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Single-cell analysis reveals gene-expression heterogeneity in microbial syntrophic dual-culture

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Microbial syntrophic metabolism has been well accepted as the heart of how methanogenic and other anaerobic microbial communities function. In this work, we applied a single-cell RT-qPCR approach to reveal gene-expression heterogeneity in a model syntrophic system of *Desulfovibrio vulgaris* and *Methanosarcina barkeri*, as compared with the *D. vulgaris* monoculture. Using the optimized primers and single-cell analytical protocol, we quantitatively determine gene-expression levels of 6 selected target genes in each of the 120 single cells of *D. vulgaris* isolated from its monoculture and dual-culture with *M. barkeri*. The results demonstrated very significant cell-to-cell gene-expression heterogeneity for the selected *D. vulgaris* genes in both the monoculture and the syntrophic dual-culture. Interestingly, no obvious increase in gene-expression heterogeneity for the selected genes was observed for the syntrophic dual-culture when compared with its monoculture, although the community structure and cell-cell interactions have become more complicated in the syntrophic dual-culture. In addition, the single-cell RT-qPCR analysis also provided further evidence that the gene cluster (DVU0148-DVU0150) may be involved syntrophic metabolism between *D. vulgaris* and *M. barkeri*. Finally, the study validated that single-cell RT-qPCR analysis could be a valuable tool in deciphering gene functions and metabolism in mixed-cultured microbial communities.

Biography

Weiwen Zhang is a Professor of Microbiology and Biochemical Engineering, Head of Laboratory of Synthetic Microbiology in the School of Chemical Engineering and Technology of Tianjin University in China. Prior to joining Tianjin University, he was a Faculty with Biodesign Institute and the School of Life Science of Arizona State University for 2007-2011, and a Senior Scientist at Microbiology Department with the Pacific Northwest National Laboratory of the U.S. Department of Energy (DOE) for 2002-2007. He has broad research experience in microbial genetics, physiology and synthetic biology, has authored more than 130 peer-reviewed scientific papers. His recent research focuses on synthetic biology of photosynthetic microorganisms and analysis of microbial consortia.

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