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# Detection of resistance genes and resistant bacteria in wild birds from the French Antarctic and Austral Territories

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## Introduction

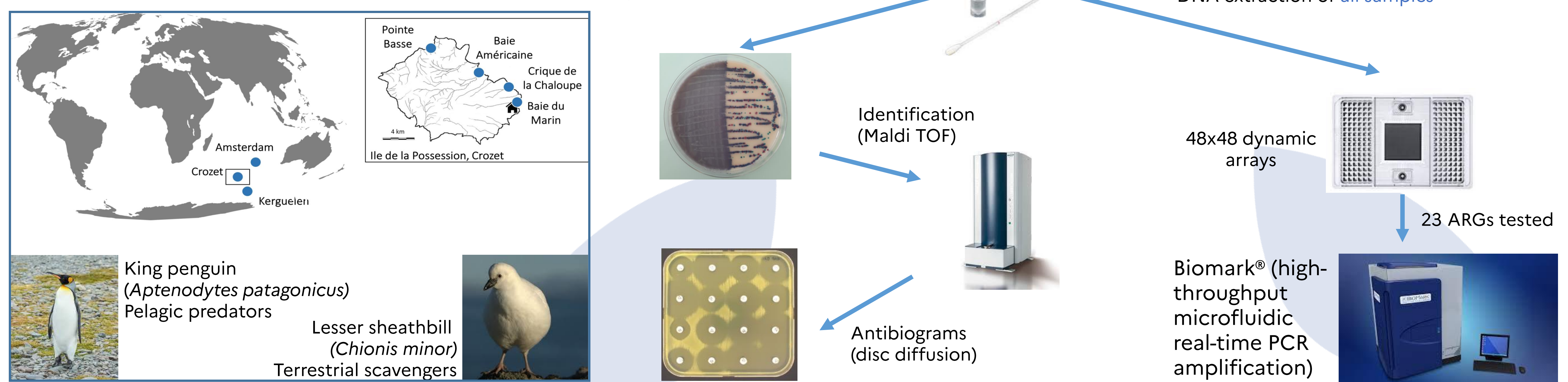
Antimicrobial resistance (AMR) in wild birds most likely reflects the contamination of their natural environment with antimicrobial resistance genes (ARGs) from anthropogenic sources.

AMR acquisition in wild birds generally occurs through foraging (scavenging, predation), but the exact source of AMR in specific wild individuals is often difficult to infer.

The aim of this study was to determine the AMR load in fecal samples of wild birds living on islands of the French Antarctic and Austral Territories, which is a highly pristine environment with limited human presence.

