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Estimating the impact of *Trypanosoma evansi* infection (surra) on buffalo population dynamics in southern Philippines using data from cross-sectional surveys.

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Abstract

Despite the widespread problem with surra (*Trypanosoma evansi*) in livestock, there are no published studies on its impact on host populations, probably because of the large financial and time cost involved in performing longitudinal studies. During 2002-6, a cross-sectional survey for *T. evansi* infection involving 1,732 buffaloes from 71 villages in southern Philippines was carried out. Other livestock animals (horses, cattle and goats) in every surveyed village were also tested for infection with *T. evansi* but domestic buffalo were the primary survey target. Seroprevalence ranged from 6% to 21% and 13% to 100% for buffalo in low and high risk areas, respectively. Key demographic parameters were estimated from the age structured distributions of the sampled buffalo population for each sex. All areas were dominated by females (69%) and the annual calving rate for areas of 100% and low seroprevalence was 15% and 47%, respectively. Males were removed at a relatively high annual rate of 27% in all areas. In the main reproductive years (4-10) female removal/mortality was <1% and 10% for low and high risk areas, respectively. Older females were removed/died at a rate similar to males regardless of area. In high risk areas there were consistently more 2-year than 1-year old females and the reverse was true for the low risk areas. This implies that females were imported to the high risk areas for breeding. By assuming a stable age structure and similar size populations in each area, it was estimated that 28% of female calves need to be moved from low to high risk areas to maintain the observed age structure. In high-risk areas, surra imposes significant financial losses due to reduced fertility, high mortality/removal rate and the necessity to import replacement buffalo.

Keywords: *Trypanosoma evansi*; Swamp buffaloes; Cattle; Horses; Seroprevalence; Host fertility; Host population demographics; Philippines
1. Introduction

Amongst the pathogenic trypanosomes, *Trypanosoma evansi* (Trypanosomatidae, Kinetoplastida), the causative agent of surra, has the largest geographical distribution and the widest range of hosts. It is endemic throughout Central and South America, Africa and Asia where it is an important constraint to the productivity of livestock, and poses a high risk of spreading to other free countries through animal movement and trade. Recently, outbreaks of the disease have occurred in camels in the Canary Islands (Spain) and mainland France (Gutierrez et al., 2006; Desquesnes et al., 2008). *Trypanosoma evansi* is mechanically transmitted from an infected to a susceptible host mainly by haematophagous tabanid flies (Family: Tabanidae) (Desquesnes et al., 2009) which are found worldwide (Mackerras, 1954). Surra does not occur in Papua New Guinea and Australia but if it enters those countries it would have a devastating effect on livestock and native marsupials that are highly susceptible to infection (Reid and Copeman, 2000; Reid et al., 2001b). Surra is an acute disease with high mortality in susceptible animal species such as horses, dogs and wallabies (Reid et al., 2001b) and a chronic but invariably fatal disease in most other livestock species (Luckins, 1988). Progressive emaciation, anaemia, reduced draft power, immuno-suppression and low reproduction due to infertility, abortions and stillbirths are also common manifestations in affected animals (Lohr et al., 1986; Luckins, 1988; Dargantes et al., 2005b). Buffalo and cattle are probably the main reservoir hosts for *T. evansi* because other infected species tend to either rapidly die (horses, wallabies, dogs) or experience a brief/low parasitaemia (pig, deer) in tissues which impedes transmission (Luckins, 1988; Reid et al., 1999, 2001b).

Surra is considered an economically important livestock disease in the Philippines. Several large epidemics have occurred, particularly in the islands of Visayas and Mindanao during the past two decades, characterised by high morbidity and mortality not only in horses but also in cattle, goats and buffaloes, the main draught animals in most areas in the country (Manuel, 1998; Reid, 2002). Yet, in spite of the widespread nature and economic importance of the disease, its impact on host population dynamics has not been evaluated. Hence, this study aimed to quantify the impact of surra on domestic buffalo populations required for agriculture and food by estimating reduced fertility, increased mortality and animal imports due to the disease using data from a 4-year cross-sectional survey conducted in various regions in Mindanao, southern Philippines. Estimates of these demographic parameters were also utilised to construct an
infectious disease model for estimating production benefits of surra control/treatment in the accompanying paper (Dobson et al., 2009).

