

***Dolphins of the kelp* - genetic diversity and population structure of Commerson's and Peale's dolphins around the Falkland (Malvinas) Islands**

Baker C. Scott¹, Steel Debbie¹, Costa Marina², Brickle Paul², Pimper Lida E.³, Pérez-Alvarez María José^{4,5,6}, Poulin Elie⁵, Acevedo Jorge⁷, Olavarria Carlos⁸. ¹Marine Mammal Institute, Oregon State University, Newport, Oregon, US. ²SAERI, South Atlantic Environmental Research Institute, Stanley, FA. ³Sede Ushuaia, Administración de Parques Nacionales, Ushuaia, Tierra del Fuego, AR. ⁴Escuela de Medicina Veterinaria, Facultad de Ciencias, Universidad Mayor, Santiago, CL. ⁵Instituto de Ecología y Biodiversidad, Facultad de Ciencias, Universidad de Chile. ⁶n/a, Centro de Investigación Eutropia. ⁷Laboratorio Mamíferos Marinos, Depto. Ecología de Ecosistemas Acuáticos, Fundación CEQUA, Punta Arenas, CL. ⁸CEAZA, Centro de Estudios Avanzados en Zonas Áridas, La Serena, CL.

The nearshore waters of the Falkland (Malvinas) Islands host a unique, and perhaps uniquely abundant, community of Commerson's dolphins and Peale's dolphins. Both species appear to be island-dependent, year-round and are observed foraging in the dense kelp forests within a few hundred meters of shore. The Falkland (Malvinas) Islands have no history of inshore fisheries and thus, no fisheries related mortality (bycatch) that threatens coastal dolphins in other parts of the world (e.g., Chilean dolphins and the New Zealand Hector's and Maui dolphins). Here we report the first genetic characterization of Commerson's and Peale's dolphins around the West and East Falkland (Malvinas) Islands. Genetic samples were collected with a minimally intrusive biopsy dart during boat surveys in early 2017. From a total of 60 samples of Commerson's dolphins and 59 samples of Peale's dolphins, we used microsatellite genotypes to identify 52 individuals and 51 individuals, respectively (no further analyses were performed with these nuclear data). From the mtDNA sequences we resolved 8 maternal lineages for the Commerson's and 11 for the Peale's dolphins. We found no evidence of population differentiation between the east and west islands for the Commerson's but highly significant difference between islands for the Peale's dolphins. We found only limited sharing of mtDNA haplotypes with populations of both species from South America. Interestingly, the population of Peale's dolphins from West Falkland (Malvinas) Island showed greater differentiation with East Falkland (Malvinas) Island than with samples from South America. The diversity of mtDNA lineages was low for the Commerson's dolphins from the Falkland (Malvinas) Islands and there was no sharing of lineages with the subspecies of Commerson's dolphin found at the Kerguelen Islands in the Indian Ocean. These patterns are consistent with an island-associated, founder event followed by genetic isolation from conspecific populations

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