

Stability in the microbiomes of temperate gorgonians and the precious red coral *Corallium rubrum* across the Mediterranean Sea

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Introduction

- Gorgonians are key habitat-forming species of temperate benthic communities¹.
- Dramatic population declines due to local human impacts and mass mortality events caused by high temperatures and disease outbreaks².
- However, relatively little is known about the microbial of gorgonians.

OBJECTIVES – Reveal the composition of the bacterial communities of 5 soft gorgonian species and the precious red coral and assess the stabilities of these associations on both spatial and temporal scales.

Material & Methods

- Study species (encompassing 4 genera, 3 families, 2 sub-orders)**
 - Eunicella cavolini*, *E. singularis*, *E. verrucosa*
 - Leptogorgia sarmentosa*
 - Paramuricea clavata*
 - Corallium rubrum*
- Sample collection over temporal and spatial scales (30-40m depth)**
 - Seasonal: every 3 months at 2 locations (Cassis & La Spezia)
 - Spatial:

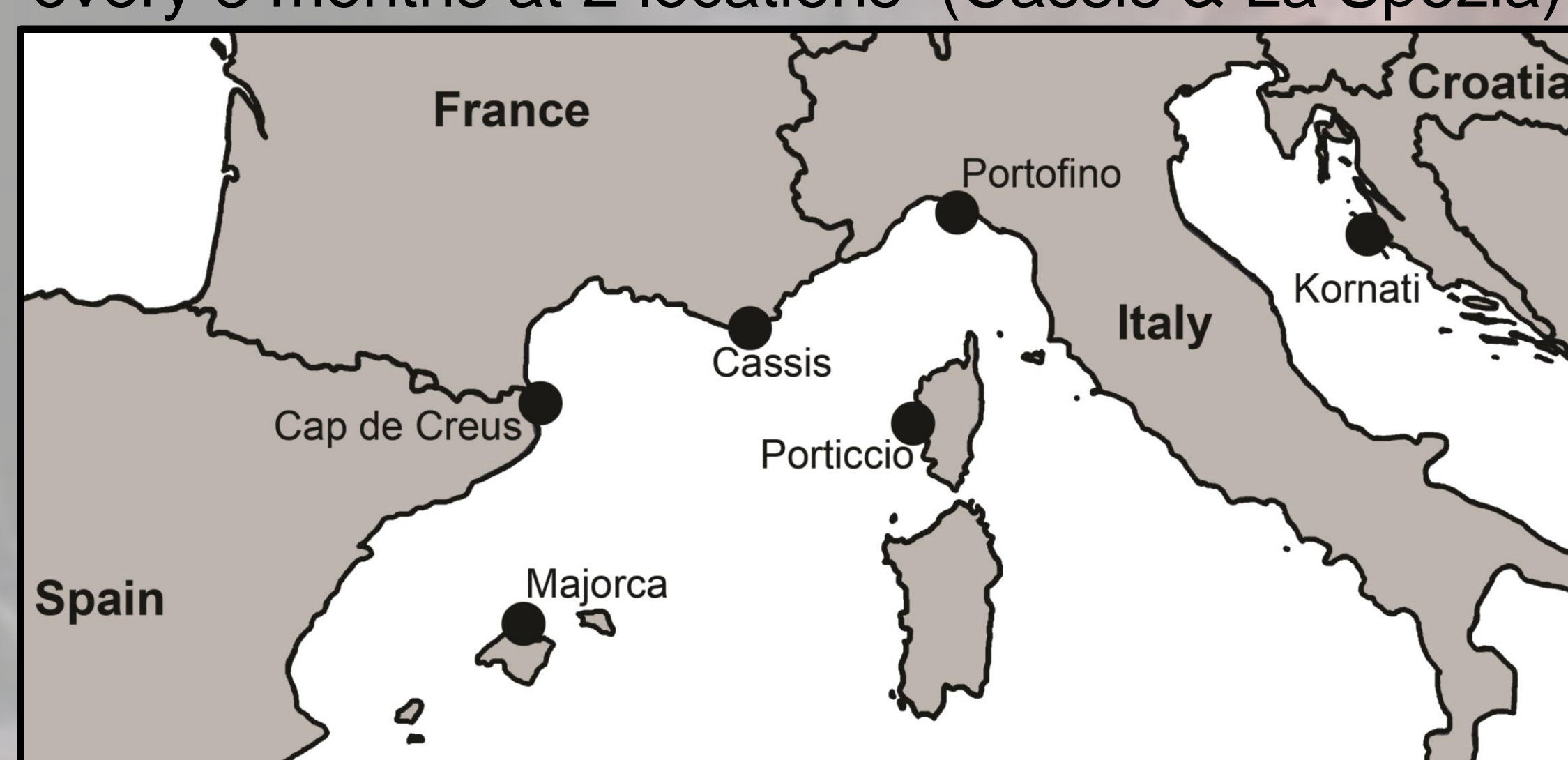


Figure 1 - Six locations spanning a 1100km distance across the western Mediterranean Sea.