2. Materials and methods

2.1. Prevalence survey

2.1.1. Study area

From 2002 to 2006, field surveys to detect *T. evansi* infection in buffaloes were conducted in 71 villages in five provinces in Mindanao. Mindanao (8°00’ N, 125°00’ E) is the second largest island in the Philippines located in the south with a total land area of 94,630 sq km. It receives 1,000 mm of rain annually with a mean annual temperature of 26.6°C and a humidity of 71-85%. The livestock industry, mainly composed of small-scale farmers, plays an important part in the overall farming and economy of the region. Most small-hold farmers own one to two buffaloes raised in a semi-extensive farming system (tethered, allowed to wallow and supplemented with crop by-products). In a village, farm animals are usually tethered in a common pasture area. Table 1 shows the areas and years in which animals were sampled.

2.1.2. Animals sampled

A total of 1,732 local swamp buffaloes (*Bubalis bubalis*), 205 cattle, 43 horses and 38 goats owned by small-hold farmers were sampled during epidemiological surveys in 2002-6. Village farmers were informed in advance through their local government officials of the sampling and animals were brought to one or two sampling sites in each village. Paired whole blood (with and without the anticoagulant EDTA) were taken from each of the animals brought to the sampling sites. Blood samples in EDTA were placed inside a cooler box until examination and blood without anticoagulant was allowed to clot for 1 h at room temperature and placed inside the cooler box until the serum was separated. A comparison of seroprevalence between buffaloes and other host animals was done by pooling results across areas and years with similar buffalo seroprevalence. It was necessary to pool data for this comparison as too few non-buffalo hosts were
sampled from each site. Additional seroprevalence data for pigs and goats was obtained from an unpublished survey currently being undertaken in Mindanao by the authors of this study.

2.1.3. Parasitological tests

The microhaematocrit centrifugation technique (MHCT) and mouse inoculation test (MIT) were used to detect *T. evansi* in blood samples. Tests were carried out within 6-8 h after collection using published protocols with slight modification (Holland et al., 2001; Reid et al., 2001a; Wernery et al., 2001). Briefly, in MHCT, two heparinised microcapillary tubes (75 x 1.5 mm) of EDTA-treated blood were examined for each sample. Capillary tubes were sealed with clay and centrifuged at 12,000 g for 15 min. Each tube was microscopically examined at 100-400x magnification for the presence of motile trypanosomes at the buffy coat-plasma interface. Blood samples positive to MHCT and those with low packed cell volume (PCVs<25%) were then tested using the MIT. Approximately 0.3 to 0.5 ml of uncoagulated blood was injected i.p. into a locally-bred, 4-6 week-old Swiss white mouse. The development of parasitaemia was monitored daily for 30-40 days after inoculation by wet smear examination of tail-tip blood. The MIT was performed with approval from the Murdoch University Animal Ethics Committee, permit No. R881/01.

2.1.4. Serological test

The card agglutination test for trypanosomiasis/*T. evansi* (CATT/*T. evansi*) (Institute for Tropical Medicine, Antwerp, Belgium) was used to determine presence of circulating anti-trypanosome antibodies in the sera as per the manufacturer’s instructions. Briefly, 25 µl of serum (1:4 dilution) was mixed with 45 µl of CATT reagent on a reaction card, gently agitated for 5 min with a card rotator and observed visually for the presence of agglutination. A sample was considered positive when blue agglutinates were visible (Verloo et al., 2000). The apparent seroprevalence of *T. evansi* infection in buffalo and other host animals was corrected based on the published sensitivity and specificity of CATT at a 1:4 serum dilution, 83 and 96%, respectively (Reid and Copeman, 2003) using the formula for true prevalence (Rogan and Gladen, 1978): True prevalence= (Apparent Prevalence + Specificity -1)/(Sensitivity + Specificity-1). Given the high diagnostic accuracy of the CATT the corrected seroprevalence was used to estimate the impact of the disease on buffalo populations.
2.2. Birth rates

From the age structured survey data, summarized in Fig. 1, calving percentages/year were estimated for each province and time by dividing the number of animals less than 1-year old by the number of females between 3 to 12 years old. Animals aged from 1-2 years could also have been included in this estimation but were excluded as there was no way to determine how many had been imported or exported etc.; this is also true for the animals less than 1 year old. However suckling calves are less likely to be removed for sale or consumption and thus should provide a less biased estimate. A linear regression to predict calving from seroprevalence was fitted to the estimates of calving percentage for each sample time and province (Fig. 2). Fitted values were also obtained by fixing the birth rates at 47.5% and 15% for individual uninfected and infected animals, respectively. The proportion in each category was then set according to the sample seroprevalence for the province/time and then the mean fertility of the pooled population was calculated. These values were chosen because 47.5% was the mean calving rate for Bukidnon (the only province sampled that historically has consistent low prevalence) and areas with 100% prevalence had estimated birth rates of 15%.

