Bacterial degradation pathways for the plant sugar sulfoquinovose

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Sulfoquinovose (SQ, 6-deoxy-6-sulfoglucose) is the polar headgroup of the sulfolipid (SQDG) in all higher plants, mosses, ferns and algae, and in most photosynthetic bacteria. SQ represents a significant proportion of the organo-sulfur in nature and, thus, plays an important role in the biogeochemical sulfur cycle. There is evidence for at least two SQ-degradative pathways in bacteria, but no enzymic reaction or gene in any pathway has been defined, though a sulfoglycolytic pathway has been proposed.

We found that *Escherichia coli* K-12, the most widely-studied prokaryotic model organism, is able to utilize SQ for growth. SQ is catabolized through "sulfoglycolysis", involving four newly discovered reactions that we established using purified, heterologously expressed enzymes: 6-deoxy-6-sulfoglucose (SQ) isomerase, 6-deoxy-6-sulfofructose (SF) kinase, 6-deoxy-6-sulfofructose-1-phosphate (SFP) aldolase, and 3-sulfolactaldehyde (SLA) reductase. The pathway yields dihydroxyacetone phosphate (DHAP), which powers energy conservation and growth of *E. coli*, and the sulfonate product 2,3-dihydroxypropane-1-sulfonate (DHPS), which is excreted. The corresponding SQ-gene cluster is found in >90% of the known *E. coli* genomes, and in a wide range of other *Enterobacteriaceae*, e.g., *Salmonella*, *Klebsiella* and *Pantoea* species. Hence, we presume that sulfoglycolysis plays a significant role in bacteria in the alimentary tract of all herbivores and omnivores, and in human and plant pathogens.

We are currently revealing a second degradative pathway for SQ in a typical soil bacterium, *Pseudomonas putida* SQ1. This organism excretes 3-sulfolactate (SL) instead of DHPS during growth with SQ, and the present enzymic, proteomic and analytical-chemical data indicate that the pathway may proceed in analogy to the Entner-Doudoroff pathway for glucose-6-phosphate in *Pseudomonas* species, through four novel enzymes: NAD^+-dependent SQ-dehydrogenase, 6-deoxy-6-sulfogluconolactonase (SGL), 6-deoxy-6-sulfogluconate dehydratase (SG), 2-keto-3,6-dideoxy-6-sulfogluconate aldolase (KDSG), and sulfolactaldehyde (SLA) dehydrogenase.

The excreted sulfolactate and DHPS can be mineralized by other environmental bacteria. Hence, a complete degradation of SQ can be accomplished by bacterial communities.