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## Ornithogenic colony soils as an AMR baseline: an ancestral, non-mobile resistome that converges across three penguin species in Antarctica

### Inhalt

Wildlife is increasingly seen as a reservoir of environmental AMR, yet a pristine baseline to interpret it is missing. We characterized the resistome, metallome, biocidome and mobilome of 84 soil metagenomes from 24 sites and three sympatric *Pygoscelis* species on the Antarctic Peninsula, for multi-species comparison of ornithogenic soils. The resistome is dominated by a ubiquitous core (45 genes in >90% of samples; 92.8% of abundance) of intrinsic mechanisms (efflux, target alteration) in environmental psychrophilic genera with no recognized pathogens. Five independent lines show no mobility signatures: 99.3% chromosomal location, decoupling of insertion sequences, fragmented MGE candidates, marginal lysogeny, and no clinical plasmids or resistance-bearing integrons. Antibiotic, metal and biocide resistance co-vary with community phylogeny while mobile elements remain decoupled: resistance is inherited with genomes, not between them. The resistome converges across all three species: community explains ~30% of variance and guano ~3%, while the core assembles deterministically, the periphery stochastically (NST 0.05 vs 0.69). No local anthropogenic signal appeared: the resistome was unstructured by distance to stations. Resistance is a vertically inherited, ecologically integrated trait carried chromosomally, not on mobile elements, positioning Antarctica as a sentinel baseline of pre-antibiotic resistance for tracking anthropogenic and climate-driven change.

### Keywords

Antimicrobial resistance genes, metagenomics, *Pygoscelis*, Antarctica, ornithogenic soils, environmental baseline

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Yes, I am a Junior Scientist.

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