2.3. Removal rates

The removal rate represents the net removal due to death, export and slaughter for consumption. Removal rates for high and low risk areas were estimated using the pooled data from Fig. 1. However, animals aged 0-2 years were omitted from the analysis because in the high risk areas there were more 2-4 year olds than younger animals, which implies animals were imported from low risk areas to maintain herd size (breeding capacity) in the high risk areas. This analysis thus assumes that relatively few animals over 2 years old are imported. The data was also pooled into 2-year age categories (i.e. 0-2, 2-4 …) to provide some smoothing over time/age. Removal rates were fitted separately to the female (Fig. 3) and male (Fig. 4) buffalo populations from two risk areas. Two models were fitted to the data: 1) a single removal rate for all ages; 2) different removal rates for animals aged 2-8 and over 8.

2.4. Age-structured transition state model

A population projection analysis (Caswell, 1989) was performed using PopTools (CSIRO, Australia) in Excel (Microsoft Inc., USA) to fit female immigration/emigration rates to the same data used in Section
2.3 but including the 0-2 year olds as they represent the age group most likely to be moved between provinces. It was assumed that the observed population structure from the surveyed population was representative of the two risk areas and that the areas have similar size buffalo populations. Rather than fit birth and death rate parameters for each age cohort, which would over-parameterize the model, for each area, a single birth rate was estimated. For young (3-4 years) and old (over 14 years) buffaloes the common birth rate was halved to simulate reduced fertility in these groups. In each area, separate death rates were fitted for animals less than 9 or over 9 years old. Parameters were estimated by minimizing the residual sums of squares for the proportion of animals in each age cohort in each area. Because there were few animals 19 years or older, this group was pooled as a single cohort for analysis. To estimate the goodness of fit of the model the total chi-square across both areas was determined from the observed and fitted number of animals in each age cohort in each area.

3. Results

3.1. Prevalence survey

Table 1 shows the apparent prevalence based on parasitological tests (combined MHCT and MIT) and the corrected seroprevalence (CATT) for various provinces. All samples were examined using CATT and MHCT. However, the MIT was only performed on MHCT-positive samples and samples from animals with low PCVs. A sample that was positive for either MHCT or MIT was counted as positive to estimate the apparent prevalence based on the presence of trypanosomes in Table 1. Except for Compostela Valley, in the provinces regarded as high risk for surra, trypanosomes were confirmed by MHCT or MIT. A comparison of corrected seroprevalence for buffalo and other hosts is given in Table 2.

3.2. Birth rates

Estimated birth rates are plotted against seroprevalence in Fig. 2. Calving percentages/year were estimated for females aged 3-12 years old. For uninfected animals fertility was estimated to be 40.4% (obtained from the intercept of the linear model fitted to the data). There was a significant regression ($P = 0.042$, $R^2 = 0.4694$) for calving versus seroprevalence. Similar fitted values to the regression model were
obtained by setting birth rates to 47.5% and 15% for uninfected and infected animals, respectively, and then calculating the mean fertility of the pooled population (shown in Fig. 2). If 40% was used, instead of 47.5%, then the “predicted” value would be the same as that determined by the fitted linear model. The mean calving rate for areas of historically high prevalence was 20.4%. A number of areas had 100% seroprevalence with estimated calving rates of 15%.

3.3. Removal rates

The best fit to the female populations was obtained by fitting separate removal rates for animals aged 2-8 and over 8 years (Fig. 3). The total chi-square was 21 \( (P = 0.013) \) and 15 \( (P = 0.093) \) for the high and low risk areas, respectively; fitting a single removal rate more than doubled the chi-square \( (P < 0.001) \) in both cases. The removal rates for 2-8 year olds was 0.091 and 0.001 for the high and low risk areas, respectively, this difference can be attributed to surra-related deaths in the high risk areas as females of this age are highly valued for draft power and breeding. The removal rate for the older females was 0.251 and 0.231 for the high and low risk areas, respectively. In contrast, for males (Fig. 4), a single removal rate of approximately 0.266 for all ages in the high and low risk areas best fitted the data. The total chi-square was 5 \( (P = 0.915) \) and 12 \( (P = 0.263) \) for the high and low risk areas, respectively. Unlike the females, fitting the additional removal rate gave a poorer fit for the male data, i.e. slightly increased the total chi-square and reducing \( P \).

