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Investigation of the Central Carbon Metabolism of *Sorangium cellulosum*: Metabolic Network Reconstruction and Quantification of Pathway Fluxes

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Abstract:

In the present work, the metabolic network of primary metabolism of the slow-growing myxobacterium *Sorangium cellulosum* was reconstructed from the annotated genome sequence of the type strain So ce56. During growth on glucose as the carbon source and asparagine as the nitrogen source, So ce56 showed a very low growth rate of 0.23 d^{-1} , equivalent to a doubling time of 3 days. Based on a complete stoichiometric and isotopomer model of central metabolism, ^{13}C metabolic flux analysis was carried out for growth with glucose as carbon and asparagine as nitrogen sources. Normalized to the uptake flux for glucose (100 %), cells recruited glycolysis (51 %) and the pentose phosphate pathway (48 %) as major catabolic pathways. The Entner-Doudoroff pathway and glyoxylate shunt were not active. A high flux through the TCA cycle (118 %) enabled a strong formation of ATP, but cells revealed a rather low yield for biomass. Inspection of fluxes linked to energy metabolism revealed that *S. cellulosum* utilized only 10 % of the ATP formed for growth, whereas 90 % is required for maintenance. This explains the apparent discrepancy between the relatively low biomass yield and the high flux through the energy-delivering TCA cycle. The total flux of NADPH supply (216 %) was higher than reactions for balancing of NADPH. The cells further exhibited a highly active metabolic cycle, interconverting C_3 and C_4 metabolites of glycolysis and the TCA cycle. The present work provides the first insight into fluxes of the primary metabolism of myxobacteria, especially for future investigation on the supply of cofactors, building blocks, and energy in myxobacteria, producing natural compounds of biotechnological interest.

Key-words: Myxobacteria, primary metabolism, flux, NADPH, maintenance