rates of animal in-moves per capita (here, > 17% of herd replaced by purchases in the past year) were identified as significant risk factors for recent (within the last three years) BoHV-1 circulation. Previous studies had indicated a herd-level prevalence in Ireland of up to 80%. The lower prevalence estimates identified in this study may reflect improved biosecurity and vaccination uptake in recent years. The findings from this survey, although showing that BoHV-1 is still endemic in Irish beef herds, provide updated prevalence figures which are considerably lower, indicating that a higher number of farms would be in a position to achieve freedom from BoHV-1 in a relatively short period. These results offer essential epidemiological insights to inform the design and implementation of a national BoHV-1 control programme in Ireland.

Keywords IBR, BoHV-1, Cattle, Beef, Ireland, Prevalence, Eradication, NBWS

*Correspondence:
Jonas Brock
jbrock@animalhealthireland.ie
[1]Animal Health Ireland, Carrick-On-Shannon, Co. Leitrim, Ireland
[2]Helmholtz Centre for Environmental Research GmbH - UFZ, PG Ecological Epidemiology, Leipzig, Germany
[3]Department of Agriculture, Food and the Marine, Virology Division, Backweston laboratories, Virology Division, Celbridge, Republic of Ireland
[4]Department of Agriculture, Food and the Marine, One Health One Welfare Scientific Support Team, Agriculture House, Kildare St, Dublin 2, Ireland
[5]Anvil Consulting Services Limited, Ballynahinch, County Down, Northern Ireland

Introduction

IBR is a highly infectious disease caused by BoHV-1 that not only imposes substantial economic losses through reduced production and increased veterinary costs, but also contributes to respiratory distress, reproductive failure and overall compromised animal welfare [1–4]. The virus typically spreads by close contact between animals although airborne transmission may occur over distances of up to 5 m and it can also be spread by using contaminated semen, and indirectly by equipment and people [4]. Once an animal becomes infected, it remains infected for life despite developing immunity [4]. The virus establishes a lifelong latent infection in the nerve cells within the animal's central nervous system. During this period the latent carrier is not shedding virus. However, at times of stress, such as transport, mixing of stock, calving, nutritional stress and inter-current disease, the virus may be reactivated and can begin to multiply and be re-excreted, generally in nasal and ocular secretions [4–6]. This can lead to new infection and disease in other susceptible cattle, which in turn will also become latent carriers [4]. These latently infected carriers play a central role in maintaining BoHV-1 in infected herds, where they act as a reservoir of infection, and in spreading infection between herds.

In Ireland, infection with BoHV-1 is widespread in both dairy and beef herds with previous studies having found evidence that 75–80% of herds have been exposed to BoHV-1 and contain carrier animals [7–10]. One study estimated the mean within herd prevalence (the mean proportion of seropositive carrier animals per herd) in Irish beef herds to be 40% and found a positive association between seroprevalence to BoHV-1 and the herd size and mortality rate [10]. Although our focus is on beef herds, previous dairy herd estimates offer useful national benchmarks for BoHV-1 seroprevalence and facilitate comparison across production systems. A study of Irish dairy herds found a within herd seroprevalence in BoHV-1-positive, unvaccinated dairy herds of 31.7% [11]. Regarding the most relevant factors for introduction of BoHV-1 into cattle herds, a recent literature review found that these include herd size, purchase of cattle, cattle density, age of cattle, distance to neighbouring cattle herds and professional visitors [12].

In Ireland, beef breeding herds (commonly called suckler herds) represent the largest cattle enterprise, with nearly 50 000 registered herds in 2019 [13]. Five subtypes reflect the progression from birth to sale or slaughter: Beef Suckling to Weanling (BSW), Beef Suckling to Youngstock (BSY), Non-rearing BSY (BSY-nR), Suckling to Beef (BSB), and Beef Pedigree (BP). BSW herds rear calves to weaning (September–October sales), while BSY herds retain calves up to 12–20 months. BSY-nR herds sell female calves at weaning, replacing breeders by purchase; BSB cover the full cycle to slaughter; and BP herds supply pedigree breeding stock [13]. Data on IBR vaccine usage specifically in beef herds are lacking, although national vaccine sales have risen in recent years.

The economic losses associated with BoHV-1 can be substantial, with infected herds experiencing reduced milk yields, increased culling rates, and higher veterinary costs [2, 14, 15]. In Ireland, farmers are estimated to be spending around 10 million Euros annually on BoHV-1 vaccines, highlighting the significant financial burden of the disease.

