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Potential geographic distributions of two parthenogenetic weevils (Coleoptera: Curculionidae) associated with citrus in Argentina and Brazil

María G. del Río¹, Noelia V. Guzmán², Sara I. Montemayor^{1,*}, Viviana A. Confalonieri², and Analía A. Lanteri¹

Abstract

Parapantomorus fluctuosus (Boheman) and *Pantomorus cinerosus* (Boheman) (both Coleoptera: Curculionidae) are parthenogenetic broad-nosed weevils native to South America, and they damage citrus in Argentina and Brazil. The objectives of this contribution are to apply ecological niche modelling to compare the suitable areas of occurrence of these species with those of other parthenogenetic Naupactini distributed in similar areas, and to analyze their potential range in relation to the distribution of citrus groves, mainly in Argentina and Brazil. *Pantomorus cinerosus* and *P. fluctuosus* were predicted to be distributed in tropical and subtropical South America, Mexico, Central America, Cuba, southeastern USA (Florida), southern Africa, Madagascar, eastern Australia, and southern China. However, neither has colonized other countries outside the native range. The potential distribution of *P. fluctuosus* is broader than that of *P. cinerosus*, and the predicted areas of both species are partially coincident with main production areas of citrus in Argentina, Brazil, and throughout the world. Although ecological niche modelling is an effective tool for predicting the potential spread and colonization of weevils in distant cultivated areas, weevil establishment is most likely the result of multiple factors.

Key Words: invasive weevils; ecological niche modelling; Naupactini; agricultural pests; orange trees

Resumen

Parapantomorus fluctuosus (Boheman) y *Pantomorus cinerosus* (Boheman) (ambos Coleoptera: Curculionidae) son gorgojos partenogenéticos de rostro corto nativos de América del Sur, que causan daños en cítricos, en Argentina y Brasil. Los objetivos de esta contribución son realizar un análisis de modelado de nicho ecológico de estas especies, comparar las áreas óptimas modeladas con las de otras especies partenogenéticas de Naupactini de similar distribución, y analizar sus distribuciones potenciales con respecto a las zonas productoras de cítricos principalmente de Argentina y Brasil. De acuerdo con nuestros resultados, *Parapantomorus fluctuosus* y *Pantomorus cinerosus* presentan condiciones ambientales favorables en Sudamérica tropical y subtropical, América Central, México, Cuba, sureste de Estados Unidos (Florida), sur de África, Madagascar, este de Australia, y sur de China; sin embargo ninguna de ellas ha colonizado otros países fuera de su rango natural. La distribución potencial de *P. fluctuosus* es mas amplia que la de *P. cinerosus* y las áreas predichas para ambas especies son parcialmente coincidentes con las regiones de cultivo de cítricos en Argentina, Brasil y a lo largo del mundo. El modelado de nichos ecológicos es una herramienta de utilidad para estimar la posible dispersión y colonización a distancia de plagas de gorgojos, sin embargo, su establecimiento en dichas áreas sea probablemente el resultado de múltiples factores.

Palabras Clave: insectos invasivos; modelado de nicho ecológico; Naupactini; plagas agrícolas; naranjos

Human activities, especially commercial trade, increase the risk of spreading invasive agricultural pests. The implementation of appropriate phytosanitary regulations concerning non-native phytophagous insects (e.g., integrated pest population management) requires information on

habitat suitability (Baker et al. 2000), and niche modelling analysis has become a useful tool to address this subject (Peterson 2003; Thuiller et al. 2005). Ecological niche models are used to infer ecological requirements of species based on known occurrence, and to project potential

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distribution of species into different landscapes. In particular, ecological niche models provide valuable insights for planning and establishing priorities for the monitoring and management of insect pests. However, the successful establishment of a non-native species in a new environment also depends on other factors, such as the presence of predators and competitors, food availability, human footprint, and climatic similarity with the native region (Rödger & Lötters 2009).

