

Ralfuranone biosynthesis in *Ralstonia solanacearum* suggests functional divergence in the quinone synthetase family of enzymes.

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Abstract

Ralstonia solanacearum is a destructive crop plant pathogen and produces ralfuranone, i.e., a monophenyl-substituted furanone. Extensive feeding experiments with (13)C-labeled L-phenylalanine now proved that all carbon atoms of the heterocycle derive, after deamination, from this aromatic amino acid. A genetic locus was identified which encodes the aminotransferase RalD and the furanone synthetase RalA. The latter is a tridomain nonribosomal peptide synthetase (NRPS)-like enzyme which was characterized (1) biochemically by the ATP-pyrophosphate exchange assay, and (2) genetically through gene inactivation and transcriptional analysis in axenic culture and in planta. This is the first study to our knowledge on the biochemical and genetic basis of *R. solanacearum* secondary metabolism. It implies new chemistry for NRPSs, as RalA-mediated biosynthesis requires C-C-bond and subsequent C-O-bond formation to establish the furanone ring system.

Beteiligte Forschungseinheiten

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