3.4. Age-structured transition state model

Fig. 3 also shows the fitted values for the age-structured state transition model from which it was estimated that 28% of female calves were moved from the low to the high risk areas to maintain the observed age structure in both areas. The total chi-square across both areas was 49 \( (P < 0.001) \) however, in the high risk area the 15-16 year old cohort contributed over half the total chi-square (32), so the total chi was re-estimated by excluding this value to give 17 with \( P = 0.103 \); this shows the age-structured state transition model reasonably fits the data if the high risk 15-16 year cohort was ignored (Fig. 3). Fitted parameter estimates: birth rates 29% and 38%; death rates for females less that 9 years old were 10% and 0% for high and low risk areas, respectively; for animals over 9 years the removal rate was 30% (both areas).
4. Discussion

All groups from the high surra risk areas in the sampled provinces had more 2-year old than 1-year old calves, while in the low risk area (sampled on two occasions) there were more 1 year olds as would normally be expected in a stable or growing population. What these observations probably represent are stable populations, one maintained by imports and the other by exports. Coen et al. (2001) reported a seroprevalence of about 70% from buffalo populations in Indonesia where animals over 7 years were pooled and results were not segregated by sex. From their data it can be seen that there were more animals aged 1-2 than 0-1 year old (see Table 3) which is similar to our observations in the surra-high risk areas. Table 3 shows that a model with different removal rates for young and old animals better fitted the population age structure than a single removal rate for all ages, also in agreement with our results. It is not possible to determine from the data what the principal cause of animal removal was, i.e. death (disease or natural) or harvest (sale or food). However, restricting the Philippine data to females is likely to provide an estimate of death or removal attributed to surra, particularly in the young female population that is highly valued and kept for work and breeding. For males in particular, the harvest rate probably dominates the combined removal rate, since owners would generally maintain females for breeding. In this study, the demographic inferences were derived from data which was primarily a prevalence survey in Mindanao that focused on high risk areas where there was sporadic drug treatment. While a longitudinal survey over many years would best serve to estimate such demographic parameters, its cost would be prohibitive so estimating parameters as best we can from cross-sectional survey data is reasonably justified.

The halving of calving rate in high surra risk areas compared with the low risk area (Bukidnon) may be attributed to several factors (e.g. poor nutrition and management, infections). However, the consistently low calving rate in high surra risk areas suggests a strong association between the disease and poor reproductive performance. Surra has been associated with reproductive problems (i.e. abortions, stillbirths) in buffaloes (Lohr et al., 1986; Kashiwazaki et al., 1998) and in other animals (Arunasalam et al., 1995; Kashiwazaki et al., 1998; Suteeraparp et al., 1999; Gutierrez et al., 2006). Reduced calving rate in high surra risk areas could also be attributed to reduced fertility of infected bulls. While there is no available information as to the effect of surra on buffalo male fertility, *T. evansi*-infected bucks and dromedary bulls
manifested testicular enlargement, poor semen quality and even aspermia that may indicate infertility (Ngeranwa et al., 1991; Al-Qarawi et al., 2004; Dargantes et al., 2005a). Emaciation and anaemia associated with surra (Damayanti et al., 1994) may have also contributed to low reproduction performance of buffalo cows. In Indonesia, emaciation due to surra was believed to cause cessation of oestrus in one *T. evansi*-infected heifer (Payne et al., 1993). In high risk areas in Mindanao, buffalo cows are commonly emaciated and anaemic. Since buffaloes were surveyed from provinces with more or less similar farming and management practices, and forage is abundant all year round, management and nutrition factors are unlikely to cause the observed lower calving performance in the high surra risk areas. Other infections (e.g., brucellosis, neosporosis) that can cause low reproductive performance in buffaloes may also be implicated. However, a recent survey in Luzon showed no strong association between abortion in buffaloes with these diseases (Konnai et al., 2008). While other pathogenic trypanosome species (*Trypanosoma vivax*, *Trypanosoma congolense*) have also been reported to cause reproductive problems in animals elsewhere (Ogwu et al., 1986, 1996; Llewelyn et al., 1988), only *T. evansi* was observed in this study based on parasitological examination and confirmed by molecular analysis (unpublished data).

