

Modeling an Electrosynthetic Microbiome

KBase analysis explains how a 13-species electrosynthetic community can fix carbon dioxide and scrub oxygen.

The Science

Microbial electrosynthesis is a renewable energy and chemical production platform that employs communities of microbes to generate valuable products (such as biofuels or commodity chemicals) from carbon dioxide and electrons from the cathode. In this [study](#), researchers applied KBase annotation and metabolic modeling pipelines to analyze a 13-species electrosynthetic community and discovered that *Acetobacterium* is the primary carbon fixer for the community, excreting large amounts of acetate, which serves as the main carbon source for the rest of the community.

The Impact

Microbial electrosynthesis technology has potential for the renewable generation of biofuels and industrially important commodity chemicals using excess electricity. The molecular discoveries and metabolic modeling techniques used in this research could serve as a foundation for designing electrosynthetic microbial communities to produce specific chemicals. The analysis showed that electrosynthetic microbiomes could also potentially provide a valuable ecosystem service by scrubbing oxygen, as well as cheaply and sustainably synthesizing important chemical products such as biofuels.

Summary

This study utilized KBase's annotation and metabolic modeling capabilities to characterize the genomic features of a high-performing microbial electrosynthesis system that can generate commodity chemicals from carbon dioxide. These metagenomes were used to construct a metabolic flux model of the most abundant members of the microbial community, and transcript expression data were used to validate these models. Metabolic models of the predominant community members revealed that *Acetobacterium* is the primary carbon fixer, excreting large amounts of acetate which serves as the main carbon source for the rest of the community (see Figure 1). The results demonstrated that a diverse set of microorganisms can be active in limited niche space with carbon dioxide as the only carbon source and the electrode as the only electron donor.

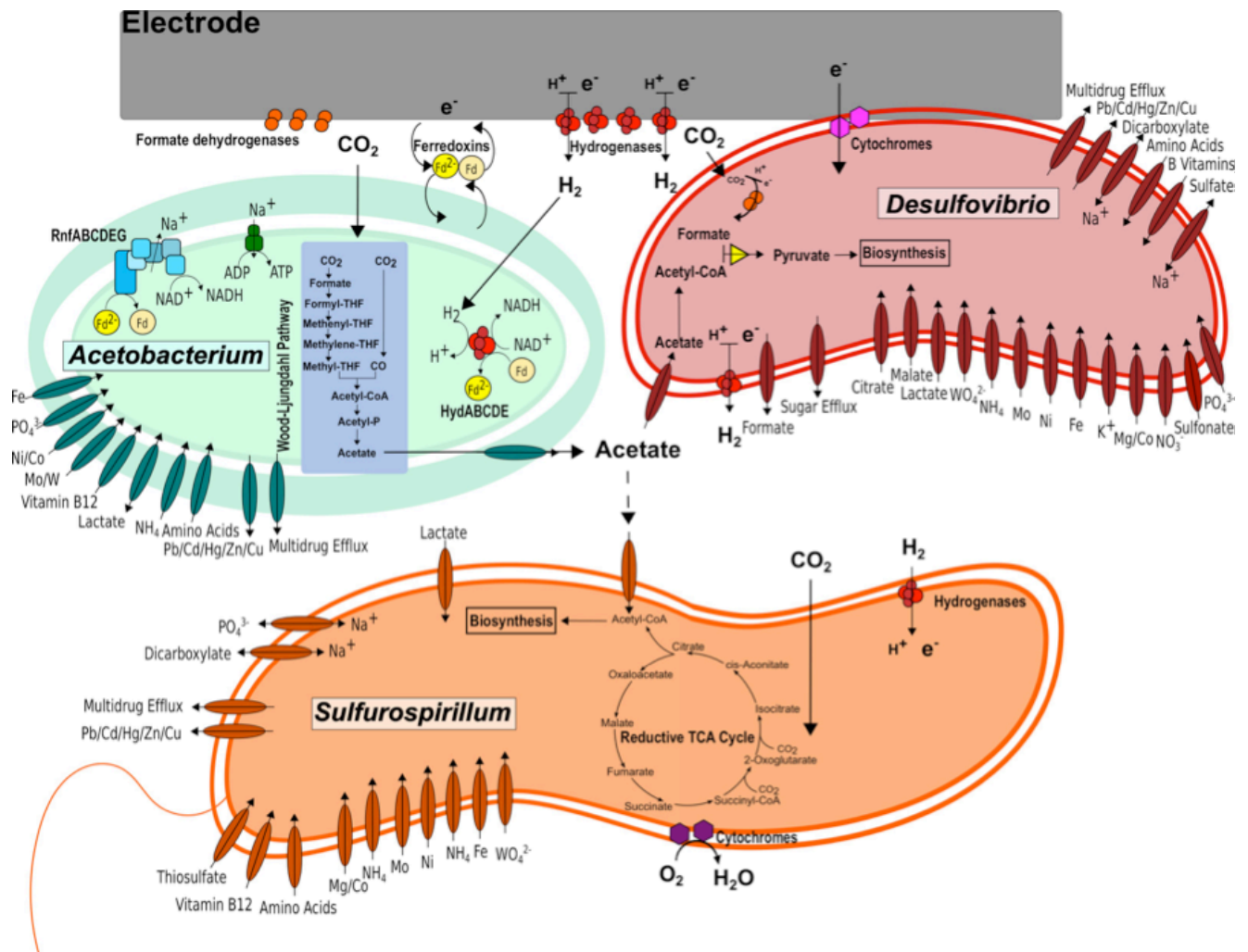


Figure 1: Hypothetical model of key metabolic activities and interactions among dominant members of the electrosynthetic microbial community.

