

Latitudinal variation in the microbiome of the sponge *Ircinia campana* correlates with host haplotype but not anti-predatory chemical defense

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Supplement 1.

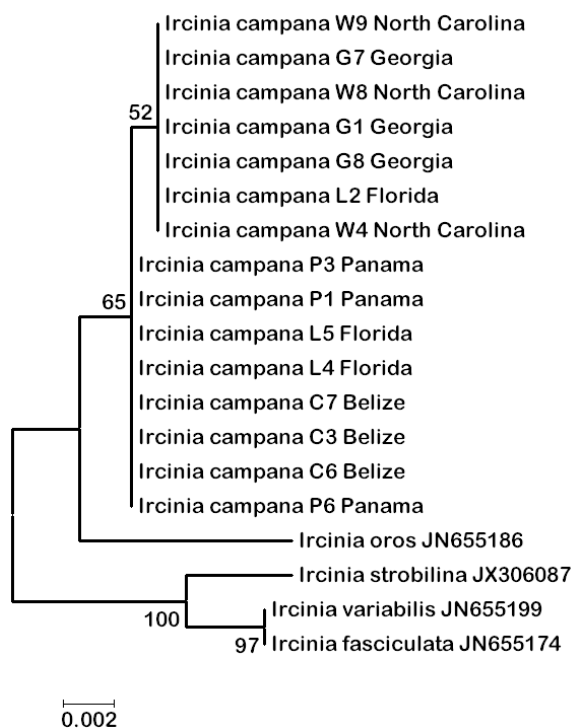


Figure S1. Host phylogeny based on partial COI gene sequences. Tree topology was obtained through ML analysis and numbers on the nodes indicate bootstrap support percentages. Labels on terminal nodes indicate the *Ircinia* species, sample code (for sequences obtained in this study) or GenBank accession number, and sample location. Scale bar indicates number of substitutions per site

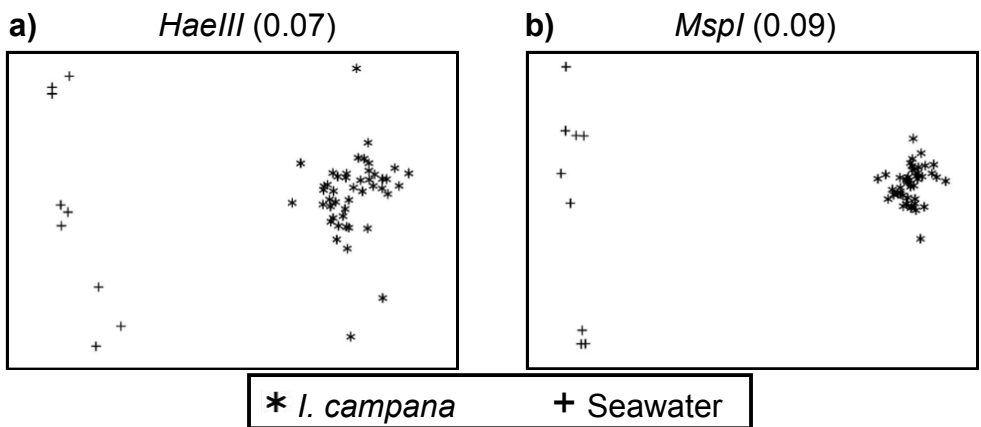


Figure S2. nMDS plots of bacterial community structure in *I. campana* and surrounding seawater based on Bray-Curtis similarity of T-RFLP profiles using the restriction enzymes **a) *HaeIII*** and **b) *MspI***. Stress values are shown in parenthesis.

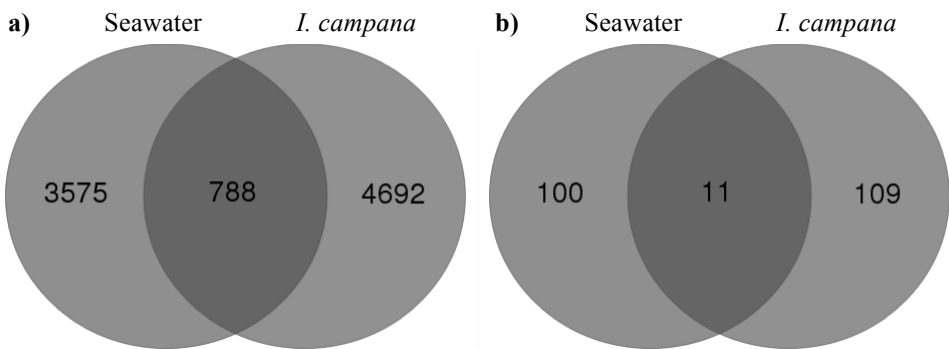


Figure S3. Comparison of the seawater and *I. campana* OTU profiles showing the number of OTUs that are unique to each source and shared between them when **a) all OTUs** are considered and when **b) only OTUs** that contribute at least 0.1% of the total reads for a source.

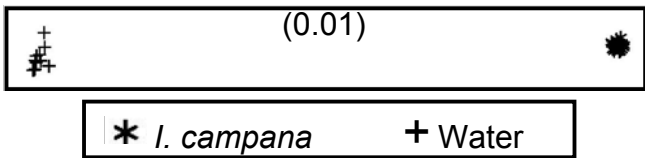


Figure S4. nMDS plot of microbial community structure in *I. campana* and surrounding seawater based on Bray-Curtis similarity of OTU profiles compiled from Illumina sequences. The stress value is shown in parenthesis.