Metagenomics of the line islands

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and a cast of thousands...

How do we screw up the environment?

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Metagenomics of the line islands

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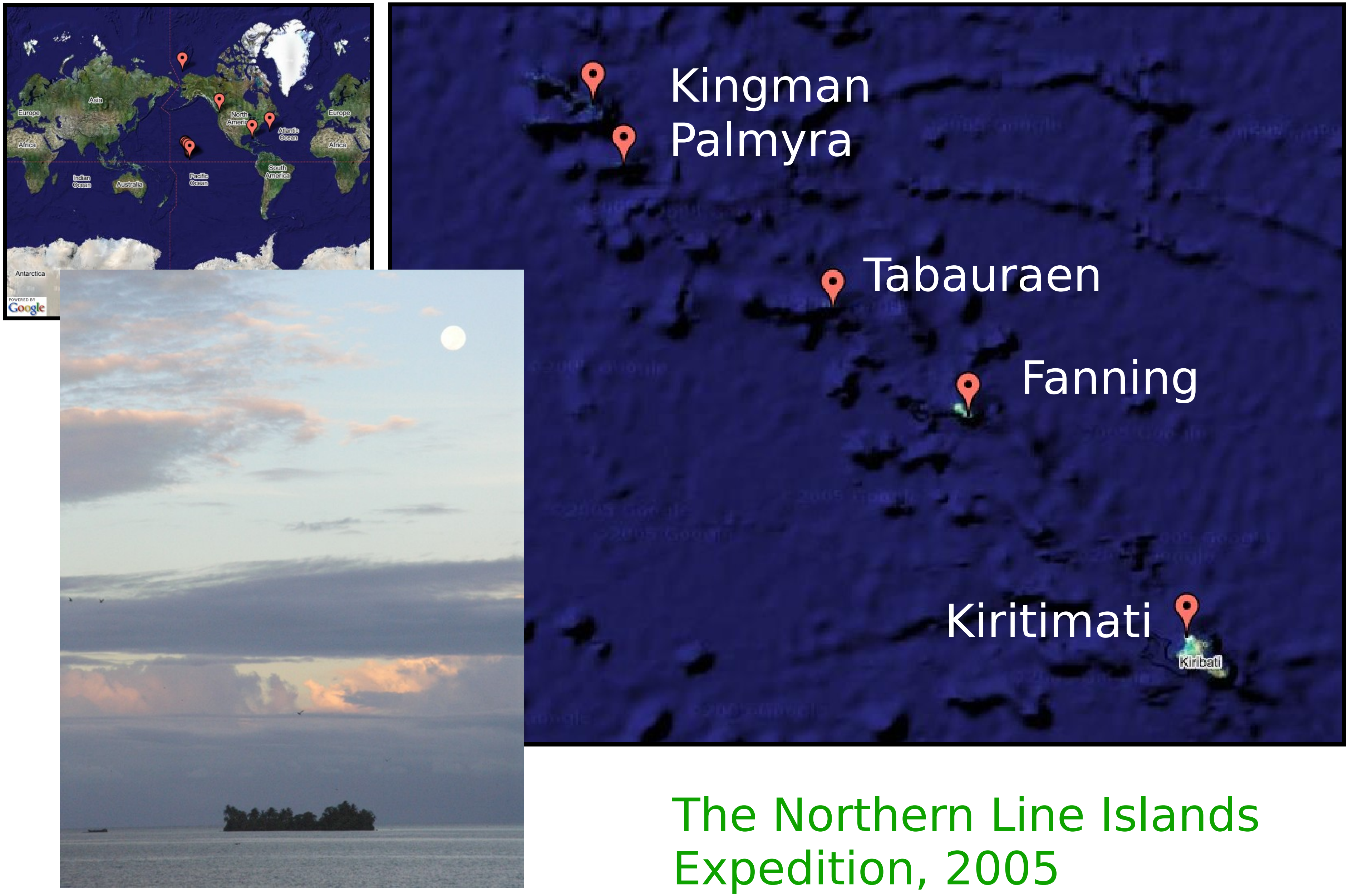
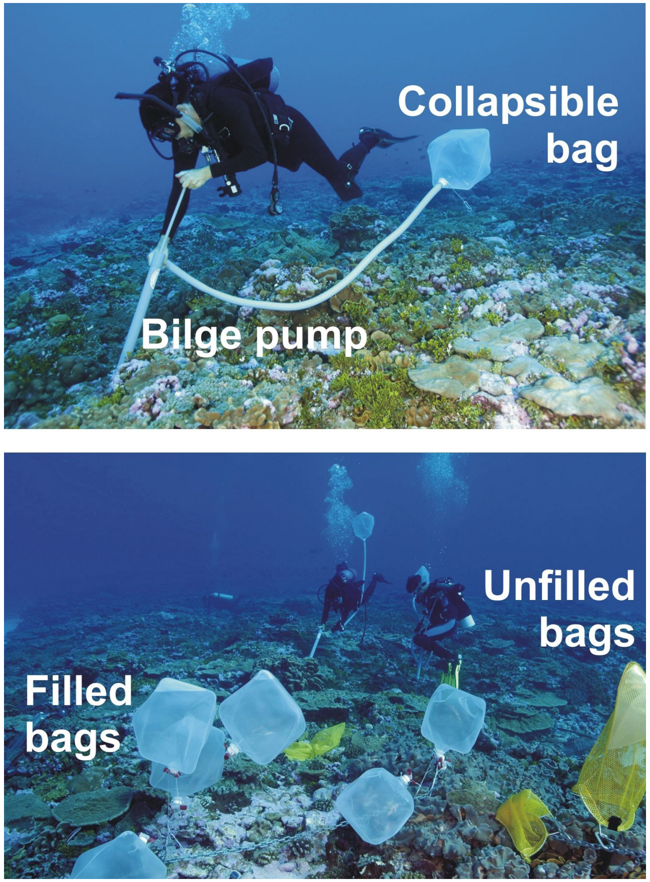