Generally, the negative reproductive impact of surra represents a considerable loss of benefit for small-scale farmers in surra-endemic areas who expect to produce surplus animals for sale as additional income or for consumption. Consequently the need to import replacement stock from other sources is a financial burden for marginally low income farmers. Additionally, the higher death rate of valuable young buffalo cows in high risk areas (10% versus <1%) during their most productive stage implies a shortening of their life expectancy (almost half). Losses to farmers are not restricted to income but also draught output, milk and reproduction losses. Considering that small-scale farmers in developing countries, dependent on oxen or buffaloes, own few animals (Filipino smallholder farmers own one to two buffaloes on average), premature deaths of buffalo due to surra will have a great economic and social impact on the farmer’s family viability. Findings of this study are important for estimating the overall economic losses of surra and the financial benefits of its control not only in buffaloes but in other affected domestic animals as well. In the accompanying paper (Dobson et al., 2009) we describe a disease model of surra for buffaloes and other farm animal species. This simulation model was run over a time-frame sufficient to forecast demographic impacts on host populations and has allowed the net-benefit of surra control on production to be assessed.
Acknowledgements

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References


Table 1

Apparent *Trypanosoma evansi* prevalence in buffaloes in Mindanao determined by detection of trypanosomes using either the microhaematocrit centrifugation technique (MHCT) or mouse inoculation test (MIT). Corrected *T. evansi* seroprevalence was determined by card agglutination test for trypanosomiasis (CATT). The female proportion of the population and the historical surra risk status are also given.

<table>
<thead>
<tr>
<th>Number. Province</th>
<th>Year</th>
<th>Risk</th>
<th>MHCT/MIT</th>
<th>CATT ((n))</th>
<th>Apparent Surra Prevalence</th>
<th>Corrected Seroprevalence</th>
<th>Female Sero-prevalence</th>
<th>Male Sero-prevalence</th>
<th>Female Proportion</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Agusan del Sur</td>
<td>2002</td>
<td>High</td>
<td>0.126</td>
<td>0.996 (104)</td>
<td>1.000</td>
<td>0.934</td>
<td>0.766</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. Agusan del Sur</td>
<td>2005</td>
<td>High</td>
<td>0.027</td>
<td>0.130 (294)</td>
<td>0.113</td>
<td>0.154</td>
<td>0.578</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3. Agusan del Sur</td>
<td>2006</td>
<td>High</td>
<td>0.194</td>
<td>1.000 (103)</td>
<td>1.000</td>
<td>1.000</td>
<td>0.661</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4. Compostela Valley</td>
<td>2002</td>
<td>High</td>
<td>0.00(^a)</td>
<td>0.818 (303)</td>
<td>0.906</td>
<td>0.818</td>
<td>0.728</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5. Surigao del Norte</td>
<td>2004</td>
<td>High</td>
<td>0.086</td>
<td>0.276 (128)</td>
<td>0.288</td>
<td>0.258</td>
<td>0.677</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6. Surigao del Norte</td>
<td>2005</td>
<td>High</td>
<td>0.035</td>
<td>0.521 (228)</td>
<td>0.582</td>
<td>0.401</td>
<td>0.692</td>
<td></td>
<td></td>
</tr>
<tr>
<td>7. Surigao del Sur</td>
<td>2006</td>
<td>High</td>
<td>0.139</td>
<td>1.000 (274)</td>
<td>1.000</td>
<td>0.959</td>
<td>0.628</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Mean</strong></td>
<td></td>
<td></td>
<td><strong>0.111</strong></td>
<td><strong>0.677</strong></td>
<td><strong>0.698</strong></td>
<td><strong>0.646</strong></td>
<td><strong>0.676</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8. Bukidnon(^b)</td>
<td>2004</td>
<td>Low</td>
<td>0.000</td>
<td>0.209 (39)</td>
<td>0.255</td>
<td>0.076</td>
<td>0.744</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9. Bukidnon(^b)</td>
<td>2005</td>
<td>Low</td>
<td>0.000</td>
<td>0.059 (220)</td>
<td>0.039</td>
<td>0.105</td>
<td>0.716</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Mean</strong></td>
<td></td>
<td></td>
<td><strong>0.000</strong></td>
<td><strong>0.134</strong></td>
<td><strong>0.147</strong></td>
<td><strong>0.091</strong></td>
<td><strong>0.730</strong></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\(^a\)MHCT only; animal mortalities due to surra were reported in this province

\(^b\)No case of surra was reported/confirmed in this area
Table 2
Comparison between corrected observed surra seroprevalence for different host species.

