Genome mining and heterologous expression reveal two distinct families of lasso peptides highly conserved in endofungal bacteria.

Bratovanov EV, Ishida K, Heinze B, Pidot SJ, Stinear TP, Hegemann JD, Marahiel MA, Hertweck C (2019) Genome mining and heterologous expression reveal two distinct families of lasso peptides highly conserved in endofungal bacteria. *ACS Chem Biol* 15(5), 1169-1176.

Abstract

Genome mining identified the fungal-bacterial endosymbiosis Rhizopus microsporus-Mycetohabitans (previously: Burkholderia) rhizoxinica as a rich source of novel natural products. Yet, most of the predicted compounds have remained cryptic. In this study we employed heterologous expression to isolate and characterize three ribosomally-synthesized and post-translationally modified peptides (RiPPs) with lariat topology (lasso peptides) from the endosymbiont M. rhizoxinica: burhizin-23, mycetohabin-16 and mycetohabin-15. Through coexpression experiments it was shown that an orphan gene product results in mature mycetohabin-15, albeit encoded remotely from the core biosynthetic gene cluster. Comparative genomics revealed that mycetohabins are highly conserved trait among M. rhizoxinica and related endosymbiotic bacteria. Gene knockout and reinfection experiments indicated that the lasso peptides are not crucial for establishing the symbiosis; instead, the peptides are exported into the environment during endosymbiosis. This is the first report on lasso peptides from endosymbiontic

bacteria.

Beteiligte Forschungseinheiten

Biomolekulare Chemie Christian Hertweck Mehr erfahren

Leibniz-HKI-Autor*innen

Evgeni Bratovanov

Details

Christian Hertweck

Details

Keishi Ishida

Details

Identifier

doi: 10.1021/acschembio.9b00805

PMID: 31800204