The Northern Line Islands Expedition, 2005

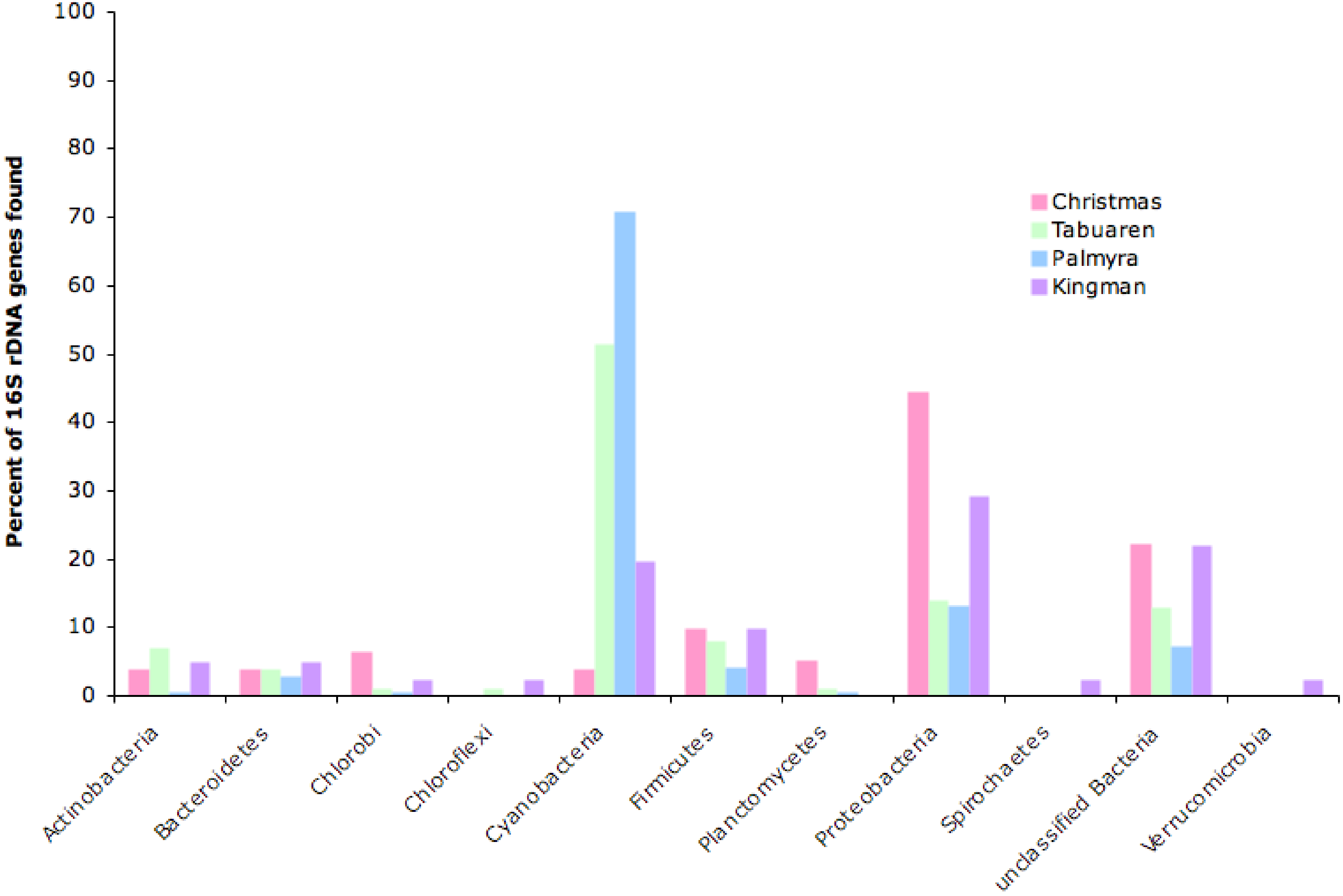
Metagenomic samples

Four microbial metagenomes included organisms >0.45 µm – Bacteria and Archaea, some small Protists and virus like particles

