

Diversity in carbon dioxide concentrating mechanisms among gammaproteobacterial chemolithoautotrophs from the deep-sea hydrothermal vents and elsewhere

Kathleen M. Scott, Juliana Leonard, Ryan Keeley, and USF MCB 4404L

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

Six autotrophic carbon fixation pathways are known among members of domains Bacteria and Archaea. The 'front-end' of these pathways, delivery of dissolved inorganic carbon (DIC; = $\text{CO}_2 + \text{HCO}_3^- + \text{CO}_3^{2-}$) from the environment to the cytoplasm, has only been described in cyanobacteria, in which CO_2 concentrating mechanisms (CCMs), consisting of DIC transporters and carboxysomes, facilitate growth under low DIC conditions. CCMs are likely to be common beyond the cyanobacteria, since the concentrations of DIC vary considerably among the habitats where autotrophic Bacteria and Archaea are active, and could impact the rate at which they catalyze reactions of geochemical importance. Deep-sea hydrothermal vent gammaproteobacterium *Hydrogenovibrio crunogenus* was the first proteobacterium to have its CCM characterized. Like cyanobacteria, and many autotrophic proteobacteria, *H. crunogenus* has carboxysomes. Its DIC transport system consists of a novel two-subunit transporter whose genes are downstream from its carboxysome operon. Other *Hydrogenovibrio* species, as well as some members of *Thiomicrospira* and *Thiomicrobacter* also carry these genes, and they are upregulated when grown under DIC limitation. Indeed, homologs of this transporter are present in 14 phyla in Bacteria and one phylum in Archaea. Some members of *Thiomicrobacter* and *Thiomicrospira* carry distantly related homologs of cyanobacterial SbtA-family and/or BicA-family bicarbonate transporters downstream from their carboxysome operons, and these are upregulated when cells are grown under DIC limitation, raising the possibility that three evolutionarily distinct DIC transporters facilitate the growth of the closely related genera *Thiomicrospira*, *Hydrogenovibrio*, and *Thiomicrobacter*.