

Niche Partitioning in the Rimicaris Exoculata Holobiont: The Case of the First Symbiotic Zetaproteobacteria

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Research

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Abstract

Background Mutualistic symbioses between invertebrate animals and chemosynthetic bacteria are the basis of life in hydrothermal vent ecosystems. The shrimp *Rimicaris exoculata*, which dominates animal communities along the Mid-Atlantic Ridge, houses a complex bacterial community in its enlarged cephalothorax, including the dominant Campylobacteria, *Desulfobulbia* (formerly Deltaproteobacteria), Alpha proteobacteria, Gammaproteobacteria and some recently discovered iron oxyhydroxide-coated Zetaproteobacteria. This epibiotic consortium uses iron, sulfide, methane, and hydrogen as energy sources. Here, we generated shotgun metagenomes from *Rimicaris exoculata* cephalothoracic epibiotic communities to reconstruct and investigate symbiotic genomes. We collected specimens in three geochemically contrasted vent fields, TAG, Rainbow, and Snake Pit, to unravel the specificity, variability, and adaptation of *Rimicaris* –microbe associations.

Results Our data enabled us to reconstruct 49 metagenome-assembled genomes (MAGs) from the TAG and Rainbow vent fields, including 16 with more than 90% completion and less than 5% contamination based on single copy core genes. These MAGs belonged to the dominant Campylobacteria, *Desulfobulbia*, Thiotrichaceae as well as some novel candidate phyla radiation (CPR) lineages. In addition, most importantly, two MAGs in our collection were affiliated to Zetaproteobacteria and had no close relatives (average nucleotide identity ANI < 77% with the closest relative *Ghiorsea bivora* isolated from TAG, and 88% with each other), suggesting potential novel species. Genes for Calvin-Benson Bassham (CBB) carbon fixation, iron, and sulfur oxidation, as well as nitrate reduction, occurred in both MAGs. However, genes for hydrogen oxidation and multicopper oxidases occurred in one MAG only, suggesting shared and specific potential functions for these two novel Zetaproteobacteria symbiotic lineages. Overall, we observed highly similar symbionts co-existing in a single shrimp at both the basaltic TAG and ultramafic Rainbow vent sites. Nevertheless, further examination of the seeming functional redundancy among these epibionts revealed important differences.

Conclusion These data highlight microniche partitioning in the *Rimicaris* holobiont and support recent studies showing that functional diversity enables multiple symbiont strains to coexist in animals colonizing hydrothermal vents.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the latest manuscript can be downloaded and [accessed as a PDF](#).