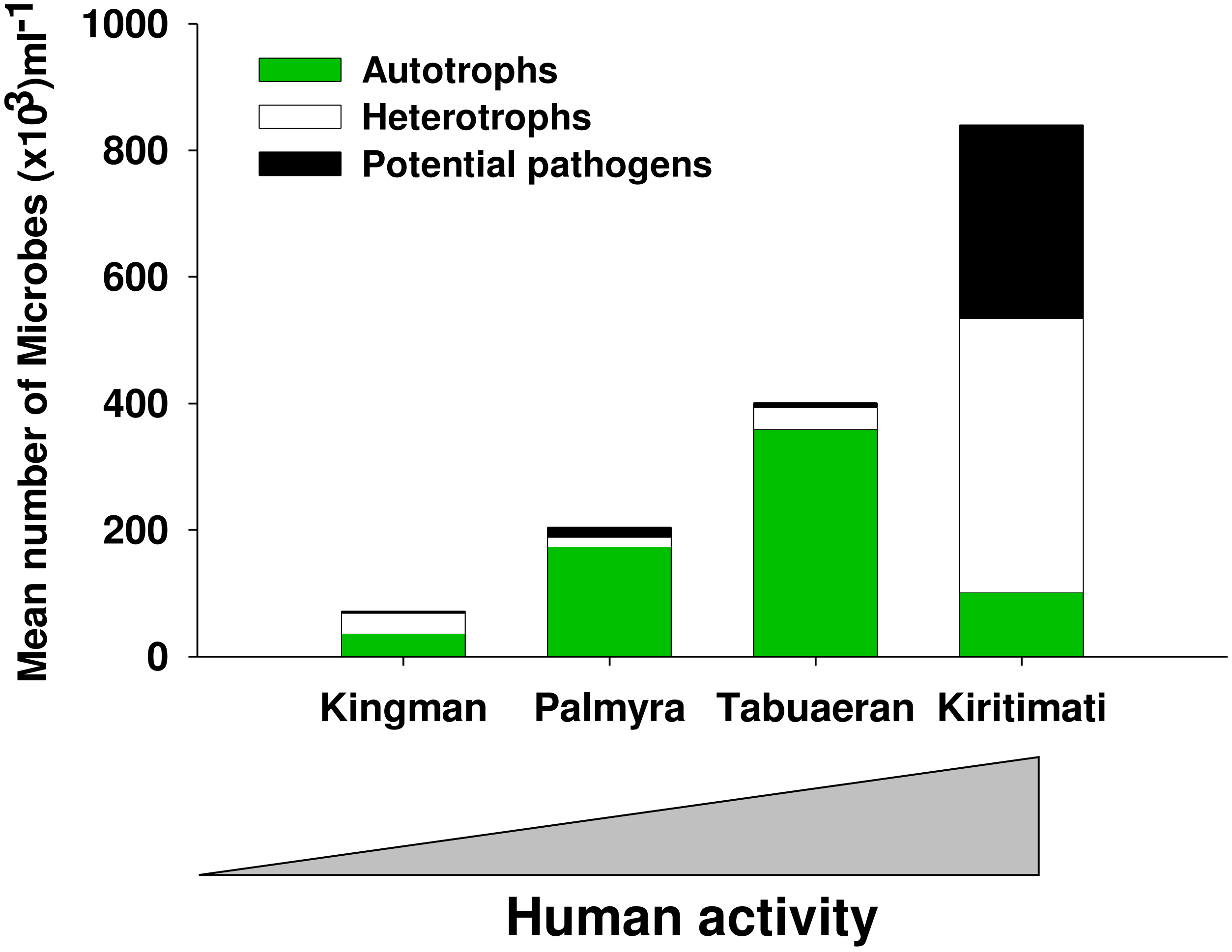
Four viral metagenomes included organisms <0.45 µm, Chloroform treated and cesium chloride gradient – virus like particles



16s rDNA at each island



Trophic structure from 16S rDNA



Method
16S rRNA gene from metagenomes

↓

Blastn

↓

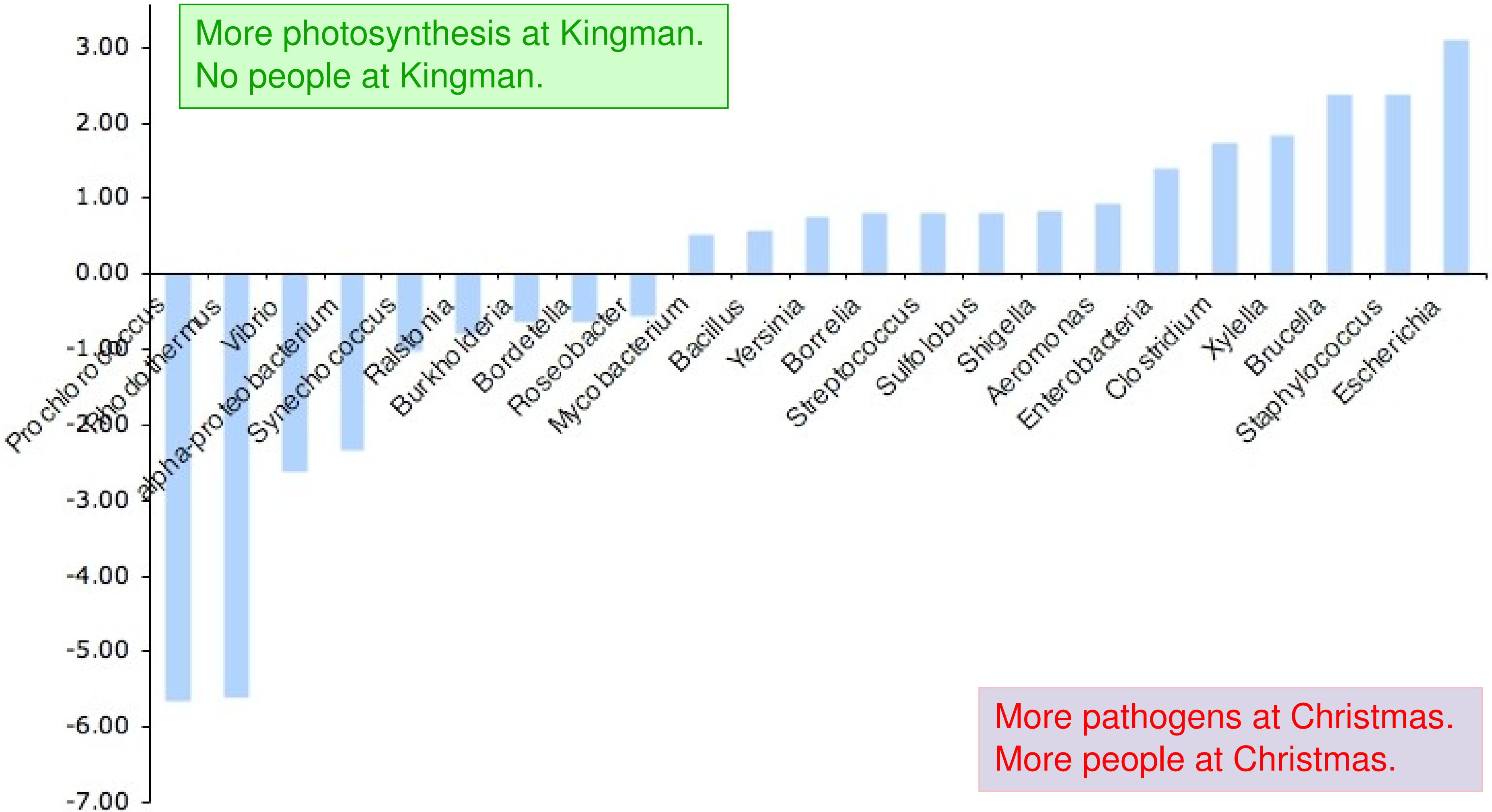
Taxonomic assignment

↓

Placed into guilds using Bergey's manual
Potential pathogens – eg *Vibrio* spp., *E. coli*

