



## Spatial association between malaria vector species richness and malaria in Colombia



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### ABSTRACT

Malaria transmission in Colombia is highly variable in space and time. Using a species distribution model, we mapped potential distribution of five vector species including *Anopheles albimanus*, *Anopheles calderoni*, *Anopheles darlingi*, *Anopheles neivai*, and *Anopheles nuneztovari* in five Departments of Colombia where malaria transmission remains problematic. We overlaid the range maps of the five species to reveal areas of sympatry and related per-pixel species richness to mean annual parasite index (API) for 2011–2014 mapped by municipality (n = 287). The relationship between mean number of vector species per municipality and API was evaluated using a Poisson regression, which revealed a highly significant relationship between species richness and API (p = 0 for Wald Chi-Square statistic). The results suggest that areas of relatively high transmission in Colombia typically contain higher number of vector species than areas with unstable transmission and that future elimination strategies should account for vector species richness.

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### 1. Introduction

Malaria remains an important vector-borne disease in Colombia with an annual case burden ranging between 50,000–100,000 over the past decade (WHO, 2014). With a wide range of climates, highly variable topography and land cover, Colombia also has relatively high number of anopheline species with some 47 species described (Gonzalez and Carrejo, 2009). Of these, three primary vectors account for the majority of infections—*A. albimanus* Wiedemann, *Anopheles nuneztovari* Gabaldon (known now as *A. nuneztovari* s.l.), and *Anopheles darlingi* Root, with a number of other species and species complexes also implicated in transmission of both *Plasmodium vivax* and *Plasmodium falciparum* (Naranjo-Diaz et al., 2013). The Pacific region, where nearly one-third of cases occur in Colombia, is a particularly diverse region for anophelines, although relatively little is known about the current spatial distribution of vector species there (Naranjo-Diaz et al., 2013). Recent field surveys in the region suggest that three other

anophelines are important malaria vectors including *Anopheles neivai* Howard, Dyar & Knab 1912, *Anopheles punctimacula* Dyar & Knab 1906 and *Anopheles calderoni* Wilkerson 1991 (Escovar et al., 2013; Naranjo-Diaz et al., 2013; Orjuela et al., 2015).

While these field collection efforts have advanced understanding of transmission dynamics in the region, field sampling is typically non-random and highly clustered in small localities where malaria is endemic. Therefore, the results from individual surveys typically do not translate well into a spatially comprehensive assessment of vector distribution, which is important for design of future elimination strategies (Clements et al., 2013). However, various geospatial methods exist to generate continuous vector distribution surfaces using occurrence data in combination with spatial covariates such as climate, vegetation type (biome) and function, and land cover/use (Sinka et al., 2010; Conley et al., 2014; Alimi et al., 2015). Here we present the results of an analysis of vector distributions for *A. albimanus*, *A. calderoni*, *A. darlingi*, *A. neivai*, and *A. nuneztovari* s.l. in the five departments of Colombia (Antioquia, Chocó, Valle del Cauca, Cauca, and Nariño) that cover 191,396 km<sup>2</sup> of coastal Pacific and one contiguous interior region (Antioquia department) where malaria remains endemic. The specific aim of this analysis, therefore, is to utilize the wealth of

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species occurrence data available in these five departments to generate accurate species distribution surfaces and analyze these with respect to malaria incidence.

## 2. Materials and methods

We utilized the Maxent species distribution model to produce the potential distribution surfaces. Maxent is a presence-only model that estimates spatial distribution in a defined geographic space subject to the constraint that the expected value of each predictor variable matches its empirical average (Phillips and Dudik, 2008). Maxent produces a projected distribution surface such that each pixel provides a probability of presence. Anopheline points were obtained from survey data acquired under the auspices of an International Center of Excellence in Malaria Research (ICEMR) project (Herrera et al., 2012) as well as the Malaria Atlas Project, 2015 (<http://www.map.ox.ac.uk/>) and included both larval and adult records obtained over the last 30 years. Sample sizes varied by species, with *A. albimanus* (n=624), *A. calderoni* (n=61), *A. darlingi* (n=425), *A. neivai* (n=70), and *A. nuneztovari s.l.* (n=544). Environmental covariates included topography from the Shuttle Radar Topographic Mission, precipitation, temperature from WorldClim (Hijmans et al., 2005) and biomes and hydrological basins from national GIS databases (SIGOT, 2015 [igotn.igac.gov.co/sigotn/](http://igotn.igac.gov.co/sigotn/)). Other covariates include the 2013 annual mean, maximum, minimum and standard deviation of Enhanced Vegetation Index (EVI), which is provided by the Moderate Resolution Imaging Spectroradiometer (MODIS) on board the Terra satellite, a topographic wetness index derived from the digital elevation data, and a deforestation data set (Hansen et al., 2013). All covariates were gridded to 1-km spatial resolution consistent with the highest resolution of the WorldClim dataset. Model accuracy was assessed using the area-under-the-curve statistic (AUC) and the omission rate.