- Profiling of the host-associated bacterial communities based on 16S rRNA amplicon sequencing**
 - Libraries generated with 8F/338R (V1-V2 regions) and 784/1061R (V5-V6 regions) primer sets
 - 2x300bp paired-end sequencing - Illumina MiSeq
- Data processing:** QIIME pipeline³ and phyloseq/DESeq2⁴

Discussion & Conclusions

- Gorgonian-associated bacterial communities are highly structured and relatively stable on both temporal and seasonal scales, suggesting tight regulation of holobiont membership.
- Microbiome impacted by / acclimated to local environmental conditions.
- Composition of *C. rubrum* microbiome unique in phylum Cnidaria.
- Ancient host-microbe associations, conserved through evolutionary times, but divergence in microbiome composition is clear along distant phylogenetic lines.
 - > Significant overlap in the microbiome among species from the same family.
 - > Support 'Holobiont Model' over 'Hologenome Theory of Evolution'.
- Roles of the microbial symbionts to host health remain to be elucidated.

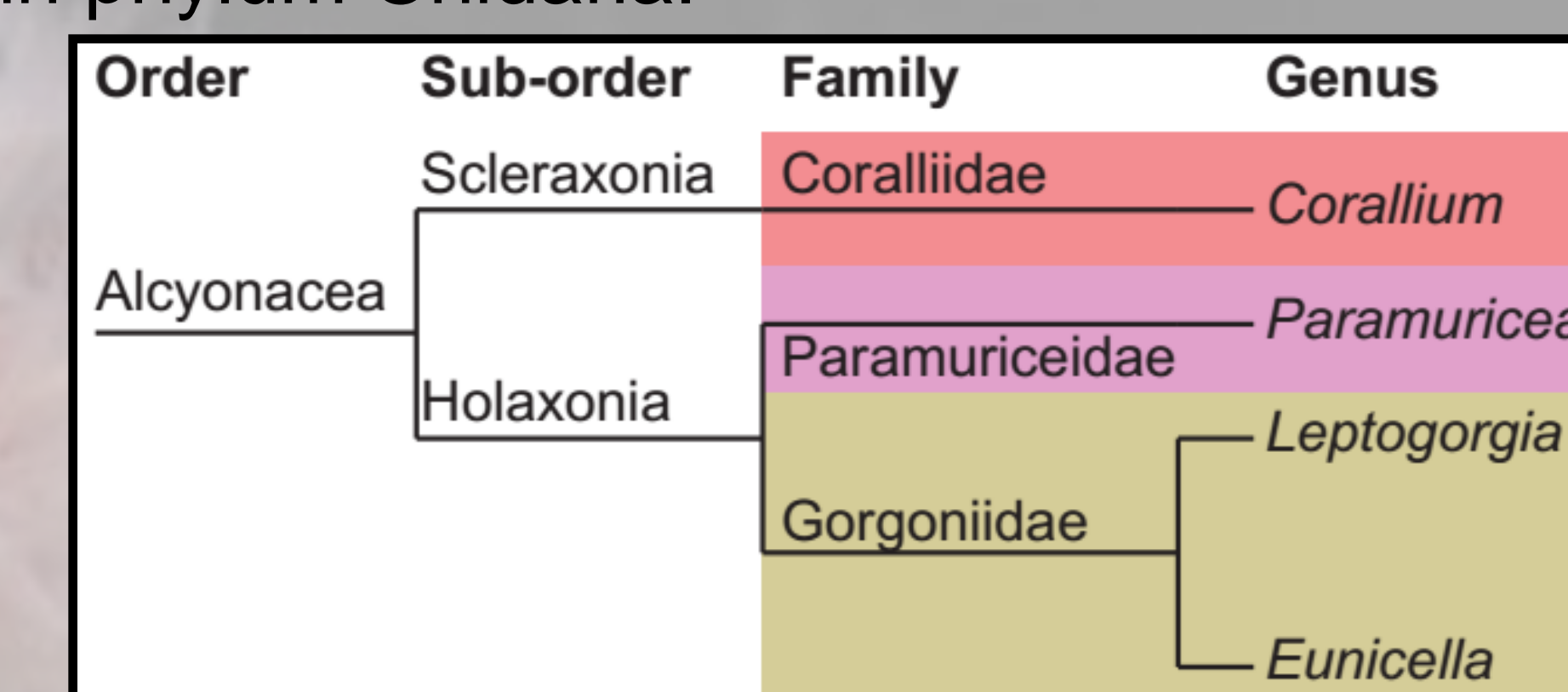


Figure 6 - Schematic overview of Mediterranean gorgonian taxonomy. The different colours identify taxa harbouring distinct core microbiomes.

Results II - Seasonal patterns in bacterial community composition

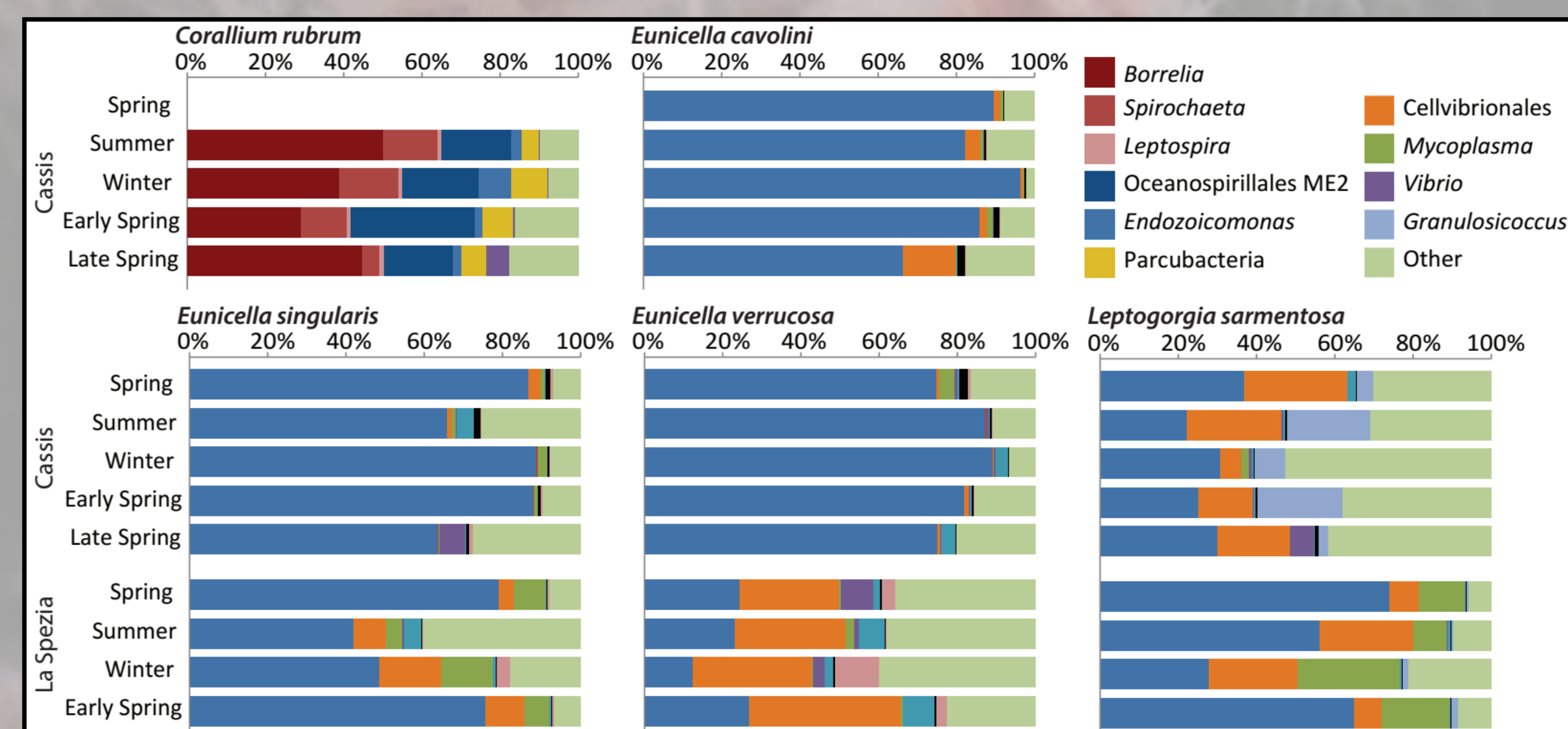


Figure 4 - Composition of the bacterial communities associated with five different gorgonians over time at two different locations – Cassis and La Spezia.

