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Participatory Risk Mapping of Malaria Vector Exposure in Northern South America using Environmental and Population Data

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Abstract

Malaria elimination remains a major public health challenge in many tropical regions, including large areas of northern South America. In this study, we present a new high spatial resolution (90 × 90 m) risk map for Colombia and surrounding areas based on environmental and human population data. The map was created through a participatory multi-criteria decision analysis in which expert opinion was solicited to determine key environmental and population risk factors, different fuzzy functions to standardize risk factor inputs, and variable factor weights to combine risk factors in a geographic information system. The new risk map was compared to a map of malaria cases in which cases were aggregated to the municipio (municipality) level. The relationship between mean municipio risk scores and total cases by municipio showed a weak correlation. However, the relationship between pixel-level risk scores and vector occurrence points for two dominant vector species, *Anopheles albimanus* and *An. darlingi*, was significantly different ($p < 0.05$) from a random point distribution, as was a pooled point distribution for these two vector species and *An. nuneztovari*. Thus, we conclude that the new risk map derived based on expert opinion provides an accurate spatial representation of risk of potential vector exposure rather than malaria transmission as shown by the pattern of malaria cases, and therefore it may be used to inform public health authorities as to where vector control measures should be prioritized to limit human-vector contact in future malaria outbreaks.

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Keywords

Participatory GIS; malaria; risk mapping; multi-criteria decision analysis; *Anopheles species*

1. Introduction

Malaria represents a major global health threat that resulted in some 219 million cases and 660,000 deaths in 2010 (WHO, 2012). While most mortality and morbidity associated with the disease occur in Sub-Saharan Africa, parts of the Neotropics experience significant case burdens, particularly in the Amazon Basin and western Colombia (Herrera et al., 2012; Oliveira-Ferreira et al., 2010). Unlike Africa, where the principal malaria parasite is *Plasmodium falciparum*, most cases in Latin America and the Caribbean involve infection by *Plasmodium vivax*, which may produce relapsing infections in some patients. All *Plasmodium* parasites are transmitted to humans through the bite of several species of mosquitoes in the genus *Anopheles* and some dominant species are highly effective in transmitting malaria parasites (Sinka et al., 2010). While application of control measures aimed at limiting exposure to vectors such as use of insecticide treated nets (ITNs), indoor residual spraying (IRS), and early detection, diagnosis, and treatment have reduced malaria incidence in the region over the past decade, elimination of malaria remains elusive as uneven application of control measures may limit their effectiveness in reducing transmission (Ulrich et al., 2013). Further, anopheline vectors may develop insecticide resistance or behaviors that lead them to avoid control measures, thus making elimination in some areas extremely challenging (Govella et al., 2013).

In large parts of northern South America, transmission of malaria is considered low and unstable, thus malaria is generally hypoendemic and *Plasmodium* infection rates of anophelines are typically low relative to parts of Africa where vectors such as *An. gambiae* are involved in transmission (Arévalo-Herrera et al., 2012). In addition, vectors and human populations vary in space and time, so that outbreaks may occur, especially in frontier agricultural areas or where extractive activities such as mining and logging take place (Caldas de Castro et al., 2006; da Silva-Nunes et al., 2012). Nevertheless, some areas are prone to malaria endemicity because they possess a confluence of socioeconomic and environmental factors such as slow-flowing water bodies, wetlands, frontier settlements, resource-extractive activities, and warm-humid climates that favor mosquito breeding and contact between vectors and humans. Over the past decade, data on such environmentally based risk factors have become publically available for most parts of the globe, such that they may be incorporated into decision-support algorithms within geographic information systems (GIS) and combined in various ways to depict composite risk of diseases such as malaria that have strong environmental components. However, many different methods exist for modeling and mapping disease risk, including probabilistic models, deterministic models, and knowledge-based approaches that rely on a combination of expert opinion (EO) and statistics. The choice of approach is generally determined by the availability of georeferenced disease data (Stevens & Pfeiffer, 2011), which is often limited in developing countries either to small localities where intensive field studies have taken place or to national-level data, which are often aggregated to variably-sized political units like states

and counties. Spatial representation of risk using limited disease data may result in maps that are highly generalized, contain artifacts relating to human-defined boundaries (i.e., political units), and broad risk categories (e.g., high risk, moderate risk, low risk, etc.). For example, the Pan American Health Organization (PAHO) produced a malaria risk map for South America that embodies all these characteristics, including highly generalized polygons that follow international borders along with broad risk categorization (da Silva-Nunes et al., 2012). Thus, given the public availability of high-resolution environmental data, there is great potential and need to produce more highly detailed maps that depict spatial patterns of malaria risk consistent with landscape features that may influence vector ecology and human activities.

