Genome-wide analyses reveal drivers of penguin diversification

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Ver número de ResearcherID y ORCID de Web of Science

PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA
Volumen: 117
Número: 36
Páginas: 22303-22310
DOI: 10.1073/pnas.2006659117
Fecha de publicación: SEP 8 2020
Tipo de documento: Article
Ver impacto de la revista

Abstract

Penguins are the only extant family of flightless diving birds. They currently comprise at least 18 species, distributed from polar to tropical environments in the Southern Hemisphere. The history of their diversification and adaptation to these diverse environments remains controversial. We used 22 new genomes from 18 penguin species to reconstruct the order, timing, and location of their diversification, to track changes in their thermal niches through time, and to test for associated adaptation across the genome. Our results indicate that the penguin crown-group originated during the Miocene in New Zealand and Australia, not in Antarctica as previously thought, and that Aptenodytes is the sister group to all other extant penguin species. We show that lineage diversification in penguins was largely driven by changing climatic conditions and by the opening of the Drake Passage and associated intensification of the Antarctic Circumpolar Current (ACC). Penguin species have introgressed throughout much of their evolutionary history, following the direction of the ACC, which might have promoted dispersal and admixture. Changes in thermal niches were accompanied by adaptations in genes that govern thermoregulation and oxygen metabolism. Estimates of ancestral effective population sizes (N-e) confirm that penguins are sensitive to climate shifts, as represented by three different demographic trajectories in deeper time, the most common (in 11 of 18 penguin species) being an increased N-e between 40 and 70 kya, followed by a precipitous decline during the Last Glacial Maximum. The latter effect is most likely a consequence of the overall decline in marine productivity following the last glaciation.

Palabras clave

Palabras clave de autor:penguin; Antarctica; genome; ancestral niche; ancestral distribution

KeyWords Plus:FORAGING BEHAVIOR; EXTANT PENGUINS; HISTORY; MITOCHONDRIAL; PERFORMANCE; ANTARCTICA; PHYSIOLOGY; PHYLOGENY; PATTERNS; PACKAGE

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Financiación

Entidad financiadora Mostrar más información	**Número de concesión**
Instituto Antartico Chileno	INACH RT_12-14
Comision Nacional de Investigacion Cientifica y Tecnologica (CONICYT) CONICYT FONDECYT	1150517
Genomics Antarctic Biodiversity/Programa de Investigacion Asociativa/Comision Nacional de Investigacion Cientifica y Tecnologica (GAB PIA CONICYT)	ACT172065
National Science Foundation (NSF)	DEB-1441652
French Polar Institute Paul-Emile Victor (IPEV)	137 354
California Academy of Sciences	
National Council for Scientific and Technological Development (CNPq)	
Instituto Nacional de Ciencia e Tecnologia Ecologia, Evolucao e Conservacao da Biodiversidade (INCT-EECBio) Brazil	

Ver texto de financiación

Editorial

NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON, DC 20418 USA

Información de la revista

- **Impact Factor:** Journal Citation Reports

Categorías / Clasificación

Áreas de investigación: Science & Technology - Other Topics

Categorías de Web of Science: Multidisciplinary Sciences

Información del documento

Idioma: English

Número de acceso: WOS:000572968600001

ID de PubMed: 32817535

ISSN: 0027-8424