At the time of writing, the establishment of a national BoHV-1 control programme is being considered in Ireland, in line with the efforts of many European countries that have already implemented successful BoHV-1 control programmes. Several countries or regions within the European Union (EU) are considered free from BoHV-1 following the implementation of EU-approved eradication programmes. These include Austria, Germany, Denmark, Finland, Sweden, Czechia and the Italian regions of Valle d'Aosta and the Province of Bolzano. As a result, these countries/regions are granted additional trade guarantees. Other EU countries and regions, such as Belgium, Luxembourg, multiple regions of France and the Italian provinces of Friuli-Venezia Giulia and Trento, are currently implementing Commission-approved BoHV-1 eradication programmes [16, 17]. The BoHV-1 trade restrictions and additional guarantees for BoHV-1-free countries/regions impact the trade of live cattle from countries or regions that are not free from the disease, particularly when there are not an approved eradication programmes in place.

A national programme to control BoHV-1 does not currently exist in Ireland, but is under active discussion, co-ordinated by Animal Health Ireland (AHI; www.animalhealthireland.ie), a not-for-profit public–private partnership established to improve the profitability and sustainability of the Irish farming and agri-food sector. This study was specifically designed to inform those national-level discussions and to support stakeholders in assessing the feasibility, structure, and strategic targeting of a future BoHV-1 control or eradication programme in Ireland.

Understanding the prevalence and epidemiology of BoHV-1 is crucial for the development of effective control and prevention strategies. The objective of this study was to conduct a descriptive analysis of BoHV-1 infection in Irish beef cattle herds, providing valuable insights into the status of the disease in the country, and to perform a risk factor analysis to identify herd characteristics that explain recent within-herd BoHV-1 circulation. Given that earlier seroprevalence studies in Irish beef herds were smaller in scale and are now outdated, and that national IBR vaccine uptake has increased recently,

these updated figures—covering approximately 25% of all beef herds—are essential to inform the planning of a potential eradication programme.

Methods

Data and testing

This study was conducted as part of the National Beef Welfare Scheme (NBWS) in 2023, a government-funded and voluntary programme in Ireland that aims to further increase the economic efficiency of and enhance animal health and husbandry on suckler farms. The NBWS provided financial support for the testing of cattle herds for BoHV-1 antibodies. In total 10,659 beef breeding herds participated in the testing programme, which is approximately 20% of the entire Irish beef herd population [13].

To determine the herd-level BoHV-1 status, a'snapshot'test was performed using a blood sample from up to 20 randomly selected animals from each herd, ideally 9 months old or above to avoid maternally derived antibodies, or all ages if there were fewer than 20 on the holding on the day of testing. Where a herd had twenty or more bovines, a minimum of twenty were to be tested and where a herd had less than twenty bovines, all were tested. Sampling took place between 3rd August 2023 and 20th December 2023, thus covering the late summer to early winter period. While guidance was provided to encourage random selection of animals, all sampling was carried out by local practicing veterinarians. As the study authors were not directly involved in the sampling process, we cannot confirm the extent to which true randomisation or systematic selection procedures were implemented in practice.

The decision to sample a maximum of 20 animals per herd was made by the Department of Agriculture, Food and the Marine (DAFM), who administered the NBWS. The study authors were not involved in determining this sampling threshold. While no formal sample size calculation was shared with the authors, it is understood that the 20-animal limit was determined primarily.

The collected samples were submitted to one of the laboratories listed in the Department of Agriculture, Food and the Marine's (DAFM) Terms and Conditions for the NBWS. All participating laboratories were ISO17025 accredited and used commercially available gE ELISA kits. While specific kit information was not systematically linked to individual test results, the list of accredited assays includes the IDEXX gE Competition ELISA, IDvet SCREEN ELISA, and the Indical Cattletype BHV-1 gE ELISA. All tests were applied and interpreted according to the respective manufacturers' thresholds for sample-to-negative (S/N) ratios.

The gE ELISA was selected because it enables differentiation between wild-type BoHV-1 infection and vaccination with marker (gE-deleted) vaccines. Since 2004, only marker vaccines have been authorised for use in Ireland [18], making the gE test appropriate for identifying field virus exposure. As individual vaccination records for participating herds were not available, this test provided the most reliable estimate of field infection prevalence under the given conditions.

