



Metal resistance mechanisms in hydrothermal microbial communities

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Hydrothermal environments are associated with volcanic active sites, and are known for being highly rich in toxic metals. Several recent studies have revealed a diverse range of microorganisms that can exist in such environments, although the mechanisms by which these organisms tolerate high metal concentrations are poorly understood. The aim of this study is to characterise the metal resistance determinants in bacteria isolated from a shallow hydrothermal embayment, located at Santorini Island (Greece). A collection of 25 aerobic heterotrophic bacteria were isolated from fresh sediment collected from the transition zone of the hydrothermal embayment, using a minimal marine medium solidified with agar. After PCR amplification and sequencing of the *16S rRNA* genes from the isolates, many of the organisms were found to be most closely related to Firmicutes and previously uncultured bacteria. All pure cultures were tested for their tolerance to elevated concentrations of Arsenic (As), Mercury (Hg), Cadmium (Cd), Silver (Ag) and Zinc (Zn). The highest tolerance to metal ions was recorded and amplification of metal resistance determinants performed by PCR using a suite of primers. Although in some examples we were able to detect genes for heavy metal transporter proteins including P-Type ATPases (CadA) and metal reductases (MerA and ArsC), they were absent in many isolates, suggesting the presence of novel metal resistance mechanisms in these organisms. A range of approaches, including proteomics techniques, are now being used to identify novel proteins expressed by these organisms in the presence of toxic metals. Ultimately, results from these studies will contribute to a better understanding of the fate of trace metals in marine sediments, and may provide microbial systems for use during the bioremediation of toxic metals.