Results I - Spatial patterns in bacterial community composition

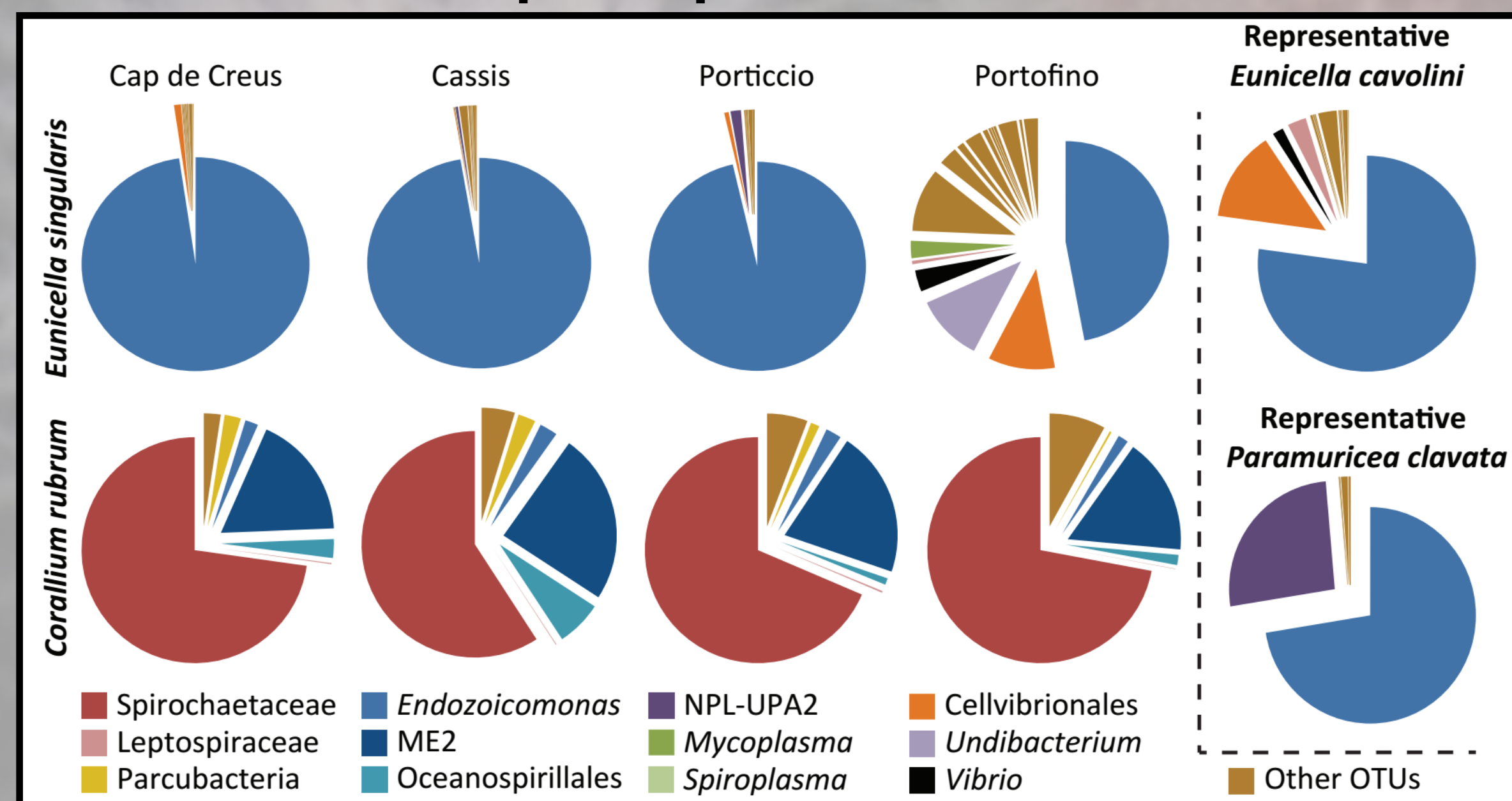


Figure 2 – Spatial patterns in bacterial community composition of *E. singularis* and *C. rubrum*. Similar results obtained for other gorgonian species and representative samples is shown.

