



Investigating carbon monoxide (CO) consumption in the marine bacteria *Silicibacter pomeroyi* with *coxL* gene expression

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A cycle of photochemical production and microbial consumption results in carbon monoxide (CO) supersaturation in the surface ocean. This concentration gradient drives a global flux of CO from the ocean to the atmosphere. Understanding bacterial CO consumption is critical for evaluation of the oceanic CO cycle. *Silicibacter pomeroyi*, a member of the marine Roseobacter clade, represents an important group of bacteria that consume CO as an energy source. Genomic analysis of *S. pomeroyi* reveals the presence of two operons encoding aerobic carbon monoxide dehydrogenase, the enzyme regulating oxidation of CO to CO₂. Here we describe the carbon monoxide dehydrogenase large subunit (*coxL*) gene expression of *S. pomeroyi* in response to varying [CO]. Gene expression was examined in *S. pomeroyi* inoculated into seawater media with and without CO. Various primer sets were designed and screened through reverse transcription polymerase chain reaction for examination by gel electrophoresis. Three of the *coxL* gene primer sets targeting different clades of *coxL* were successful in producing bands from extracted RNA of *S. pomeroyi* at the predicted amplicon size. Initial results suggest that expression of *coxL* by *S. pomeroyi* may be constitutive. The *coxL* gene was expressed in all experimental conditions thus far, indicating that CO oxidation may be a continuous process in marine surface waters that is not regulated by ambient CO concentrations.