Proteome allocation and the evolution of metabolic cross-feeding

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Résumé

In a common instance of metabolic cross-feeding (MCF), an organism incompletely metabolizes nutrients and releases metabolites that are used by another to produce energy or building blocks. Why would the former waste edible food, and why does this preferentially occur at specific locations in a metabolic pathway have challenged evolutionary theory for decades. To address these questions, we combine adaptive dynamics with an explicit model of cell metabolism, including enzyme-driven catalysis of metabolic reactions and the cellular constraints acting on the proteome that may incur a cost to expressing all enzymes along a pathway. After pointing out that cells should in principle prioritize upstream reactions when metabolites are restrained inside the cell, we show that the occurrence of permeability-driven MCF is rare and requires that an intermediate metabolite be extremely diffusive. Indeed, only at very high levels of membrane permeability (consistent with those of acetate and glycerol, for instance) and under distinctive sets of parameters should the population diversify and MCF evolve. These results help understand the origins of simple microbial communities, such as those that readily evolve in short-term evolutionary experiments, and may later be extended to investigate how evolution has progressively built up today's extremely diverse ecosystems.

Mots-Clés: metabolism, specialization, division of labor, gene expression, proteome optimization

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