

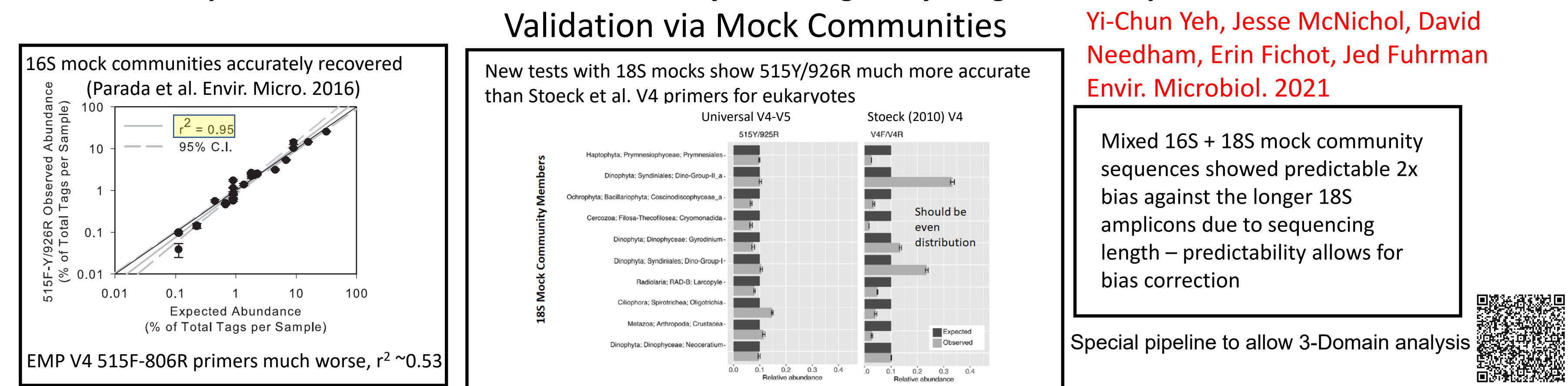
Ecological Patterns of Marine Bacteria, Archaea, Protists and Viruses on Small to Large Temporal and Spatial Scales

