Identification and mobilization of a cryptic antibiotic biosynthesis gene locus from a human-pathogenic nocardia isolate.

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Details

Abstract

The genus Nocardia contains >50 human pathogenic species that cause a range of illnesses from skin and soft tissue infections to lung and brain infections. However, despite their membership of the most prominent family of secondary metabolite producers (the Actinomycetes), the ability of Nocardia species, especially those that cause human infections, to produce secondary metabolites has not been well studied. Using genome mining, we have investigated cryptic secondary metabolite biosynthesis gene clusters from Nocardia species and identified a conserved locus within human pathogenic strains of Nocardia brasiliensis and Nocardia vulneris. Direct capture and heterologous expression in a Streptomyces host activated the biosynthetic locus revealing it to be the source of the brasiliquinones, benz[a]anthraquinone antibiotics whose biosynthetic path-way has remained hidden for over two decades, until now. Our findings highlight these hitherto neglected human pathogenic Nocardia as a source of diverse and important natural products.

Beteiligte Forschungseinheiten

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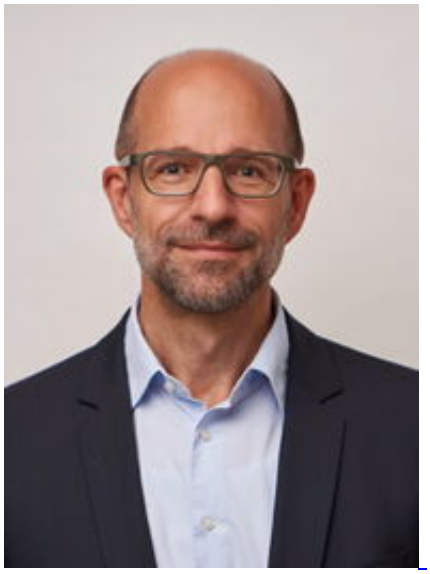

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