

Available online at www.sciencedirect.com



MOLECULAR PHYLOGENETICS AND EVOLUTION

Molecular Phylogenetics and Evolution 46 (2008) 503-514

www.elsevier.com/locate/ympev

Genetic structuring in the threatened "Lagartijo del Bosque Seco" (*Anolis cooki*) from Puerto Rico

Javier A. Rodríguez-Robles^{a,*}, Tereza Jezkova^a, Manuel Leal^b

^a School of Life Sciences, University of Nevada, LasVegas, 4505 Maryland Parkway, Las Vegas, NV 89154-4004, USA ^b Department of Biology, Duke University, Durham, NC 27708-0338, USA

> Received 9 April 2007; revised 2 November 2007; accepted 14 November 2007 Available online 22 November 2007

Abstract

Species with restricted geographic distributions consisting of isolated populations are particularly susceptible to extinction because these demes face an increased risk of disappearing due to environmental, demographic, and genetic stochasticity. We used partial DNA sequences of the cytochrome b (1083 bp) and ND2 (1041 bp) mitochondrial genes to investigate the phylogeography and population genetics of Anolis cooki, a threatened lizard endemic to the southwestern coast of the Caribbean Island of Puerto Rico. Maximum likelihood and Bayesian methods revealed relatively shallow genetic differentiation among 27 unique haplotypes (from 52 individuals) from the known extant populations of A. cooki in mainland Puerto Rico. Despite this pattern, specimens from the same geographic area tended to nest together. The most basal division within A. cooki is between haplotypes from the three westernmost populations (Punta Águila, Morrillos, Playa Santa) and the remainder demes (Bahía Ballena, La Cueva, Punta Verraco). The three westernmost populations of A. cooki are separated from their conspecific demes by the Guánica Bay and the Loco River drainage system, which together may represent a physiographic barrier for A. cooki. Each population of A. cooki only has private haplotypes; in other words, there are no shared mitochondrial types between populations. Because the number of private haplotypes can be used as an indirect measure of gene flow, this finding suggests that currently there is no migration among demes, and that each is an independent demographic unit, despite the relatively short distances (ca. 2 km) that separate some of them. Pairwise F_{ST} values and spatial analyses of molecular variation confirmed the existence of distinct groups of genetically defined sampling areas, and of significant molecular variation among populations within groups and within populations. The conservation status of the populations of A. cooki varies greatly. The demes from Punta Águila, Morrillos, and Bahía Ballena inhabit protected areas, and are larger, genetically diverse, and seemingly stable. The population from Playa Santa showed a high level of genetic diversity, but it occurs in an area that has been intensively developed for residential and touristic purposes, and its long-term survival is uncertain. A. cooki is also known from Caja de Muertos, an island off the southcentral coast of Puerto Rico. Surveys conducted on September 2006 and March 2007 did not produce any specimens, and a thorough assessment of Caja de Muertos is needed to determine the present status of A. cooki on the island. © 2007 Elsevier Inc. All rights reserved.

Keywords: Anolis cooki; Conservation; Cytochrome b; Caribbean sea; ND2; Phylogeography; Population genetics; Puerto Rico

1. Introduction

[Anolis cooki] clearly survives as of now. But is this a stable situation? It is easy to see climatic change wiping cooki out. But even without climatic change is

cooki holding its own? It is not possible to answer this question on any current evidence, but the existence of *cooki* may already be marginal. It may be the very model of a species about to submerge (Williams, 1972, p. 83).

Species with restricted geographic distributions consisting of small, isolated populations are particularly susceptible to extinction because these demes face an increased risk of disappearing due to environmental, demographic, and

^{*} Corresponding author. Fax: +1 702 895 3956.

E-mail addresses: javier.rodriguez@unlv.edu (J.A. Rodríguez-Robles), jezkovat@unlv.nevada.edu (T. Jezkova), mleal@duke.edu (M. Leal).

