

Blow microbiota of free-ranging short-finned pilot whales: comparison of two 16S rRNA primers for studies of blow prokaryotic communities



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Pipeline optimization for metabarcoding analysis of prokaryotic community harbored in the respiratory tract of short-finned pilot whales.

Globicephala macrorhynchus



suitable matrix to discover the microbial communities within cetaceans' respiratory tract

1. Sampling

3. DNA extraction 4. Quality and quantitative DNA assessment

6. Microbial Communities analysis



R Studio



2. Storage -80°C



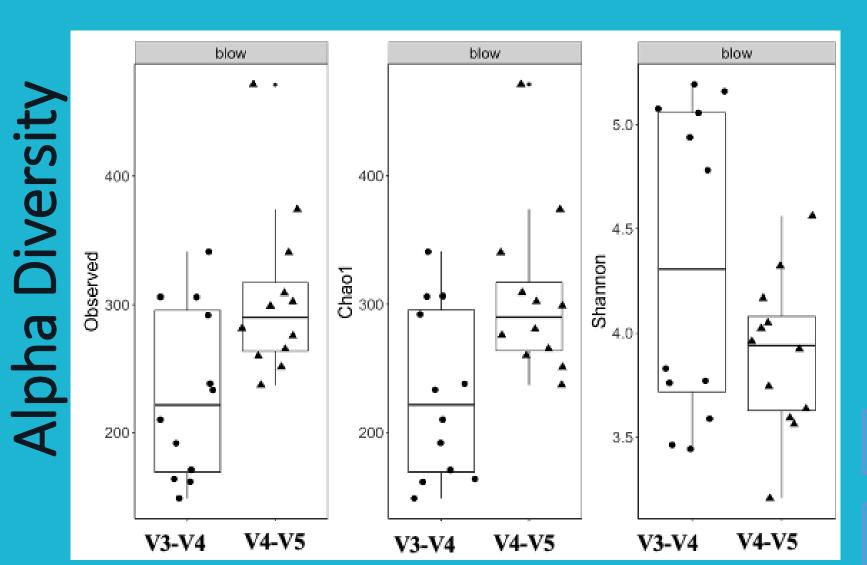
5. Illumina MiSeq

Metabarcoding (Amplicon sequencing V3-V4 and V4-V5 regions of 16S rRNA)

COMPARISON of 16S rRNA primers (Blow Samples)

V3-V4 16S rRNA gene Primers: 341F/806R

V4-V5 16S rRNA gene Primers: 515F-Y/926R



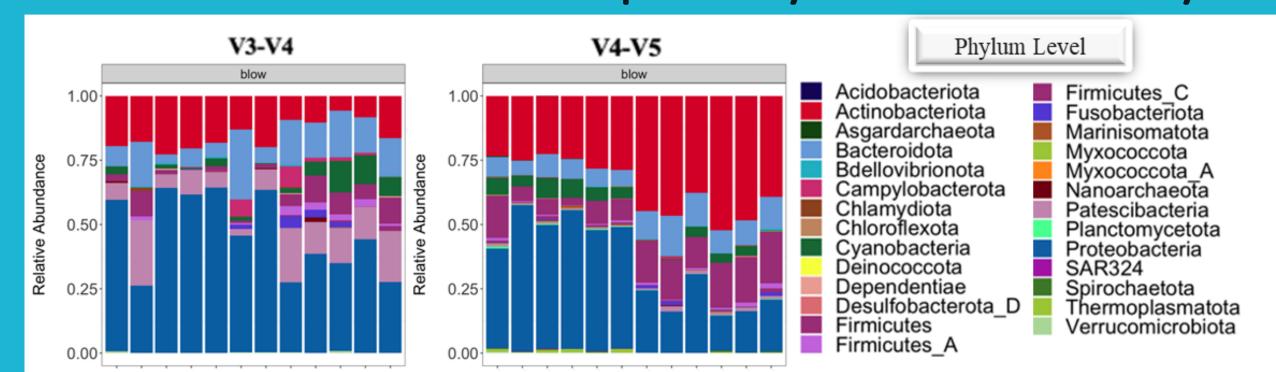
Blow community richness (ASV observed; Chao1) and diversity (Shannon)

significantly different between the two primers sets.