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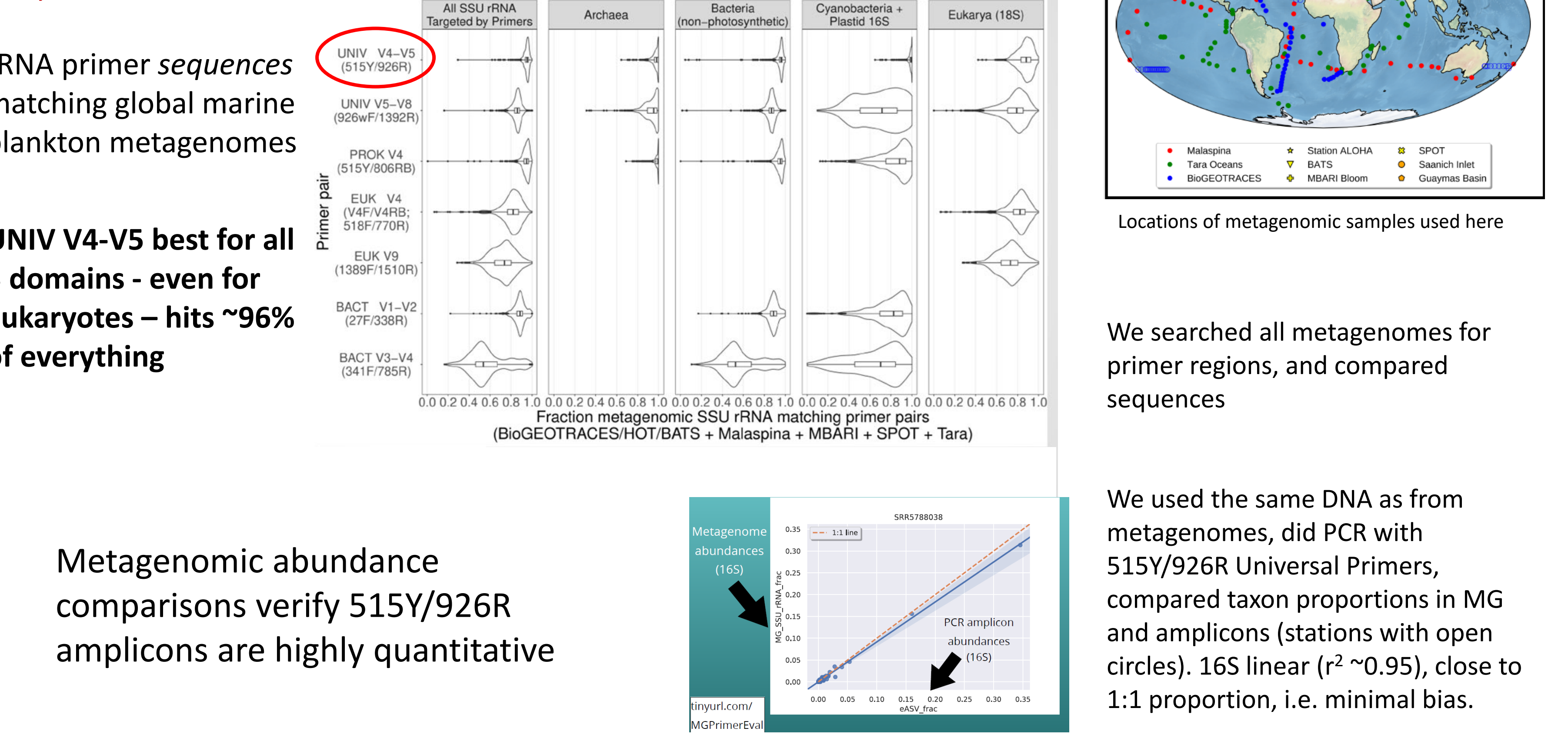
Abstract: We used metagenomes and mock communities to validate the use of universal 3-domain rRNA primers which simultaneously amplify bacteria, archaea, and protist sequences with excellent overall coverage. Amplicons and metagenomes were used to study patterns in distributions of microbes and viruses on a wide range of scales. At the San Pedro Ocean Time Series site, the prokaryotic and viral communities have had a remarkably stable and resilient average community composition for more than a decade, with superimposed seasonality at the "species"-like level; however, viruses show Red Queen dynamics, constantly changing strains, suggestive of an "arms race." In contrast to prokaryotes and viruses, eukaryotes were surprisingly unstable in their community composition, and showed an opposite pattern with depth in Shannon Diversity. Large-scale ocean transects of "whole seawater" samples (>0.2 μm) analyzed with universal primers were able to discern global patterns in the distribution of organisms present, relative to each other and the community as a whole, providing ground-truth data for improvement of global biological-physical models, and showing that prokaryotic rRNA genes dominate quantitatively in most of the world's oceans.

PRIMER VALIDATION: Universal V4-V5 515Y/926R amplifies from all three domains in a single reaction.

Advantages: Excellent coverage, remarkable quantitative accuracy vs other tested primers, and abundances reported relative to the total community, allowing everything to be compared to each other

