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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

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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

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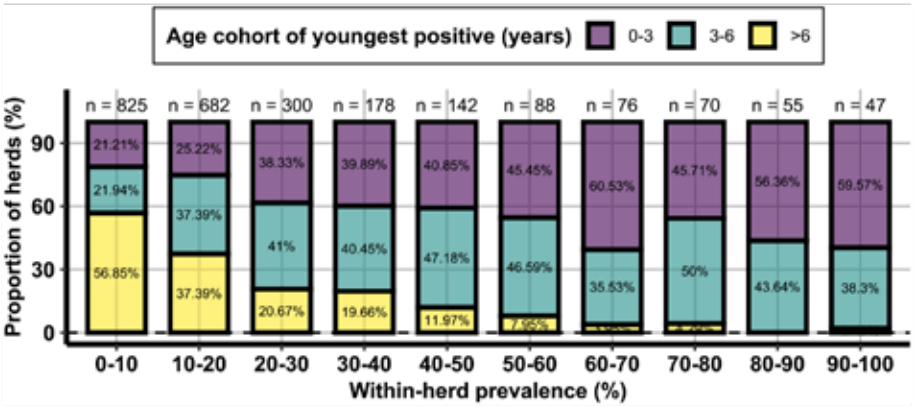

Fig. 5 Stacked bar chart showing the age-cohort of the youngest positive animal per herd, structured by within-herd prevalence group

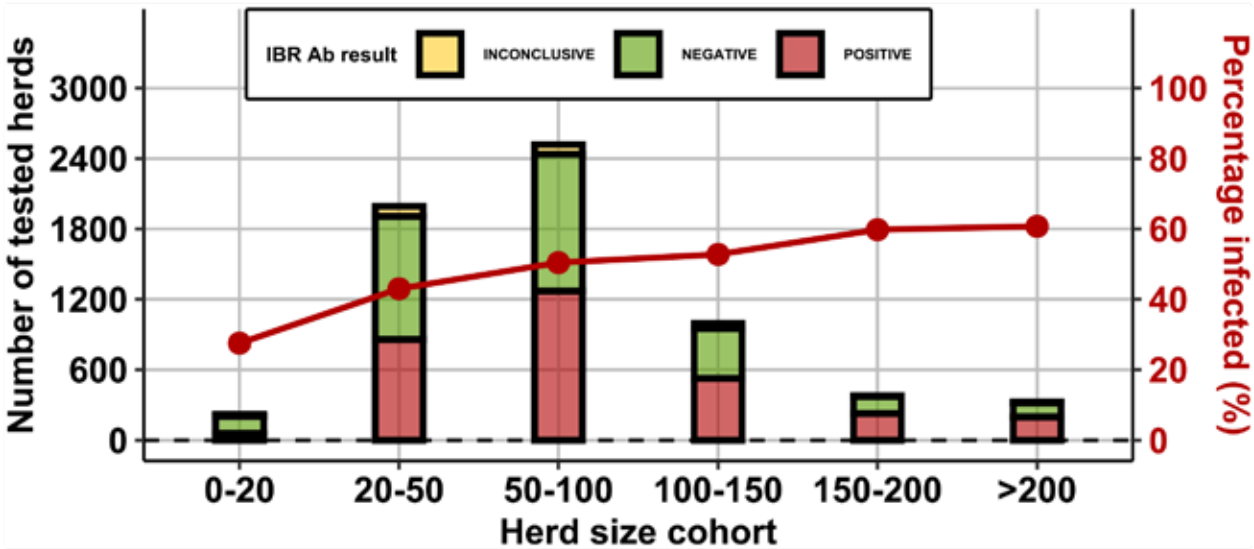

Fig. 6 Proportion of seropositive herds by herd size

The analysis revealed a strong positive association between herd size and recent BoHV-1 circulation. Herds in the largest size cohort (greater than 102 animals) had the highest odds of recent active virus circulation (OR = 1.73, 95% CI: 1.36–2.21) compared to the smallest herds (1–41 animals), which served as the reference category.

The proportion (%) of animal movements into a herd (in-moves) per capita was the other significant risk factor (Table 3). Herds in the highest quartile of in-moves per capita (more than 16.9%) were more than three times as likely of having recent virus circulation (OR = 3.05, 95% CI: 2.37–3.95) compared to herds with the fewest in-moves per capita (0%–2.6%), which served as the reference group.