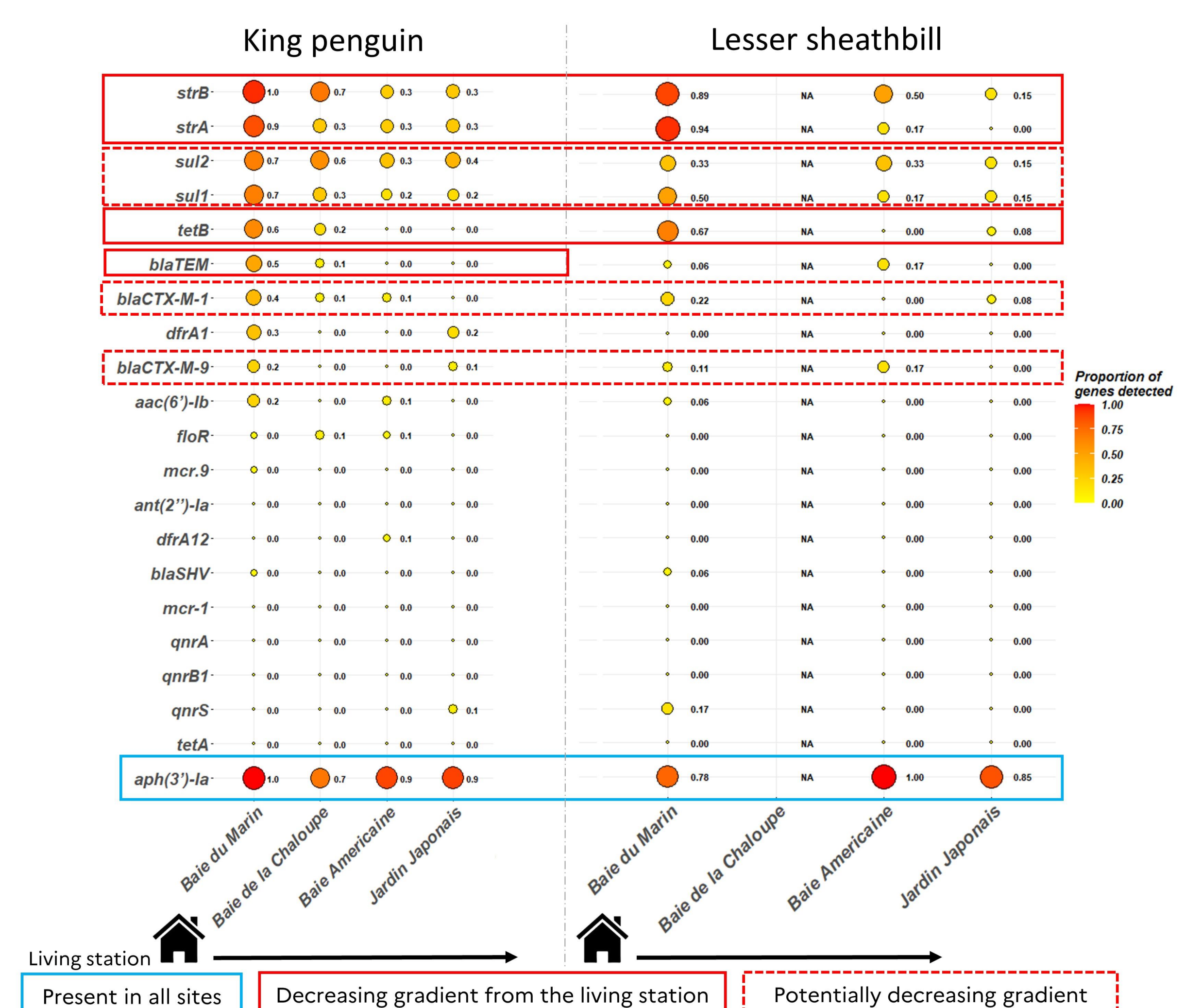
## Material and Methods

- 346 samples (E-swab®)
- Mostly king penguins and lesser sheathbills
- Crozet, Kerguelen and Amsterdam Islands



## Results

- No extended-spectrum beta-lactamase (ESBL) producing isolate was identified on selective plates. However, ESBL genes *bla*<sub>CTX-M-1-group</sub> and *bla*<sub>CTX-M-9-group</sub> were sporadically identified (n=25 and n=54) by qPCR.
- A total of 546 different bacteria were collected on non-selective plates, including 182 *Enterococcus* spp and 73 *Escherichia* spp isolates. Antibiograms revealed very few resistance phenotypes.
- All tested ARGs, except *mcr-1* and *tetA*, were detected at least in one sample. The most frequent ones were those conferring resistance to aminoglycosides (*aph(3')-Ia*, n=311; *strA* n=169; *strB*, n=190), sulfonamides (*sul1/sul2*, n=144/167) and tetracyclines (*tetB*, n=115).
- The class 1 and class 2 integrons were respectively found in 147 and 286 samples.
- Analysis of the qPCR data from Possession Island only (Crozet Archipelago) showed that the proportion of ARGs decreased with distance from the scientific station (Figure 1).



**Figure 1.** Proportion of resistance genes identified by qPCR in the king penguins (left panel) and lesser sheathbills (right panel) from Possession Island. Different sampling sites located further and further away from the scientific station were included in this analysis.

## Discussion

ARGs have percolated in the most pristine environments, even though the AMR burden is still low.

Indeed, direct plating of the samples without an enrichment step did not allow the isolation of ESBL-producing isolates. However, ESBL genes could be identified using HT-qPCR, indicating that these AMR genes are still restricted to the sub-dominant flora. Interestingly, our results showed that the proportion of ARGs decreased with distance from the scientific station, suggesting the role of anthropization in the spread of ARGs.

A new sampling campaign is currently being conducted to provide more evidence for this hypothesis.