Identifying invertebrate prey of hydrothermal vent gastropods

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Identifying invertebrate predator-prey relationships is critically important for determining the effects of changing environmental conditions on community structure, food web dynamics, and the transfer of energy in deep-sea chemosynthetic ecosystems. Stable isotopes and lipid profiles have been useful for identifying the prey of some predators, but in cases where prey have similar stable isotopic or lipid composition, these methods are more limited. We employed PNA-mediated PCR with universal eukaryotic primers to amplify DNA, extracted from the dissected stomachs of hydrothermal vent gastropods, sampled from diffuse-flow vents at the East Pacific Rise (9°50'N) in 2007, to identify their ingested invertebrate prey. With the PNA-clamp, only the DNA of eukaryotic prey, and not the predator, was amplified, cloned, and sequenced. While sample sizes were limited in this pilot study, the DNA sequences obtained from the stomachs of Lepetodrilus tevnianus matched with high similarity to Tevnia jerichonana, Riftia pachyptila and Bathymodiolus spp. Thus, our results supported the hypothesis that Lepetodrilus spp. (limpets) at the East Pacific Rise could inhibit colonization of siboglinids, but also bathymodiolins, in established hydrothermal vent communities.