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Eduardo Sánchez Murrieta
Universidad de Sonora

Alberto Macías-Duarte
Universidad Estatal de Sonora

Reyna A. Castillo-Gómez
Universidad de Sonora

Angel B. Montoya
Partners for Fish and Wildlife Program

Alejandro Varela-Romero
Universidad de Sonora

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Authors

Eduardo Sánchez Murrieta, Alberto Macías-Duarte, Reyna A. Castillo-Gómez, Angel B. Montoya, Alejandro Varela-Romero, and Nohelia G. Pacheco Hoyos

VARIABILITY AND GENETIC STRUCTURE OF THE MONTEZUMA QUAIL IN THE NORTHERN LIMIT OF ITS DISTRIBUTION

Eduardo Sánchez-Murrieta^{1, 2}

Departamento de Investigaciones Científicas y Tecnológicas de la Universidad de Sonora, Avenida Luis Donaldo Colosio S/N, edificio 7G, colonia Centro, Hermosillo, Sonora 83000 Mexico

Alberto Macías-Duarte

Universidad Estatal de Sonora, Unidad Académica Hermosillo, Avenida Ley Federal del Trabajo S/N, Hermosillo, Sonora, 83000, Mexico

Reyna A. Castillo-Gámez

Departamento de Investigaciones Científicas y Tecnológicas de la Universidad de Sonora, Avenida Luis Donaldo Colosio S/N, edificio 7G, colonia Centro, Hermosillo, Sonora 83000, Mexico

Angel B. Montoya

Partners for Fish and Wildlife Program, U.S. Fish and Wildlife Service, 1800 Marquess Street, Las Cruces, NM 88005, USA

Alejandro Varela-Romero

Departamento de Investigaciones Científicas y Tecnológicas de la Universidad de Sonora, Avenida Luis Donaldo Colosio S/N, edificio 7G, colonia Centro, Hermosillo, Sonora 83000, Mexico

Nohelia G. Pacheco Hoyos

Departamento de Investigaciones Científicas y Tecnológicas de la Universidad de Sonora, Avenida Luis Donaldo Colosio S/N, edificio 7G, colonia Centro, Hermosillo, Sonora 83000, Mexico

ABSTRACT

A species' geographic distribution of genetic variability is influenced by different factors including size of geographic distribution, dispersal capability, mating system, and migration. For instance, a low migration rate among populations may cause a decrease in genetic variation. Such is the case of the Montezuma quail (*Cyrtonyx montezumae*), a popular game bird with a limited flight capacity that prevents long-distance dispersal. In the northern limit of the species' distribution in Arizona, New Mexico, and Texas in the United States, the species inhabits oak forests that are separated from one another by deserts. Consequently, Montezuma quail populations are distributed in patches or islands. Knowledge of the species' genetic structure is likely to help inform habitat management decisions. The objective of this study was to determine patterns of genetic variation in populations of the Montezuma quail using 9 microsatellite DNA loci. We genotyped 119 individuals harvested from 4 populations: Arizona (AZ), western New Mexico (WNM), eastern New Mexico (ENM), and west Texas (WTX). Montezuma quail populations had low observed heterozygosity ($H_o = 0.22 \pm 0.04$) and a low number of alleles per locus ($A = 2.41 \pm 0.27$) compared to other quail species. A global population genetic differentiation index (R_{ST}) of 0.045 suggests a weak genetic structure. $\text{Max}(R_{ST})$ occurred among pairwise comparisons AZ-WTX, AZ-ENM, and WNM-WTX. A Bayesian allocation analysis indicates that individuals were separated into 3 groups ($K = 3$), placing the populations of Arizona and Texas in distinct groups apart from the 2 populations of New Mexico, which are in the same group. Despite this differentiation, the Bayesian allocation analysis suggests admixture among populations, which may be an indicator of migration between them, especially between the populations in New Mexico and Arizona. An isolation-by-distance analysis indicates that there is a strong correlation ($R^2 = 0.84$) and suggestive evidence ($P = 0.08$) of non-independence between geographical and genetic distances, though Montezuma quail populations in the southwestern United States may not be isolated. Climate change projections indicate an increase in aridity conditions in this region, especially in temperate ecosystems where the species occurs. In this scenario, corridors between the populations may disappear, thus causing their complete isolation.

¹ E-mail: edusm04@gmail.com

² Present address: Calle 2 #247, Caborca, Sonora 83600, Mexico

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