

## High Throughput Isolation and Microbial Community Enrichment Platforms

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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.**

Generating models that can accurately predict how environmental perturbations will affect the microbial communities and their natural ecosystems will require a representative set of characterized microbial strains found in the field. To that end, we have developed microbial isolation strategies to quickly generate and catalogue thousands of isolates using a variety of standard growth media and a scalable characterization pipeline including high quality genome sequences, growth data over a standard set of conditions, and accompanying exometabolomics. To date, this approach has generated > 1000 isolates, from commonly isolated genera (i.e. *Pseudomonas*, *Cupriavidus*), to isolates assigned to a genus that is new to our ENIGMA strain collection (i.e. *Zoogloea*, *Xylophilus*, *Cellovibrio*). The commonly cultured genera, which in some cases are abundant at the site, can be used to pinpoint the genomic signatures that account for differences in their growth profiles, while the rare members provide a valuable strain resource to discover novel genes and pathways. In parallel, we are also using microbial enrichments, that expand the spectrum of growth conditions tested and microbial membership, to increase the culturable microbial diversity in the lab. This enrichment dataset provides a wealth of information about the microbial growth parameters ideal for capturing microbes important in the field, while at the same time generating the microbial community materials that can be used for generating isolates using the high throughput pipeline. In addition, the microbial enrichments-when done at the scale we are doing here- can provide insight into microbial interactions, the conditions that drive those interactions, and the raw materials to start dissecting those interactions. All of this work, complements the targeted approach of other ENIGMA researchers and provides them the bandwidth to go after the very difficult and slow growing microbes that are important at the field site. With the successful development of these platforms, we have begun the routine processing of isolates and enrichments adding to the shared ENIGMA resource of a diverse and tractable microbial collection.

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