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Detection in and circulation of Bluetongue virus among domestic ruminants in Madagascar

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ABSTRACT

So far, no published data was available concerning the circulation of Bluetongue virus (BTV) in Madagascar. During a survey on Rift Valley Fever, we were able to detect a virus belonging to BTV. Therefore, we conducted a study aiming at characterizing molecularly the BTV isolated and assess the importance of circulation of BTV in Madagascar. A total of 4393 sera from ruminants selected randomly by stratification and sampled in 30 districts of Madagascar were tested for BTV. Moreover, 175 cattle were followed during 11 months. Phylogenetic analyses were performed from virus isolated from unfed pools of mosquitoes.

Overall, the estimated mean seroprevalence of infection at the national level was 95.9% (95% CI: [95.2–96.5]) in cattle and 83.7% (95% CI: [81.4–85.9]) in small ruminants. Estimation of incidence rate was 54 per 100 cattle-years assuming that the incidence rate is constant all year along. Phylogenetic analyses revealed that BTV detected belong to serotype 2.

In conclusion, our results showed that BTV is endemic in Madagascar and highly prevalent among cattle. In our study we did not work on the vector involved in transmission of BTV in cattle. Thus, research should be conducted to better describe epidemiology of BTV in Madagascar including vectors and assess economic impact of the disease associated to BTV infections.

1. Background

Bluetongue disease is a disease of ruminants caused by Bluetongue Virus (BTV). This arthropod-borne virus is transmitted primarily by biting midges belonging to the *Culicoides* genus (reviewed in Coetzee et al., 2012a,b). BTV is circulating widely and its distribution pattern is related to the distribution of its vectors. BTV is believed to have expanded in recent years as a possible result of climate warming (Purse et al., 2005; Tabachnick, 2004). Areas like

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Northern and Western Europe, previously BTV-free were recently affected by the disease (Wilson and Mellor, 2009). Direct or indirect economic impacts were important in some areas of the world (Dungu et al., 2004a; Maclachlan, 2010; MacLachlan and Osburn, 2006; Tabachnick et al., 1996). BTV can cause severe disease in certain species of sheep, especially European fine wool and mutton breeds; however in endemic regions, local ruminants do not express clinical disease (Coetzee et al., 2012b). The clinical signs of BTV infection can vary between species. Sheep may have mainly fever, serous bloody nasal discharge, edema erosions and ulcers. Cattle and other ruminants may have ocular discharge, conjunctivitis, oral mucosal congestion, ulceration of muzzle, and teats (reviewed in Maclachlan et al., 2009). Previous studies showed that ruminants of African origin are apparently resistant to the infection (Fernandez-Pacheco et al., 2008; Mauroy et al., 2008). This resistance to BTV might explain why the disease was never described in Madagascar. In this study, we describe for the first time the detection of BTV serotype 2. Moreover, serosurvey amongst cattle revealed high seroprevalence of BTV infection and large distribution of the virus in Madagascar.

2. Methods

2.1. Specimen collection

A total of 12,785 adults mosquitoes were collected on April 2009 in Fianarantsoa and Ambalavao (Central South of Madagascar) during investigations due to Rift Valley Fever outbreaks. Mosquitoes were pooled (23–30) by species and then stored at −80 °C. A total of 390 pools containing monospecies of unfed female mosquitoes were grinded and supernatants were collected for subsequent viral analysis.

To address seroprevalence of BTV infection, we used sera from cattle and small ruminants collected in Madagascar in August 2008 during Rift valley fever outbreak. Sampling methods were described in Jeanmaire et al. (2011). Briefly, Madagascar was divided into 10 sampling areas representing the combination of two stratification factors, the cattle density and the different ecozones. In these 10 sampling areas, 30 districts were randomly sampled. In each district 33–200 animals were sampled. Only animals that were born and lived in the same sampling area were considered.

For estimation of incidence, we included retrospectively sera collected from a cohort of cattle from 5 and 3 villages located respectively in the Southwestern (Tulear II district) and Northwestern (Mampikony district) regions of Madagascar (Fig. 1A). These two districts were chosen because of their agro-system differences. Tulear II is a semi-arid ecosystem and Mampikony has an environment of a dry and deciduous forest. In these study sites, 20 to 30 cattle were sampled and followed up monthly from May 2010 to April 2011. In collaboration with veterinary service and the farmers, cattle included in this cohort study were firstly identified and marked using number hooked around

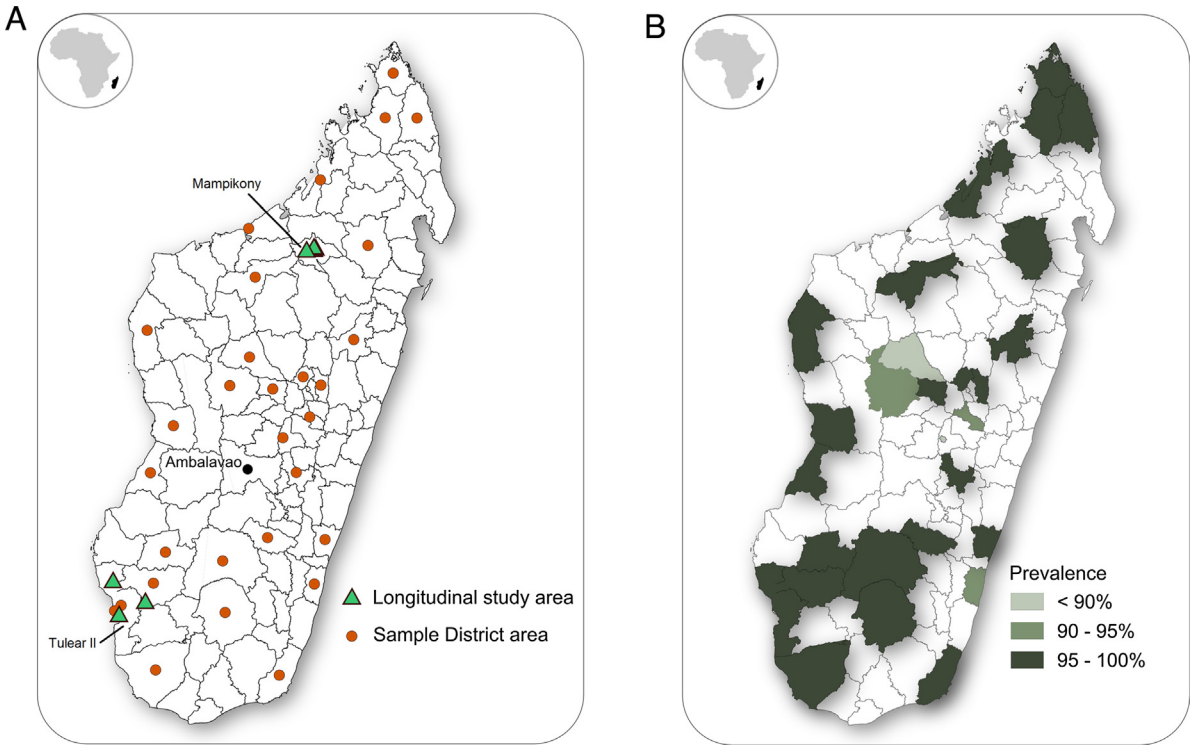

Fig. 1. Seroprevalence of Bluetongue virus infection, Madagascar 2008–2009. (A) Sampled area. Longitudinal study area: Tulear II in the Southern region (3 sites) and Mampikony in the Northern Region (2 sites). Sample district area: 30 districts sampled for the survey. (B) Seroprevalence of BTV in sampled area. White areas represent districts where no sample was collected.