Experimental methods

Cultures of the bacterium, *Eggerthella lenta*, were grown on unsupplemented brain heart infusion (BHI) media, ferulate-supplemented media, and itaconate-supplemented media, as described elsewhere.[1] Samples of trypsin-digested proteins were prepared using a modified version of the filter-aided sample preparation procedure.[2] Samples of trypsin-digested proteins were analyzed using a Synapt G2-Si ion mobility mass spectrometer that was equipped with a nanoelectrospray ionization source (Waters, Milford, Massachusetts). The mass spectrometer was connected in line with an Acquity M-class ultra-performance liquid chromatography system that was equipped with trapping (Symmetry C18, inner diameter: 180 µm, length: 20 mm, particle size: 5 µm) and analytical (HSS T3, inner diameter: 75 µm, length: 250 mm, particle size: 1.8 µm) columns (Waters). The mobile phase solvents were water and acetonitrile, both of which contained 0.1% formic acid (volume/volume). Data-independent, ion mobility-enabled, high definition mass spectra and tandem mass spectra were acquired in the positive ion mode.[3-7] Samples were run in biological duplicate. Data acquisition was controlled using MassLynx software (version 4.1, Waters). Data were processed using Progenesis QI for Proteomics software (version 4.2, Waters Nonlinear Dynamics). Data were searched against the *Eggerthella lenta* protein database to identify peptides using the following parameters: digest reagent: trypsin; maximum number of missed cleavages: two; fixed post-translational modification: carbamidomethyl cysteine; variable post-translational modification: methionine oxidation; target false discovery rate: less than four percent, number of fragment ions per peptide: three or more; number of fragment ions per protein: seven or more; number of peptides per protein: one or more.[8] The resulting protein and peptide ion lists were exported from Progenesis QI for Proteomics software in comma-separated values (csv) format.

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