



Quantifying the risk of spread of bovine viral diarrhoea virus (BVDV) between contiguous herds in Ireland

Graham D.A.^{a,*}, Clegg T.A.^b, Thulke H.-H.^c, O'Sullivan P.^d, McGrath G.^b, More S.J.^b

^a Animal Health Ireland, Main St, Carrick on Shannon, Co. Leitrim, Ireland

^b UCD Centre for Veterinary Epidemiology and Risk Analysis, UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland

^c Department of Ecological Modelling, UFZ—Centre for Environmental Research Leipzig-Halle, D-04318 Leipzig, Germany

^d Irish Cattle Breeding Federation, Shinagh House, Bandon, Ireland

ARTICLE INFO

Article history:

Received 19 October 2015

Received in revised form 5 January 2016

Accepted 18 January 2016

Keywords:

Bovine viral diarrhoea virus

Infection risk

Spread

Contiguous herds

ABSTRACT

The control of bovine viral diarrhoea virus (BVDV) mainly focuses on the identification and restriction of persistently infected (PI) animals. However, other transmission pathways can also result in new break-downs, including the movement of animals pregnant with PI calves (Trojan animals) and the spread of infection between contiguous farms. Contiguous spread is likely an important problem in the BVD eradication programme in Ireland, given the spatial distribution of residual infection, and the highly fragmented nature of land holdings on many Irish farms. In this study, we seek to quantify the risk of BVD spread between contiguous herds in Ireland.

Multivariable logistic models were used to estimate the risk of a herd having BVD positive calves in January to June 2014 (the study period) when contiguous to a herd that had at least one BVD positive calf born in 2013. The models included risk factors relating to the study herd and to neighbouring herds. Separate multivariable models were built for each of four “PI-neighbour” factors relating to the presence of BVD+ animals and/or the presence of offspring of PI breeding animals.

In total, 58,483 study herds were enrolled. The final model contained the province, the log of the number of calf births born during the study period, the number of cattle purchased between January 2013 and January 2014, and with a two-way interaction between the number of animals of unknown BVD status in the study herd and the PI-neighbour risk factor. When the number of PI-neighbour herds was used as the PI-neighbour risk factor, the odds ratio (OR) associated with the number of PI-neighbour herds ranged from 1.07 to 3.02, depending on the number of unknown animals present. To further explore the risk associated with PI-neighbour factors, the models were repeated using a subset of the study herds ($n = 7440$) that contained no animals of unknown status. The best fitting model including “any PI-neighbour” as the PI-neighbour factor and also contained the log of the number of calf births born during the study period and the number of cattle purchased. The OR associated with “any PI-neighbour” was 1.92 (95% C.I. 1.37–2.70).

This study provides the first quantitative information on the risks posed by the presence of BVD+ animals in neighbouring herds and also highlights the importance of clarifying the BVD status of animals that have not yet been tested in the context of the Irish eradication programme.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

Infection of susceptible cattle with bovine viral diarrhoea virus (BVDV), a member of the genus Pestivirus, family Flaviviridae

(Neill, 2012), may result in either transient or persistent infections, depending on circumstances. Significant economic losses associated with transient infection (TI) may occur mainly due to a range of negative reproductive outcomes including fertilisation failure, early embryonic death, abortion, foetal mummification and a range of teratogenic effects on the central nervous system, and also as a consequence of a virus-induced immunosuppression (Gunn et al., 2004; Stott et al., 2010; Lanyon et al., 2014). A further consequence of transient infection of susceptible females in the first trimester of pregnancy is the creation of calves with a specific immune-

* Corresponding author.

E-mail addresses: david@animalhealthireland.ie (D.A. Graham), tracy.clegg@ucd.ie (T.A. Clegg), hans.thulke@ufz.de (H.-H. Thulke), posullivan@icbf.com (P. O'Sullivan), guy.mcgrath@ucd.ie (G. McGrath), simon.more@ucd.ie (S.J. More).

tolerance to the virus which, if they survive to term, are born persistently infected (PI) with BVDV and typically shed virus at high levels throughout their lifetime (Peterhans and Schweizer, 2010; Lanyon et al., 2014). These PI animals have a markedly reduced life expectancy relative to their non-PI comrades, with many dying before 24 months of age either from mucosal disease or other intercurrent ailments, adding further to the losses associated with infection (Houe, 1993; Taylor et al., 1997; Presi and Heim, 2010).

PI calves are recognised to be central to the epidemiology and control of BVD infection at herd, regional or national level. The coordinated identification and removal of PI calves, allied to the implementation of appropriate biosecurity measures and supported by on-going surveillance, is recognised to be crucial to the successful implementation of co-ordinated programmes of eradication (Lindberg and Alenius, 1999; Houe et al., 2006; Lindberg et al., 2006). A number of European countries have now either completed eradication programmes based on these principles or have programmes underway (Lindberg et al., 2006; Stahl and Alenius, 2012; Norström et al., 2014). Elsewhere, other countries are currently considering the merits of control at national level (Lanyon and Reichel, 2014), or have implemented voluntary regional programmes in the absence of national consensus (Van Campen, 2010).