Curculionidea is one of the most diverse groups of Coleoptera, with 62,000 species, (Marvaldi et al. 2002, 2014). The tribe Naupactini (Entiminae) is represented by broad-nosed weevils that are highly diversified in the Neotropical region (Lanteri & del Río 2017), and includes several species harmful to agriculture (Lanteri et al. 2002a). Parthenogenetic reproduction is quite common among entimines (Marvaldi et al. 2014), and about 30 species of Naupactini native to South America show this reproductive mode (Lanteri & Normark 1995). Parthenogenesis may increase the probability for a species to establish in new areas, because a single female at any stage of development has the potential to start a new population without male fertilization (Kearney 2005). Parthenogenetic weevils are expected to display higher colonization capacity than their sexual counterparts, especially in marginal areas with low species biodiversity (Stenberg & Lundmark 2004).

In a previous paper, we studied the potential distributions of 10 parthenogenetic species of South American Naupactini native to central Argentina, southern Brazil, Uruguay, and Paraguay that are harmful to several crops, such as cereals, alfalfa, soybean, and other legumes (Lanteri et al. 2013b). They are mainly found in 1 of the agricultural heartlands of the world, the Pampas, which is a vast treeless plain dominated by grassy prairies and steppes. Some of these species (e.g., *Aramigus tessellatus* [Say], *Atrichonotus taeniatulus* Berg, *Naupactus leucoloma* Boheman, and *Naupactus peregrinus* Buchanan [all Coleoptera: Curculionidae]) have spread to distant locations where they became established, including prairies and steppes of Australia, New Zealand, and the USA (Buchanan 1939; Chadwick 1965; Guzmán et al. 2012; Lanteri et al. 2013a, b). Other species (e.g., *Aramigus conirostris* [Hustache], *Eurymetopus fallax* Boheman, *Pantomorus auripes* Hustache, and *Pantomorus ruizi* [Brèthes] [all Coleoptera: Curculionidae]) are not found outside South America even though our niche modelling analysis predicted that some areas of the southeastern USA, southern Africa, and southeastern Australia would be moderately suitable for their occurrence (Lanteri et al. 2013b).

The principal objectives of this paper are to recognize, at a global scale, areas with suitable climatic conditions for 2 parthenogenetic species of Naupactini native to South America, *Parapantomorus fluctuosus* (Boheman) and *Pantomorus cinerosus* (Boheman), to compare their predicted suitable ranges with those of parthenogenetic species previously modelled, and with the most important areas of citrus production in Argentina, Brazil, and the rest of the world.

Both species are naturally distributed in Argentina and Brazil, where they cause damage to citrus groves, particularly orange, *Citrus sinensis* (L.) Osbeck (Rutaceae) (Lanteri et al. 2002a, b; Guedes et al. 2005). Fruit production is reduced due to the damage caused by the larvae feeding on roots, with subsequent plant infection by pathogens (e.g., the fungus *Phytophthora* spp.; Peronosporales). Brazil is the principal exporter of orange juice in the world (Lanteri et al. 2002b; Guedes et al. 2005).

Parapantomorus fluctuosus is one of the most frequent Naupactini associated with citrus groves in the states of São Paulo and Minas Gerais, Brazil (Lanteri et al. 2002b; Guedes et al. 2005). It also occurs in Bolivia, and was recently found damaging oranges in Corrientes Province in Argentina. *Pantomorus cinerosus* occurs in the Citrus Belt of Brazil, although less frequently than the former species, and also in Uruguay and central Argentina. It was reported to attack orange plants in Entre Ríos Province in Argentina, and soybean *Glycine max* (L.) Merr.

(Fabaceae), and alfalfa, *Medicago sativa* L. (Fabaceae) in central Argentina (Lanteri et al. 2002a).

