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THE CELL ENVELOPE PROTEOME OF *BIFIDOBACTERIUM LONGUM* IN AN IN VITRO BILE ENVIRONMENT

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Host-bacteria interactions are often mediated via surface-associated proteins. The identification of these proteins is an important goal of bacterial proteomics. To address how bile can influence the cell-envelope proteome of *Bifidobacterium longum* biotype *longum* NCIMB8809, we analysed its membrane protein fraction using stable isotope labelling of amino acids in cell culture (SILAC). We were able to identify 141 proteins in the membrane fraction, including a large percentage of the theoretical transporters of this species. Moreover, the envelope-associated soluble fraction was analysed using different subfractionation techniques and differential in-gel fluorescence electrophoresis (DIGE). This approach identified 128 different proteins. Some of them were well known cell wall proteins, but others were highly conserved cytoplasmatic proteins likely displaying a "moonlighting" function. On the other hand, we were able to identify 11 proteins in the membrane fraction and 6 proteins in the envelope-associated soluble fraction whose concentration varied in the presence of bile. Bile promoted changes in the levels of proteins with important biological functions, such as some ribosomal proteins and the enolase. Also, oligopeptide binding proteins were accumulated on the cell surface, which was reflected in a different tripeptide transport rate in the cells grown with bile. The data reported here will provide the first cell-envelope proteome map for *B. longum*, and might contribute to understanding the bile tolerance of these bacteria.