We applied presence-absence thresholds based on the equal sensitivity and specificity threshold produced by Maxent. This

particular threshold is considered among the most robust for determining presence/absence from probability surfaces (Liu et al., 2005). Each occurrence pixel for the five species was assigned a value of 1 and the five species layers were combined in additive fashion to provide an estimate of partial anopheline species richness (SR) for each pixel with values ranging from 0 (no vectors present) to 5 (all vectors present). The Annual Parasite Index (API) was obtained from government data (Sivigila) for all municipalities within the five departments (n=287) and the mean API was calculated for 2011–2014. Mean SR was then compared to the mean API for each municipality and the relationship was evaluated using a Poisson regression model (in SPSS version 22), which is appropriate for count data (i.e., species richness or SR in this case) and in situations where the data are overdispersed.

## 3. Results

The AUC for the five projected vector surfaces ranged from 0.87 for *A. darlingi* to 0.99 for *A. calderoni*. Similarly, the omission rates ranged from 0.14 for *A. calderoni* to 0.25 for *An. neivai*. Taken together, these results suggest highly accurate distribution projections. Further, in four out of five distribution projections, altitude contributed the most to each model, with the exception of *A. nuneztovari s.l.*, in which hydrologic basin contributed 51.2 percent to the model with altitude contributing 23.9 percent. In addition, biome type was either the second or third most important contributor to each model surface, while EVI, TWI, precipitation or temperature typically contributed less than 10 percent for each species projection. This result suggests that altitude serves as an effective proxy of temperature and precipitation and remains an important limiting factor to species dispersal. Further, basin and habitat type (biome) also suggest that these categorical variables relate well to distribution and that vectors are restricted somewhat in their distribution by watersheds and biogeographic properties.

