EXPLORING NEW PATHWAYS OF SULFOQUINOVOSE BIODEGRADATION

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Sulfoquinovose (SQ), a sulfosugar that forms polar head group of plant sulfolipid SQDG, plays a critical role in the global sulfur cycle with an estimated 10 billion tonnes production per year [1]. We present a desulfonation pathway in *Agrobacterium tumefaciens* that can grow solely on SQDG as carbon source, through complete SQ catabolism to glucose and sulfite [2]. This pathway involves a 'gateway' GH31 glycoside hydrolase [3] and a central two-component FMN-dependent SQ monooxygenase that recognize the distinguishing 'sulfonate' group in SQ and facilitate the direct cleavage of C–S bond, releasing inorganic sulfite and glucose, allowing direct entry into glycolysis (**Figure 1**). Structural and biochemical analyses provide insights into enzyme-substrate interactions and specific sulfonate-binding motifs. Our recent work also uncovered the founding members of new GH188 family in the CAZy database that utilize alternative mechanisms to hyrolyse SQ from the sulfolipids [4]. Strikingly different to GH31 SQases, these NAD^+-dependent SQases from GH188 CAZy family operate through transient oxidation at C3. We will present bioinformatic data that show that this pathway is widespread among alpha- and beta-proteobacteria, particularly within the Rhizobiales order and marine Roseobacter clades, suggesting a broad ecological significance of SQ biology.

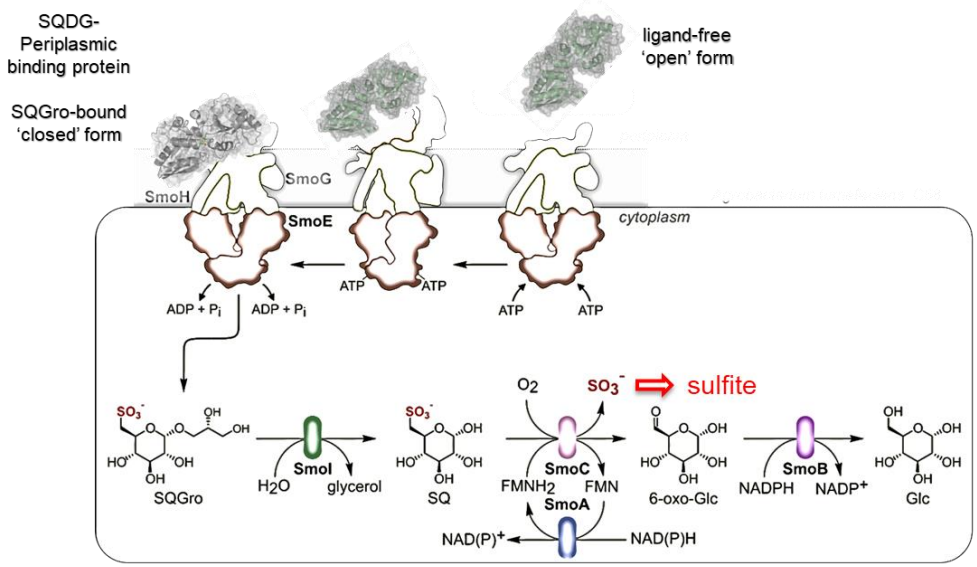

Figure 1. Schematic summary of SMO pathway in A. tumefaciens. SQGro, a metabolite of SQDG, is imported into the cell and hydrolysed to liberate SQ, which is further metabolized to release sulfite and glucose.

References:
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