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# An integrated approach to assessing the viability of eradicating BVD in Scottish beef suckler herds[☆]

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ABSTRACT

The viability of eradicating bovine viral diarrhoea (BVD) in Scottish suckler herds is dependent on the continued compliance with eradication schemes. At the farm level, the costs of BVD have been identified in previous studies and show a substantial financial imperative to avoid infection. At a regional level the incentives of BVD eradication to individuals are unclear, for example the requirement for vaccination strategies despite achieving disease-free status. Ensuring farmer compliance with an eradication scheme is therefore difficult. Experience of eradicating BVD from beef-dominated areas is limited and theoretical models have tended to focus on the dairy sector. Here we present a stochastic epidemiological model of a typical beef suckler herd to explore the interaction of a farm with a regional pool of replacements, utilising information from a BVD virus seroprevalence survey of Scottish beef suckler herds. Our epidemiological model is then used to assess the relative costs to individuals assuming different regional endemic prevalences, which are used to represent the likelihood of BVD re-introduction. We explore the relative cost of BVD, taken as likelihood and consequence, at an endemic steady state in contrast to previous models that have assumed the introduction or control of BVD in an epidemic state (e.g. a closed and mostly susceptible population). Where endemic, BVD is unlikely to affect all farms evenly and will cost most farmers very little due to herd immunity or self-clearance of the virus. Compliance is likely to be boosted by pump-priming to initiate and complete eradication schemes with cost-sharing.

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## 1. Introduction

Bovine viral diarrhoea (BVD) is an endemic livestock disease causing substantial economic losses in dairy and beef cattle herds worldwide (Bennett and Ijpelaar, 2005). The biggest losses occur through reduced fertility and the generation of persistently infected (PI) animals that are a source of continued infection and can suffer high mortality from the development of mucosal disease (Brownlie, 1985; Roeder and Drew, 1984). BVD virus (BVDV) causes immunosuppression (Chase et al., 2004), predisposing animals to a wide range of disease and resulting losses will often be attributed to secondary causes. As a consequence, economic as well as animal health impacts of BVD are often underestimated in herds with endemic infection.

A comparative study of the economic challenge of BVD in several European countries or regions (Gunn et al., 2005), suggests that the UK may be at a relative disadvantage both in terms of the current challenge from BVD and in the costs to individual farmers of unilateral attempts to establish and maintain disease freedom. This highlights the need for a more detailed study of the economics of BVD at regional rather than just at individual

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farm level. Regional control has tended to focus on areas dominated by the dairy industry. This is not the case in Scotland, which has a much larger beef sector and where there is limited practical experience of eradicating BVDV from beef herds, although some success has been had on the Shetland and Orkney islands (Synge et al., 1999).

Based on the guidance of the OIE (2008), we use a risk analysis framework to integrate studies from complimentary disciplines to explore the feasibility of a regional eradication scheme in the context of Scottish beef suckler herds. McInerney (1996) has suggested that the marginal costs of an eradication scheme might increase considerably towards the end as prevalence decreases and it becomes more difficult to find and eliminate the last and most intransigent infected herds. The problems experienced on the Shetland islands during the eradication of BVD (Synge et al., 1999) lend weight to this argument. Marginal costs at the start of an eradication programme may also be higher as maintaining disease-free herds will be more expensive whilst regional prevalence, and thereby challenge, of BVDV remains high (Gunn et al., 2005). At both extremes of the scheme farms are, therefore, less likely to either embark on or comply with the protocol because the balance of 'risks' is less favourable than midway through the programme. Identification of the relative cost, or their inverse benefits, to individuals and to the public (i.e. a wider farming community) may enable appropriate 'beneficiary pays' cost-sharing to pump-prime an eradication scheme at its start and end. However, estimates of the potential extent of this effect are needed to inform policy.

We explore the financial incentives to control BVD, as an individual farm or a region and the identification of the 'beneficiary' who ought to pay based on the level of endemic disease. Endemic disease represents both the *status quo*, that which is accepted as the norm, and then by reducing the prevalence it represents stages of an eradication scheme which aims to reduce prevalence of disease to zero. For this purpose, we present a stochastic model of a typical Scottish beef suckler herd that interacts with a regional pool of replacement animals of known BVDV prevalence. Previous models (Gunn et al., 2004; Innocent et al., 1997; Viet et al., 2004) have dealt with the incentives to control BVDV on a single closed farm and have explored the consequences of introducing BVDV into a wholly susceptible farm. Here we present a model of a farm that introduces animals from an external source to explore the longer term consequences of different likelihoods of re-introducing BVDV. Our model also explores the endemic state of BVDV, at which point there is an approximately stable prevalence of infected herds even though for any given farm the incidence of BVDV is very low.

## 2. Materials and methods

### 2.1. Data

#### 2.1.1. BVD seroprevalence in Scotland

The starting point for an eradication programme is to identify the prevalence level in order to assess the scale of the challenge and to establish a benchmark from which to estimate the changing marginal benefits of eradication postulated above. This study is based on the results of a survey estimating the national prevalence of active BVDV herd infection in Scottish beef suckler herds (Brülisauer et al., 2009).

A survey comprising 301 beef suckler herds, stratified by geographic region and herd size, was carried out in 2006–2007. Blood samples were taken from a randomised sample of between seven and ten youngstock (6–16 months old) from each management group within the enterprise. Samples were tested by BVDV antibody ELISA and information gathered on farm characteristics and herd management factors using a standardised questionnaire.

One-third of beef suckler herds showed evidence of recent BVDV exposure, with at least one animal testing BVDV seropositive. Sixteen percent (95CI: 11.6, 19.7%) of herds had youngstock with a seroprevalence of more than 90%. This group therefore showed evidence for recent active BVDV infection and presently or in the past harbouring a PI animal.

### 2.2. Modelling

#### 2.2.1. Epidemiological modelling

Following Gunn et al. (2004), we modelled a typical Scottish 100 cow beef suckler herd, using a state transition approach for the BVDV dynamics in an age stratified population. Our stochastic simulation model was designed to account for the small finite population of beef cattle and featured a daily, rather than annual, time step to allow greater emphasis on the timing of (re-)introduction of BVDV via the purchase of animals. These features allowed us to better explore the importance of variability in the timing and likelihood of introduction of infectious animals from off-farm relative to rebreeding and other significant management activities on farm. We modelled BVDV dynamics on a single typical farm using no BVDV control measures, which interacted with a regional pool of herds that were the source of replacement animals. The proportion of animals in each of the mutually exclusive disease states (susceptible, S; transiently and persistently infected/infectious, TI and PI respectively; and immune animals, *R*) on the farm was dynamic based on the assumptions in Table 1.

### 2.3. Regional pool properties

The regional pool was designed as a collection of replacement animals and modelled as a separate set of disease-state classes. Both the number of animals and the prevalence of BVDV in the regional pool were assumed to be static during a given model scenario. The rationale was to mimic the risk of BVDV infection/re-infection to which an individual farm is exposed when buying replacements from a large pool of other farms (the region) assuming an endemic (i.e. steady) prevalence of BVDV equal to, or below, the current level. The regional herd in this model represented any large collection of available animals from a local cooperative to a national herd that can be assumed to have relatively stable, endemic, BVDV prevalence. The

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