On receipt of samples, the laboratories recorded the identity of each animal sampled in the Irish Cattle Breeding Federation (ICBF) database in each herd in advance of testing of the samples. A sample-to-negative (S/N) ratio was calculated for each test, and the numeric value was classified into interpreted results of positive, negative, or inconclusive depending on the manufacturers' thresholds. The herd-level BoHV-1 status was determined based on the presence of BoHV-1 antibodies in the tested animals. Following testing, results were uploaded to the ICBF database where they were accessible to herd owners. Herds were classified as BoHV-1 positive if at least one animal within the herd tested positive for BoHV-1 antibodies. For the following analysis, inconclusive results were considered negative. Furthermore, only herds with either complete results or a single missing test result were included in the analysis. This was the case when all expected test results were available for a herd (up to 20 tests depending on herd size), or if only one result was missing, based on a comparison of the number of samples initially logged for each herd against the number of results that were subsequently uploaded. The rationale for including herds with a single missing result—but excluding those with more—was based on a review of the distribution of missing test data across herds and consultation with an expert panel overseeing the analysis.

Descriptive analysis

A descriptive analysis of the BoHV-1 antibody data was conducted to provide a comprehensive understanding of the status of the disease within the tested cattle herds.

To assess the extent to which results could be considered representative of the national population, the representativeness of the herds tested was assessed by comparing the distribution of herd types (as described in [13]) and herd sizes in the NBWS herds to the distribution of all beef breeding herds in Ireland. For this analysis, herd demography data for all registered beef breeding herds was obtained from the Animal Identification and Movement (AIM) national database maintained by the DAFM in Ireland. The intention of this analysis was to ensure that the results could be extrapolated to the national level.

In a second step, the herd- and animal-level apparent prevalences were calculated, along with their respective 95% confidence intervals. The animal-level prevalence calculation process involved dividing the number

of animals testing positive for BoHV-1 antibodies by the total number of animals tested. Similarly, the herd-level prevalence was determined by considering the presence of at least one animal testing positive for BoHV-1 antibodies within a specific herd. The corresponding 95% confidence intervals (CIs) were calculated using the exact Clopper–Pearson method, which is appropriate for binomial proportions.

Risk factor analysis

To identify potential risk factors associated with recent (within the last three years) BoHV-1 antibody positivity, a case–control study at the herd level was conducted in accordance with the guidelines laid down in the STROBE statement [19, 20].

Cases were defined as herds that had serological evidence of active BoHV-1 circulation within the past three years, while control herds were those that tested negative for BoHV-1 antibodies. The three-year timeframe was selected pragmatically by the study team, with input from the expert panel overseeing the analysis. This threshold was not based on a specific published framework but was chosen to focus on more recent virus circulation, which is most relevant for informing control and eradication strategies. The intention was to exclude historical infections that may no longer reflect the current epidemiological risk in herds.

To determine whether a herd had active BoHV-1 circulation in the past three years, a filtering process was applied to all seropositive herds. The age of the youngest homebred positive animal within each herd was calculated to approximate the time since the last active virus circulation. This approach was based on the following theoretical framework.

Previous studies indicate that once BoHV-1 is introduced into a herd, it is likely to spread and affect all animals on the farm, resulting in seropositivity across all age cohorts [11]. Infected animals remain antibody-positive for life, serving as indicators of past virus circulation. As viral circulation ceases, newborn animals will be seronegative. By assessing age-dependent seroprevalence patterns, step-wise increases in seropositivity can be observed within herds, as described by [11] This pattern allows the approximation of the timing of the last active BoHV-1 circulation within a given herd. By employing this methodology, herds were classified accurately into case and control groups, providing a reliable basis for further analysis of potential risk factors associated with recent BoHV-1 circulation.

An initial univariable analysis was performed to explore the distribution of variables and visually examine differences between case and control herds using boxplots and bar charts. Statistical comparisons between cases and controls were also conducted. Throughout, linear predictors were categorised based on quartiles. This was done to accommodate non-normal distributions and to meet the assumptions of the logistic regression model, while also facilitating interpretation of the effect sizes across different value ranges. The chi-squared ($\chi 2$) test of independence was employed to determine whether there is a statistically significant relationship between each of the selected herd characteristics and the herd's BoHV-1 status. The variables analysed in the univariable analysis included: herd size (at the time of the test), herd type, number of animal movements into the herd per capita and proportion of non-homebred animals in the herd. All risk factor data were sourced from the Animal Identification and Movement (AIM) database, Ireland's national cattle registry maintained by the Department of Agriculture, Food and the Marine. After checking for variable collinearity using the variance inflation factor with a threshold of 5 applied to identify potentially collinear variables, a multivariable logistic regression model was trained on the data using a stepwise backward variable selection approach. The backward variable selection approach was based on Akaike's Information Criterion (AIC). The results of the final model were presented as odds ratios with corresponding 95% confidence intervals, indicating the strength and direction of the association between each risk factor and recent BoHV-1 circulation.

