In vitro co-cultures of human gut bacterial species as predicted from co-occurrence network analysis

Network analysis of large metagenomic datasets generated by current sequencing technologies can reveal significant co-occurrence patterns between microbial species of a biological community. These patterns can be analyzed in terms of pairwise combinations between all species comprising a community. Here, we construct a co-occurrence network for abundant microbial species encompassing the three dominant phyla found in human gut. This was followed by an in vitro evaluation of the predicted microbe-microbe co-occurrences, where we chose species pairs Bifidobacterium adolescentis and Bacteroides thetaiotaomicron, as well as Faecalibacterium prausnitzii and Roseburia inulinivorans as model organisms for our study. We then delineate the outcome of the co-cultures when equal distributions of resources were provided. The growth behavior of the co-culture was found to be dependent on the types of microbial species present, their specific metabolic activities, and resulting changes in the culture environment. Through this reductionist approach and using novel in vitro combinations of microbial species under anaerobic conditions, the results of this work will aid in the understanding and design of synthetic community formulations.