Materials and Methods

SPECIES DATA

Two occurrence datasets were compiled for *P. fluctuosus* and *P. cinerosus*. For each species, a total of 40 and 35 occurrence localities were assembled, corresponding to 365 and 160 specimens, respectively. This information was compiled from specimens collected by the authors and data housed in several entomological collections, i.e., American Museum of Natural History (New York, USA), Charles W. O'Brien Collection (Green Valley, Arizona, USA), Departamento de Zoología da Universidade Federal do Paraná (Curitiba, Brazil), Museo de La Plata (La Plata, Argentina), Museu de Zoologia da Universidade de São Paulo (São Paulo, Brazil), United States National Museum (Washington, DC, USA), and Universidad de la República (Montevideo, Uruguay).

In order to avoid biases due to spatial autocorrelation, occurrences closer than 10 km were discarded. The final datasets used to train the models constituted 37 records for *P. fluctuosus* and 29 for *P. cinerosus*. Tables of supplementary material, with information on the locations and geographic coordinates of the samples studied are available at http://www.museo.fcnym.unlp.edu.ar/uploads/docs/georreferencias_naupactini.pdf.

SELECTION OF VARIABLES

To build the models, we used the set of 19 bioclimatic variables available at WorldClim database (Hijmans et al. 2005); the resolution of the layers was 5 arc-min (10 km²). To avoid multi-collinearity, correlated variables were excluded for both species. Pearson's correlation coefficient (r) was calculated between each pair of the 19 WorldClim (Hijmans et al. 2005) variables for all the points from the geographical extent of both species. For each comparison with $r \geq 0.90$, 1 variable was selected for modelling. The excluded variables for *P. fluctuosus* were Bio3, Bio8, Bio9, Bio10, Bio11, Bio13, Bio14, and Bio16, and for *P. cinerosus* were Bio2, Bio4, Bio10, and Bio19.

ECOLOGICAL NICHE MODELLING

Ecological niche models were prepared according to Maxent v3.4.1k (Phillips et al. 2018). To calibrate the models, we defined an area based on the ecoregions where the known records are distributed, following the World Wildlife Foundation hierarchical classification of ecoregions (Olson et al. 2001), and on this area a 10-km buffering zone was applied. After calibrating, models were transferred globally. To avoid over-parameterization, models were tuned by exploring the performance of different beta-regularization multiplier values (0.5 to 4), and of different feature classes (L, H, LH, and LQH). Model performance for each combination of regularization multiplier and feature class were evaluated, following the recommendations of Shcheglovitova and Anderson (2013), through the omission rate and the AUC, and by analyzing the model predictions in the known distribution of the species. Optimal model complexity was estimated for *P. fluctuosus* with a regularization multiplier of 0.5 and the feature class of HLQ, and for *P. cinerosus* with a regularization multiplier of 0.5 and the feature class of H.

Models were converted into binary maps considering the "minimum training presence logistic threshold". Values above this threshold were considered as presence, and below as absence. Values above the minimum training presence logistic threshold indicate that climate conditions are suitable for the survival of the modelled species, guar-

anteing that all records used to train the models are predicted as suitable. A multivariate environmental similarity surface analysis was performed to identify the regions with environmental conditions outside the range of the training area. Cells on the binary map where the multivariate environmental similarity surface analysis recovered novel climates were identified and discarded in the final maps because both species are considered highly conservative of their climatic niche.

MODEL VALIDATION

Models were validated by applying the partial ROC procedure (pROC). For each species, 1,000 random iterations with 50% sub-sampling were performed to determine if the real models are statistically significantly better than random (higher than 1.0) ($P < 0.001$) (Peterson et al. 2008). These evaluations were carried out in Niche Toolbox available on the Web at <http://shiny.conabio.gob.mx:3838/nichetoolb2/> (Osorio-Olveda et al. 2018).