With the advent of high-resolution environmental data sets originating from orbital platforms, such as the Shuttle Radar Topography Mission (SRTM) global elevation data, highly detailed environmental information now exists for discerning landscape-level spatial patterns that influence disease risk. However, at national-to-regional scales, detailed georeferenced data on location of transmission in northern South America is generally unavailable in part because patients can only speculate as to where they were bitten by infected anophelines, geocoding of patient addresses is limited by low availability of street-level GIS data, and ethics policies may restrict data to ensure patient confidentiality. And, even if available, data on patient addresses may not represent the location of transmission (Wesolowski et al., 2012). Although georeferenced malaria data for Colombia and surrounding countries are generally restricted or unavailable, environmental data are relatively abundant, thus we elected to use a knowledge-based approach with EO known as multi-criteria decision analysis (MCDA). MCDA provides a way to combine different environmental covariates (e.g., elevation, hydrography, population density, etc.) to evaluate disease risk. Further, EO is becoming a more widely used input to disease modeling as a way to incorporate insights of epidemiologists, vector biologists, and other public health specialists in the decision-making process (Hay et al., 2013; Sinka et al., 2010). MCDA is a preferred method for participatory problem solving as it provides a means for expert interaction, it is computationally fast and easy to understand, and involves a mix of statistical methods and human intuition (Stevens & Pfeiffer 2011). For example, MCDA methods have been used to predict suitable areas for Rift Valley Fever in Africa (Clements, Pfeiffer, & Martin, 2006) and for prioritizing areas for malaria vector control in Madagascar (Rakotomanana et al., 2007). Moreover, because MCDA methods produce data on a continuous scale, small differences in risk can be mapped and parametric statistics may be used to validate MCDA outputs if suitable disease or vector data are available (Stevens & Pfeiffer, 2011). Cell- or pixel based methods such as these also can elucidate gradients and hotspots independent of political boundaries and therefore may provide improved guidance for *post-hoc* analysis that seeks to identify causation associated with model outliers. Thus, the over-arching objective of this research effort was the production of a new high-resolution malaria risk map for Colombia and surrounding areas of Ecuador, Venezuela, Panama, Brazil, and Peru based on EO guidance and participatory decision-support methods implemented with GIS raster-based software.

2. Materials and Methods

Twenty-seven malaria scientists from seven countries (Colombia, Honduras, Guatemala, Panama, Costa Rica, the United States of America, and Peru) participated in a three-day risk mapping workshop in Cali, Colombia, in January 2013. The workshop was designed primarily to incorporate EO on environmental risk factors affecting malaria transmission and vector ecology in the region. Malaria remains problematic in Colombia and therefore we centered our investigation there (Fig. 1). According to the Colombian National Health Service (INS in Spanish), 85% of Colombia's rural land area is below 1,600 m elevation, which the INS uses as a rough threshold to assess areas suitable for malaria transmission; i.e., where transmission may potentially occur (INS 2014). Further, the average annual number of malaria cases reported for 2003-2007 was close to 120,000 with a predominance of *P. vivax* cases (80%) (Arévalo-Herrera et al., 2012). As part of the MCDA mapping exercise, workshop participants were asked about the types of environmental risk factors to include in the analysis, how they should be scaled, and their relative importance. Six risk factors were utilized, including layers depicting possible vector breeding sites (rivers, streams and wetlands), sources of human blood meals (urban areas, population density, and major roads) and thermal gradients and limits controlled by elevation that affect vector distributions (Table 1). To avoid loss of spatial detail from vector GIS data, all coverages were gridded to 90 m spatial resolution and projected to Universal Transverse Mercator projection zone 18 north. We resampled the population data, originally provided at 1000 m resolution, to 90 m using a nearest neighbor algorithm, which was done to maintain consistency with other layers for subsequent analysis. Downscaling gridded data in this way may introduce spatial artifacts in the final map in the form of a coarse-grid square pattern, especially if large weights are assigned to the downscaled layer. Details on the specific data sources and layers are provided in Table 1.

