

Characterization and expression analysis of the cytochrome bd oxidase operon from *Desulfovibrio gigas*

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Abstract: Although classified as anaerobic, *Desulfovibrio gigas* contains a functional canonical membrane respiratory chain, including a cytochrome bd quinol oxidase as its terminal element. In the present study, we report the identification of the operon *cydAB* encoding the two subunits of cytochrome bd from this bacterium. Two hypothetical promoter regions and sequences resembling transcriptional regulators-binding sites have been identified. Amino acid sequence analysis revealed a high similarity to cytochrome bd from other organisms, presenting the conserved residues typical from these proteins. Reverse transcription polymerase chain reaction (RT-PCR) and Northern blot analysis confirmed the operon transcription. Gene expression was assessed by real-time RT-PCR in cells grown in different media and under exposure to oxygen and nitric oxide. mRNA levels were slightly enhanced in the presence of 150 μ M NO. However, in the presence of 10 μ M NO, a decrease was observed of the steady-state population of *cydAB* mRNA. No considerable effect was observed in the presence of fumarate/sulfate medium, 60 μ M O₂ or 10 μ M NO.

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