

Food-poisoning bacteria employ a citrate synthase and a type II NRPS to synthesize bolaamphiphilic lipopeptide antibiotics.

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Abstract

Mining the genome of the food-spoiling bacterium *Burkholderia gladioli* pv. *cocovenenans* revealed five non-ribosomal peptide synthetase (NRPS) gene clusters, including an orphan gene locus (*bol*). Gene inactivation and metabolic profiling linked the *bol* gene cluster to novel bolaamphiphilic lipopeptides with antimycobacterial activity. A combination of chemical analyses and bioinformatics elucidated the structures of bolagladin A and B, lipocyclopeptides featuring an unusual dehydro- β -alanine enamide linker fused to an unprecedented tricarboxylic fatty acid tail. Through a series of targeted gene deletions we proved the involvement of a designated citrate synthase (CS), priming ketosynthases (KS III), a type II NRPS including a novel desaturase for enamide formation, and a multimodular NRPS generating the cyclopeptide. Network analyses

revealed the evolutionary origin of the CS and identified cryptic CS/NRPS gene loci in various bacterial genomes.

Beteiligte Forschungseinheiten

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