WHY IS THE POPULATION OF *PANSTRONGYLUS GENICULATUS* OF THE SOUTHERN CENTRAL CORRIDOR OF THE ATLANTIC FOREST IN BRAZIL ISOLATED AND ITS OCCURRENCE RESTRICTED TO A SMALL AREA?

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INTRODUCTION

Triatomines (Insecta, Reduviidae, Triatominae) are hematophagous insects that are widespread in several natural and artificial ecotopes, mainly on American continent. They are vectors of Chagas disease, an endemic anthropozoonotic disease that affects 15 million individuals in Latin America. The etiologic agent of this parasitosis is *Trypanosoma cruzi* (Chagas, 1909), a flagellate protozoan that circulates in sylvatic cycles, and, more recently, in domestic cycles involving humans.

Panstrongylus geniculatus (Latreille, 1911) is one of the most widely distributed species of Triatominae on South and Central America. Its known range extends from southern Mexico to northern Argentina, including the Caribbean islands. Although it occasionally invades houses, this triatomine has not adapted to colonize human domiciles, an important factor in limiting its potential as a vector of Chagas disease to man. Colonization of pigsties near to and contiguous with human domiciles in the Amazon River floodplain, however, has been reported (Valente et al. 1998).

Because of its wide distribution in the neotropics, *P. geniculatus* occurs in several biomes with different climatic characteristics (*e.g.*, Amazon and Atlantic forest, Caatinga, and Cerrado). Despite this wide distribution, the population of the southern Central Corridor (SCC) of the Atlantic forest in Brazil is, for unknown reasons, isolated and its occurrence restricted to a small area. The determination of its fundamental ecological niche can help us to find evidence about the factors that might be important role in limiting its occurrence in this region.

We then addressed the following questions: Why is the population of *P. geniculatus* of the SCC of the Atlantic forest in Brazil isolated and its occurrence restricted to a small area? Do topographic and climatic conditions limit its distribution? Or its distribution is limited by other factors? We expected to find that this population is locally adapted, presenting narrow tolerance limits to environmental conditions, which limit its distribution in this region.

MATERIAL AND METHODS

Our study area comprises the SCC of the Altantic forest in Brazil, which has about 4.8 million ha. We obtained and georeferenced the occurrence data of *P. geniculatus* in the study area from the database of the Fundação Nacional de Saúde of the Brazilian state of Espírito Santo (1996-2005). This database originates from the entomological surveillance program, which is provided with records of triatomines that people have caught in their houses. We obtained 21 environmental data layers of the study area from the WorldClim database and from IBGE, both accurate to 30 arc-seconds (~ 1 km). We then calculated Pearson correlation coefficients for all combinations of the layers and eliminated highly correlated ones (*r* e"0.95). The ten layers remaining and used for the modeling included: altitude, terrain slope variability (TSV), isothermality (ISO), temperature seasonality, maximum temperature of warmest month, temperature annual range, annual precipitation (PAN), precipitation seasonality, precipitation of wettest quarter and of driest quarter.

To produce a model of the fundamental ecological niche of *P. geniculatus*, we used DesktopGarp, a software based on the Genetic Algorithm for Rule-Set Prediction (GARP). This algorithm uses as input a set of point localities where the species is known to occur and a set of digitized maps of environmental variables of relevant ecological dimensions. It searches for nonrandom associations between environmental characteristics of localities of known occurrence versus those of the overall study region. The output model represents the environmental conditions where the species should be able to maintain populations, and when projected onto a landscape, it provides a potential geographic distribution of the species (Guisan & Zimmermann 2000). We inserted the obtained occurrence data of *P.*

geniculatus and the environmental data layers into the program and configured it with 50 generations, 2000 iterations and a convergence limit of 0.001, using the rule types range, negated range and logistic regression. The models were based on random 50%-50% splits (training/test) of available occurrence points. Because of the stochastic elements in the algorithm and the multiple solutions with the same value for the optimization criterion, no unique solution is produced. Then we used the function Best Subset to select the ten models with the best accuracy of prediction - the optimized relationship between omission and commission errors. We imported and summed these models into ArcGis to visualize the potential distribution.

We performed a jackknife procedure to assess the relative importance of the individual environmental variables. This procedure involved the construction of a series of ecological niche models, each systematically omitting one of the ten layers. This manipulation resulted in ten model combinations and 500 models for the analysis (10 model combinations x 50 generations). For the analysis, we used Hierarchical Partitioning, a robust statistical technique that avoids the path-dependence of multiple regression approaches by calculating all possible regression models, and decomposing the effects of each independent variable into independent and joint effects (Chevan & Sutherland 1991). This technique identified variables most important to accurate distributional prediction at varying numbers of variables included in a particular analysis.

RESULTS AND DISCUSSION

Of the 91 occurrence points of *P. geniculatus*, 56 were considered geographically distinct for model generation. Based on the 50%-50% subsets of training/test points set aside before modeling, the GARP models were highly significant. Compared with random models, the probability of such high predictivity was very low (x^2 tests, 2.2^{-30} d"p d"1.3^{-24}), showing that the models were highly predictive and that our ecological niche models indeed summarize the requirements of the species.

The potential distribution of *P. geniculatus* in the SCC based on our ecological niche modeling appears to be very realistic. It included all known areas where the species occurs, even areas where we did not input records for the model but other authors had reported its occurrence. According to the Hierarchical Partitioning randomization, the most important variables for the occurrence of *P.*

geniculatus were TSV, ISO, and PAN (*Z*-score = 13.2, 5.2, and 1.7, respectively). The southern study area is mainly compounded by a mountainous region with irregular relief and is the most suitable region for this population, which was not predicted to occur in the northern study area, a plainer region with low elevation.

The high predictivity of our niche models and the confirmed importance of topographic and climatic conditions in limiting the occurrence of *P. geniculatus* support our following statement: there is a wide area unsuitable for *P. geniculatus* in the SCC because of the narrow tolerance limit of the studied population to climatic and topographic conditions. The other populations of *P. geniculatus* geographically closest to the studied population are in transition areas between Atlantic forest and Cerrado or Caatinga (Leite et al. 2007), supporting the idea that the studied population is locally adapted to climatic characteristics of the Atlantic forest. Because of the local adaptation of this population, the spatial partitioning was a useful approach in determining its ecological niche. As species could extend their distribution by local adaptations to limiting environmental factors, we suppose several populations of *P. geniculatus* should exist in the neotropics, locally adapted to different environmental conditions (ecotypes). If the conditions of a geographic area to which an ecotype is adapted are similar to the conditions of an anthropic environment, this preadapted ecotype could be most important to Chagas disease epidemiology (Aragão 1983).

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