

ENIGMA: New technologies for the large-scale screening of microbial interactions

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Project Goals: ENIGMA -Ecosystems and Networks Integrated with Genes and Molecular Assemblies use a systems biology approach to understand the interaction between microbial communities and the ecosystems that they inhabit. To link genetic, ecological, and environmental factors to the structure and function of microbial communities, ENIGMA integrates and develops laboratory, field, and computational methods.

Abstract: Environmental microbial community is normally composed of thousands of species and affected by a wide variety of biotic and abiotic factors, which make untangling all interactions an herculean task. A frequently used strategy to reduce the complexity is, similar like untangling a ball of yarn, to start at a single point, a single interaction between two microbes. Although this can be very insightful, the implications of this single interaction on the total community may be impossible to predict. A reversed approach, where a large number of microbes are screened on their interactions would be a better way to identify possible relationships. Here we present two novel platforms for the large-scale screening of microbial interactions. In one method, acoustic printing is used to create paired colonies in agar filled multi-well plates, which allows to make visual observations of interactions such as changes in colony size, shape, texture and pigmentation. Metabolite usage and exchange during the interactions are screened by mass spectrometry. In another method, taking advantages of droplet generation rate of 20 million per hour, the microbes are coupled into small drops, enriched, barcoded, and eventually sequenced in one pool. The composition, abundance, and cell interactions are revealed through the high throughput sequencing. Both new techniques allow us obtain thousands to millions interactions in days, which will make mapping out microbial community structure possible.