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Emergent behavior in a synthetic gut community

Due to its complexity and the impact of the human host, it is hard to obtain a mechanistic understanding of the gut microbial community from sequencing data alone. Synthetic communities are an excellent tool to complement in vivo studies. Their dynamics can be accurately monitored while exerting a degree of control that is impossible to achieve in vivo. Here, I will present an in vitro study of a synthetic microbial community consisting of three human gut bacterial strains. We monitored each community member growing in isolation and in co-culture and developed a kinetic model to describe their dynamics. The experiments validate cross-feeding interactions and highlight the special role of *Blautia hydrogenotrophica* as an interaction partner. When parameterized on mono- and bi-culture data, our model describes well the observed community dynamics, but fails to predict community dynamics from mono-cultures alone. RNA-seq applied to mono- and tri-culture samples confirmed a change in behavior. In conclusion, we showed that gut bacteria respond to their interaction partners, giving rise to emergent behavior.

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