<table>
<thead>
<tr>
<th>Province &amp; Year Number</th>
<th>Host</th>
<th>Seroprevalence</th>
<th>Buffalo Seroprevalence</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>%</td>
<td>n</td>
</tr>
<tr>
<td>1, 3 &amp; 4</td>
<td>Horse</td>
<td>92</td>
<td>43</td>
</tr>
<tr>
<td>1 &amp; 4</td>
<td>Goat</td>
<td>68</td>
<td>38</td>
</tr>
<tr>
<td>1, 4 &amp; 7</td>
<td>Cattle</td>
<td>58</td>
<td>76</td>
</tr>
<tr>
<td>2 &amp; 6</td>
<td>Cattle</td>
<td>11</td>
<td>31</td>
</tr>
<tr>
<td>9</td>
<td>Cattle</td>
<td>10</td>
<td>98</td>
</tr>
<tr>
<td>a</td>
<td>Goat</td>
<td>32</td>
<td>211</td>
</tr>
<tr>
<td>a</td>
<td>Pig</td>
<td>17</td>
<td>96</td>
</tr>
</tbody>
</table>

*a Unpublished data from a recent survey conducted by the authors.

*b Data was pooled for these provinces/years to estimate seroprevalence (see Section 2.1.2). The numbers here refer to those given in Table 1 that defines specific provinces and years.
Table 3

Age structured buffalo numbers (male and female) sampled for 2G6-ELISA in Indonesia (Coen et al., 2001) to which a two or single removal rate model was fitted after excluding 0-1 year olds from the analysis. The two-rate model estimated removal rates of 0.123 and 0.435 for 1-7 and 8+ year old animals, respectively. The fitted removal rate for the one-rate model was 0.223.

<table>
<thead>
<tr>
<th>Age</th>
<th>Numbers</th>
<th>2-rate</th>
<th>1-rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-1</td>
<td>255</td>
<td>na</td>
<td>na</td>
</tr>
<tr>
<td>1-2</td>
<td>390</td>
<td>407</td>
<td>480</td>
</tr>
<tr>
<td>2-3</td>
<td>403</td>
<td>354</td>
<td>373</td>
</tr>
<tr>
<td>3-5</td>
<td>548</td>
<td>574</td>
<td>515</td>
</tr>
<tr>
<td>5-7</td>
<td>442</td>
<td>432</td>
<td>311</td>
</tr>
<tr>
<td>7+</td>
<td>401</td>
<td>401</td>
<td>458</td>
</tr>
</tbody>
</table>

Total chi-square 9 83

| P   | 0.011 | <0.001 |

*na – not applicable
Legends to Figures

Fig. 1. Numbers of buffalo by age and sex sampled from surra high and low risk areas. Data was pooled over provinces and years as given in Table 1 for each of the surra risk areas.

Fig. 2. Plot of observed corrected seroprevalence (▲) versus calving percentages/year estimated for females aged 3-12 years and linear regression (—— Linear (Observed)) fitted to the data. Predicted values obtained by setting birth rates to 47.5% and 15% for uninfected and infected animals, respectively, then calculating the mean fertility of the pooled population are shown by ■.

Fig. 3. Number of female buffalo for each 2-year age category (♦ shows the category mid-point) to which a single (---) or different (——) removal rates for animals aged 2-8 and over 8 years were fitted. Removal rate models were fitted separately to animals from high and low surra risk areas and animals aged 2 years or less were excluded from the analysis. × shows the predicted values for all the data fitted by the age-structured state transition model used to estimate import or export of females to the different areas; this model estimated 28% of female calves were moved to the high risk area to maintain the observed age structure.

Fig. 4. Number of male buffalo for each 2-year age category (♦ shows the category mid-point) to which a single (---) or different (——) removal rates for animals aged 2-8 and over 8 years were fitted. Removal rate models were fitted separately to animals from high and low surra risk areas and animals aged 2 years or less were excluded from the analysis.
Figure 1

Areas with History of High Prevalence Mindanao 2002-6 n=1446

Areas with History of Low Prevalence Mindanao 2002-6 n=257
Figure 2

% Calving vs. seroprevalence 3-12 y.o.

\[ y = 40.41 - 0.2519x \]

\[ R^2 = 0.4694 \]
Figure 3

High Risk Area Females

Low Risk Area Females
Figure 4.

High Risk Area Males

- Observed
- Predicted 1-rate
- Predicted 2-rates

Removal Rate 0.268

Low Risk Area Males

- Observed
- Predicted 1-rate
- Predicted 2-rates

Removal Rate 0.264
Figure 5.