Kiritimati to Kingman Bias in No. Phage Hosts

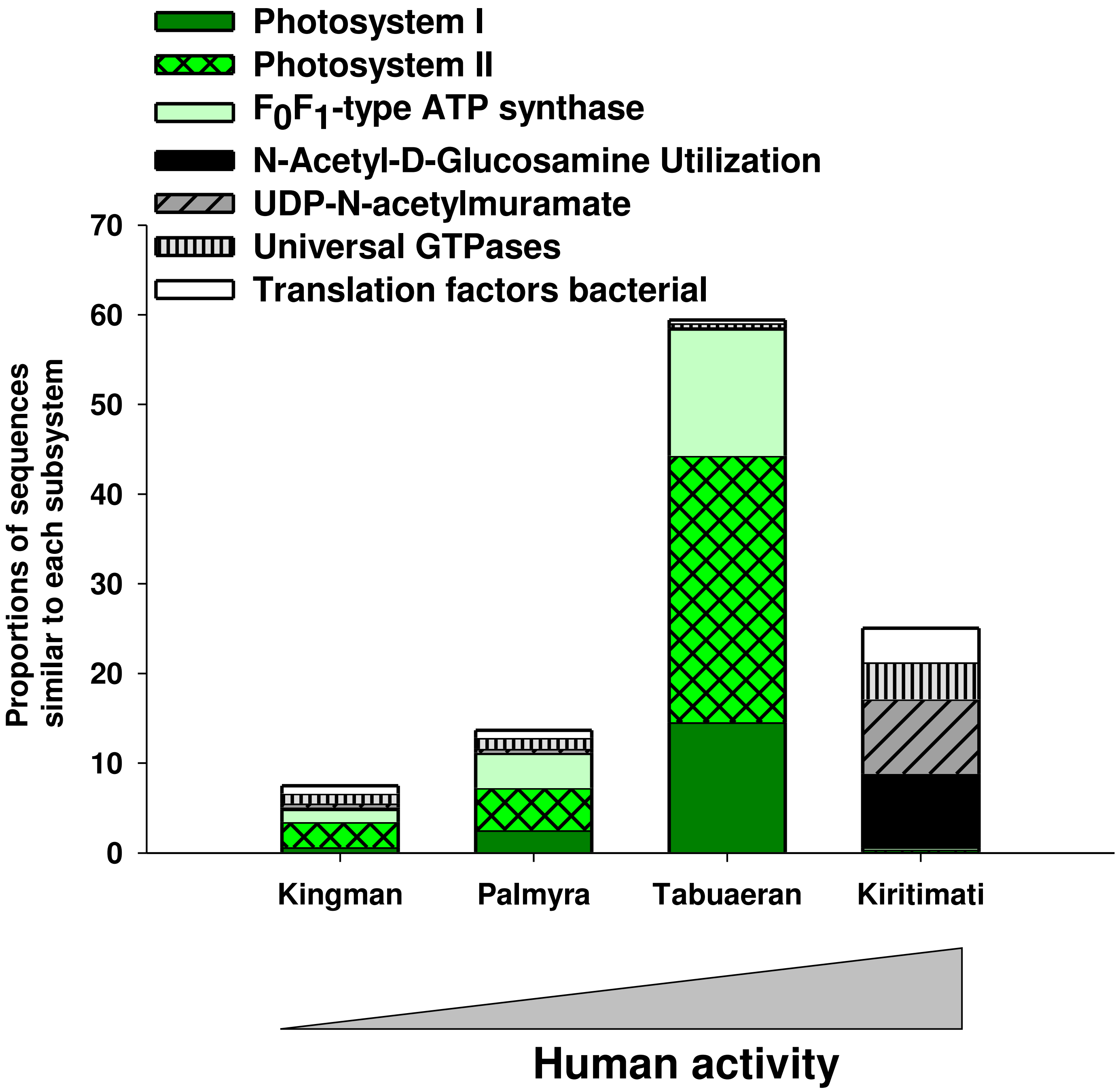
Negative numbers mean relatively more phage hosts at Kingman