Fuzzy membership functions (FMF) were employed to scale spatial data layers in terms of degree of risk membership along an 8-bit number range (0-255), with the shape of the FMF determined by control points guided by EO. Different fuzzy functions were used, which assume that the degree of risk membership ranges from 0 (no risk) to 255 (full membership). The shape and direction (i.e., increasing or decreasing) of the functions was selected experimentally with control points informed through EO and through previous experience using fuzzy set methodology in different risk mapping applications (Fuller, Williamson, Jeffe, & James, 2003; Fuller, Meijaard, Christy, & Jessup, 2010). Thus, for example, linear decreasing functions were used to scale risk from potential breeding sites such as wetlands and streams by assuming maximum risk proximate to such features and zero risk more than 3000 m from the feature. The elevation layer from SRTM was used as a constraint (or mask) to eliminate areas where risk of transmission is assumed to be vanishingly small in high-elevation areas (>1,800 m). As the underlying method relies on fuzzy logic, each cell value depicts degree of risk membership rather than probability of malaria transmission. EO was critical to determine the different FMF shapes and control points that govern degree of risk for each factor. Table 1 shows the different spatial data layers incorporated in the analysis along with the fuzzy functions and breakpoints agreed upon by the workshop participants.

Risk factor weights were assigned using the Analytical Hierarchical Process (AHP) of Saaty (1994), in which a matrix of pairwise factor comparisons was used to determine relative importance of each factor pair. Each factor pair was judged such that the one factor was assigned a number using a continuous nine-point rating scale ranging from extremely less important to extremely more important relative to the other paired factor. The final weights were produced by means of the principal eigenvector of the pairwise comparison matrix. A consistency ratio for the AHP was used to avoid conflicts among different trade-offs, and a threshold of 0.10 was utilized to indicate good consistency within the pairwise matrix. The pairwise matrix shows how the individual ratings would have to be changed if they were to be perfectly consistent with the best fit weightings achieved. If the overall consistency ratio is greater than 0.1, it is recommended that the matrix be reexamined to determine the pairwise comparison with the largest deviations (Eastman, 2012). Combination of different, weighted “fuzzy” layers was then achieved through weighted linear combination or WLC, which is a linear function where fuzzy values for each factor or risk membership score is multiplied by a weight that signifies importance (Fuller, Meijaard, Christy, & Jessup, 2010; Robinson, van Klinken, & Metternicht, 2010). In the WLC, factor weights sum to one. FMF, AHP, and WLC portions of the analysis were implemented in the decision-support modules of the GIS software IDRISI 17: The Selva Edition (Eastman, 2012).

Participatory multi-criteria decision analysis (MCDA) was conducted during the workshop in Cali that focused on the Valle del Cauca (VDC) department (Fig. 1a) in southwestern Colombia where the cities of Cali and Buenaventura are located. The FMF, factor weights determination, and WLC for VDC were established iteratively using different combinations of factors to: 1. Demonstrate the MCDA methodology to malaria experts for a department of Colombia that is characterized by both high and low intensity transmission (Arévalo-Herrera et al., 2012); 2. Allow rapid evaluation and immediate feedback from workshop participants, which otherwise would have been impractical using standard computer processors if applied to the entire study region in a workshop setting (i.e., typical raster files sizes ranged from 300MB – 1.2GB for the entire study area); 3. Incorporate local knowledge of malaria transmission and epidemiology based on a number of on-going field and laboratory investigations (Arévalo-Herrera et al., 2012). Risk factors, FMFs, and weights derived from this process were later applied after the workshop to the entire study region to scale-up the results obtained for the VDC Department (shown in Figs. 1a and 2).