Figures

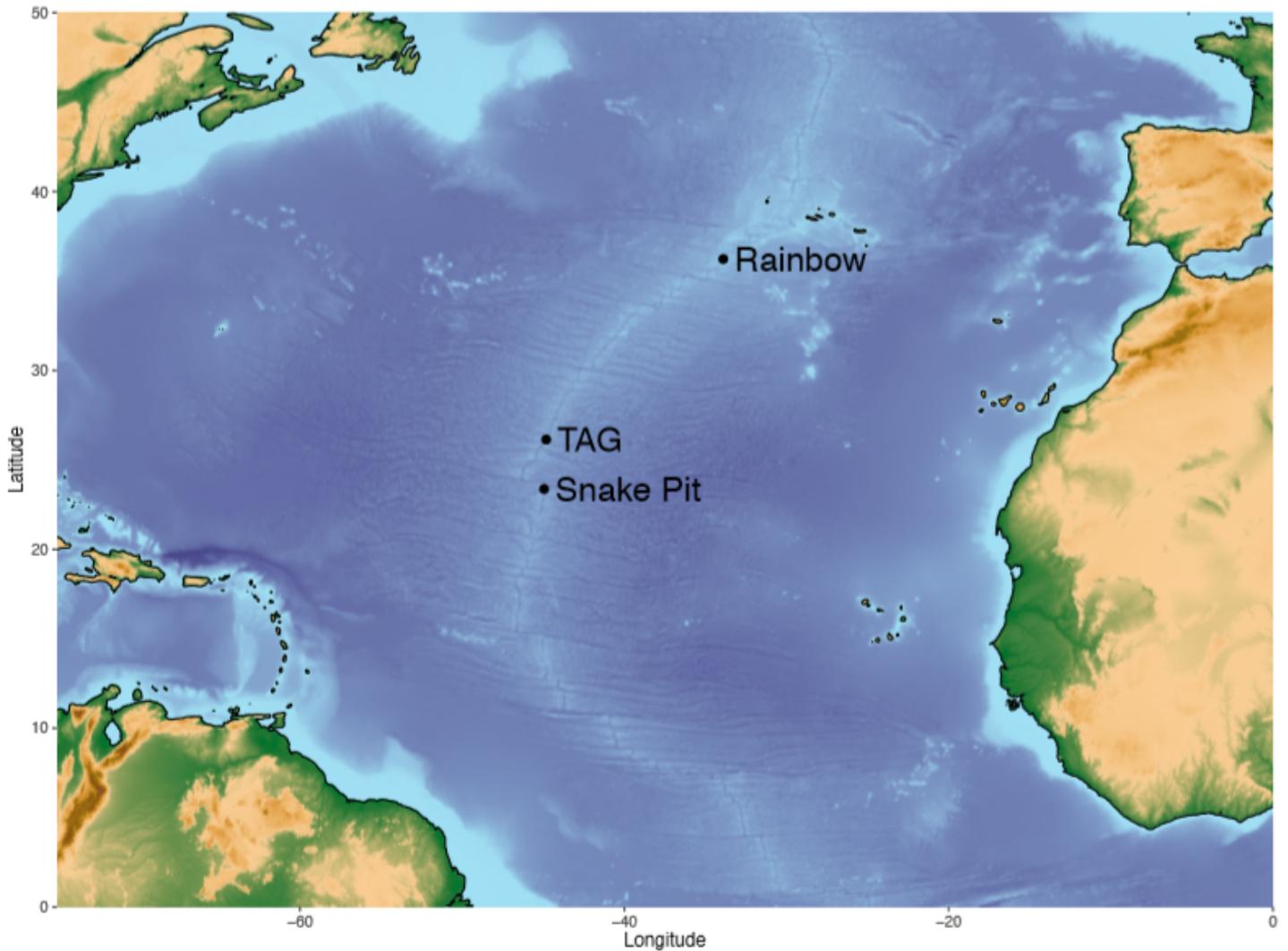


Figure 1

Geographic locations of Mid-Atlantic Ridge hydrothermal vent sites Rainbow, TAG and Snake Pit where *Rimicaris* specimens were sampled. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

