

New insights in the formate dehydrogenases family: lessons from *Bacillus subtilis*

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Formate is a readily available substrate in many ecological niches and particularly used by anaerobic or facultative anaerobic prokaryotes for growth or in energy-conserving pathways. The formate dehydrogenases family (Fdh) are the key enzymes involved in these metabolic processes and despite of intense study, a large group of the Fdh's family has remained uncharacterized. This group is largely spread in the Firmicutes phylum, with YjgC from *Bacillus subtilis* being the paradigmatic member as shown by in-depth phylogenetic analysis.

To understand the physiological function of these enzymes in Firmicutes, the YjgC from *B. subtilis* was targeted and studied after purification. Surprisingly, YjgC is co-purified with YjgD, which was discovered to be essential for FDH activity with a turnover rate of 5000 min⁻¹. Noteworthy, none of the FDHs described so far are associated with a YjgD homologue. As such, the YjgCD complex forms a previously uncharacterized FDH. We also demonstrate that insertion of a molybdenum cofactor and several iron-sulfur clusters of the YjgCD complex largely require the activity of the sulfurtransferase FdhD. In its absence, the metal content of YjgCD is reduced by half and the activity by 90%. To conclude, we were able to produce, purify and characterize a new FDH from *B. subtilis*. This paves the way for bringing new insights into firmicutes metabolic or adaptation pathways.