

2021 SMALL GRANT IN AID OF RESEARCH – SUMMARY REPORT

Untangling the complex speciation process of the Peruvian-Chilean fur seals hybrid group and the role of Isla Foca in its population dynamics

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From a total of 23 samples of fur seals sequenced, one individual was from *Arctocephalus forsteri*, seven from *Arctocephalus galapagoensis*, and 15 from *Arctocephalus australis*. From the whole distribution of *A. australis*, 12 samples were from the Peruvian coast and three from Southern Pacific and Atlantic coast (Chubut, Falkland/Malvinas, and Southern Chile). From the Peruvian coast, four samples were collected in Isla Foca. The sequencing of the genomes was outsourced, and all samples were sequenced in an Illumina NovaSeq 6000 platform at the Hospital for Sick Children, Toronto - Canada. The reads were mapped against the reference genome of *Zalophus californianus* available at chromosome level on GenBank (GCA_009762305.2). The depth average was 16.6 X (SD \pm 4.8) and 80% of the reference genome was covered by the sequenced reads. Around 93% of the reads were mapped in the reference genomes and 7% were discarded. Besides that, around 1.4% of the reads were PCR duplicates and were also discarded from the downstream pipeline. Given the depth of chromosome X, we can assume that the individuals having half of the mean depth for this chromosome (\sim 7X) are males. Taking this into account, six of the 23 sampled individuals can be considered males. Of the four individuals from Isla Foca, two can be considered males and two females. PCA for nuclear and mtDNA showed that some individuals grouped with Galapagos fur seals and others between Galapagos and Peruvian fur seals, indicating that further analyses to investigate genomic introgression are needed and will be conducted in this project.