ca. 32% more bacterial ASVs

Shannon index 11% higher V3-V4

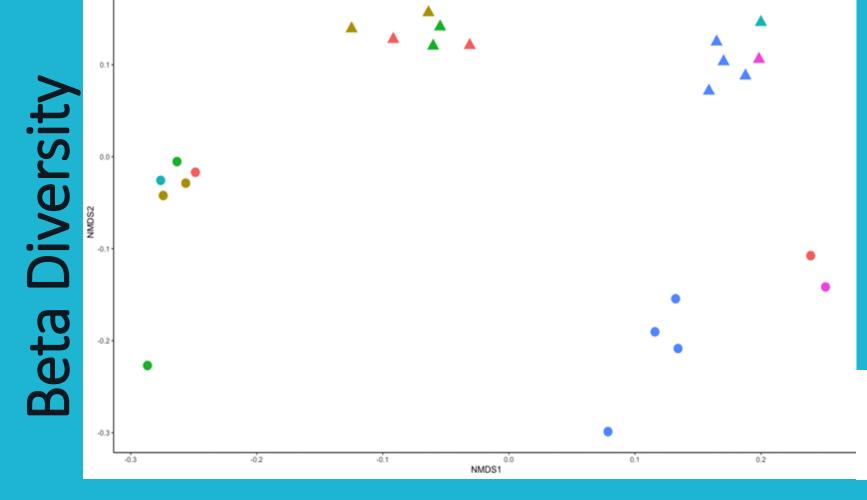
Characterization of the prokaryotic community



samples from both datasets shared a main core microbiota in their blow

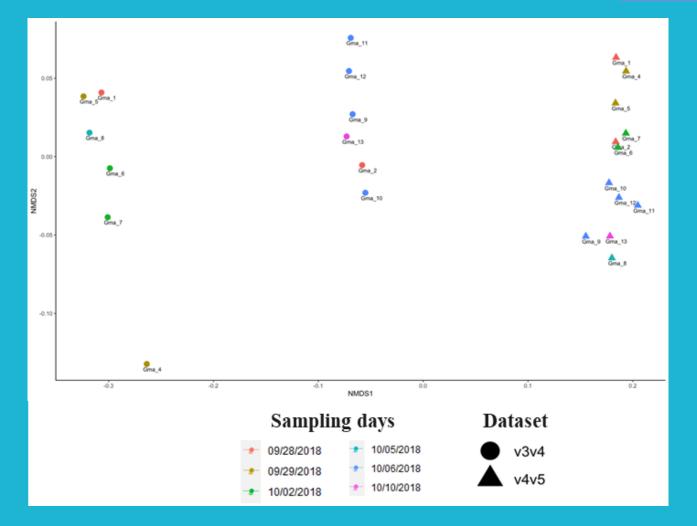
Actinobacteriota, Bacteroidota, Firmicutes, Proteobacteria

V4-V5 Detected a higher number of taxa however, the majority of them had a relative abundance <1%.



Distinction of primer sets communities

Individuals traveling together sampled, when they were appeared in the same cluster in the V4-V5 dataset.



Core Microbiota

All samples of the V4-V5 the cluster (at Genus Level)

CONCLUDING REMARKS

1st study describing the blow microbial diversity in **short-finned pilot whales**.

The selection of the primer set to use to analyze blow samples depends on the main goal of the study:

- capture more diversity: V3-V4 primers set;
- higher microbial richness (microbial rare biosphere): V4-V5 primers set.

Preliminary evidence that cetaceans host a core group of bacteria associated with the respiratory system.

The characterization of the respiratory-associated microbial communities can be used as a **future** biomarker for the physiological state of the airways in cetaceans.