All statistical analyses and data visualisations were conducted using R software.

Results

Herds and animals included

Blood samples were received for 10,659 beef herds and individual test results were available for 188,796 animals. Of the 10,659 herds for which results are available, 6,455 herds (60,5% of all NBWS participating herds) had complete records or only a single result missing. For the remaining 4,204 herds at least two results were missing. In the following analysis, data for the 6,455 herds with complete or nearly complete data is presented and are referred to as 'study herds and animals. In these herds a total of 126,028 individual tests results are available.

Representativeness of study herds and animals

The herds surveyed in the NBWS appear to be a representative subset of all beef breeding herds in Ireland in terms of herd type composition. Figure 1 shows the distribution of herd types in NBWS herds in comparison with the distribution of all beef breeding herds in Ireland. Beef suckling to weanling (BSW) herds, which maintain a herd of cows and raise calves from birth to weaning, are by far the most common herd type in both populations.

While the overall distribution of herd types is broadly consistent between NBWS herds and all beef herds, NBWS herds tend to be larger on average (mean herd

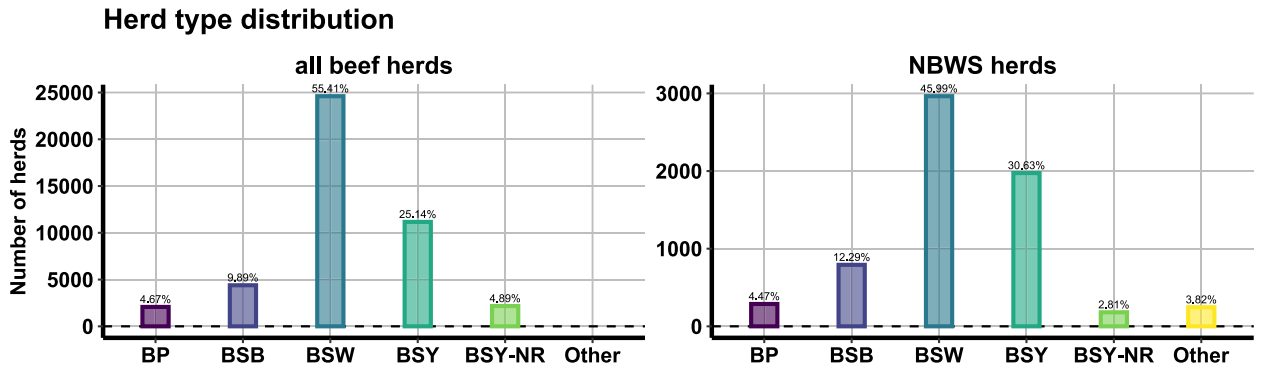

Fig. 1 Herd type distribution. The figure compares the distribution of herd types in NBWS-participating herds with all registered beef breeding herds in the Republic of Ireland at the time of sampling (data from the AIM database). Five different subtypes of beef herds have been identified in Ireland, which are consistent with recognised production systems which differ in their management characteristics including when animals are sold for further production. Beef suckling to weanling (BSW) producers maintain a herd of cows and raise calves from birth to weaning, with the majority sold as weanlings at autumn sales during September and October while a proportion of female calves is kept as heifer replacements. The beef suckling to youngstock (BSY) subtype is similar to BSW, including retaining a proportion of females as replacements, with the key difference being that calves are kept for a longer period, to allow weaned calves to gain weight prior sale. These animals are usually yearlings (12–20 months of age) by the time they leave their birth herd. Non-rearing suckling to youngstock (BSY-NR) herds are a variation of the BSY herd type, with the difference that female calves are sold after weaning and replacement bred females are purchased. The suckling to beef (BSB) herds follow the full beef production cycle, from birth through to the age of slaughter. Finally, representing only a small proportion of the beef sector in Ireland, beef pedigree (BP) herds are an important source of pedigree breeding stock to other commercial cattle producers in both the dairy and beef sectors

