MauG, a novel diheme protein required for tryptophan tryptophylquinone biosynthesis in methylamine dehydrogenase

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Methylamine dehydrogenase (MADH) is an enzyme containing a quinone cofactor tryptophan tryptophylquinone (TTQ) derived from two Trp residues (βTrp^{57} and βTrp^{108}) within the polypeptide chain (Fig 1). During cofactor formation the two Trp residues become covalently linked, and two carbonyl oxygens are added to the indole ring of βTrp^{57}. Expression of active MADH from *Paracoccus denitrificans* requires four other genes in addition to those that encode the polypeptides of the MADH $\alpha_2\beta_2$ heterotetramer. One of these, *mauG*, has been shown to be involved in TTQ biogenesis. It contains two covalently attached *c*-type hemes, but exhibits unusual properties compared to *c*-type cytochromes and diheme cytochrome *c* peroxidases, with which it shares some sequence similarity. When loss-of-function mutations are introduced into *mauG* or it is knocked out of the wild-type MADH expression system, the majority species is a TTQ biogenesis intermediate containing a monohydroxylated βTrp^{57} (Fig. 1), suggesting this is the natural substrate for MauG. Aerobic and anaerobic *in vitro* studies, in which purified MauG is added to this partially biosynthesized MADH, have shown that MauG, in an oxygen dependent reaction, can complete TTQ biosynthesis. This is consistent with MauG being a monooxygenase.

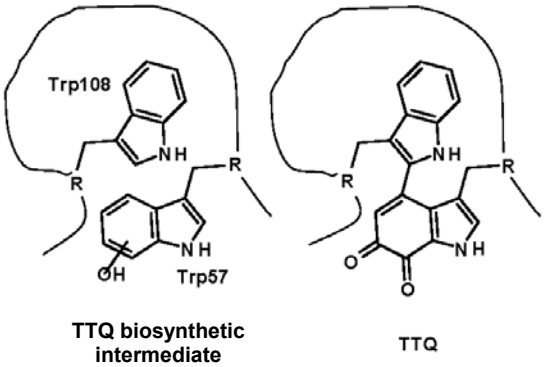

Fig. 1. TTQ and its biosynthetic intermediate formed in the absence of *mauG*.

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