For the two variables retained in the final model, univariate plots were generated to illustrate the relationship between the outcome (recent BoHV-1 circulation) and each predictor variable individually (Fig. 8).

The final logistic regression model demonstrated good overall fit, with a residual deviance of 3045.4 on 2887 degrees of freedom and an AIC of 3059. The distribution of deviance residuals did not indicate major violations of model assumptions (range: −1.04 to + 2.06). The model's area under the ROC curve (AUC) was 0.74, indicating modest discriminatory ability to distinguish between herds with and without recent BoHV-1 circulation.

Discussion

Herd and animal apparent prevalence

In the context of the Irish beef cattle sector, BoHV-1 remains endemic albeit at a lower prevalence than previously reported. While previous studies reported notably high prevalence rates (e.g. [7–10]) the current herd-level prevalence of 49% reflects a decrease from previous findings. This decline in prevalence may be attributed to

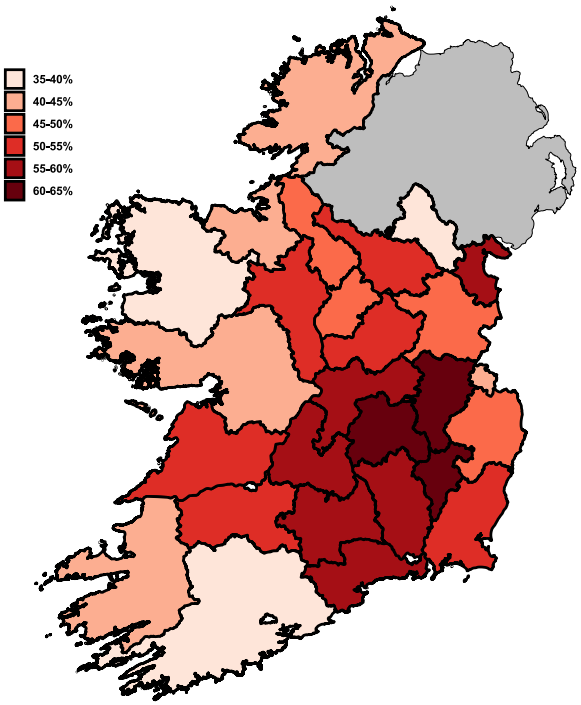

Fig. 7 Proportion of BoHV-1 positive study herds (in relation to all tested herds) by county

Table 2 Apparent prevalence by county

County	Tested herds	Positive herds	Prevalence in % (95% CI)
Carlow	103	65	63.1 (53.4—71.8)
Laois	198	122	61.6 (54.5—68.2)
Kildare	62	38	61.3 (48.4—72.6)
Tipperary	339	202	59.6 (54.3—64.9)
Waterford	110	65	59.1 (50.0—68.2)
Offaly	137	78	56.9 (48.9—65.0)
Kilkenny	171	96	56.1 (48.5—63.7)
Louth	40	22	55.0 (40.0—70.0)
Wexford	193	105	54.4 (47.2—61.7)
Westmeath	212	115	54.2 (47.6—60.8)
Roscommon	401	214	53.4 (48.4—58.4)
Clare	562	296	52.7 (48.6—56.8)
Limerick	201	106	52.7 (45.8—59.7)
Cavan	261	132	50.6 (44.4—56.7)
Meath	153	76	49.7 (41.8—57.5)
Longford	222	107	48.2 (41.4—55.0)
Leitrim	168	81	48.2 (40.5—56.0)
Wicklow	94	45	47.9 (38.3—57.4)
Galway	757	339	44.8 (41.2—48.3)
Donegal	240	105	43.8 (37.5—50.0)
Dublin	14	6	42.9 (21.4—71.4)
Kerry	327	139	42.5 (37.3—48.0)
Sligo	260	109	41.9 (35.8—48.1)
Mayo	510	204	40.0 (35.7—44.3)
Cork	511	204	39.9 (35.6—44.2)
Monaghan	199	71	35.7 (29.1—42.2)

Table 3 Conditional associations between retained predictor variables and infection status