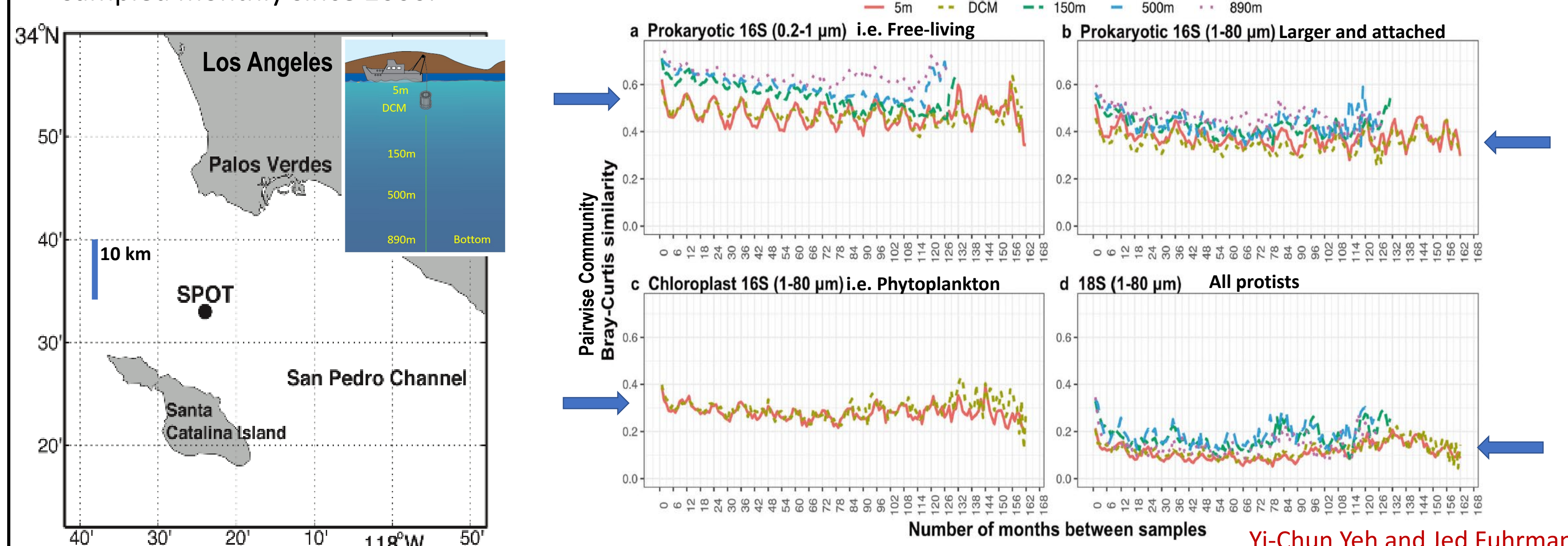


Jesse McNichol, Paul Berube, Steven Biller, Jed Fuhrman mSystems 2021



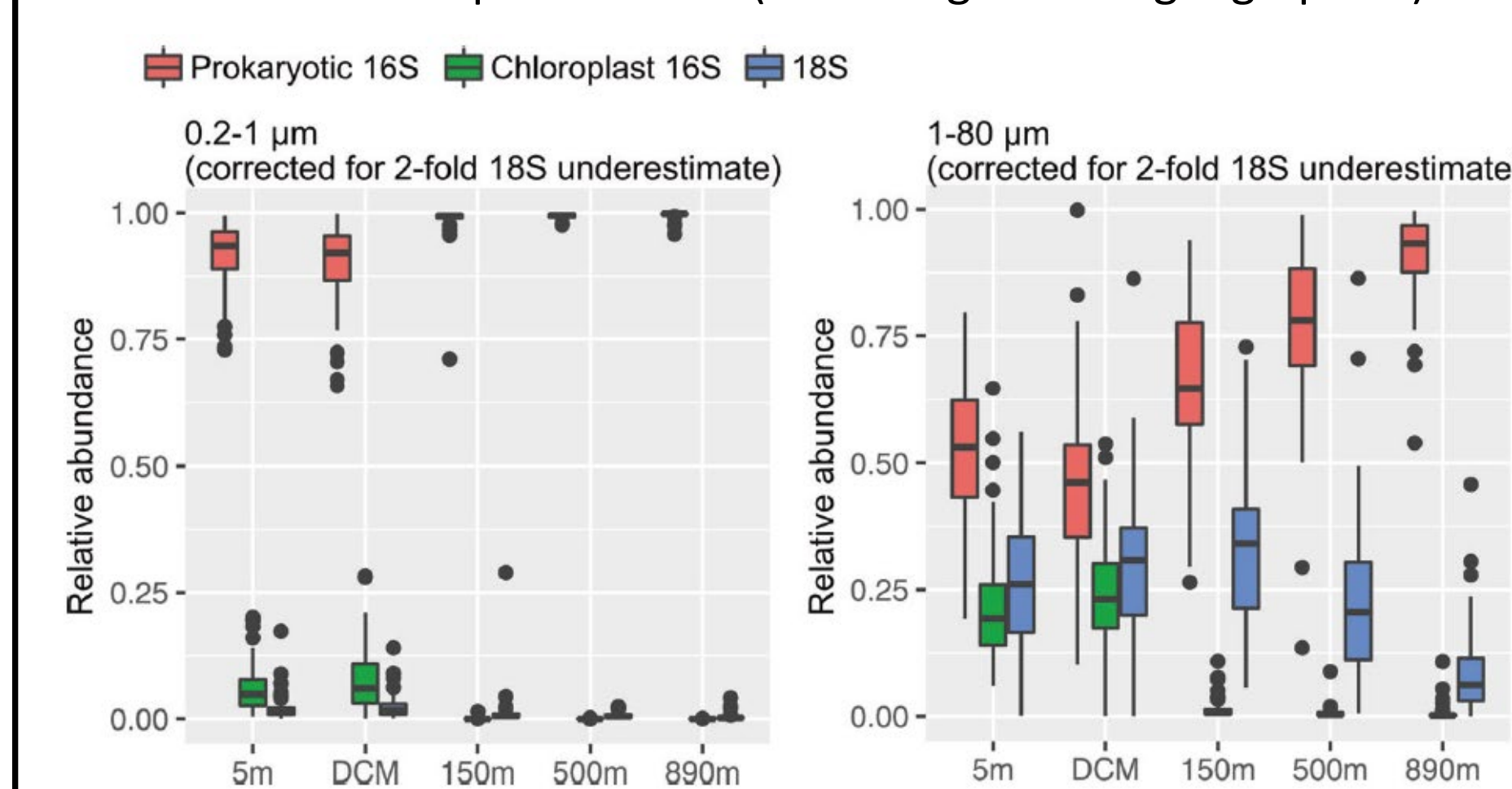
San Pedro Ocean Time-series (SPOT): Ecological patterns of whole microbial community composition

Prokaryotes, Eukaryotes and viruses, sampled monthly since 2000. Universal V4-V5 Primer-based whole microbial community stability and seasonality shown by pairwise community similarity vs. increasing intervals between samples (2005-2018)

