

P007 Function of individual *nap* gene products in NapC-independent nitrate respiration of *Wolinella succinogenes*
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In various proteobacteria including *Escherichia coli*, *Paracoccus pantotrophus* and *Rhodobacter sphaeroides*, electron transport to periplasmic nitrate reductase (NapA) is dependent on NapC, a membrane-bound tetrahaem cytochrome c that catalyses hydroquinone oxidation. In *Wolinella succinogenes*, which grows by respiratory nitrate ammonification with formate or H₂ as electron donor, the sole respiratory nitrate reductase NapA is encoded by the first open reading frame of the *napAGHBFLD* gene cluster that lacks a *napC* gene. Using appropriate mutants, it was shown that the electron transport chain from formate to nitrate is independent of a NapC homologue. In order to determine the alternative pathway of electron transport from menaquinol to NapA in *W. succinogenes*, a genetic system was established that allows non-polar inactivation of each *nap* gene product. The corresponding mutants were examined for their capability of growth by nitrate respiration and their nitrate reductase activity. The amount of NapA was determined by Western blot analysis. The results contribute to a more detailed model of the unusual electron transport chain of *W. succinogenes* nitrate respiration.