

Letters & Notices



BOVINE TB

Questioning badger culling and vaccination

PAUL Torgerson's letter re-evaluating proactive badger culling in the Randomised Badger Control Trial (RBCT) 1998–2005¹ has led to calls for collective dialogue and inquiry (M Brewer, unpublished observations) or to agree to differ.²

However, the recent bovine TB (bTB) strategy review update by Charles Godfray and others² sets out to promote its own statistical re-evaluation, preferring a different (binomial) statistical model. While one basic reporting error in the update has now been corrected,² the problem of the missing variable 'time at risk' (TAR), the treatment of which is crucial,^{3,4} remains uncorrected. TAR is the time that the RBCT experiment ran for in each of the 10 paired cull–control comparisons as it varied from under three years to close to seven years. The new analysis by Godfray and others effectively repeats the oversight of the RBCT analysis, and it looks as if the reviewers of the new analysis were not given sight of the TAR data as they are absent from the update's data table.

When the binomial model from Godfray is corrected to adjust for TAR data (with cloglog adjustment), the culling of badgers had no measurable effect on herd TB incidence, in line with most models. Likewise, the once widely accepted badger-mediated bTB 'perturbation effect' hypothesis disappears, whether TAR is included or not. This should now put an end to what has become habitual references to badgers being a significantly known vector in cattle TB transmission.^{5,6}

The diminished conclusion of the 2025 review update was that badger culling was only 'likely' to have had some effect on herd breakdowns, without direct evidence, and with selective use of scientific reports. For example, it appears to have overlooked the gross under-



“Badger vaccination must be considered an unevidenced and highly speculative high-cost option

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declaration of γ -interferon testing in the APHA reporting of the post-2013 badger culls,^{7,8} which is likely to be responsible for the disease reduction recorded. Also it uses a newly preprinted narrative (with simulations based on uncorrected RBCT assertions and avoiding post-2013 data), to try to undermine, in my view, more plausible forms of analysis checking.⁹

More balanced appraisal shows badger intervention 'benefit' has not been measurable. Evidence overlooked by the Godfray review and Natural England, which coordinates culling, suggests that ongoing Low Risk Area badger culling and vaccination was also founded on the same RBCT science.⁴

The review update and its findings should be independently investigated. Veterinarians cannot have confidence in any strategy proposals based on the suggestions of disease control benefit from badger interventions. The APHA data suggest that cattle measures have assisted to a degree, with improvements required, but as badger culling has been ineffective,^{3,9} badger vaccination must be considered an unevidenced and highly speculative high-cost option.

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CHARLES GODFRAY AND COLLEAGUES RESPOND

WE acknowledge the letter from Tom Langton and encourage people interested in the details of the statistical analysis of the Randomised Badger Control Trial (RBCT) to look at our report¹ (and note that in our analysis the time at risk is taken into account because it is included within the triplet effect).

We would like to reiterate several points made in the report:

■ Reasonable people can disagree about the best way to analyse complex data such as those from the RBCT.

■ There are likely diminishing returns from further analysis of a now 30-year-old experiment.

■ In assessing the degree to which badgers pose an epidemiological threat to cattle, a total evidence approach is needed using information from multiple sources including culling programmes and mycobacterial whole genome sequencing studies.

■ Assessing this threat is important, irrespective of where one stands on culling as a permissible intervention. For example, it informs the need for, and design of, interventions such as badger vaccination and on-farm biosecurity measures.

■ The debate has often become polarised to the point where any suggestion that badgers can transmit bovine TB to cattle is considered evidence of bias and of support for culling. This false implication is detrimental to the development of an evidence base upon which better livestock and wildlife disease policy can be formulated.

