

Who is doing what in microbial communities?

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Bacterial life is determined by environmental factors and other bacteria with whom they live in more or less complex communities. Thus, the exosystemic function of communities depends on the interaction within the community. The interactions range from competition over mutualism to synergism, and the analysis of who is doing what is key to untangling the cooperation.

The intestinal microbiome is an example of a highly complex microbial community, which is shaped by host-derived factors and cooperation within the community. I will present insights into how host-derived factors like bile acids modulate the community and how metabolic interactions determine the overall metabolic capacity of the community.

For this purpose, we established continuous anaerobic cultivation of complex and simplified cultures and a wide set of metabolic analyses and meta-proteome linked protein stable isotope probing (Protein-SIP). The combination of cultivation and meta-omics allows insights into the functionalities of microbial communities, not only from the intestine but from other environments as well.