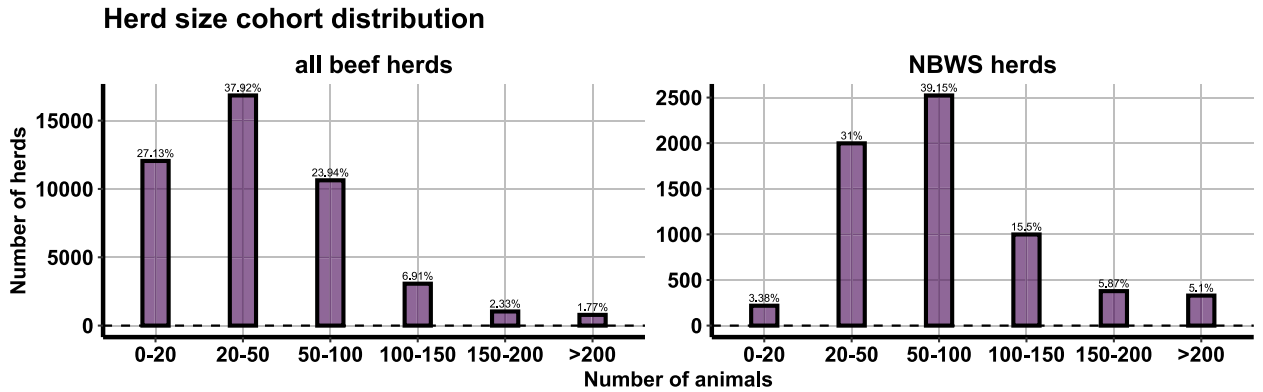

Fig. 2 Comparison of herd size cohort distribution

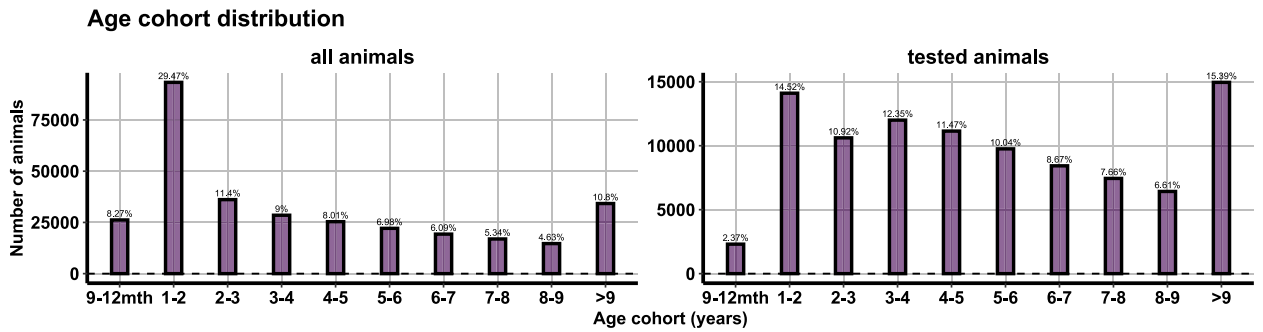

Fig. 3 Comparison of age distribution of all animals in tested herds versus tested animals including only animals over 9 months old

size: all beef herds—49.2 animals vs. NBWS herds—81.7 animals). This is mainly due to small herds (0–20 animals) being underrepresented in the NBWS sample (see Fig. 2).

Figure 3 provides a comparison between the age distribution of all animals in the tested herds at the time when the herd was sampled in comparison to the age distribution of those tested. Upon excluding the very young animals (0–9 months old) from the comparison due to

Table 1 Animal- and herd-level apparent prevalence

Animal-level results		
BoHV-1 animal status	**Number of animals**	**Proportion**
(Sample)-Negative	110,592	87,8%
(Sample)-Positive	14,371	11,4%
(Sample)-Inconclusive	1,065	0.8%
Total	126,028	
Herd-level results		
BoHV-1 herd status	**Number of herds**	**Percentage**
(Sample)-Negative	3,056	47.3%
(Sample)-Positive	3,150	48.8%
(Sample)-Inconclusive	249	3.9%
Total	6,455	

the applied sampling strategy, the age distribution of the tested animals in the NBWS aligns closely with the age distribution of all animals in the tested herds. However, a slight age discrepancy between the groups can be observed, which is also represented in the average age-figures. The average age of tested animal was 5 years, whereas the average age of all animals in the herd at time of testing was 3 years.

