

Scientific Note

Global potential distribution of the mosquito *Aedes notoscriptus*, a new alien species in the United StatesA. Townsend Peterson[✉] and Lindsay P. Campbell*Biodiversity Institute, University of Kansas, Lawrence, KS 66045, U.S.A., town@ku.edu*

The Australian mosquito *Aedes notoscriptus* ranges across Australia, New Guinea, and off-lying islands. Females of this dark mosquito, with conspicuous light markings, banded legs, and a white band across the proboscis, bite humans chiefly by day in shaded areas. This species is an effective vector of dog heartworm (*Dirofilaria immitis*) and has been shown to be competent as a vector of Barmah Forest virus (Watson and Kay 1999) and Ross River virus (Watson and Kay 1998), but is markedly less competent as a vector of dengue virus types 1-4 (Watson and Kay 1999). In sum, this mosquito can potentially play a role of importance in human or veterinary health.

Aedes notoscriptus has been reported recently from the Los Angeles area as a new alien mosquito species in the United States (http://www.sgvmosquito.org/upload_pdf/1039913098_2014_09_15_Aussie_Mozzie_Discovered_in_Los_Angeles_County.pdf). After initial reports by local residents, two southern California vector control districts made an initial identification that was later confirmed (Cameron Webb and John Clancy, University of Sydney). Indeed, this record appears to be the first record of the species outside of its native range (Australia, New Guinea, and off-lying islands), save for appearances in New Zealand that have seen immediate attention with an eye to containment (Derraik 2004). In view of its potential role in vectoring pathogens, the appearance of this species in California represents a novel situation that merits some evaluation and attention.

Here, we use ecological niche modeling approaches to assess the species' potential distribution globally (Peterson et al. 2011). We calibrated models across the native geographic distribution of the species (Australia and New Guinea), omitting the few occurrences in New Zealand; this area was our hypothesis of the accessible area M (Barve et al. 2011). We accumulated 1,480 records from the Atlas of Living Australia (<http://www.ala.org.au/>) and MosquitoMap (<http://www.mosquitomap.org/>), regardless of subspecies or lineage identity (Endersby et al. 2013), which may result in overestimation of niche dimensions if the subspecific populations have at all differentiated in niche dimensions. The occurrence data was reduced to 522 spatially unique records. We then reduced the data set to 197 points that were no closer to one another than 0.5° , or about 50 km. In light of broad spatial autocorrelation inherent in climate data, we did not differentiate between gazetteer-derived and GPS-based geographic coordinates. To represent global climates, we considered the so-called bioclimatic variables 1-7 and 10-17 from the WorldClim climate data archive (Hijmans et al. 2005) at $10'$ spatial resolution. Preliminary Maxent models (see below) with a jackknife manipulation of environmental variables indicated that bioclimatic variable 1 (annual mean temperature)

was not informative, so it was not considered further. We then developed a principal components analysis of the 14 remaining variables in ArcGIS 10.1 to reduce dimensionality and derive non-collinear environmental variables for analysis.

Niche models were fit in Maxent (version 3.3.3k). In preliminary analyses, we explored fitting models with the first nine and the first five principal component axes, summarizing 99.99% and 99.9999% of the cumulative variance, respectively. We developed a surface that summarized collecting intensity for the genus *Aedes* across the calibration region from the same two data sources and provided this data set (0.5° resolution) to the modeling algorithm as a 'bias surface' (Boria et al. 2014). To provide an evaluation of model predictive ability prior to interpretation of global implications, we subset the available, distance-filtered occurrence data at random into two equal subsets, calibrated models based on one subset, and tested model predictions based on the other subset via partial receiver operating characteristic approaches, using an expected error frequency among calibration data E of 10% (Peterson et al. 2008). Finally, we transferred significant models world wide, checking for extrapolative situations that should not be interpreted via the mobility oriented parity (MOP) metric (Owens et al. 2013).

Initial models based on the random subsampling of available occurrence data showed good correspondence with evaluation data points (Figure 1). Although some inland Australian points were consistently omitted from model predictions to the degree that such inland populations are frequent, their omission may signal problems in the models that we have developed. Whereas nine-component models were not significantly better than random expectations, five-component models yielded highly statistically significant results ($P < 0.001$), likely reflecting the common tendency for models based on too many environmental data layers to be overfit and of limited predictive value (Peterson and Nakazawa 2008). The first five principal components reflected high loadings of temperature seasonality (principal component 1) and annual precipitation (principal component 2), and contrasts between aspects of temperature and precipitation. Corresponding five-component models incorporating the bias surface were not statistically significant ($P = 0.099$). Reasons behind this reduced performance are not clear, but perhaps the *Aedes* data that we assembled to summarize relevant sampling effort did not provide a metric useful to the algorithm in incorporating sampling effort into analyses.

Transferring models globally (Figure 2), we noted that the species is reconstructed as having broad distributional potential across the Tropics worldwide, but not in desert regions. Broad areas of apparent potential distribution across far northern