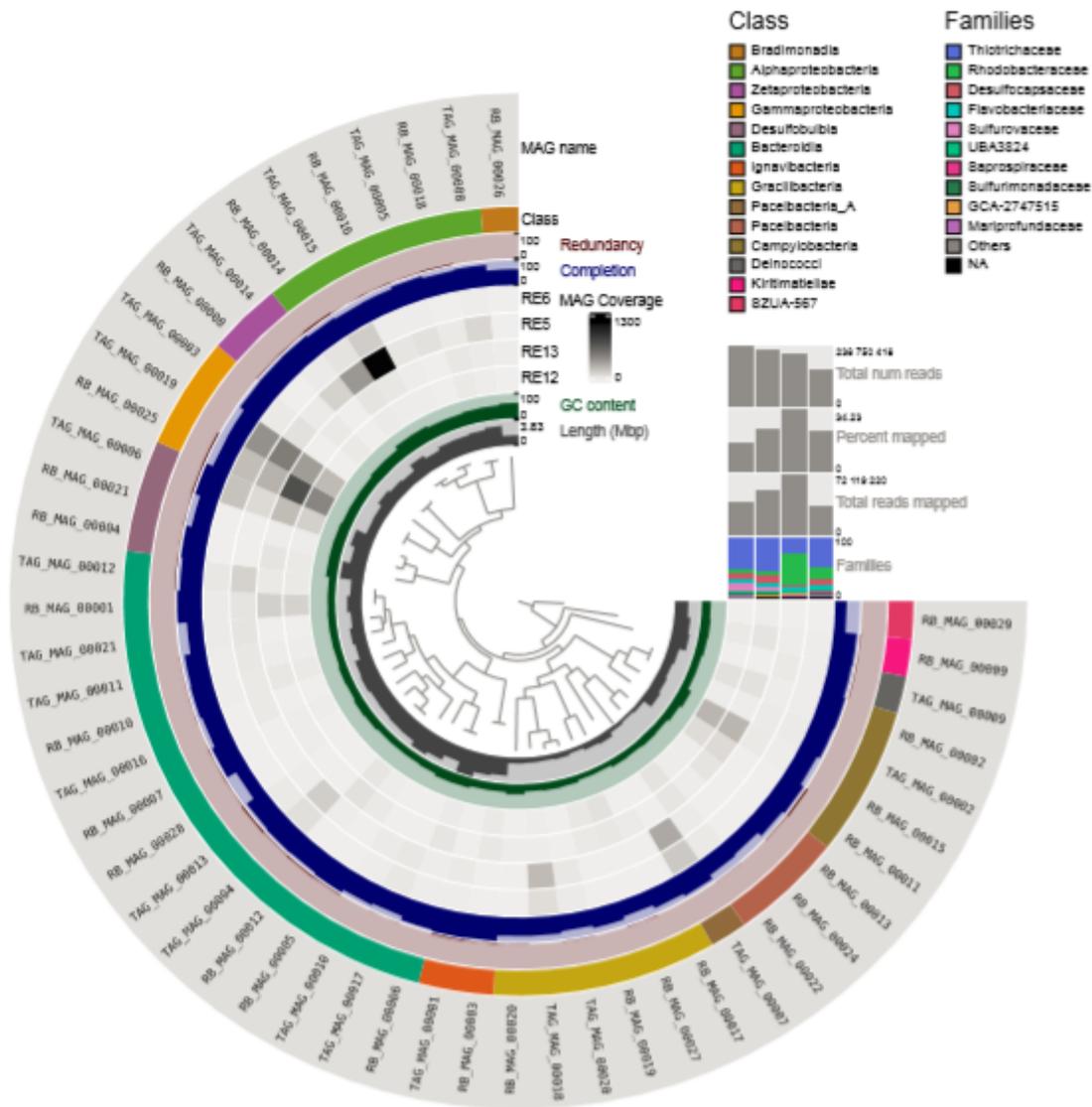


Figure 2

Static image from the anvio interactive display for the Rimicaris datasets with the 49 genome bins retained for this study. From inner to outer layers: phylogenomic tree based on concatenated marker proteins according to the GTDB-Tk genome phylogeny, length layer (shows the actual length of a genome), auxiliary layer with information about contigs stored in the contig database (GC-content), four view layers with information about MAGs across samples stored in the profile database (mean coverage), completion, redundancy, and bacterial genome bin layers. The horizontal layers show genome bin taxonomy based on GTDB-Tk for the ten most abundant families, total number of reads for each sample, total number of reads mapped and corresponding mapping percentage of reads. Relative abundances of families are noted as the percentages of reads recruited to the bins for each sample.

