

BIOCHEMICAL CHARACTERIZATION OF MYXOBACTERIAL DEVELOPMENT

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Myxobacteria are a rich source for secondary metabolites with interesting biological activities. Although several compounds have been isolated from different myxobacterial strains, genome analysis of the two model strains *Myxococcus xanthus* DK1622 and *Sorangium cellulosum* So ce56 revealed the potential to produce many more than the known compounds previously described from both strains. Our goal is to isolate these unknown secondary metabolites which might be produced only under very specific growth conditions. Because myxobacteria have probably the most complex life cycle of all prokaryotes with the formation of sometimes highly complex fruiting bodies and the formation of spores within these structures, we are especially interested in the biochemical characterization of this process in order to induce the production of additional compounds. We have already identified secondary metabolites produced specifically during the fruiting body formation. Additionally, changes in the fatty acid and lipid composition have been observed and their role in the developmental process is discussed. Furthermore, we have identified a new pathway to precursors of fatty acids and secondary metabolites which is also induced during development and which branches from the well-known mevalonate-dependent isoprenoid biosynthesis.