Towards an Evolutionary Ecology of Bacterial Mobile Genetic Elements

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Abstract

Antimicrobial resistance represents a threat to our healthcare systems. In bacteria, resistance genes are often carried by mobile genetic elements (MGEs). These are genetic entities capable of horizontal transfer between host cells, and which have their own evolutionary trajectory independent of those of their bacterial host. MGEs are highly diverse in terms of horizontal transmission mechanisms (conjugation, transduction, natural transformation) and horizontal transfer rate. Additionally, they differ in their vertical transmission efficiency and genetic content. On the basis of these properties, some MGEs may appear exclusively parasitic, while others may be mutualistic (e.g. by conferring multidrug resistance on their host bacteria). While conventional genomics tools can describe MGEs, the eco-evolutionary mechanisms underlying their diversity remain elusive.

Using a theoretical model, we propose a paradigm shift by mobilizing the concepts and tools of ecology to understand the eco-evolutionary dynamics of MGEs and the maintenance of their diversity. MGEs are then defined as species competing for bacterial resources under environmental stress. All MGEs then form a community that circulates within a bacterial (meta-)population. In our model, the ecological niche of MGE species is defined by the combination of two traits: their rate of horizontal transfer and their content in resistance genes, each of which incurs a cost in terms of replication to their bacterial hosts.

First, we show that competition between MGEs is the cause of strong erosion of diversity. Furthermore, the most competitive MGE depends on the stress regime. Finally, when we model a meta-population of bacteria, subjected to different stress regimes, we see the emergence at the global level of the stable coexistence of different clusters of MGEs. This result is in line with the theory of emergent neutrality, which unifies ecological niche theory and neutral biodiversity theory.

Finally, this modeling work underlines that concepts and tools from ecology could contribute to a better understanding of bacterial genome dynamics.

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