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Microbial interaction networks in soil and in silico

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Soil harbors a huge number of microbial species interacting through secretion of antibiotics and other chemicals. What patterns of species interactions allow for this astonishing biodiversity to be sustained, and how do these interactions evolve? I used a combined experimental-theoretical approach to tackle these questions. Focusing on bacteria from the genus *Streptomyces*, known for their diverse secondary metabolism, I isolated 64 natural strains from several individual grains of soil and systematically measured all pairwise interactions among them. Quantitative measurements on such scale were enabled by a novel experimental platform based on robotic handling, a custom scanner array and automatic image analysis. This unique platform allowed the simultaneous capturing of $\sim 15,000$ time-lapse movies of growing colonies of each isolate on media conditioned by each of the other isolates. The data revealed a rich network of strong negative (inhibitory) and positive (stimulating) interactions. Analysis of this network and the phylogeny of the isolates, together with mathematical modeling of microbial communities, revealed that: 1) The network of interactions has three special properties: “balance”, “bi-modality” and “reciprocity”; 2) The interaction network is fast evolving; 3) Mathematical modeling explains how rapid evolution can give rise to the three special properties through an interplay between ecology and evolution. These properties are not a result of stable co-existence, but rather of continuous evolutionary turnover of strains with different production and resistance capabilities.