Malaria case data aggregated to municipio level for 2000-2009 were obtained from Colombian Ministry of Health sources and was mapped using ArcGIS 10 software (ESRI 2011). Annual case means were calculated for each municipio to reduce the interannual variability typically associated with areas of hypoendemic malaria. Correlations between this information and MCDA scores were analyzed as a way to assess the validity of the risk map. Malaria vector collection points were obtained from the Malaria Atlas Project (MAP) for three dominant vector species (DVS), *An. albimanus*, *An. darlingi*, and *An. nuneztovari*. Collections of these DVS included immatures (larvae) as well as adult specimens collected in and around Colombia since 1985 (Fig. 1b). We also utilized a set of additional collection points obtained from Montoya-Lerma et al. (2011) for *An. albimanus*, which is one of the most common vectors in the study region. These vector points were then compared to the

EO-based risk map using a t-test for difference of means. Spatial autocorrelation of DVS collections was assessed using Moran's I statistic calculated in ArcGIS software. Moran's I indicates spatial autocorrelation when the Z statistic is not significant and in such cases vector point layers were resampled systematically by removing points until DVS samples were spatially independent. Reduced samples (RS) and complete samples with spatially independent DVS distributions were then used to evaluate the hypothesis that mean MCDA risk scores for DVS points differed significantly from a random point distribution.

3. Results

Workshop participants determined FMFs based on their knowledge of malaria case and vector distribution in the study region (Table 1). Monotonically decreasing, linear functions were selected for potential vector breeding sites including rivers, streams, and wetlands. Major roads represent corridors along which vectors and infected humans spread and dwell, and risk was considered to decline linearly from 0-3000 m from these features. However, in the case of population and urban areas, the workshop participants suggested that sigmoidal FMFs were most appropriate as malaria cases and vectors are generally absent in densely populated urban areas, they tend to increase in the urban periphery, reaching a peak at moderate population densities, and then decline in areas of very low population density. In the case of elevation, which served as a proxy for temperature, a decreasing J-shaped function was selected as the risk of malaria was assumed to decline slowly at low elevations (0-500 m) and decline steeply at elevations exceeding 1800 m. During the AHP weight derivation, workshop participants elected to weigh wetlands and population density as more important variables relative to rivers, roads, and urban areas. Elevation was also considered important relative to rivers, streams, and major roads, but equally important to population density and wetlands. The final factor weights were therefore 0.1766 for population density, 0.0478 for rivers and streams, 0.0554 for roads, 0.2606 for elevation, 0.0921 for urban areas, and 0.3675 for wetlands, with a consistency ratio of 0.07, which is considered acceptable.

These weights, when applied in a weighted linear combination of six environmental and population-based risk factors, resulted in Fig. 2, which indicates a spatial pattern generally consistent with the distribution of cases shown in Fig. 1a. Consistent with understanding of malaria risk in Colombia, workshop participants noted the zones of relatively higher risk along the Pacific Coast within Valle del Cauca and south near the city of Tumaco. Both areas are known to have relatively high levels of transmission within Colombia (Arévalo-Herrera et al. 2012). Fig. 2 also reveals areas of relatively high risk including a large area in Venezuela associated with the Llanos, an area of seasonally flooded wetland. In addition, the map shows elevated risk in east-central Colombia consistent with Fig. 1a, as well as high risk in the flooded forests along stretches of rivers in the Amazon basin (várzeas) in Brazil and Peru and large areas of wetland in northern Colombia adjacent to the border with Panama and descending between the Cordilleras. Low-to-moderate risk is shown in large areas of the Colombian and northwest Brazilian Amazon (Amazonas State) where human population density is very low and large wetlands are generally absent. Areas in light blue in Fig. 2 indicate either oceanic areas or areas above 1800 m, where risk was assumed to be zero. In addition, by examining the map in detail at 500 percent zoom, we did not notice any obvious effects of the downscaling of the coarse-resolution population layer, which suggests

balanced weighting between the different input layers. However, certain differences between the malaria case distribution shown in Fig. 1a and risk shown in Fig. 2 are apparent including an area of high malaria cases in northern Colombia to the east of the Colombia-Panama border known as Tierralta. The similarities and differences between mean case distribution and mapped risk prompted further investigation using municipio-level information.

Fig. 3 shows the scatterplot of mean risk score against mean malaria cases for all 1116 Colombian municipios. The Pearson correlation coefficient for $N = 1116$ was 0.138, which is significant at the 0.01 level (2-tailed); however, the high number of observations likely influenced this result. When a subset of municipios with average cases greater than 250 ($n = 85$) was examined, the Pearson correlation coefficient decreased to 0.053, which was not significant at $p < 0.01$ (two-tailed). However, more spatially precise information associated with DVS occurrence points produced more coherent results. Fig. 4 reveals the mean risk values for locations where specimens of *An. albimanus*, *An. darlingi*, and *An. nuneztovari* have been reported. Also shown in Fig. 4 is the mean risk value for 173 randomly sampled points and the mean risk score for all three vectors. The results were evaluated using a t-test for differences between means, which revealed that the relationship between pixel-level risk scores at vector occurrence points for two dominant vector species, *Anopheles albimanus* and *An. darlingi*, was significantly different ($p < 0.05$) from the random point distribution, as was a pooled point distribution for these two vector species and *An. nuneztovari*. In the case where autocorrelation was detected in the point distribution of *An. darlingi* and the pooled distribution of the three DVS, the significance of the Z-score from Moran's I, t-statistics for reduced samples (RS) were also significant at $p < 0.05$, which indicates that spatial autocorrelation did not significantly affect the results.

