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INSTITUT DE BIOLOGIE INTÉGRATIVE ET DES SYSTÈMES
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CONFÉRENCE

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Quantifying the coupling of ecological and evolutionary dynamics in microbiomes

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Pavillon Charles-Eugène Marchand, salle Hydro-Québec (1210)

Abstract:

A microbiome's composition, stability, and response to perturbations are influenced by the community interaction matrix that is commonly assayed by pair-wise species competition. In their natural environment however, microbes concurrently experience multiple species, face conditions that may be difficult to mimic *in vitro*, and have members that are impractical to isolate. Due to the overlap of evolutionary and ecological timescales, the community interaction matrix is also influenced by intra-species diversity, although how and to what extent this occurs remains poorly understood.

We recently developed a general approach called Dynamic Covariance Mapping (DCM) to estimate the interaction matrix of a multispecies microbiome community in its natural environment from abundance time-series data. Together with intra-species high-resolution lineage tracking via chromosomal barcoding, we quantified the inter- and intra-species community interaction matrix during *E. coli* colonization of the mouse gut microbiome with increasing complexity: germ-free, antibiotic-perturbed, and innate microbiota. With DCM, we differentiated broadly three temporal phases of invasion: 1) initial loss of community stability as *E. coli* enters; 2) recolonization of some gut bacteria; and 3) recovery of stability with *E. coli* clones coexisting with resident bacteria in a quasi-steady state. These phases were influenced by specific interactions between *E. coli* sub-lineages with other species in the community. These results highlight the transient nature and time-dependence of community interaction networks in microbiomes, driven by the persistent coupling of ecological and evolutionary dynamics.

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