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Unravelling the molecular basis of metabolic interactions in synthetic consortia dedicated for bio-H₂ production.

Nowadays, it is well established that microbes live in the form of complex communities that sense their environment, communicate between members and exchange biological materials. This microbial cooperation often allows new function or better performance of the whole community not predictable via genome analysis. Understanding the metabolic interdependence in microbial communities becomes an important challenge to decipher the microbial behavior at the community scale, but also to unlock alternative pathways as for the biotechnological use. Based on the model of microbial biomass degradation which in Nature involved various anaerobic bacteria that sequentially degrade complex organic matter into H₂, CO₂, CO or CH₄, previous research in the group led to the construction of simplified models (also called co-culture) [1] [2]. Two synthetic co-cultures composed of *Desulfovibrio vulgaris* (*DvH*) and *Clostridium acetobutylicum* (or *Escherichia coli*) are used to investigate the metabolic interdependence between microbes. In both co-cultures, under nutritional stress conditions, cell-to-cell interactions were shown to occur between bacteria allowing bidirectional exchange of biological materials. These interactions are essential for *D. vulgaris* growth. Interestingly, this also led to increase bio-hydrogen production. The establishment of the physical interactions is crucial and depends on the AI-2 quorum sensing (QS) molecules produced by *D. vulgaris*' partners. To get insight the different mechanisms as the communication, the physical interactions, the cross feeding (allowing *D. vulgaris* to resume growing under starvation) global approaches as transcriptomic, proteomic, and targeted metabolite analysis are in progress. Here we show the breakthrough on the communication mechanism achieved by bioinformatics approach.

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