

Formation of methyl and hydride metal(loid) compounds of the elements arsenic, selenium, antimony, tellurium and bismuth is widespread in the environment – especially under anaerobic conditions – and lead to a notable modulation of mobility and toxicity of these metal(loid)s (Bentley and Chasteen 2002; Chasteen and Bentley 2003). The capability to form volatile methyl metal(loid)s – and in some cases also volatile hydrides – was shown for numerous methanoarchaea (Meyer et al. 2008). This thesis aimed towards elucidating the cause of the exceptional versatility of methanoarchaea to form metal(loid) methyl and hydride derivatives.

The comparison of inorganic metal(loid) reactants converted into volatile derivatives by cell-free crude extracts prepared from non-induced *Methanosarcina mazei* cultures and by growing cultures of the same strain indicated no inductively elevated expression of enzymes to enable the observed metal(loid) methylation reaction. The *in vitro* assays needed only amendment by two central cofactors of methanogenesis, methylcobalamin (CH<sub>3</sub>Cob(III)) and 2-mercaptoethanesulfonate (HS-CoM), to volatilize the same metal(loid)s by methylation as growing cultures upon metal(loid) addition. Surprisingly, not only formation of volatile permethylated species like in the case of *M. mazei in vivo* but also formation of volatile hydride derivatives of arsenic, selenium and antimony was found.

As both CH<sub>3</sub>Cob(III) and HS-CoM are required for the observed multi metal(loid) methylation and hydride generation by cell-free crude extract but no multi-metal(loid) methylation and hydride generation by these cofactors alone were observed, the additional requirement of an enzyme using both cofactors was indicated. The CH<sub>3</sub>Cob(III)/HS-CoM dependent methyltransferase MtaA as an integral part of the methylotrophic methanogenesis from methanol was thereupon tested whether it is capable to substitute for the cell-free crude extract. Substitution of cell-free crude extracts by MtaA results in the formation of the same volatile metal(loid) derivatives as formed in the presence of the cell-free crude extracts. This finding supports the assumed connection between metal(loid) methylation and methanogenesis and additionally demonstrates that multi metal(loid) methylation and hydride generation can arise from a key reaction of methanogenesis, the CH<sub>3</sub>Cob(III) dependent HS-CoM methylation. The discovered multi-metal(loid) methylation and hydride generation mechanism from *M. mazei* might thus represent a common principal for metal(loid) methylation and in some cases also for hydride generation in all methanoarchaea.

The closer analyses of arsenic methylation and hydride generation by MtaA in the presence of CH<sub>3</sub>Cob(III) and HS-CoM revealed a decisive role of the CH<sub>3</sub>Cob(III) demethylation product Cob(I). Moreover, the data from the performed experiments points towards a non-oxidative methylation mechanism. The role of Cob(I) is probably to supply electrons to enable the methylation and hydride generation reactions.

Analyses of the transcriptional response of *M. mazei* towards bismuth and arsenic were performed to investigate whether the discovered *in vitro* multi-metal(loid) methylation pathway is also feasible for the observed *in vivo* multi metal(loid) methylation. The analyses revealed no expression of genes that hint to an alternative pathway leading to multi-metal(loid) methylation. Even the *arsR/arsM* operon of *M. mazei* which was previously described as being capable to form volatile methyl arsenic derivatives from arsenite (Qin et al. 2006; Yuan et al. 2008) is not inductively more expressed at arsenite and arsenate concentrations at which notable methylation by *M. mazei* was demonstrated previously (Meyer et al. 2008). Instead, genes encoding enzymes participating in cob(I)alamin remethylation and HS-CoM recycling/de-novo syntheses were noticeably up-regulated in the presence of bismuth, thus supporting the assumption that multi-metal(loid) methylation also *in vivo* is directly coupled to methanogenesis. The transcriptional analyses also indicate some general stress responses towards exposure to elevated bismuth and arsenic concentrations and points towards imbalance of the iron metabolism in *M. mazei*.