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Reference

- 1 Godfray HCJ, Hewinson G, Silverman B, et al. Bovine TB Strategy Review Update 2025. Defra. 2025. <https://bit.ly/4oz9VuP> (accessed 2 December 2025)

SQUIRRELPOX

Suspected change in squirrelpox virus threat to red squirrels

SQUIRRELPOX virus (SQPV) asymptomatically infects grey squirrels (*Sciurus carolinensis*) with high prevalence. In Britain, ELISA testing typically reveals 60 per cent have SQPV antibodies.¹ Transmission of SQPV from grey squirrels causes disease (squirrelpox) and high mortality in red squirrels (*Sciurus vulgaris*).^{2,3}

Lower SQPV seroprevalence (ie, viral exposure) has been observed in small and relatively geographically isolated grey squirrel populations.⁴ Studies have shown that sitka spruce forest habitat types support low-density squirrel populations.^{5,6} We have data suggesting a concomitantly low SQPV seroprevalence in grey squirrel populations within such forests: in 2011/12, only 26.4 per cent of ELISA-tested individuals (n=129) were positive for antibodies in Clocaenog Forest (Wales).⁷

Elevated sero-prevalence of SQPV is likely to reflect immigration from adjacent populations

In subsequent years, annual culling of grey squirrels occurred within Clocaenog Forest and intensive habitat surveillance detected grey squirrel incursions from adjacent broad-leaved habitats where densities were typically high.^{5,6} We have recorded pronounced annual camera-based detection peaks within Clocaenog Forest and associated numbers of grey squirrels being caught in reactive trapping operations (Fig 1). ELISA testing of samples in 2025 revealed 73 per cent of grey squirrels (n=15) were seropositive for SQPV. This elevated seroprevalence is likely to reflect immigration from adjacent populations in broad-leaved habitats that support high grey squirrel densities,⁵ which encourage SQPV transmission.

Clocaenog Forest is one of two key mainland habitats for red squirrel conservation in Wales. Given SQPV transmission from grey to red squirrels, potentially involving environmental contamination,⁸ regular grey squirrel incursions from habitats with high SQPV seroprevalence clearly increase the risk from squirrelpox disease epidemics to sympatric red squirrels.

Red squirrel numbers were perilously low in Clocaenog Forest in 2011/12,⁷ but have increased following a translocation reinforcement programme.⁹ However,

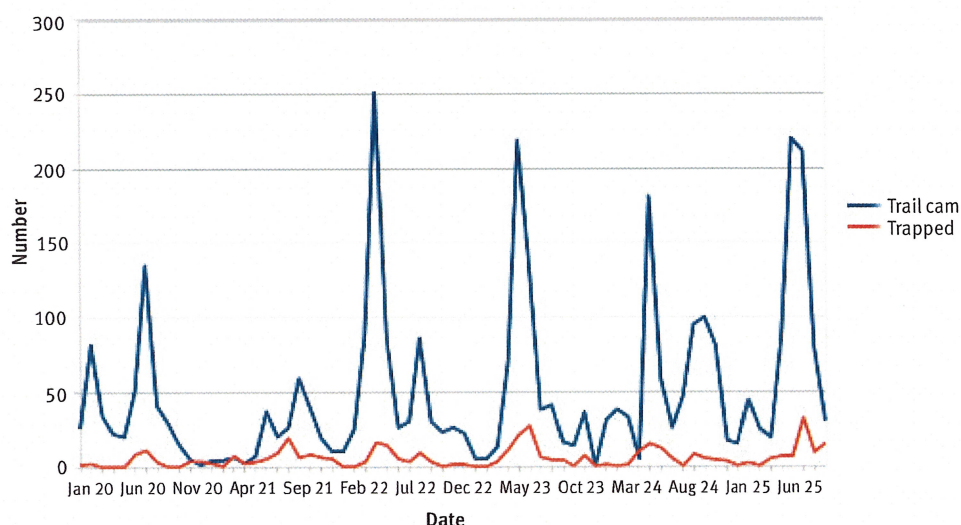


Fig 1: Number of grey squirrel sightings recorded on forest trail cameras and individuals caught in Clocaenog Forest, Wales, in the period 2020 to 2025