^{1055-7903/\$ -} see front matter © 2007 Elsevier Inc. All rights reserved. doi:10.1016/j.ympev.2007.11.006

genetic stochasticity. Environmental stochasticity is random, unpredictable variation in environmental factors, such as rainfall and food supply. Demographic stochasticity is variation in birth and death rates and sex ratios due to chance alone. Genetic stochasticity encompasses the deleterious impact of inbreeding, loss of genetic diversity, and mutational accumulation on populations (Fischer and Matthies, 1998; Shrestha et al., 2002; Johansson et al., 2007). Small, disjunct populations are also more likely to be decimated by catastrophes (extreme forms of environmental fluctuation such as hurricanes. floods, landslides, severe cold, and forest fires), disease outbreaks, and destruction or degradation of their habitat due to anthropogenic activities (Young, 1994; Lande, 1999). For these reasons, island populations are more prone to extinction than mainland populations. Indeed, island endemics have higher extinction risks than nonendemic species (Frankham, 1998).

Genetic variation within a species is considered to be of great importance for its long-term survival (Lande, 1999). Without an appropriate amount of genetic diversity, species have reduced potential to adapt to environmental change and to cope with evolving predators, competitors, and parasites (Hudson, 1996; Kirkpatrick, 1996). Small population size can lead to random changes in gene frequencies (genetic drift), which results on average in a loss of genetic variance from a population (Lande, 1999; Frankham et al., 2002). Because future evolutionary adaptation depends on the existence of genetic diversity, loss of variation increases the possibility of extinction. The primary objective of conservation biology is thus to preserve both evolutionary processes and the ecological viability of populations by maintaining as many distinctive genetic "units" as possible within a species (Moritz, 2002; Forest et al., 2007; Lankau and Strauss, 2007).

Anolis cooki Grant ("Lagartijo del Bosque Seco," Dry Forest Anole) is a moderate-size, sexually dimorphic lizard (snout-to-vent length up to 70 mm in males, up to 59 mm in females; Schwartz and Henderson, 1991) endemic to the southwestern coast of Puerto Rico, the smallest and easternmost of the Greater Antilles, in the Caribbean Sea. The species has a discontinuous distribution on Caja de Muertos Island (located off the municipality of Juana Díaz in southcentral Puerto Rico) and between the municipalities of Cabo Rojo and Guayanilla on mainland Puerto Rico (Gorman et al., 1968; Jenssen, 1990; Schwartz and Henderson, 1991; Rivero, 1998; Fig. 1). Currently, there are only a few known populations of *A. cooki*, and all

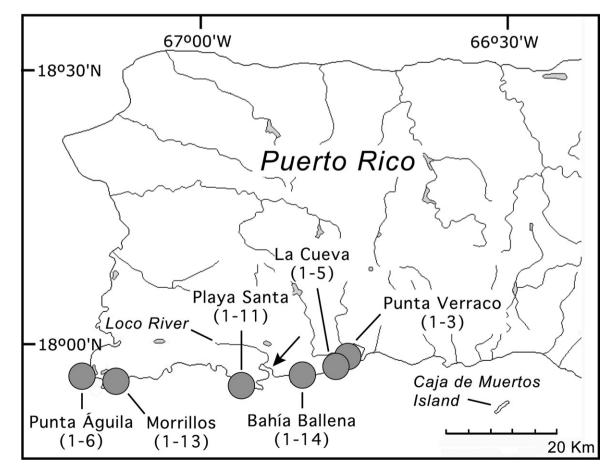


Fig. 1. Map of western Puerto Rico. Circles indicate the approximate locations of the specimens of *Anolis cooki* included in this study (see Table 1 for specific locality information). The arrow indicates the location of Guánica Bay.

Download English Version:

https://daneshyari.com/en/article/2835328

Download Persian Version:

https://daneshyari.com/article/2835328

Daneshyari.com