

Plasticity of the Malleobactin Pathway and its Impact on Siderophore Action in Human Pathogenic Bacteria.

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Abstract

The human pathogenic bacteria *Burkholderia mallei*, *Burkholderia pseudomallei*, and *Burkholderia thailandensis* harbor a highly conserved gene cluster coding for the biosynthesis of the long sought-after malleobactins. Four new, unexpected congeners of the malleobactin family that were isolated and fully characterized in this study feature unusual deviations from the parent, ornibactin-like architecture. Thus, the malleobactin non-ribosomal peptide synthetase (NRPS) has a rare flexibility that yields diverse peptide backbones, of which one candidate confers pronounced siderophore activity (EC_{50} : 8.4 μ M, CAS assay). These findings not only unveil a highly diverse assembly line but also are an important addition to the knowledgebase of the pathogens' metabolomes.

Beteiligte Forschungseinheiten

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