In Ireland, an industry-led compulsory national eradication programme (www.bvdfree.ie), supported by legislation (Anon, 2012, 2014), began on 1st January 2013 (Graham et al., 2015a,b). It immediately followed a one-year voluntary programme in 2012 (Graham et al., 2014) during which approximately 25% of the national calf crop of 2.1 million calves were tested. The movement of cattle born during the programme without a negative BVDV test, and of other animals with positive or inconclusive results or which have been assigned a suspect status in the database, is prevented, except to slaughter. It is not however required by legislation to cull PI calves, and a minority of herd owners have elected to retain them (Graham et al., 2015a). This is despite extensive communications on the importance of doing so and the provision by the Department of Agriculture, Food and the Marine (DAFM) of limited financial incentives (Anon 2015a,b). In early 2015, DAFM announced its intention to begin placing movement restrictions on herds retaining PI animals and notifying neighbouring herds of their proximity to PI animals, with implementation commencing in June 2015.

While control programmes that identify PI animals and prevent their movement can largely address spread through trade, other transmission pathways can result in new breakdowns. A variety of direct and indirect means of BVDV spread between herds has been described. Trade in animals that are either themselves PI or that are pregnant with PI calves (Trojan animals) are considered to be the most significant (Lindberg and Houe, 2005; Lindberg and Alenius, 1999). This was confirmed in a recent risk factor study in Ireland (Graham et al., 2013). The presence of infection in herds contiguous to non-infected herds logically presents a risk to the latter group, through close contact with a TI or PI animal (for example, animal contact over a boundary fence), although Lindberg and Alenius (1999) suggest that it is likely to be of lower importance than use of common grazing. Nonetheless, contiguous spread is empirically considered to be an important problem in the Irish programme, given the spatial distribution of residual infection, and the highly fragmented nature of land holdings on many Irish farms. Its importance has been recognised in recent modelling studies on BVD transmission within beef cow-calf herds (Smith et al., 2009, 2014; Damman et al., 2015). As yet, this risk remains unquantified, reflecting the lack of sufficient data on neighbourhood contact structures and herd-level BVD data, requiring these modelling studies to rely on expert opinions to provide values for this model parameter.

In this study, we seek to quantify the risk of BVD spread between contiguous herds in Ireland. We estimated the infection risk of a

herd having BVD positive calves in 2014 when contiguous to a herd that had at least one BVD positive calf born in 2013.

2. Methods

2.1. Data sources

Data for the selection of study herds and the status of individual animals therein and in contiguous herds were obtained from the database of the Irish Cattle Breeding Federation (ICBF; www.icbf.com). Contiguity of herds was determined by shared land parcel boundary between farms. It was calculated from the Land Parcel Identification System (LPIS) of the Department of Agriculture, Food and the Marine using the Near Analysis in ArcGIS 10.1 (ESRI, Redlands, California, USA).

2.2. Animal level statuses and definitions

Individual calf status was defined according to the results of the initial and confirmatory diagnostic tests recorded in the programme database. In detail, calves that were positive at the initial test and had a further positive result when subjected to retest were identified as BVDPI. Calves positive for BVDV at the initial test that were not subject to a retest were identified as BVDPOS. For the purposes of this study, both BVDPOS and BVDPI calves were collectively identified as BVD+ and considered to be persistently infected with BVDV. Calves which tested positive or inconclusive initially but negative on retest were identified as BVDTI and considered as transiently infected. The dams of BVD+ calves were assigned a DAMPI status. Where a DAMPI animal was tested with positive results, any live offspring on the database that had not been subject to a direct BVD test were assigned an OFFPI status (offspring of a PI dam) and were themselves considered to be PI. Where a negative test result was recorded for a calf, the registered dam was assigned an indirect negative status (INDINEG). Finally, those animals for which no valid test result was available were assigned an UNKNOWN status.

2.3. Study population

The records of the approximately 82,000 breeding herds in Ireland were interrogated to identify the study herds, which met all of the following criteria: at least one calf was born between 1st January and 30th June 2014 (the study period); the herd had not participated in the voluntary year of the Irish BVD eradication programme in 2012 (ensuring that all herds were in the first year of testing and removing potential variability in relation to farmer experience of the programme, awareness of the disease and approach to biosecurity); and there was no evidence of BVD infection in the herd in 2013. This last criterion was based on the absence of the following known or suspect sources of BVD infection: BVD+ calves born in 2013 or in previous years; animals with DAMPI or OFFPI status; animals with a BVDTI status. Herds were also excluded if all BVD+ calves born in the study period were born within 5 months of the dam being introduced into the study herd (exclusion of Trojan introductions, Lindberg and Alenius, 1999), since in these cases animal movement rather than contiguous spread accounted for the PI birth(s).

2.4. Outcome measure

The outcome measure was the birth of one or more BVD+ calves in the study herd between 1st January and 30th June 2014 (the study period).

Download English Version:

<https://daneshyari.com/en/article/5792950>

Download Persian Version:

<https://daneshyari.com/article/5792950>

[Daneshyari.com](https://daneshyari.com)