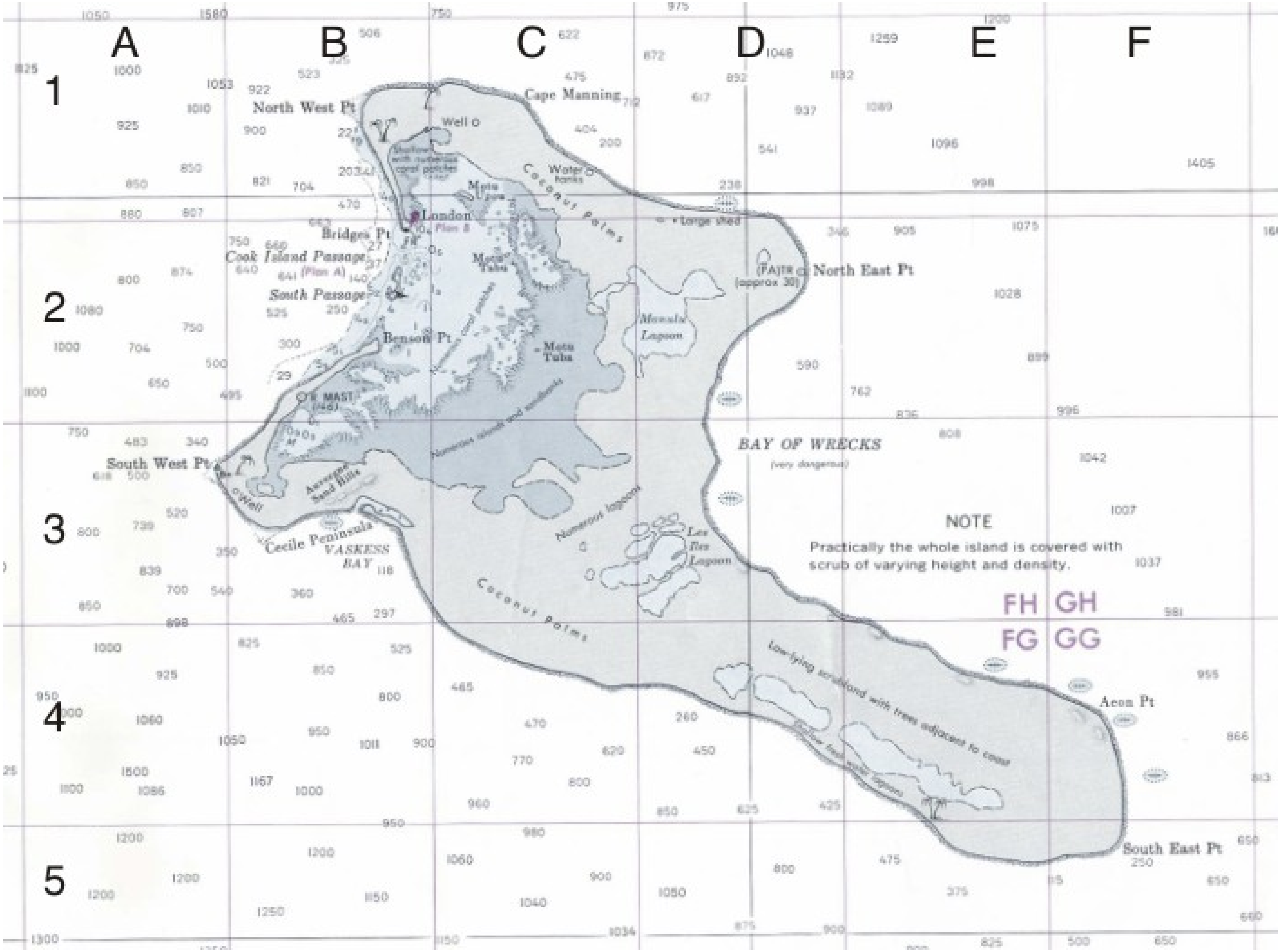
More photosynthesis at Kingman.
No people at Kingman.

More pathogens at Christmas.
More people at Christmas.

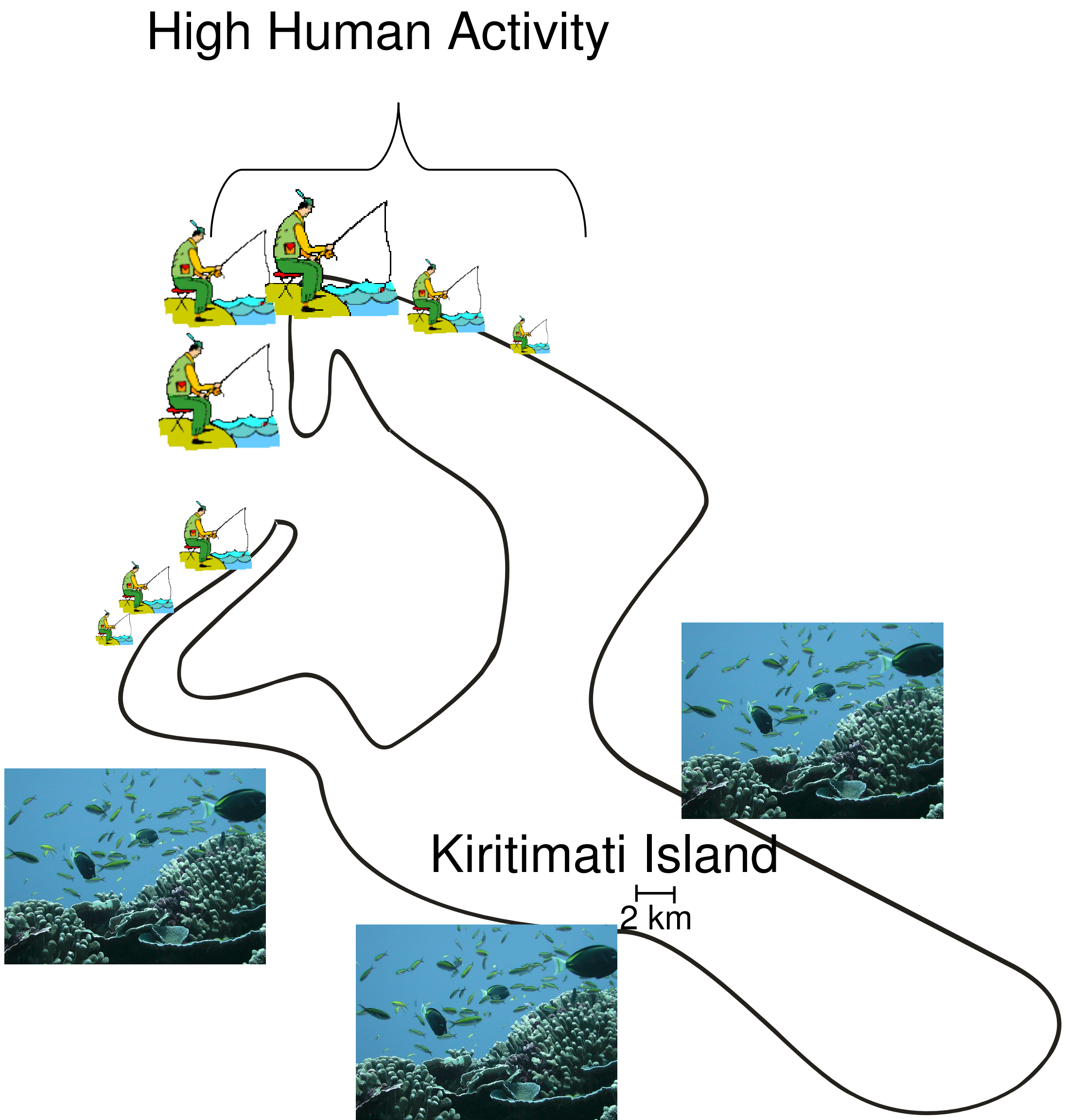
It's not just 16S genes and phages ...



