

Phylogeography of the Marine Otter (*Lontra felina*): Historical and Contemporary Factors Determining Its Distribution

JULIANA A. VIANNA, PAULA AYERDI*, GONZALO MEDINA-VOGEL, JEFFREY C. MANGEL, HORACIO ZEBALLOS, MANUEL APAZA, AND SYLVAIN FAUGERON

From the Departamento de Ecología y Biodiversidad, Facultad de Ecología y Recursos Naturales, Universidad Andrés Bello, Republica 440, código postal 8370251, Santiago, Chile (Vianna and Ayerdi); the Center for Advanced Studies in Ecology and Biodiversity, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile (Vianna, Ayerdi, and Faugeron); the Escuela Medicina Veterinaria, Facultad de Ecología y Recursos Naturales, Universidad Andrés Bello, Santiago, Chile (Medina-Vogel); the Pro Delphinus, Lima, Peru (Mangel); the Centre for Ecology and Conservation, School of Biosciences, University of Exeter, Cornwall Campus, Penryn, Cornwall, UK (Mangel); the Centro de Estudios y Promoción del Desarrollo—DESCO, Umacollo, Arequipa, Peru (Zeballos); and the Centro de Ornitología y Biodiversidad (CORBIDI), Peru (Apaza).

*Deceased

Address correspondence to J.A. Vianna at the address above, or e-mail: jvianna@unab.cl.

Abstract

The evolutionary history of a species can be revealed by phylogeographical analysis; nevertheless, not only historical but also contemporary processes can imprint on the distribution of genetic diversity. We report on the phylogeny of *Lontra* spp. in South America, and the role of spatial heterogeneity in shaping the distribution and population structure of the endangered marine otter, *Lontra felina*. Analyzing a total of 2261 bp of mitochondrial DNA (mtDNA) revealed the recent divergence of *L. felina* from *L. provocax*. A strong population structure ($\Phi_{st} = 0.83$, $P < 0.0001$) and a significant pattern of isolation by distance were described for *L. felina* ($n = 168$) across a wide geographical distribution (13°53'S to 43°36'S). *Lontra felina* mtDNA phylogeny is composed of 2 main clades: a clade from Peru and another composed of Chilean haplotypes. Northern populations show different divergent lineages and higher genetic diversity when compared with more recently colonized southern populations. Furthermore, long sandy beaches seem to act as barriers to dispersal, creating 2 evolutionary significant units in agreement with subspecies previous description, and at least 5 different management units (MUs). At a fine spatial scale, the size of rocky seashore patches, the distance between patches and anthropogenic factors also play important roles in species gene flow.

Key words: climatic change, conservation, fragmented habitat, phylogeny, phylogeography, otter

A total of 13 otter species are found in the world in 7 distinct genera, with *Lontra* the most representative genus in America. Most of these charismatic species are top predators in their respective communities and are vulnerable or at risk of extinction (IUCN 2010). Otters are widespread in aquatic environments from tropical to cold-temperate regions. Although otters are mostly dependent on freshwater habitats, all but 4 species have also been recorded along seacoasts (Kruuk 2006). Only 2 species, however, are adapted to a strictly marine existence: the sea otter (*Enhydra*

lutris) distributed along the North Pacific Ocean and the marine otter (*Lontra felina*) found in the southeast Pacific Ocean.

The evolution of the Lutrinae led to 3 major clades, based on nuclear and mitochondrial markers: a clade grouping the sea otter and river otters of Eurasia and Africa (*Aonyx*, *Enhydra*, *Hydricis*, *Lutra*, and *Lutrogale*); a second clade grouping the marine otter and river otters from North, Central, and South America (*Lontra*), and a basal lineage of *Pteronura brasiliensis* (Koepfli and Wayne