

**TITLE:** RIDERS ON THE WINGS: INTERCONTINENTAL MICROBIAL DISPERSION BY ANTARTIC BROW SKUA

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**ABSTRACT:**

Brown skuas are migratory sea birds breeding at moderate to high latitudes. Together with their partner, they defend areas around their nest and places where penguin colonies are found, since their food habit mainly includes eggs and penguins chick, besides krills and fish. During the austral summer (breeding season) that these birds migrate from southern South America to the Antarctic peninsula. Due to this migration, the skuas act as dispersing agents of microorganisms, due to the microbiota present in feathers. The aim of this work was to evaluate the microbial community present in feathers of a Brow Skua population in two consecutive years in the Elephant Island, Antarctica. A total of 23 feather samples were collected from *Catharacta antarctica*, 10 of which were obtained in 2012 and 13 samples in 2013. Each feather was washed in saline solution and the microbial DNA was extracted from this wash using PowerSoil DNA Isolation kit (MO BIO, Carlsbad, CA). The amplification of the V4 region of the 16S rRNA gene was done and the amplicons were sequenced using the Ion Torrent PGM platform. Sequences were processed using the pipeline of the Brazilian Microbiome Project and library comparisons were performed using the QIIME. A total of 295,776 sequences were obtained which were grouped into 646 OTUs. In general, the microbial composition of the samples was very similar, taking into account the phylogenetic distance among samples. The *Proteobacteria* phylum was the most abundant, with a total frequency of 52.4%, followed by *Firmicutes* (16.1%) and *Bacteroidetes* (10.4%). The most abundant taxonomic unit (OTU) in both years, with a frequency of 25.8% in 2012 and 17.2% in 2013, belongs to the *Moraxellaceae* family, which includes species that colonize mucous membranes or skin of humans and other animals and are found in the general environment, but can cause a variety of infections in these. The second most abundant OTU was classified to the *Psychrobacter* genus (with a sample mean of 11.2%) and is commonly found on ornithogenic soils of Antarctica and on ice sea. Our data has shown that microbiota in feathers of skuas is mostly composed by microorganisms psychotropic and chemoorganotrophic, present in the nutritious soil around their nests, in regions when they seek food and in their prey. Although the important role in dissemination of diversity, skuas also must be crucial transporters of pathogen species over the sites when they fly.

**Keywords:** Bird migration, Breeding, Dispersion pathogens, Feathers, 16S rRNA.

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