Engineering an applicable bacterial bioremediator through Artificial Selection.

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One of the most stimulating aspects of microbiology is to employ bacterial genetic potential for our contingent needs. Rhodococcus erythropolis is a bacterial strain that harbors a wide enzymatic inventory and an ample catabolic potential. Aflatoxin B1 (AFB1) is a stable fungal secondary metabolite (a mycotoxin) that contaminates about 50% of crops around the world. It is the most carcinogenic metabolite in nature. We intend to exploit R. erythropolis potential to engineer an efficient and applicable AFB1 bioremediator through the process of Artificial Selection; our final objective is identification of essential variables and modelization of general principles to inform future works aimed at applications in bioremediation.
Developing an effective bioremediator compels us to a deep understanding of the mechanics underlying the detoxification process. We shed light on such mechanics trying to answer essential, single-instance questions. We use the information to set up proper selection schemes for optimizing bioremediation efficiency, and finally we formulate theoretical predictions about how selection, in each of these schemes, would influence the trajectory of evolution. Through adaptation experiments, we will isolate clones from evolving populations at different times. To identify what genes or regulatory mechanisms might be involved in improving the bioremediation efficiency, we intend to compare phenotypic and genotypic changes across different populations during the course of adaptation (using the ancestral strain as the reference). Correlating this information with phenotypic data of degradation efficiency for the same clones, we will establish what genetic changes impact the bioremediation potential and, possibly, how to induce them.