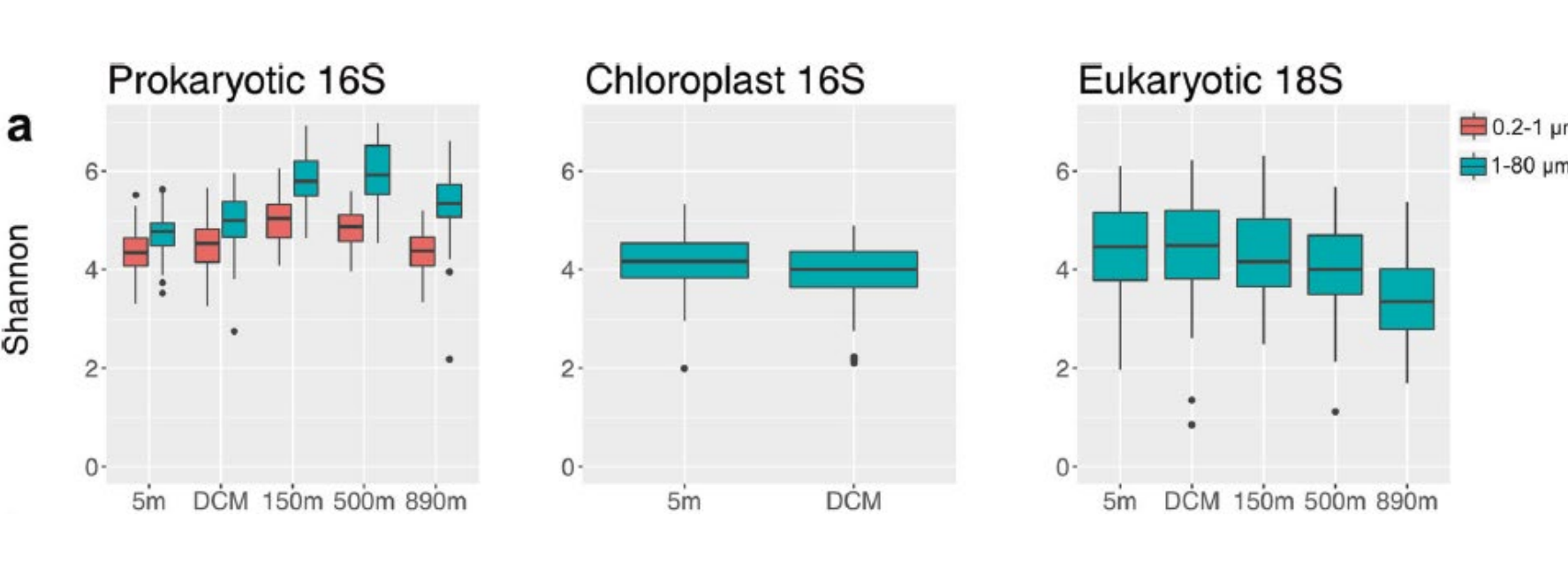


- Free prokaryotes have particularly stable communities – average B-C similarities are high (0.5-0.7) and steady.
- Highest stability seen in deep prokaryotes (150, 500, and especially 890 m).
- >1 μm prokaryotic community (largely attached) is less stable than free (B-C ~0.4), but still seasonal.
- Phytoplankton (chloroplasts) communities less stable than prokaryotes, average B-C similarity ~ 0.3.
- Total protists (18S) communities least stable - sample pairs average only about 10-20% B-C similarity.
- Seasonality, i.e. peaks in similarity at 12,24,36 etc. month intervals, apparent for euphotic zone prokaryotes and phytoplankton.

Prokaryotes unexpectedly dominate rRNA genes of both size fractions at all depths at SPOT (see also global biogeographies)



