

Prevalence of antibiotic resistance genes in East Antarctic seabirds

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Recent studies have highlighted the presence of antibiotic resistance genes (ARGs) in Antarctica, which are typically indicative of human activity. However, these studies have concentrated in the Antarctic Peninsula region and relatively less is known about ARGs' prevalence in East Antarctica, where human activity levels are lower compared to the Antarctic Peninsula. In addition, the mechanisms of ARGs' transmission to Antarctica through natural or anthropogenic pathways remain unclear. In our study, we analyzed the fecal samples of Adélie penguins and South polar skuas using high-throughput real-time PCR at their breeding colony near Syowa Station in East Antarctica. We found a significant number of ARGs in the intestinal feces of both Adélie penguins and South polar skuas, with higher detection rates in skuas than in penguins. To better understand how these birds might be acquiring and transmitting these genes, we analyzed the migratory patterns of South polar skuas from geolocator tracking. We found that these skuas migrate from the Lutzow-Holm Bay to the tropical and subtropical regions of the Indian Ocean during the austral winter. On the other hand, Adélie penguins exhibited a more localized migration pattern, mainly staying within Antarctic waters (Takahashi et al. 2018). The Indian Ocean is considered one of major reservoirs of ARGs (Calero-Cáceres et al. 2019). This suggests that South polar skuas might be exposed to these ARGs during their winter migration, potentially acting as carriers when they return to Antarctica.

References

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