

sporulation. Some sulfate reducing bacteria have never been tested for syntrophic growth, but as all crucial domains were found in their genomes, it is possible that these are able to grow in syntrophic association with methanogens. In addition, profiling domains involved in electron transfer mechanisms revealed the important role of the Rnf-complex and the formate transporter in syntrophy, and indicates that DUF224 may have a role in electron transfer in bacteria that show syntrophic growth.

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A genomic view on syntrophic versus non-syntrophic lifestyle of anaerobic fatty acid-degrading bacteria

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In sulfate-reducing and methanogenic environments complex biopolymers are degraded by fermentative micro-organisms that produce hydrogen, carbon dioxide and short chain fatty acids. Degradation of short chain fatty acids can be coupled to methanogenesis or to sulfate reduction. We applied a genomic approach to understand why some bacteria are able to grow in syntrophy with methanogens and others are not. Bacterial strains were selected based on genome availability and upon their ability to grow on short chain fatty acids alone or in syntrophic association with methanogens. Systematic functional domain profiling allowed us to shed light on this fundamental and ecologically important question. Extra-cytoplasmic formate dehydrogenases, including their maturation protein are a typical difference between syntrophic and non-syntrophic butyrate and propionate degraders. Furthermore, two domains with a currently unknown function seem to be associated with the ability of syntrophic growth. One is putatively involved in capsule or biofilm production and a second in cell division, shape-determination or