6 January 2012

Defra TB Programme
c/o Nobel House
17 Smith Square
London SW1P 3JR

Dear TB Programme staff,

**Estimated proportion of confirmed herd breakdowns attributed to infectious badgers**

Following our discussions, I have brought together the details to document my calculations. Based on mathematical modelling of data collected on badgers culled in initial proactive badger culls, estimates obtained by Donnelly and Hone (2010) indicated that on average at initial proactive badger culls roughly 50% of bovine TB incidents could be attributed to infectious badgers, based on the average of trial-area-specific estimates of the proportion of bovine TB attributable to infectious badgers (49.85%, see Table 1 for the estimate obtained for each triplet).

This estimate was based on comparison of the model fitted per-herd incidence of confirmed TB herd breakdowns in the year before the initial proactive cull for each of the proactively culled trial areas with the prediction, based on the same model, for each area had there been no badger-to-cattle transmission within the area (0.034). Table 1 gives the observed and fitted confirmed TB incidence per herd for each proactive trial area and the corresponding estimated proportion of confirmed TB herd breakdowns attributed to infectious badgers.

**Table 1. The observed and model fitted per-herd incidence of confirmed TB herd breakdowns within each proactive trial area and the corresponding estimated proportion of confirmed TB herd breakdowns attributed to infectious badgers.** The observed data related to 12 months prior to the initial proactive cull (so a different 12-month calendar period in each case). The fitted values were obtained from a model, fitted by Donnelly and Hone (2010), to the relationship between the incidence of confirmed TB herd breakdowns and the prevalence of *M. bovis* infection detected among badgers culled in the initial proactive culls.

<table>
<thead>
<tr>
<th>Trial area</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
<th>H</th>
<th>I</th>
<th>J</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observed</td>
<td>0.113</td>
<td>0.099</td>
<td>0.076</td>
<td>0.113</td>
<td>0.034</td>
<td>0.029</td>
<td>0.029</td>
<td>0.175</td>
<td>0.150</td>
<td>0.070</td>
</tr>
<tr>
<td>Fitted</td>
<td>0.087</td>
<td>0.062</td>
<td>0.041</td>
<td>0.122</td>
<td>0.059</td>
<td>0.051</td>
<td>0.068</td>
<td>0.068</td>
<td>0.126</td>
<td>0.087</td>
</tr>
<tr>
<td>Estimated proportion attributed to infectious badgers*</td>
<td>60.6%</td>
<td>44.2%</td>
<td>16.8%</td>
<td>71.7%</td>
<td>41.2%</td>
<td>32.7%</td>
<td>49.0%</td>
<td>49.0%</td>
<td>72.7%</td>
<td>60.6%</td>
</tr>
</tbody>
</table>

*The proportion attributed to infectious badgers was calculated for each triplet as the difference between the fitted per-herd incidence and the predicted per-herd incidence had there been no badger-to-cattle transmission within the area (0.03447) divided by the fitted per-herd incidence. So for triplet A this would be \((0.08741 - 0.03447) / 0.08741 = 60.6\%\). I have provided further decimal places here to make the calculation clear.

I hope this information is helpful. My 2010 paper with Jim Hone published in Statistical Communications in Infectious Diseases gives more detail on the data and the model fitted but it does not go through this particular calculation (http://www.bepress.com/scid/vol2/iss1/art3/). As ever I am happy to discuss further.

Yours sincerely,

Christl A. Donnelly