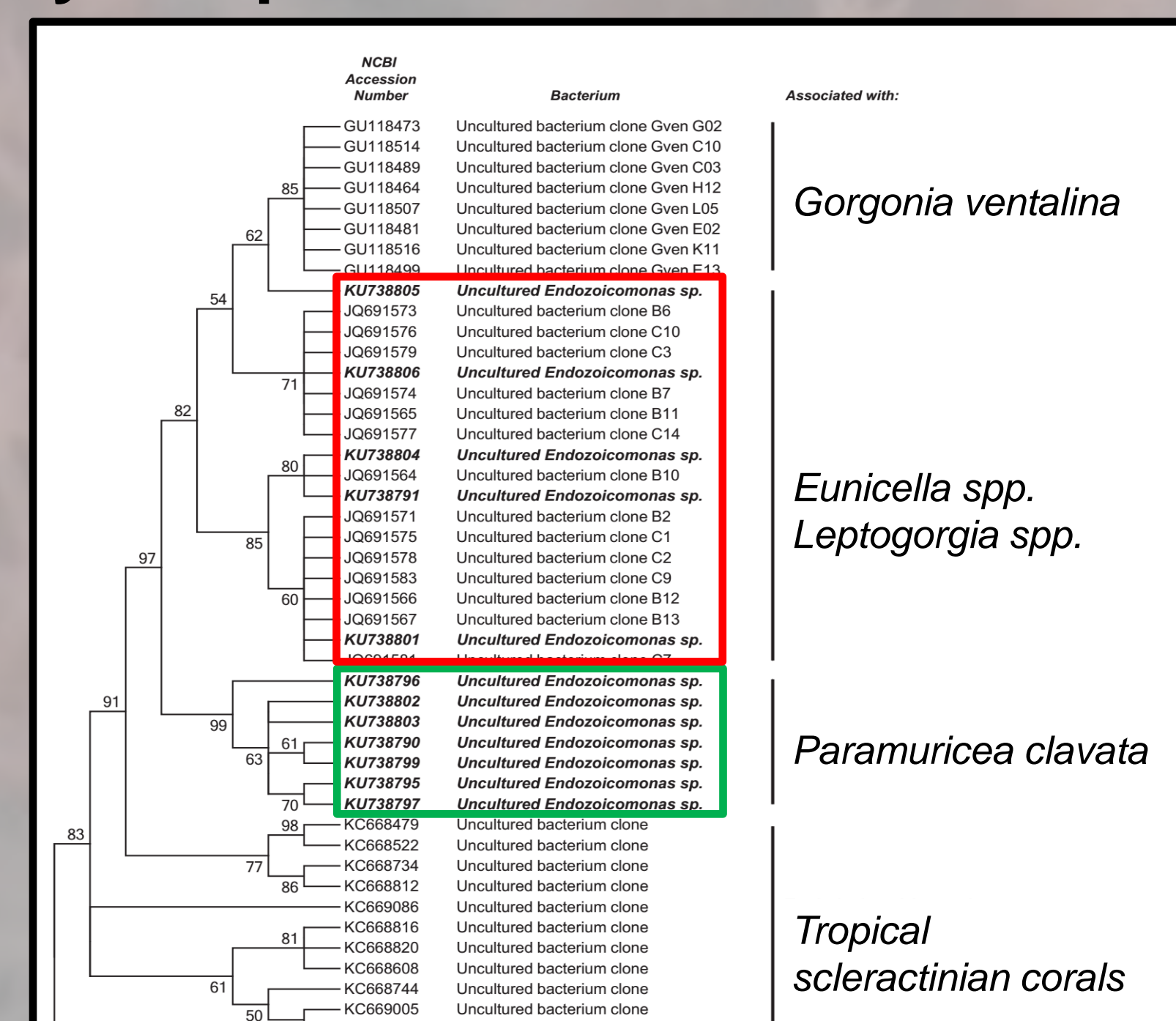


Figure 3 - *Endozoicomonas* phylogeny.

