Redox substrates and autotrophic pathways of Endoriftia Persephone, the gammaproteobacterial endosymbiont of vestimentiferan tubeworm Riftia pachyptila

<u>Juliana Leonard¹</u>, Jessica Panzarino², Roxanne Beinart³, Jon Sanders², Jennifer Delaney², Peter Girguis², Kathleen Scott¹

¹Department of Integrative Biology, University of South Florida, Tampa, FL USA; juliana10@mail.usf.edu

²Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA USA; ³Geology and Geophysics, Woods Hole Oceanographic Institution, Woods Hole, MA USA

Vestimentiferan tube worm Riftia pachyptila lives at deep-sea hydrothermal vents, which have a high degree of temporal heterogeneity in habitat chemistry. Their growth is dependent on a sulfur-oxidizing endosymbiotic gammaproteobacterium. Endoriftia persephone, that lives in the trophosome organ. E. persephone may be able to use two carbon fixation pathways, the Calvin Benson Basham cycle (CBB) and the reductive citric acid cycle (rCAC). In addition, they may also be able to use multiple electron donors (H2 and reduced sulfur compounds including H2S) and multiple electron acceptors (oxygen and nitrate). To clarify the carbon fixation pathways and redox substrates, and to infer whether these capabilities are environmentally induced, R. pachyptila were collected at hydrothermal vent sites in the East Pacific in November 2014 and October 2016 with the HOV ALVIN. The worms were incubated at sea in high pressure vessels under conditions designed to induce the relevant activities (high versus low sulfide; presence and absence of hydrogen gas; presence and absence of nitrate and oxygen). Freshly harvested symbionts were incubated in the presence of different redox substrates (H2, H2S, O2, nitrate) to determine which one(s) stimulated carbon fixation rates. Pathways were verified via stable isotope analyses and enzyme assays (RubisCO for CBB; ATP dependent citrate lyase for rCAC; hydrogenase for H2 use; nitrate reductase for nitrate utilization). Clarifying the capabilities of the symbionts to adjust to hydrothermal vent heterogeneity will in turn clarify the factors influencing the distribution of this ecosystem-structuring symbiosis.