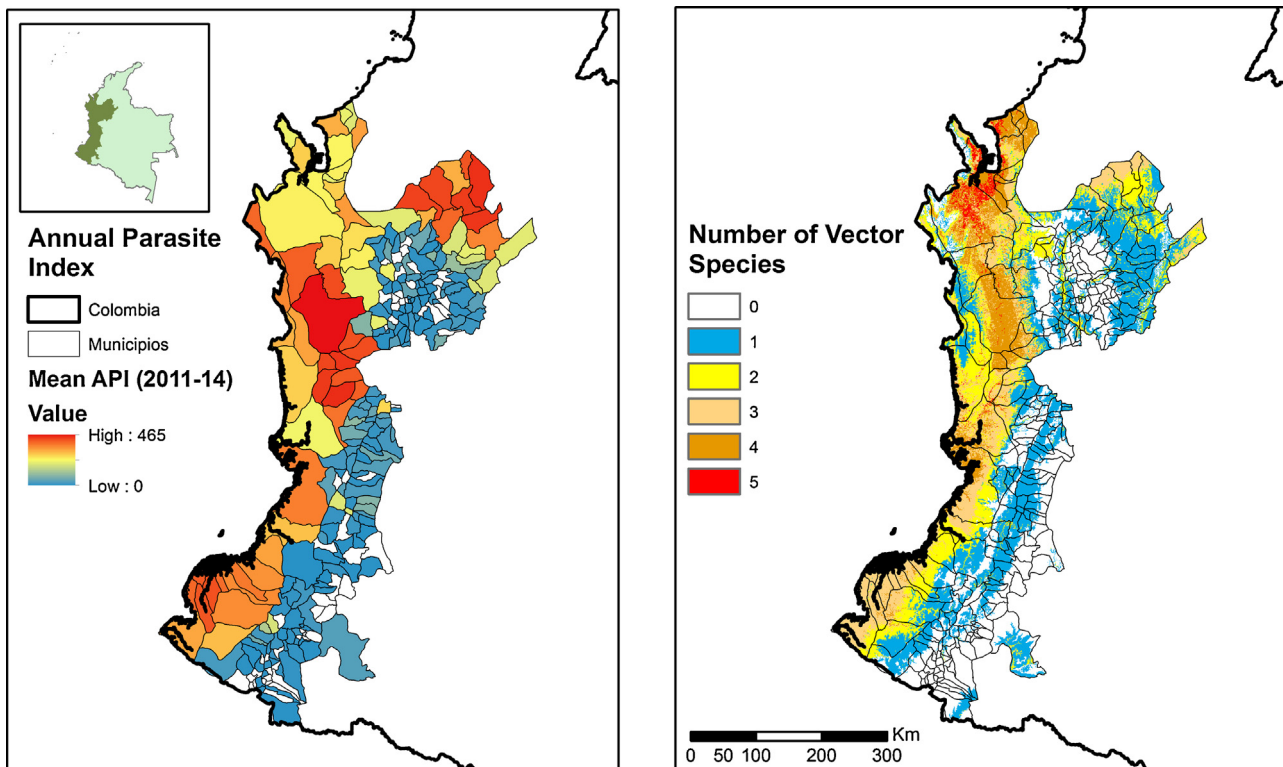
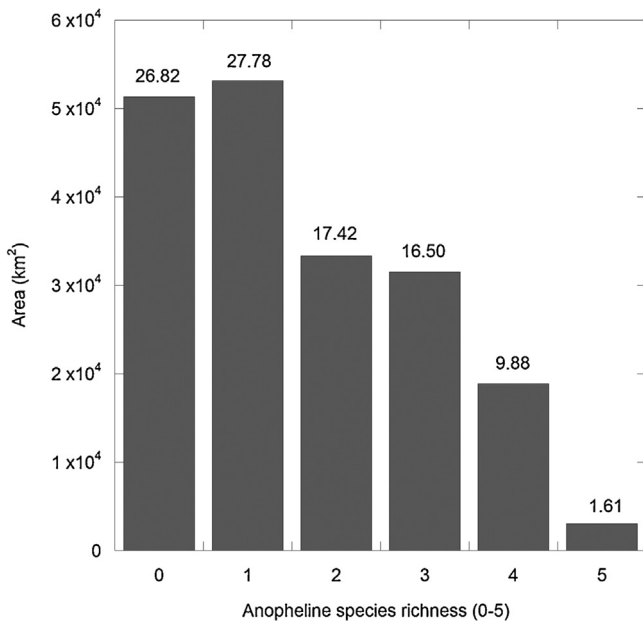


Fig. 1. Annual Parasite Index (left) and partial species richness (right) for the five vectors.



**Fig. 2.** Area covered by different levels of species richness. Numbers on top of bars indicate percent of the total study area covered.

**Fig. 1** presents the API (left panel) and the SR surface (right panel) for the study area. It clearly shows a close correspondence between the two surfaces, with generally elevated API along the Pacific coastal municipalities coincident with an area of high vector richness.

This pattern is repeated in the northeastern interior, Antioquia department, where high SR and high API typically coincide. Areas of relatively low API and low SR can be seen moving inland from the Pacific Coast, as elevation increases and becomes more variable than locations close to the coastal margin, which is dominated by mangroves, other wetlands, and lowland tropical forest. The projected area occupied by different levels of sympatry is shown in **Fig. 2**, which reveals that the most area (27.78%) is covered by one of the five anopheline species and that area of co-occurrence of 2 or more species decreases by approximately 10–11% from SR = 1 to SR = 2 or 3. However, nearly 10% of the study area contains at least four of the five vectors, with these locations found mainly in the north-central part of our study area. The amount of area occupied by all five vectors is restricted to just 1.61% of the total study area, which suggests that the habitat requirements of the five species are indeed different (Sinka et al., 2010).