Does human activity screw the reefs?



Microbial loads and human activity are coupled



High Human Activity

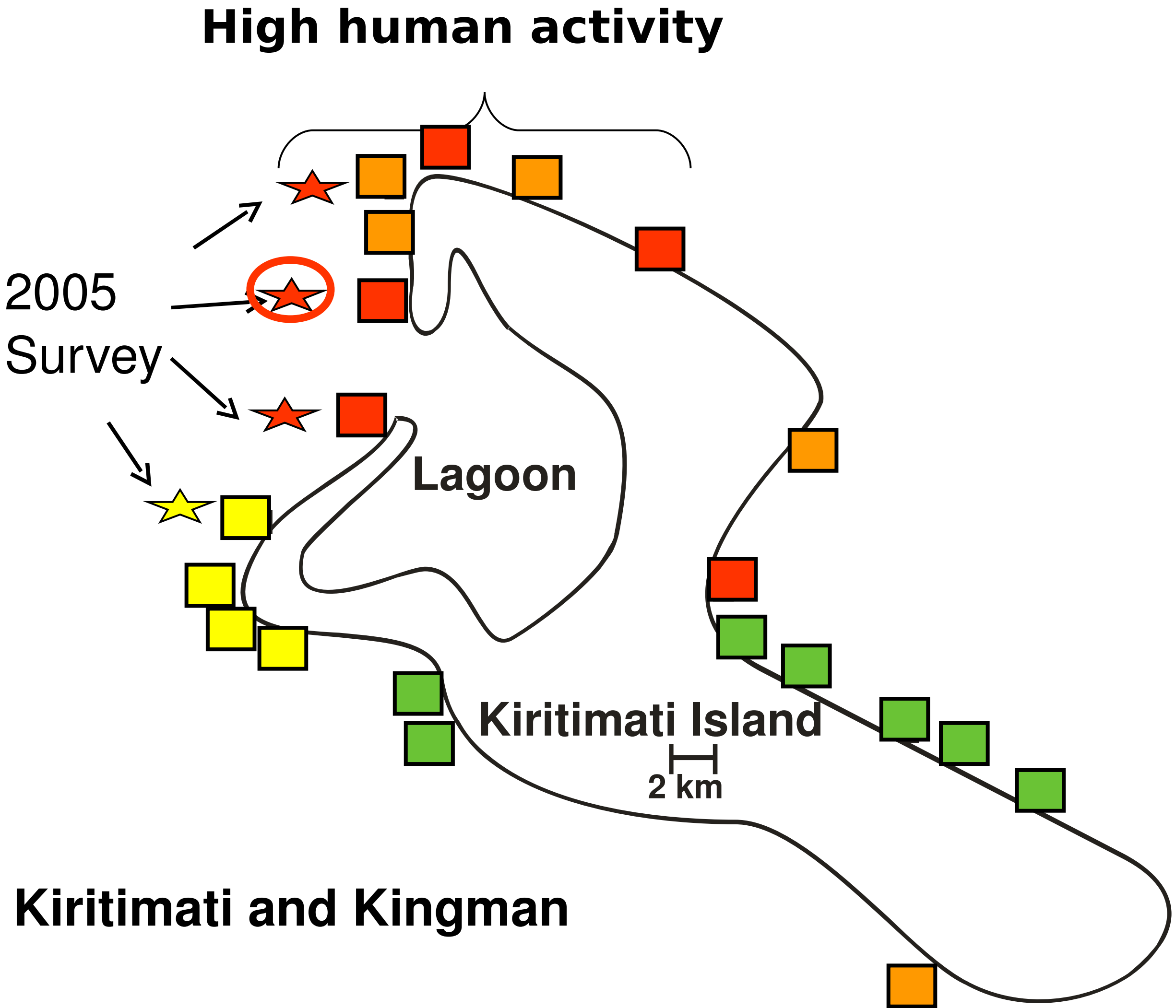
Kiritimati Island

2 km

Microbial loads and human activity are coupled

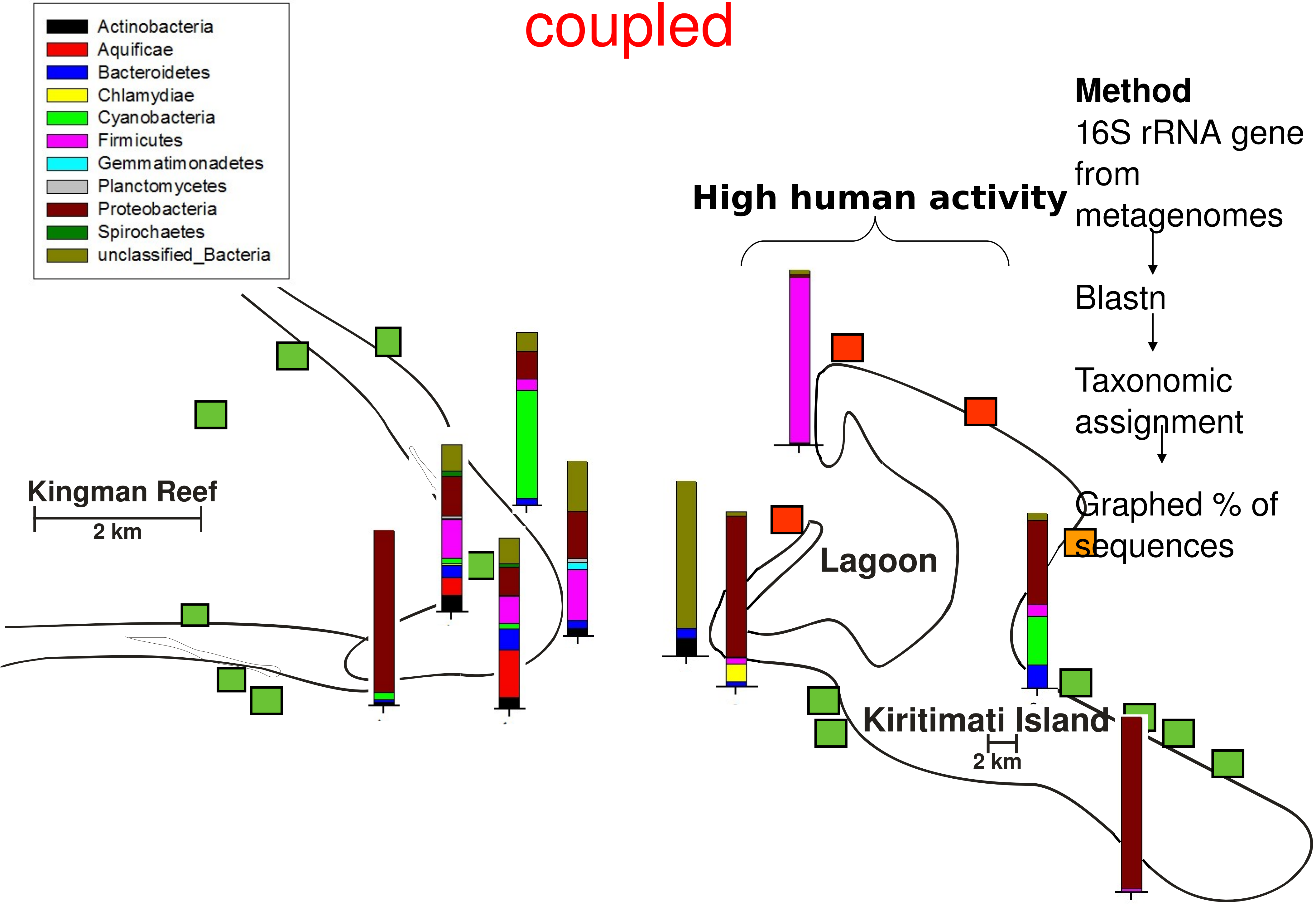
Microbial Numbers 2007 survey

- 🟥 **High > 4.31×10^6**
- 🟧 **Medium-high 1.02×10^6 to 4.31×10^6**
- 🟨 **Medium-low 6.43×10^5 to 1.02×10^6**
- 🟩 **Low < 6.43×10^5**