Prevalence estimation

Among the 126,028 study animals, 14,371 returned a positive outcome, resulting in an animal-level apparent prevalence of 11.4% (95% CI: 11.2%—11.6%) (see Table 1). The majority of animals were negative (87.8%), while 0.8% yielded inconclusive results. At the herd level, our data indicated a herd-level apparent prevalence of 48.8% (95% CI: 47.6%—50.0%).

For the 6,445 study herds, the distribution of the snapshot within herd prevalence is shown Fig. 4. In 51.2% of tested herds no positive animal was detected. In a further 15.5% of study herds, the snapshot within-herd prevalence was < 10%.

Age-cohort of the youngest positive animal

For all positive herds ($n = 3{,}150$), Fig. 5 presents the age cohort of the youngest positive homebred animal, categorised by within-herd prevalence groups. In low-prevalence herds (e.g., < 10%), infections are predominantly found in older animals. Specifically, in 57% of these low-prevalence herds, the youngest positive animal is older than six years.

Herd-size related prevalence

For the study herds, the proportion of infected herds by herd size was plotted as seen in Fig. 6. A clear size-dependent trend can be observed in the data (e.g. 60% of herds with 200 or more animals returned at least one positive test).

Proportion of BoHV-1 seropositive study herds by county

Figure 7 and Table 2 show the proportion of BoHV-1 positive study herds by county. Depending on county, the proportion of BoHV-1 positive herds among the tested herds lies between 35.7% (Co. Monaghan) and 63.1% (Co. Carlow).

Risk factor analysis

The risk factor analysis identified two key variables significantly associated with recent BoHV-1 circulation in Irish beef herds. The final logistic regression model included herd size and the proportion (%) of animal in-movements per capita (Table 3). Both of the retained variables showed a significant correlation with the likelihood of a herd experiencing recent virus circulation.

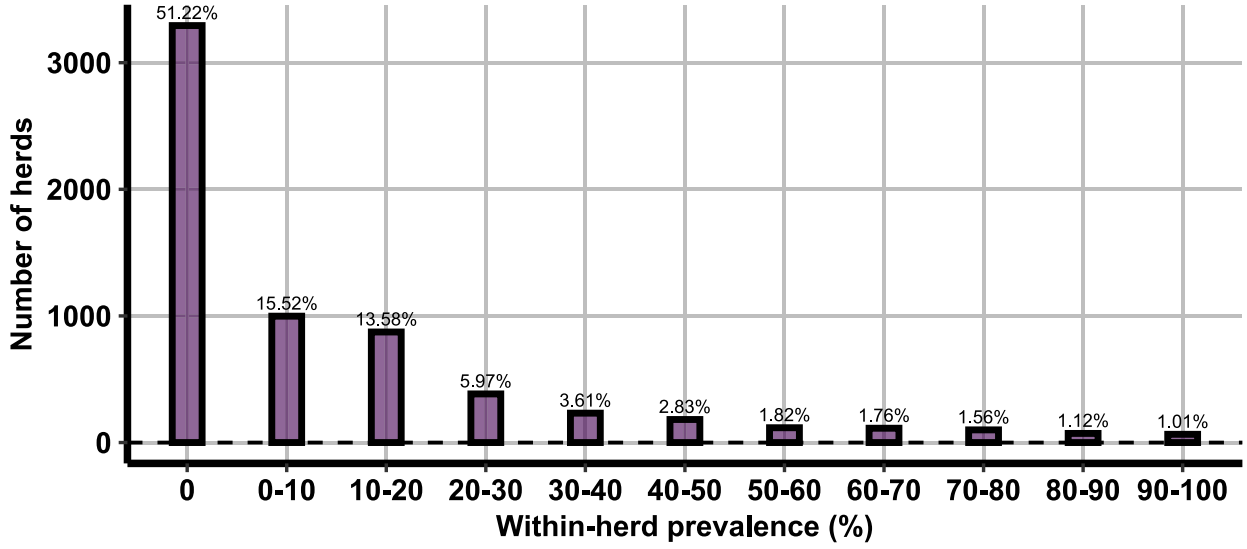

Fig. 4 Snapshot within-herd prevalence (% of samples testing positive per herd)

Part two of this paper will appear in next month's Veterinary Ireland Journal.