To perform this analysis, the researchers assembled 13 genomes from a dynamic electroacetogenic culture and mapped their transcriptional activity in a range of conditions. First, the researchers selected the three most abundant members from the 13-species community based on the relative abundance data (*Acetobacterium*, *Sulfurospirillum* and *Desulfovibrio*) and imported their genomes into KBase, followed by metabolic model reconstruction, gapfilling and metabolic flux analysis of each model. First, the assembled genome sequences for each species in the microbial electrosynthesis system were functionally annotated using RAST. The ModelSEED resource was applied to construct a draft genome-scale metabolic model for each annotated genome. Once the initial draft models were constructed, all the models were manually curated based on the available phenotype data. Gaps that appeared in the metabolic pathways of these models, due to missing or inconsistent annotations, were filled by prioritizing reactions associated with highly expressed pathways. Highly expressed pathways were identified based on normalized transcriptome data. These improved models were then integrated with transcriptome data to favor flux through highly expressed metabolic pathways. Flux balance analysis (FBA) was applied to the improved models to predict flux profiles for understanding potential key carbon sources, electron donors, electron acceptors and overall consumption and production of nutrients. The researchers used the "[Compare Flux with Expression](#)" app in KBase to assess the agreement of the model predictions with reactions based on differentially expressed genes (see Figure 2).

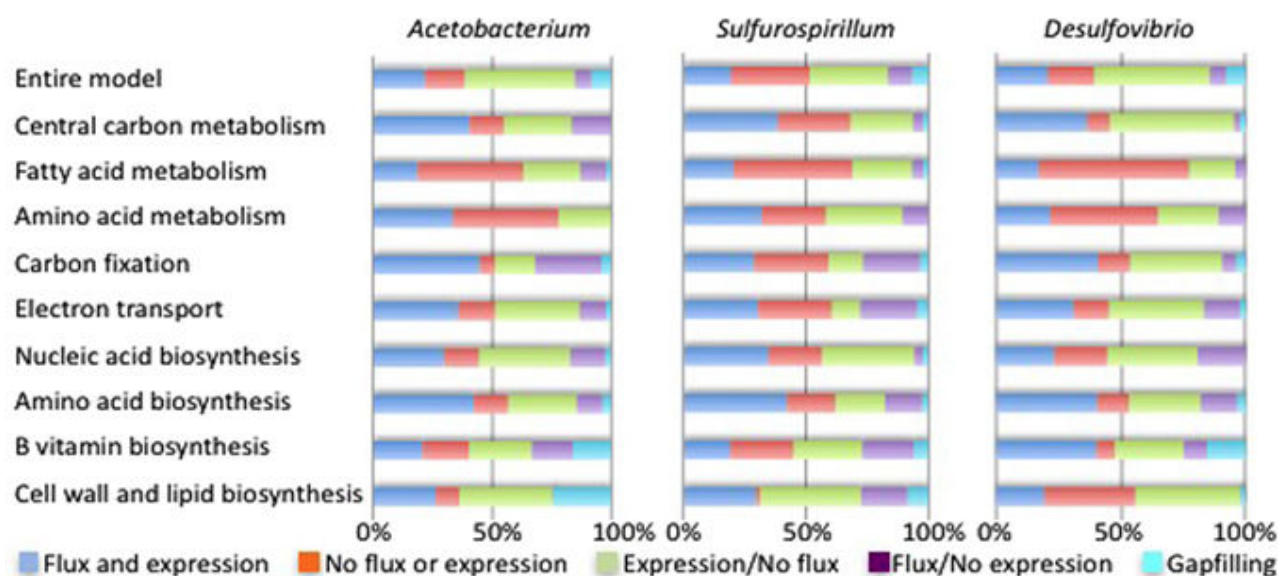


Figure 2: *Pathway flux and model agreement with expression data.* The degree of agreement between the model-based flux predictions and expression data for each of the three metabolic models is shown, both for the entire models and broken down by categories of metabolism. In the graph, reactions are divided into five categories based on their flux and the expression of their associated genes: (i) reactions that are active and associated with at least one expressed gene (dark blue); (ii) reactions that are inactive and associated only with unexpressed genes (dark red); (iii) reactions that are inactive and associated with one or more expressed genes (green); (iv) reactions that are active and associated only with unexpressed genes (purple); and (v) gapfilled reactions associated with no genes. The dark blue and dark red categories indicate agreement between the models and expression data; purple and green categories indicate disagreement.

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Publication

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<http://kbase.bmetrack.com/c/l?u=7449693&e=BC7C5A&c=8D590&t=0&l=36BF4D59&email=RFCfKMxZqhFz1yBnWE2kzciHg%2FvbFy1&seq=1>

Related Links

The analysis workflow for this study, including trophic interactions predicted between the three species based on metabolic model analyses, can be found in <https://narrative.kbase.us/narrative/ws.15248.obj.1>.