

Low genetic variability and high isolation of a post-harvest South American pinniped population as revealed by genome-wide SNPs

Diego Peralta¹, Ezequiel Ibañez¹, Sergio Lucero², Humberto Cappozzo², Santiago Ceballos³, and Juan Túnez¹

¹Instituto de Ecología y Desarrollo Sustentable

²Museo Argentino de Ciencias Naturales Bernardino Rivadavia

³Universidad Nacional de Tierra del Fuego Antártida e Islas del Atlántico Sur

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Abstract

Otaria flavescens has been one of the most heavily exploited pinnipeds during the last 200 years with depletions of about 90% in some colonies. After the prohibition on sealing in South America, populations became stabilized except for the Uruguayan population, which showed a constant decrease. The underlying causes of its decline are unknown. This study used genome-wide SNPs to assess the variability and connectivity of some of the most overexploited sea lion colonies in the Atlantic Ocean. Our results revealed low allelic richness, nucleotide diversity and heterozygosity in the Uruguayan population and evidence of complete isolation from the Argentinean populations under study. In contrast, the Patagonian populations showed a high degree of connectivity, which could explain their recovery and high levels of current diversity. Our study highlights the critical situation of the Uruguayan sea lion population, emphasizing the need for maintaining the continuous conservation efforts in the region.