LETTER

The effects of niche construction in microbial metabolism on macroevolution

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ABSTRACT

Microorganisms exhibit an amazing variety of metabolic processes. Understanding how macro evolutionary processes like innovation and diversification operate in the microbial world is necessary to comprehend the origin of this variety. The regulation of microbial resource usage by metabolic networks can occur via a variety of processes, such as horizontal gene transfers or the de novo evolution of enzymes and pathways. Environmental variables, selective pressures, and limitations imposed by the genetic design of metabolic networks all work together to control this process. A significant part of microbial innovation and diversification may also be attributed to the process of niche construction, in which organisms actively alter their own and one another's habitats and selective pressures. However, the fundamental mechanisms by which niche formation affects the patterns of microbial macroevolution are still completely unknown. Here, we describe a number of novel theories and lines of research and offer metabolic modelling techniques that may enable us to investigate extensive empirical Genotype-Phenotype-environment (G-P) spaces and analyse the macro-evolutionary consequences of niche formation. This brief essay should encourage greater systematic and quantitative characterisation of macro evolutionary patterns and processes in microbial metabolism, in our opinion.

Key Words: *Metabolic; Macro Evolutionary; Ecological Interactions; Escherichia coli; phenotypic evolution*

INTRODUCTION

On earth, prokaryotes have by far the most variety of metabolisms. Understanding the processes by which such diversity emerges is essential for comprehending the emergence of sophisticated life as well as the composition and operation of contemporary microbial ecosystems.

Numerous instances from the history of life on Earth support the theory that the process of niche creation may be crucial to diversity. One of these is the early emergence of autotrophic metabolism, which fundamentally altered the biosphere by producing intricate, energetically dense carbon molecules and releasing oxygen into the atmosphere, opening up new ecological possibilities.

There are numerous further examples in nature, ranging from the first ones outlined by Darwin in his work on earthworms to diatoms or beavers, where niche creation has been seen to play a significant role. Although theoretical research has predicted a variety of ways that niche creation may affect evolutionary outcomes, the majority of these hypotheses have not yet been empirically validated. From a general principles perspective, there are still many unanswered questions: What are the guiding concepts and methods for niche construction? How does it evolve? How does it relate to the structure of metabolic genotypes, the external environment, or metabolic strategies? How do macro-evolutionary processes like innovation and diversity interact with niche construction?

Both theoretically and practically, the short-term, micro-evolutionary effects of niche building have been thoroughly defined. Eco-evolutionary dynamics, which result from the fact that created habitats (and their impacts on selection pressures) depend, within certain bounds, on the abundance of the creatures producing them, are the most archetypal of such effects. As a result, frequency-dependent selection and density-dependent selection, which take place over similar periods, become dynamically coupled. Because single genes or mutations frequently dictate the characteristics of constructed environments in microorganisms, niche creation might connect the fate of particular alleles to the present-moment makeup of a population. A more complex phenomenon, such as the coexistence of three or more species through ecological interactions, can be produced when multiple species are involved. Unlike microevolution, the macro-evolutionary effects of niche formation, such as microbial innovation and diversity, have received less attention. The emergence of aerobic citrate consumption in Escheric-

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-hia coli during the Long Term Evolution Experiment is a rare experimental illustration of a possibly macro evolutionary event. According to recent research, the two primary mutations that caused this innovation—the aerobic expression of dctA and citt were closely related to an eco-evolutionary interaction mediated by the release of metabolites into the environment. Additionally, one of the major potentiating mutations that helped "prepare" the genetic background for the evolution of citrate use probably fixed an artificial niche because of its advantageous influence on acetate. These findings imply that niche creation may be crucial to the diversification of microbial metabolism. They demonstrate the potential of microbial research to shed light on the genetic underpinnings and mechanisms of macro evolutionary trends.

However, experiments also have significant restrictions. Only one of the 12 *E. coli* evolution lines in the LTEE, although it took about 30,000 generations, was able to utilise citrate. This demonstrates how historically conditioned and consequently uncommon combinations of mutations continue to be necessary for innovation and the discovery of undiscovered ecological prospects. In line with this, even for some of the fastest-evolving creatures on Earth, "blind" evolutionary searches of genotype space nevertheless call for timescales that are close to the boundaries of what is empirically possible.

Genome-scale metabolic models, which provide us the opportunity to quickly examine broad areas of metabolic genotype-environment space, represent a possible alternative. These models may very closely mimic the development of actual animals in silico using metabolic networks derived from the genome, giving us mechanistic understanding of how physiologically realistic Genotype-Phenotype (G-P)-fitness maps work. Genome-scale metabolic models have already been effectively used, for example, to investigate fascinating origin-of-life hypotheses and acquire understanding of long-term phenotypic evolution in bacteria.