The results of the regression using a Poisson model indicated a highly significant relationship with SR as a predictor of API. In particular, the Wald Chi-Square Statistic indicated that both the predictor variable (SR) and the intercept were significant predictors ( $p=0.00$ ) of API. The Likelihood Ratio Chi-Square, which provides an overall test of our model over a null model, also returned a highly significant value ( $p=0.00$ ). As a log-link function was used, the model parameters produced a function of the following form:

$$\text{Log(API)} = 0.75 + 1.09 \times (\text{SR})$$

$$\text{API} = \exp(0.75) \times \exp[(1.09) \times (\text{SR})]$$

such that an increase from 1 to 5 on SR, predicted API increases from 6.30 to 492.75. This suggests that the Poisson regression model tends to overestimate API near the low end of the range, but is well constrained for SR values ranging from 2 to 5.

#### 4. Discussion

The five vector species generally possess exophilic and anthropophilic behaviors and with the exception of *A. neivai*, which breeds in epiphytes, these species tend to exploit a range of water habitats for breeding, from slow-flowing streams, temporary pools to brackish water. Despite commonalities, however, there are clear differences in their projected ranges which may be the result of historical factors related to the original sites of speciation or differences in niche breadth. *A. nuneztovari* s.l. is commonly recognized as a species complex that displays a range of habitat preferences and behaviors, with some sibling species showing clear differences in biting behavior and habitat utilization (Sinka et al., 2010). Furthermore, *A. nuneztovari* s.l. and *A. darlingi*, which are among the most important vectors in Latin America, are both associated with disturbed areas such as mining sites or recently deforested locations where temporary pools are likely to be found. Our analysis suggests that ranges of these two species seldom co-occur with *A. albimanus* in our study area, although significant areas of overlap of the three dominant vectors may be found to the north of our study area in Cordoba Department (Ahumada, unpublished data) as well as the interior of the Chocó Department covered here. As *A. neivai* breeds in epiphytic plants such as bromeliads (Escovar et al., 2013), presumably this species is restricted to areas close to undisturbed forest where breeding sites would be plentiful.

The strong relationship between SR and API may be explained by the different strategies and behaviors that these vectors employ to breed and feed on humans. Exposure to an infected bite is therefore more likely when more than one species is present in a particular location as biting periods and locations (e.g., peridomestic versus indoors) vary somewhat among the vectors covered in our study. *A. albimanus* and *A. nuneztovari* s.l., in particular, appear to show the widest range of feeding behaviors during dusk and nighttime while *An. neivai* is known to feed throughout the day (Escovar et al., 2013). In addition, *A. albimanus* is known to feed both indoors and outdoors. It is also possible that vector density and SR are related such that areas optimal for more than one vector species are likely to contain a mix of suitable breeding sites and opportunities for feeding that ultimately lead to higher fecundity and thus a relatively high rate of infected bites per person. Herrera-Varela et al. (2014), for example, concluded that anopheline species composition explains differences in transmission in the northern part of Colombia and the results of our investigation appear consistent with their study.

#### 5. Conclusions

Our study demonstrates a clear qualitative and quantitative relationship between vector species richness and API in an area of Colombia where malaria transmission remains problematic. Species richness, which is one element of diversity, is relatively straightforward to map using the approach outlined above, and may therefore be used to guide vector control strategies, which may have to be adjusted for areas that have a high number of vector species. For example, a strategy that is employed against a single dominant vector such as insecticidal treated nets for an indoor-feeding species like *A. albimanus* may need to be diversified to reduce vector-human contact for daytime or dawn/dusk exophagic species such as *A. darlingi* and *A. neivai*. Thus, as the number of vectors in a particular location (e.g., **Fig. 1**) increases, so too should the strategies employed to reduce potential vector-human contact leading to transmission. Further, the same approach may be applied to analyze georeferenced subspecies data within complexes such as *A. nuneztovari* s.l., which may show high intraspecific diversity in biting, breeding, and resting behaviors. Nevertheless, it should be noted that the results of our analysis are preliminary and further

refinements of the modeling approach to account for seasonality of breeding sites and changing water levels may greatly improve the model's accuracy and utility. For example, intra-annual data on the location of breeding habitats obtained from remotely sensed observations (e.g., using radar imagery) may allow for the production of seasonal distribution maps that reveal how vector habitats are likely to shift throughout the year. In this way, the results may better inform control programs that aim to reduce the burden of vector exposure in Colombia and elsewhere.

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