Variable	OR (95% CI)	*P*-value
Herd size cohort		
Q1 (Herd size: 1—41)	Referent	
Q2 (Herd size: 42—65)	1.00 (0.77–1.29)	0.97
Q3 (Herd size: 66—102)	1.31 (1.02–1.66)	< 0.05
Q4 (Herd size: > 102)	1.73 (1.36–2.21)	< 0.05
In-moves per capita cohort		
Q1 (In-moves per capita: 0%—2.6%)	Referent	
Q2 (In-moves per capita: 2.7%—7.8%)	1.59 (1.22–2.07)	< 0.05
Q3 (In-moves per capita: 7.9%—16.9%)	2.36 (1.83–3.06)	< 0.05
Q4 (In-moves per capita: > 16.9%)	3.05 (2.37–3.95)	< 0.05

various factors such as improved biosecurity measures, vaccination strategies, or changes in farming practices that have contributed to a reduction in BoHV-1 transmission within herds. Currently in Ireland there is a continued high level of expenditure on BoHV-1 vaccination. During 2022, analysis of sales data indicates that over 3.3 million BoHV-1 vaccine doses were sold (Fig. 9). This was an increase from the previous 12 months and reflects a continuing trend seen over the past seven years, although sales dropped slightly in 2023, possibly as a reflection of lack of availability.

A previous Irish study of 6,000 beef suckler cows described an association between the presence of BVDV antibody positive animals and seroconversion to BoHV-1 [10]. This could be due to the immunosuppressive effects of BVDV and would suggest that the ongoing BVDV eradication efforts could be assisting in reducing the seroprevalence of BoHV-1. However, more recently, a study that included results from an abattoir survey from 2018 and 2020 of over five thousand animals under 30 months, found that 21% were seropositive to BoHV-1 [21]. The relationship with BVDV serological status was also explored, but the association was not sufficiently robust.

In our study we found a substantial proportion of positive herds (30%) with within-herd prevalence values below 20% (Fig. 4). The low prevalence suggests that targeted interventions in these herds could lead to rapid containment and potentially facilitate the eradication of BOHV-1 on a broader scale. A more detailed analysis of the positive, low-prevalence herds revealed that the majority of infected animals are in older age cohorts (see Fig. 5). In these herds targeted replacement strategies could result in BoHV-1 clearance without vaccination efforts.

Sampling strategy

The study's sampling strategy, although comprehensive, may have certain implications on the interpretation of apparent prevalence rates. The herds surveyed in the

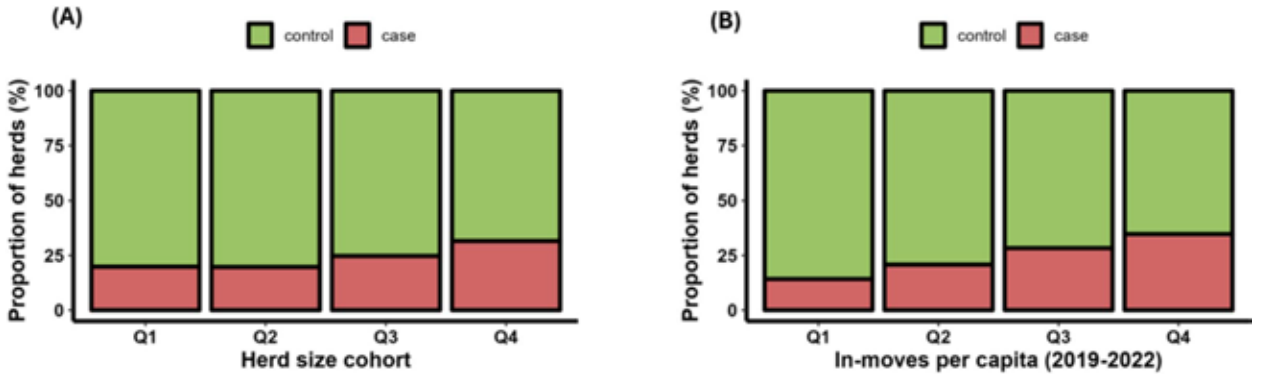

Fig. 8 Univariate plots showing the relationship between the BoHV-1 antibody status and each retained predictor. **A** Herd Size Cohort. **B** In-move per capita cohort. The value ranges for each quantile can be seen in Table 3