4. Discussion

The results indicating a very weak relationship between mean risk scores and mean malaria cases prompted extensive discussion among experts at the workshop. Although some qualitative agreement can be seen between the two data sets (i.e., Figs. 1a and 2), the low correlation as indicated in Fig. 3 suggests a number of possibilities, including the difficulty in comparing data aggregated from differently scaled units, or an ecological fallacy in which data were compared between disparately sized political units and averages calculated from samples of 90 m pixels. We hypothesize that the relationship between risk scores and malaria incidence (or cases) would be more robust if geocoded case information could be related to each individual pixel. In addition, the workshop participants knowledgeable about Colombian malaria surveillance commented that areas affected by civil unrest and internal migration of at-risk individuals (also related to economic insecurity and civil unrest) may have resulted in significant omissions in malaria case tabulations. The six environmental-population factors considered may also have failed to capture several major, local-scale drivers that tend to be associated with malaria outbreaks, including transient mining operations, logging operations, areas of civil unrest, coca cultivation, and internal migration of at-risk members of the population (da Silva-Nunes et al., 2012). However, the new risk map depicted in Fig. 2 essentially represents risk from static environmental factors that change little or gradually (such as population) over decadal time scales. Thus, the map

should be considered a general vector exposure risk map that may better represent potential risk rather than current risk as reflected in malaria case data, which appears to be driven partly by transient, local-scale exploitation of natural resources and associated human movements (da Silva-Nunes et al. 2012; Caldas de Castro, et al. 2006; Vittor et al., 2006).

Thus, although the original aim of the malaria risk mapping workshop was to develop a new high-resolution malaria risk map, the results shown in Fig. 4 suggest that the map is a better representation of where individuals are likely to be exposed to DVS than risk of transmission. Furthermore, DVS distributions are likely to relate closely to static environmental factors such as those considered in this analysis. As a public health tool, Fig. 2 has obvious advantages over other risk maps that have been published recently (da Silva-Nunes et al., 2012; Arevalo-Herrera et al. 2012) in that it provides high-level of spatial detail, clear depiction of risk gradients, and the location of potential hotspots independent of local political boundaries (i.e., municipios). This information may therefore be considered a potential tool for integrated vector management (IVM) strategies that seek to eliminate malaria insofar as it possesses much greater spatial information than traditional risk maps which typically aggregate risk categories by variably sized political units or simple thresholds based on elevation (e.g., INS 2014). Further, participatory MCDA using environmental and human population layers represents an advance since vector control is considered a highly effective control measure to prevent transmission in endemic areas (van den Berg and Takken 2008). Although IVM, which is defined by the World Health Organization as (2008) “a rational decision-making process for optimal use of resources for vector control” normally involves implementation at the community, district or neighborhood levels, broad-scale mapping at high resolution as presented here is largely consistent with this aim as 90 m is sufficient to elucidate risk patterns and gradients within and around local areas where IVM may be planned. Moreover, although Fig. 2 best represents risk of exposure to a range of vectors, adjustment of FMF control points may be considered in the future to make the map more applicable to the bionomics of different vector species that have different levels of phenotypic plasticity (i.e., the ability to change biological traits in response to environmental change) and behaviors with respect to the environment and human populations. Known limitations to MCDA include subjectivity associated with the identification of risk factors, FMFs and weights, as well as use of inter-correlated data, which may inflate risk scores for places where a number of risk factors coincide when additive models such as WLC are used (Stevens & Pfeiffer, 2011). In addition, the gridding of coarse resolution data such as the population layer used here may introduce artificial spatial discontinuities (i.e., coarse grid artifacts) in the final output map (Fig. 2), although it appears that the weights determined from AHP and the WLC mitigated this effect in this instance. We acknowledge that Fig. 2 is not comprehensive; however, it captures sufficient variation in vector locations that it represents a step forward for spatial planning for future IVM strategies in the study region.

