

Publication

A deficiency in arabinogalactan biosynthesis affects Corynebacterium glutamicum mycolate outer membrane stability

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Corynebacterineae is a specific suborder of Gram-positive bacteria that includes Mycobacterium tuberculosis and Corynebacterium glutamicum. The ultrastructure of the cell envelope is very atypical. It is composed of a heteropolymer of peptidoglycan and arabinogalactan (AG) covalently associated to an outer membrane. Five arabinosyltransferases are involved in the biosynthesis of AG in C. glutamicum. AftB catalyzes the transfer of Araf (arabinofuranosyl) onto the arabinan domain of the arabinogalactan to form terminal beta(1 -> 2)-linked Araf residues. Here we show that Delta aftB cells lack half of the arabinogalactan mycoloylation sites but are still able to assemble an outer membrane. In addition, we show that a Delta aftB mutant grown on a rich medium has a perturbed cell envelope and sheds a significant amount of membrane fragments in the external culture medium. These fragments contain mono- and dimycolate of trehalose and PorA/H, the major porin of C. glutamicum, but lack conventional phospholipids that typify the plasma membrane, suggesting that they are derived from the atypical mycolate outer membrane of the cell envelope. This is the first report of outer membrane destabilization in the Corynebacterineae, and it suggests that a strong interaction between the mycolate outer membrane and the underlying polymer is essential for cell envelope integrity. The presence of outer membrane-derived fragments (OMFs) in the external medium of the Delta aftB mutant is also a very promising tool for outer membrane characterization. Indeed, fingerprint analysis of major OMF-associated proteins has already led to the identification of 3 associated mycoloyltransferases and an unknown protein with a C-terminal hydrophobic anchoring domain reminiscent of that found for the S-layer protein PS2 of C. glutamicum.

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