Results

Partial ROC evaluation indicated that the ecological niche model of *P. fluctuosus* is robust, yielding predictions statistically significantly better than random (AUC ratios 1.17). Suitable conditions (Fig. 1A) were found mainly in tropical and subtropical areas of South America, Mexico, Central America, West Indies, and southeastern USA (Florida only). Outside America, the species is mainly predicted for south-equatorial Africa, Madagascar, eastern Australia, and southeastern Asia. Partial ROC evaluation of the ecological niche model of *P. cinerosus* also proved to be statistically significantly better than random (AUC ratios 1.90). Suitable conditions (Fig. 1B) were found in central and northern Argentina, Uruguay, eastern Paraguay, southern Brazil, Mexico, and southeastern USA (Florida only). Outside America, the species is predicted mainly for southern Africa, southern China, and eastern Australia.

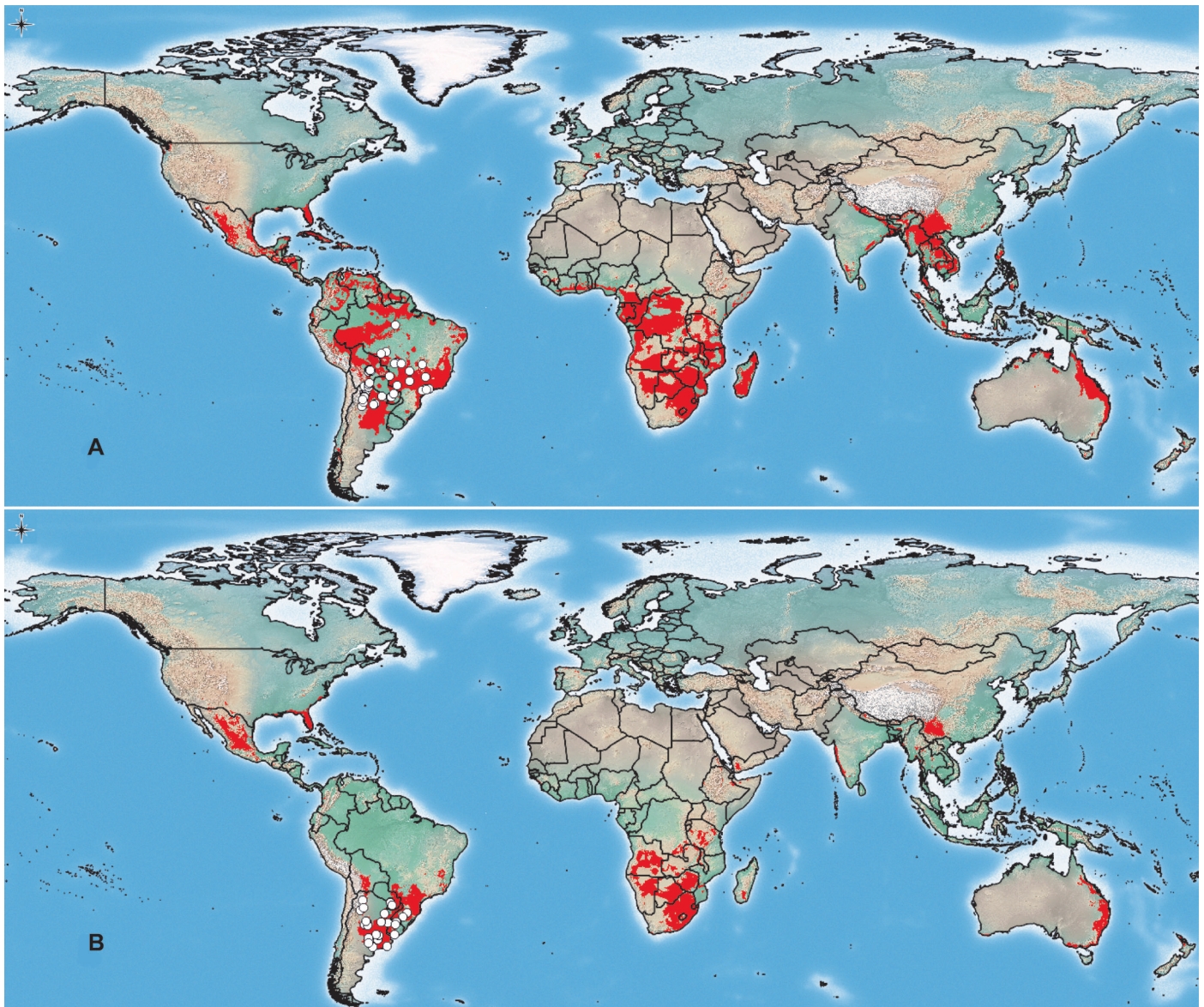


Fig. 1. Binary maps of the ecological niche models for 2 parthenogenetic weevils. (A) *Parapantomorus fluctuosus*; (B) *Pantomorus cinerosus*. Potential distributions are shown in red and occurrence records used in the model are in white circles.

Discussion

According to our models, the climatological space occupied by the 2 species analyzed herein fit with climates belonging to the subtropical forest and grasslands, but up to now neither of these species has been recorded outside their native range. Conversely, other parthenogenetic species previously modelled, such as *A. tessellatus*, *A. taeniatulus*, and *N. leucoma* (more widespread throughout the grasslands), have been able to colonize several countries outside their native range (Guzmán et al. 2012; Lanteri et al. 2013b).

Southeastern USA (Florida), southern Africa, and eastern Australia are suitable for all the parthenogenetic Naupactini previously studied, and central Europe is suitable for most of them (e.g., *A. taeniatulus*, *F. sordidus*, *E. fallax*, and *Naupactus cervinus* Boheman (all Coleoptera: Curculionidae) [Lanteri et al. 2013b; Rodriguero et al. 2016]). The predicted suitable areas for *P. cinerosus* are similar to those for the latter species, while that for *P. fluctuosus* is even broader. However, neither of them has yet colonized areas outside their native range.