5. Conclusions

By using MCDA guided by expert opinion and decision support algorithms implemented in a raster-based GIS, we produced a new, high-resolution vector exposure risk map for Colombia and surrounding areas. The map was validated using georeferenced data

representing locations where three dominant vector species have been collected. Participatory mapping exercises such as this can also be replicated for other countries since the environmental data sets used here are publicly available through online sources. Thus, the same approach may be applied in other contexts to identify areas where vectors are likely to be present and where control measures such as insecticidal spraying and distribution of ITNs should be targeted to limit human exposure. Future directions to refine participatory risk mapping for vector and/or malaria transmission include testing the results against geocoded malaria case data, incorporation of risk factors associated with malaria hotspots such as civil unrest, mining, logging, unstable populations, agricultural frontiers, and inclusion of recent land cover changes as a potential risk factor.

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- A new malaria vector-exposure risk map is presented having unprecedented spatial detail.
- Expert opinion of malaria specialists working the region was used to create the map.
- The map was evaluated using both malaria case data and vector presence points.
- The approach used provides an accurate spatial representation of risk of potential vector exposure.
- The methodology provides a robust approach to advance integrated vector management strategies.

Fig. 1.
a. Malaria cases by municipio for Colombia averaged by year for 2000-2009. b. Map of vector occurrence points found in northern South America.

Fig. 2.
Risk map of malaria vector exposure derived from multi-criteria decision analysis (MCDA) guided by expert opinion (EO).

Fig. 3. Scatterplot showing no relationship between mean risk score and mean annual cases by municipio

Fig. 4.

Bar chart showing the mean risk values for vector vs. random points.

Table 1

Risk factors, fuzzy member functions, and weights used to create the vector exposure risk map.

Data	Source	Factor	Factor Weight From AHP	Control points	Fuzzy function	Assumptions/Logic
Elevation	SRTM 90 m	Elevation	0.2606	500,500,500, 1800	J-shaped ↓	Vector exposure decreases above 500 m and is null above 1800 m
Roads	DCW	Distance	0.0554	0, 3000	Linear ↓	Transmission occurs within 3 km of roads where blood meals are available
Rivers and Streams	DCW	Distance	0.0478	0, 3000	Linear ↓	Vectors found within 3 km of rivers and streams
Wetlands	IUCN	Distance	0.3675	0, 3000	Linear ↓	Vectors occur within 3 km of wetlands
Urban areas	DeLorme, Inc.	Distance	0.0921	1000, 10000, 20000, 30000	Sigmoidal ↑↓	Vectors absent in urban areas but found in the urban periphery
Population	Landscan	Population density	0.1766	2, 50, 100, 150	Sigmoidal ↑↓	Populations between 2-150 km ² sufficient for malaria transmission
Vector occurrence points	MAP, CC	Validation point layers				

Abbreviations and Symbols: SRTM = Shuttle Radar Topography Mission, DCW = Digital Chart of the World (ESRD), IUCN = International Union for Conservation of Nature, MAP = Malaria Atlas Project, CC = Colombian collaborators. The arrows indicate that either decreasing functions (downward pointing), increasing functions (upward pointing), or symmetric functions (both upward and downward pointing arrows) were used; e.g., a decreasing function assumes that risk decreases with distance from the geographical feature of interest.

Table 2

Sample information for three dominant malaria vector species in Colombia, including information on spatial autocorrelation.

	No. of Sample Points	Mean Risk Score (sd)	Moran's I	Z-score	Moran's I RS	Z-score RS
<i>An. albimanus</i>	132	99.18 (37.75)	0.100	0.152	N/A	N/A
<i>An. darlingi</i>	53	125.89 (48.30)	1.427	3.798*	0.9274	1.437
<i>An. nuneztovari</i>	38	89.55 (28.76)	0.066	0.207	N/A	N/A
All three DVS	151		1.968	4.667*	0.2071	1.904

Notes: RS = reduced sample, sd = sample standard deviation. The total number of sample points for *An. albimanus*, *An. darlingi*, and *An. nuneztovari* does not equal the points for all three DVS because one or more DVS co-occurred in several locations.