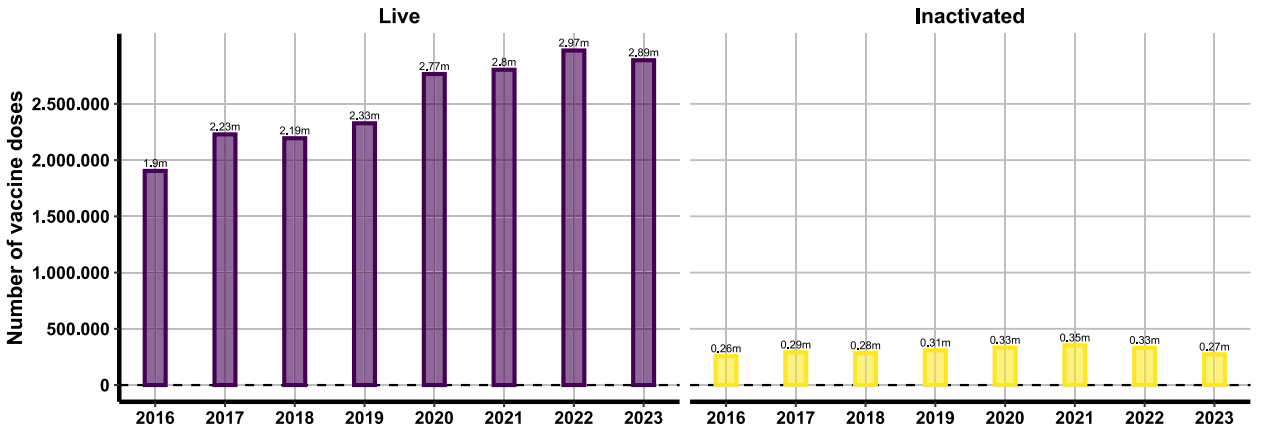

Fig. 9 Number of doses of BoHV-1 vaccine sold per year per vaccine type (inactivated, live). Data from Kynetec

NBWS appear to be a representative subset of all beef breeding herds in Ireland in terms of herd type composition (see Fig. 1). However, there are some differences in herd size distribution between NBWS herds and the overall population of beef herds (see Fig. 2). The overrepresentation of larger herds in the NBWS sample, with a notable underrepresentation of small herds (0–20 animals), could potentially skew the reported herd-level prevalence upwards. Within this study, we have seen that the level of infection is higher in larger herds. Consequently, the actual herd-level prevalence in the national beef herd might be lower than the reported 48.8% in the NBWS sample. Moreover, the overrepresentation of older animals in the tested group could influence the animal-level prevalence estimate, given that age is a known risk factor for BOHV-1 seropositivity [11, 22]. While the study adhered to guidelines recommending sampling animals over 9 months of age, this age bias should be acknowledged when interpreting the estimated animal-level prevalence of 11.4%.

In this study a'snapshot'testing strategy was employed to assess the herd-level BOHV-1 antibody status. This involved testing a random sample of up to 20 animals from each of the 10,650 beef breeding herds participating in the NBWS. If the NBWS testing approach were extrapolated to the national herd, approximately 27% of beef herds would undergo full herd testing through the snapshot, by virtue of having 20 or fewer animals, with a high proportion anticipated to return negative results.

Multivariable risk factor analysis

The multivariable risk factor analysis identified two significant factors associated with recent BoHV-1 circulation, reaffirming findings from previous studies. Herd size and the number of in-moves per capita emerged as the most influential risk factors, aligning with existing literature on BoHV-1 epidemiology [12, 21, 22]. Larger herds and those with higher per capita rates of animal movements exhibited increased odds of recently experiencing active virus circulation, emphasizing the role of herd management practices and herd dynamics in disease transmission. These results underscore the importance of targeted interventions focusing on herd size management and biosecurity measures to mitigate the spread of BoHV-1 within the Irish beef cattle sector.

This study also revealed notable geographic variation in BoHV-1 herd-level prevalence across counties, with values ranging from 35.7% in Monaghan to 63.1% in Carlow. While these differences are clearly visualised in the results, a detailed exploration of underlying drivers, such as regional variation in vaccination uptake, cattle density, biosecurity practices or interactions with other control programmes was beyond the scope of this study.