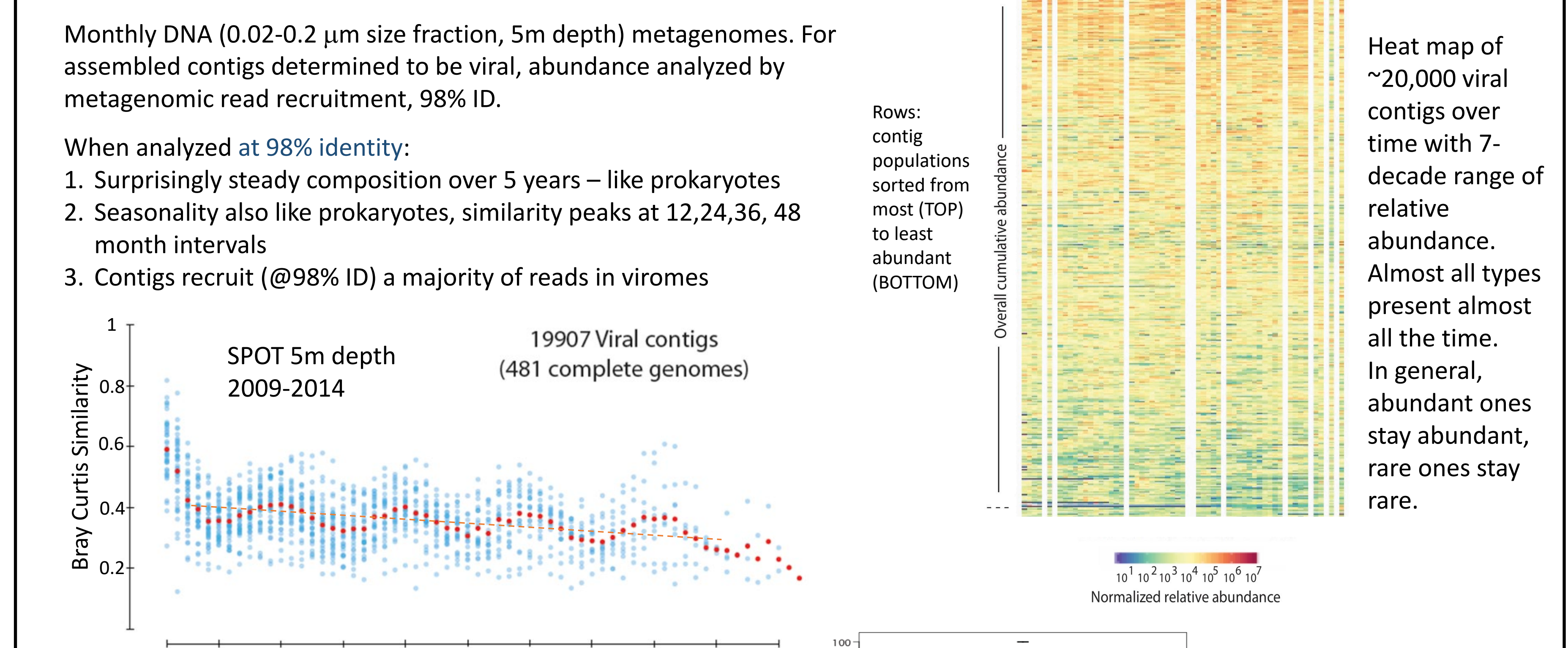
Prokaryotes and protists have similar Shannon Diversity index in the euphotic zone, but opposite patterns with increasing depth at SPOT: prokaryotes increase and protists decrease. May relate to low oxygen at depth. Note also higher prokaryote diversity in the larger size fraction, suggesting more diversity in attached prokaryotes.



Yi-Chun Yeh and Jed Fuhrman ISME Comm. 2022

Virus Community at SPOT: Steady Average, Seasonality, Red Queen Strain Dynamics

Viral Community Composition at SPOT
J Cesar Ignacio-Espinoza, Nathan Ahlgren, Jed Fuhrman
Nature Microbiology 2020



Monthly DNA (0.02-0.2 μm size fraction, 5m depth) metagenomes. For assembled contigs determined to be viral, abundance analyzed by metagenomic read recruitment, 98% ID.

When analyzed at 98% identity:

- Surprisingly steady composition over 5 years – like prokaryotes
- Seasonality also like prokaryotes, similarity peaks at 12,24,36, 48 month intervals
- Contigs recruit (@98% ID) a majority of reads in viromes

Each trace essentially follows combinations of SNVs, i.e. strains

Polymorphic sites shared with peak month

Example contig SNV abundance profiles over time

However, when examined at 100% identity, characterizing Single Nucleotide Variants, each combination of microvariants (making up the SNV profile) within a contig population is abundant only for months i.e. **Strain level Red Queen-like** dynamics. The "species" stay the same, with constantly changing strains. Almost all variations are silent. Consistent with nucleotide-level HOST DEFENSES and virus population-level responses.

The Red Queen Theory

"It takes all the running you can do, to keep in the same place. If you want to get somewhere else, you must run at least twice as fast as that!" - The Red Queen, Through the Looking-Glass

Global Marine Microbial Biogeographies, All Taxa Simultaneously Non-size-fractionated > 0.2 μm samples, Universal V4-V5 515Y/926R amplicons

Jesse McNichol, Yubin Raut