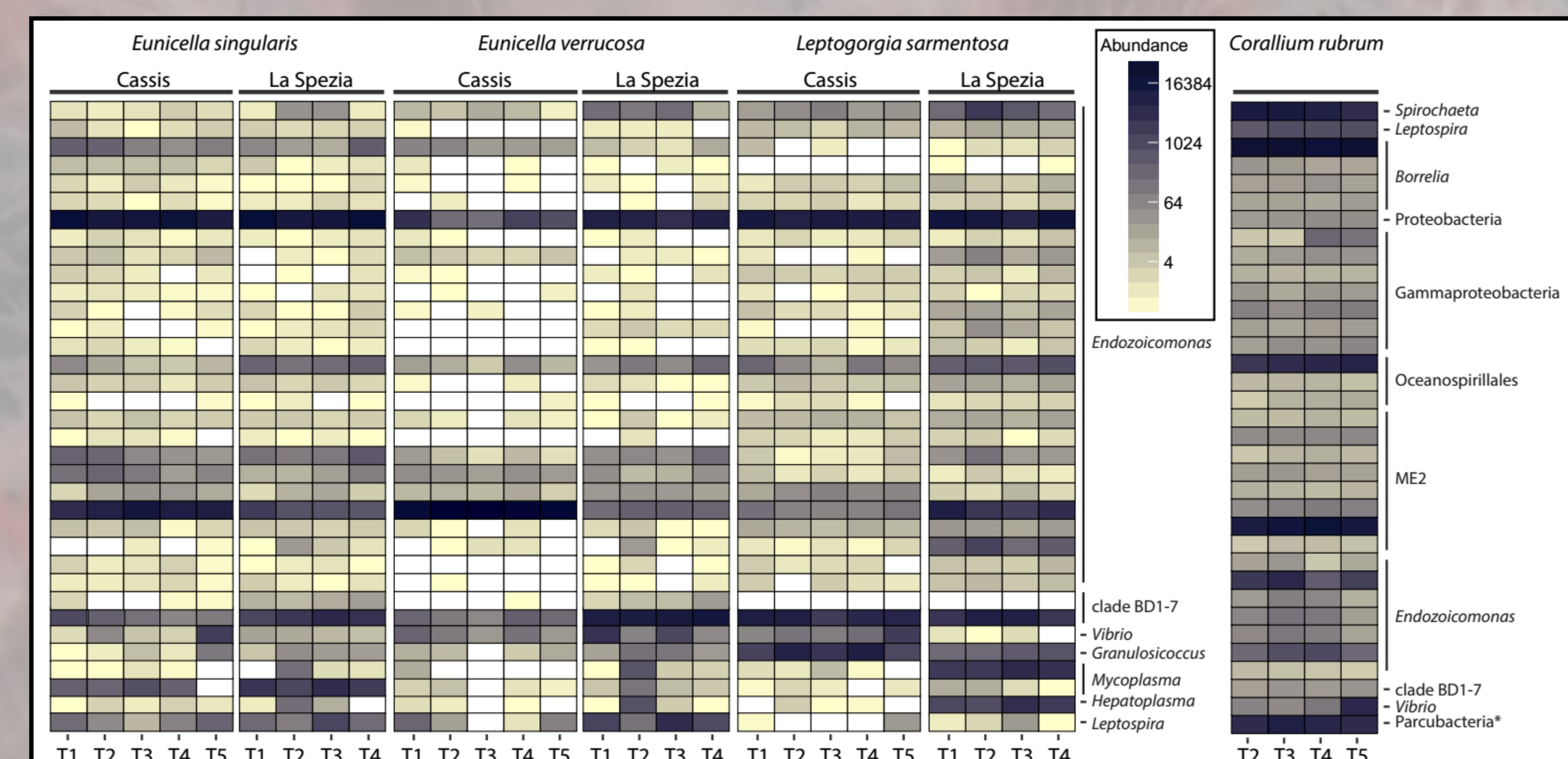


Figure 5 – Core microbiome composition at OTU level (T1-5 correspond to seasons shown Figure 4).

Relevant Publications

van de Water JAJM et al. *Microbial Ecology* - 2017 accepted
 van de Water JAJM et al. *Microbial Ecology*. 2016 October 10; 73(2): 466-478
 van de Water JAJM et al. *Scientific Reports*. 2016 June 6; 6: 27277

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 2. Bally M & Garrabou J. *Global Change Biology* 2007, 13 (10):2078-2088.
 3. Caporaso JG et al. *Nature Methods*. 2010, 7 (5):335-336.
 4. McMurdie PJ & Holmes S. *PLOS ONE* 2013, 8 (4):e61217.