Shared strategies for β-lactam catabolism in the soil microbiome

The soil microbiome can produce, resist, or degrade antibiotics and even catabolize them. While resistance genes are widely distributed in the soil, there is a dearth of knowledge concerning antibiotic catabolism. Here we describe a pathway for penicillin catabolism in four isolates. Genomic and transcriptomic sequencing revealed β-lactamase, amidase, and phenylacetic acid catabolon upregulation. Knocking out part of the phenylacetic acid catabolon or an apparent penicillin utilization operon (put) resulted in loss of penicillin catabolism in one isolate. A hydrolase from the put operon was found to degrade in vitro benzylpenicilloic acid, the β-lactamase penicillin product. To test the generality of this strategy, an Escherichia coli strain was engineered to co-express a β-lactamase and a penicillin amidase or the put operon, enabling it to grow using penicillin or benzylpenicilloic acid, respectively. Elucidation of additional pathways may allow bioremediation of antibiotic-contaminated soils and discovery of antibiotic-remodeling enzymes with industrial utility.

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