On the other hand, the model of *P. fluctuosus* predicts suitable conditions for the species in the most important area of citrus production in Brazil, the Citrus Belt, which encompasses most of São Paulo State and the eastern portion of Minas Gerais State (Guedes et al. 2005), suggesting a real threat for the citrus industry in Brazil. The Citrus Belt, also known as “Triangulo Mineiro,” provides more than 80% of the Brazilian oranges, 35% of all the oranges produced in the world, and half of the orange juice traded on the international market (Paulillo 2006; Spreen 2010). Furthermore, suitable conditions are predicted for the northwestern Argentine provinces of Salta, Jujuy, and Tucuman (Yungas biogeographic province), which are major areas of citrus production.

According to the *P. cinerosus* model, suitable conditions for this species would be found in the most important areas of citrus production in Argentina: one is the same as for *P. fluctuosus*, and the other is located in the northeastern provinces of Misiones, Corrientes, Entre Rios, and northern Buenos Aires near the Paraná, Uruguay, and La Plata rivers.

Outside South America, the predicted suitable areas for both species match areas of citrus production in southern Mexico, Cuba, southeastern USA, southern Africa, eastern Australia, and China.

The expansion of agricultural frontiers and the growth of commercial trade increase the risk of invasion by polyphagous insects, such as several parthenogenetic weevils of the tribe Naupactini. Modelling species' distributions is an effective tool for predicting potential spread and colonization of weevils in distant cultivated areas, but their successful establishment probably depends on multiple factors.

Despite the fact that *P. fluctuosus* and *P. cinerosus* may reproduce parthenogenetically, and that our models predict several of the surveyed areas (in South America and worldwide) as suitable for both species, neither of them is known to occur overseas. Indeed, only 8 of more than 30 parthenogenetic Naupactini species native to Argentina and Brazil have established populations far from their original distribution areas, the most widespread being the “fuller's rose weevil” *N. cervinus*, a serious pest of citrus and many other crops (Lanteri et al. 2002a, b; Guedes et al. 2005; Rodriguero et al. 2016).

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