Limitations

While this study provides valuable insights into the prevalence and risk factors of BoHV-1 in Irish beef herds, it is essential to acknowledge certain limitations. A key limitation of the study arises from the voluntary nature of the NBWS programme. As participation was optional, there is potential for self-selection bias in the dataset. More proactive or better-managed farms may have been more likely to engage in the scheme, possibly skewing prevalence estimates. Another limitation is the uncertainty surrounding the within-herd sampling methodology. Although guidance was issued to encourage random selection, all sampling was performed by local practicing veterinarians, and none of the study authors were directly involved. Therefore, it is possible that convenience sampling occurred in some herds, with veterinarians selecting animals that were easier to access or handle. Another limitation of this study is the exclusion of approximately 40% of participating herds due to incomplete test results. While the decision to include only herds with complete or nearly complete data (maximum one missing value) was made to ensure reliable herd-level classification, this may introduce selection bias.

Another limitation concerns the age of animals sampled in smaller herds. While the sampling protocol aimed to exclude animals under 9 months of age to avoid interference from maternally derived antibodies (MDA), this age threshold could not always be upheld in herds with fewer than 20 animals. In such cases, all animals present were sampled, irrespective of age. This may have introduced bias, as the presence of MDA in younger animals can yield false-positive results, thereby potentially inflating prevalence estimates in smaller herds.

Notably, the study lacks information on vaccine usage within the participating herds. This omission is significant, as it prevents the determination of whether vaccination strategies were employed in specific herds and, if so, how they were implemented, and their impact. The absence of this information may influence the interpretation of the results, as vaccinated herds may exhibit different seroprevalence patterns compared to non-vaccinated herds. However, the seropositive results in our study are due to exposure to the wild virus (gE) rather than vaccination, given that only marker vaccines, which allow differentiation between wild virus exposure and vaccination, have been permitted in Ireland since 2002 [18]. Future studies should consider incorporating data on vaccine use to provide a more comprehensive understanding of BoHV-1 dynamics in Irish beef herds.

A further limitation of the risk factor analysis is the absence of several potentially important confounding variables. Data on biosecurity practices, participation in other animal health programmes or detailed farm-level management were not available. These factors could influence BoHV-1 exposure risk and may confound the observed associations, particularly with respect to herd size and movement patterns.

The method used to infer recent BoHV-1 circulation in herds—based on the age of the youngest homebred seropositive animal—relies on the assumption that infection spreads uniformly across the herd and that antibody-positive animals represent past exposure. However, within-herd transmission may not be complete, especially in low-contact systems or herds with partial vaccination histories. While the age-based threshold offers a practical proxy for recent circulation, it may misclassify some herds, particularly in cases of incomplete transmission.

Finally, interaction terms between predictors were not included in the multivariable logistic regression model. The decision to exclude interaction terms was based on the exploratory nature of this analysis, the large number of potential variables, and the aim to maintain model interpretability.

Conclusion

BoHV-1 remains a significant concern within the Irish beef cattle sector. This study, conducted under the NBWS, provides a comprehensive analysis of the prevalence and risk factors associated with BoHV-1 infection in Irish beef herds. The findings highlight a herd-level prevalence of 48.8% and an animal-level prevalence of 11.4%, indicating that BoHV-1 is endemic in the population. While these prevalence rates reflect a reduction from previous studies, they underscore the persistent challenge posed by the disease. The higher case density observed in larger herds and those with frequent animal in-moves emphasizes the need for targeted interventions. Specifically, herds with evidence of recent BoHV-1 circulation should be encouraged to implement vaccination strategies to reduce transmission risk and prevent reactivation. Conversely, BoHV-1-negative herds may benefit from enhancing general biosecurity measures (e.g., controlling visitor access, quarantine of incoming animals) to maintain their free status and reduce the likelihood of virus introduction.

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Authors' contributions
DG, MG, LL, JML & MG acquired the data for this analysis. JB processed and analysed the data. All authors contributed to the interpretation of study findings. JB drafted the manuscript. DG, HHT, MG, LL, MG, JML, SB and JB contributed to the study design. All authors read and approved the final manuscript.

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Data availability
No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interest
The authors declare no competing interests.

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