Conduct survey at 20 sites around Kiritimati and Kingman

Microbial community and human activity are coupled



Method

16S rRNA gene from metagenomes

↓

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↓

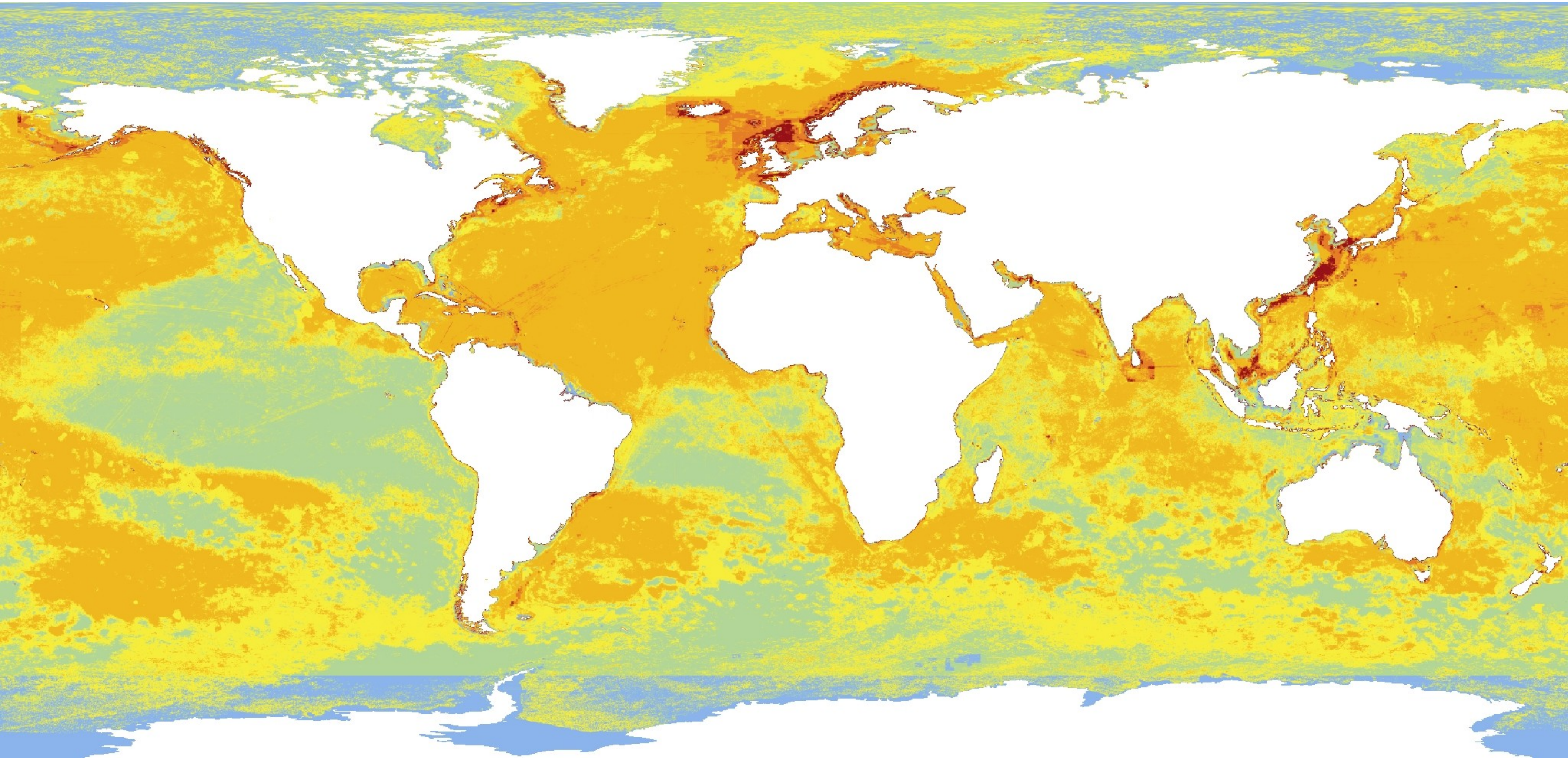
Taxonomic assignment

↓

Graphed % of sequences

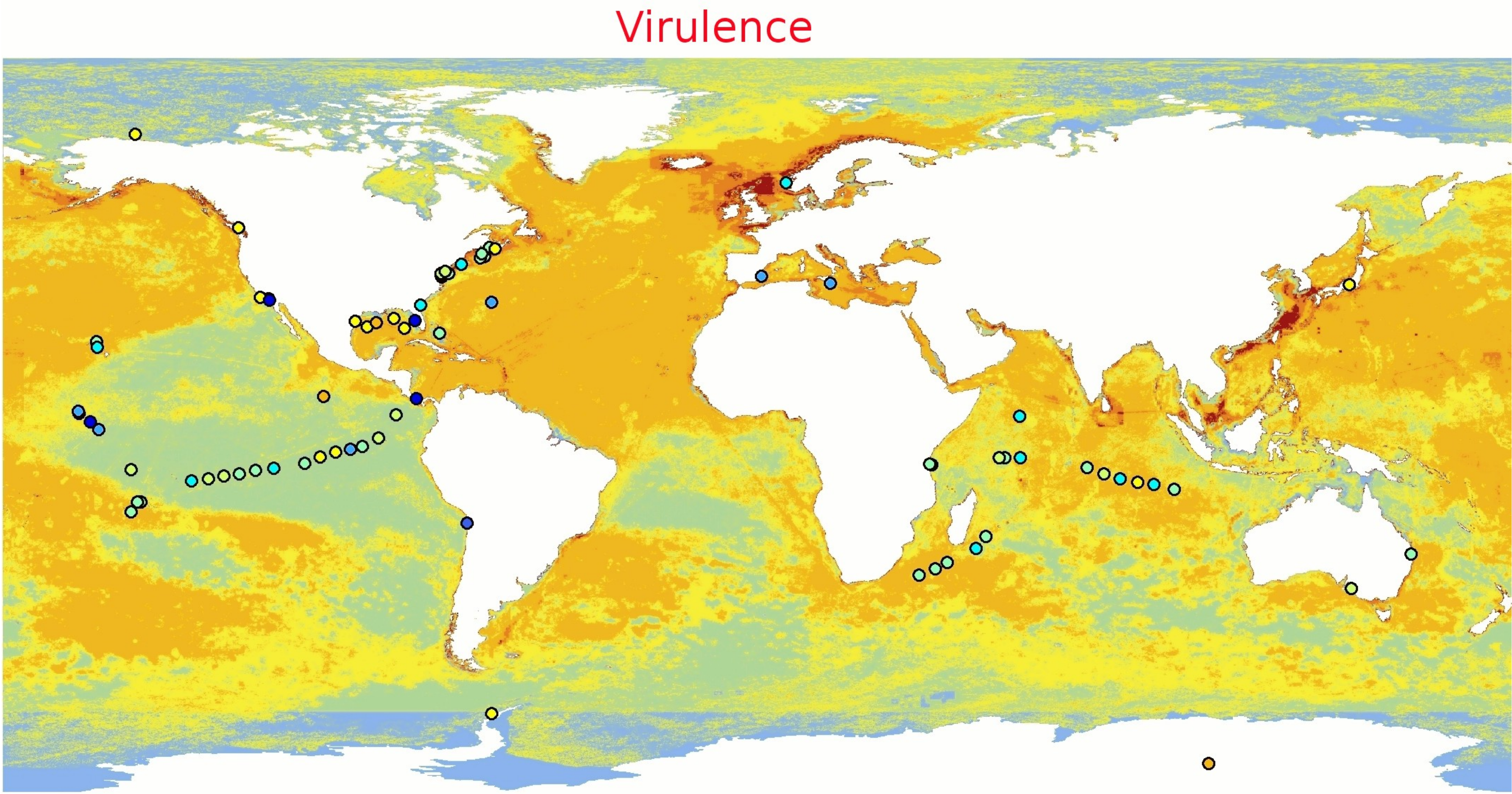
Global perspective: microbes and fishing impact

Red – high impact, Blue – low impact



Halpern *et al* 2008 Science 319:948-952

Little microbes, big planet



Take home points

- More people = less fish
- Less fish = more bad bacteria
- More bad bacteria = less corals
- Less corals = less fish

Thanks!

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BACK!