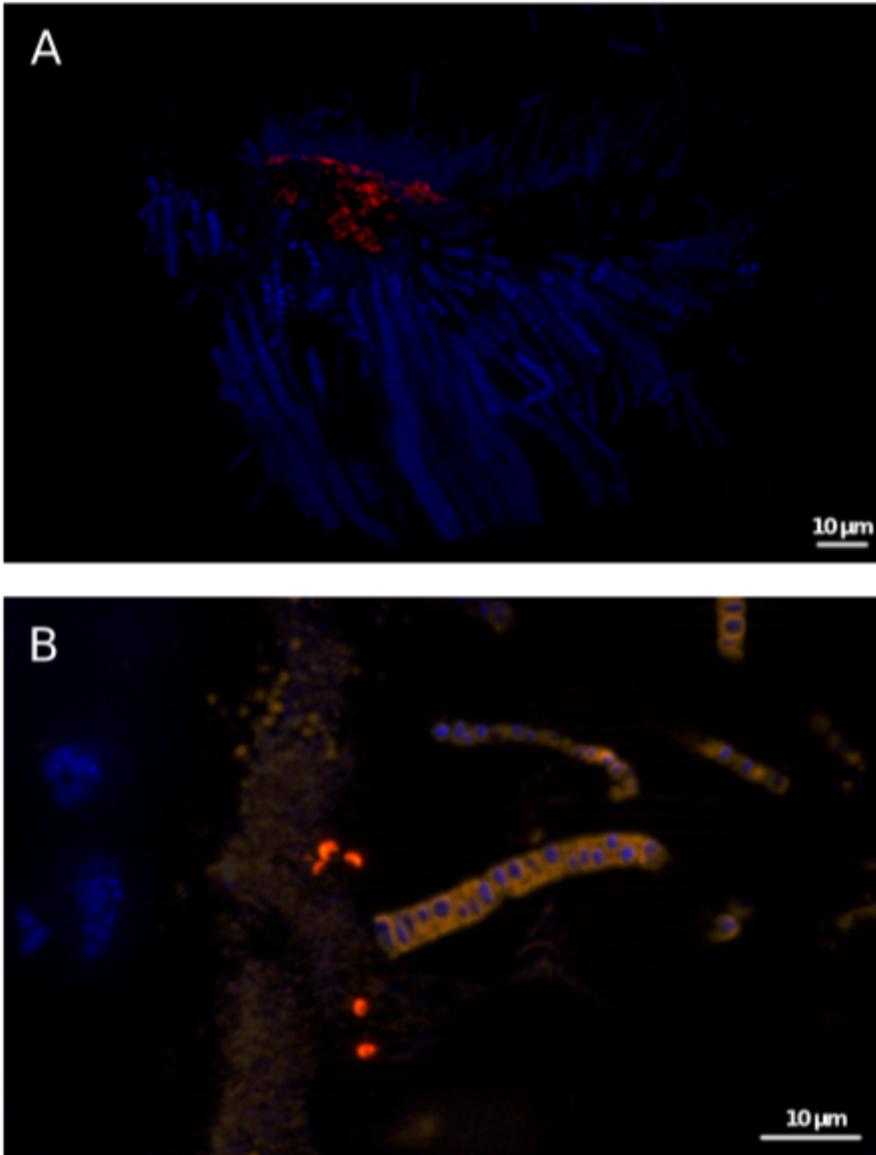


Figure 3

FISH observations of a Rainbow *R. exoculata* branchiostegite with epibionts. All cells are labelled with DAPI (blue). Zetaproteobacteria are hybridized with the Zeta123 probe (red) [28]. A. Zetaproteobacteria are closely attached to the cuticle. Dominant large filamentous bacteria (Campylobacteria) and thinner Gammaproteobacteria filaments can be seen. B. Co-hybridization of filamentous Campylobacteria with the EPSI 549 probe (orange) [53] and small Zetaproteobacteria rods (red), highlighting the co-occurrence of both lineages.

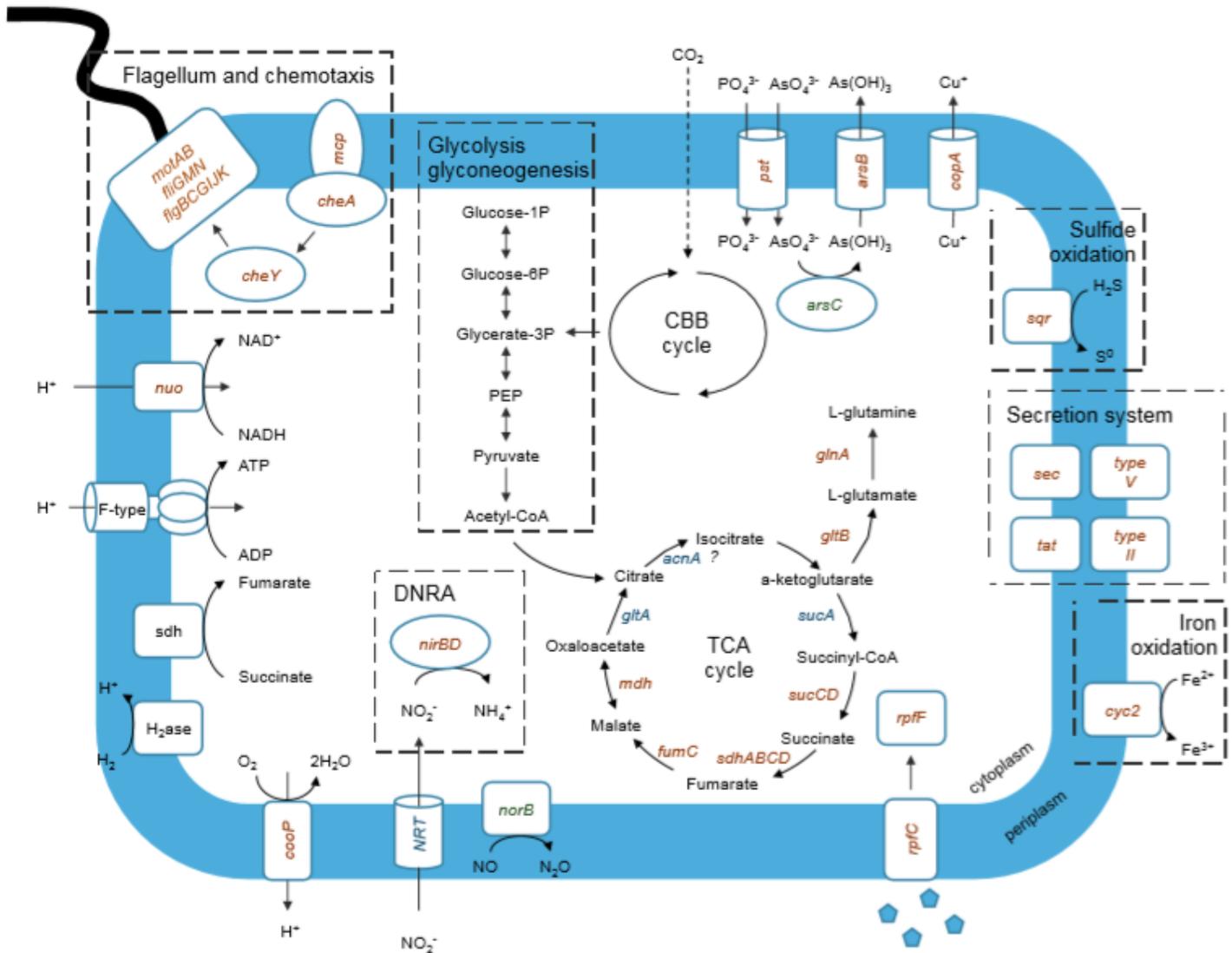


Figure 4

Schematic representation of the predicted metabolic potentials within etaproteobacteria MAGs: RB_MAG_00008 and TAG_MAG_00014. The potential metabolic traits are focused on carbon metabolism, nitrogen uptake, sulfur and iron oxidation, hydrogen utilization, flagellum, chemotaxis, and detoxification. Genes present in both MAGs are indicated in red, those present only in RB_MAG_00008 or TAG_MAG_00014 are indicated in blue and green, respectively. AHL: acyl homoserine lactone, CBB: Calvin–Benson–Bassham, H₂ase: Hydrogenase, PEP: phosphoenolpyruvate, SDH: succinate dehydrogenase.

levels are indicated and represented by the different colors. NAD-reducing hydrogenase: hoxHFUY. NiFe hydrogenase Hyd-1:hyaABC

Supplementary Files

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