ISPP 2012

14th Internacional Symposium on Phototrophic Prokaryotes

Abstract Book

August 5 to 10 - Porto, Portugal
Congress at Porto Palácio Congress Hotel & Spa

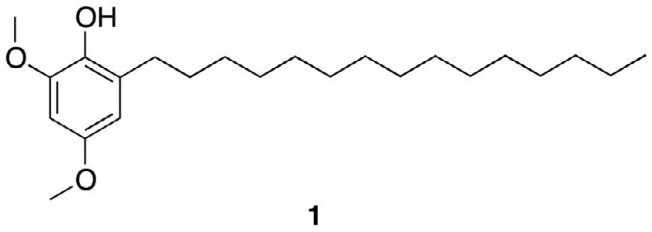
WWW.IBMC.UP.PT/ISPP2012

P179: Isolation of Hierridin B from a culturable *Cyanobium* sp. strain isolated from the Portuguese coast

Pedro N. Leão[1,2,*], Alban R. Pereira[2], Margarida Costa[1], Vitor Ramos[1], Rosário Martins[1,3,4], William H. Gerwick[2,5] and Vitor Vasconcelos[1,6]

[1]CIIMAR/CIMAR, Center for Marine and Environmental Research, University of Porto, Rua dos Bragas 289, 4050-123 Porto, Portugal; [2]Scripps Institution of Oceanography, University of California, San Diego, La Jolla, CA, 92093-0636, USA; [3]Escola Superior de Tecnologia da Saúde do Porto, Instituto Politécnico do Porto, 4400-330 Vila Nova de Gaia, Portugal; [4]IBMC - Instituto de Biologia Molecular e Celular, Universidade do Porto, 4150-180 Porto, Portugal; [5]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, La Jolla, CA, 92093-0636, USA; [6]Department of Biology, Faculty of Sciences, University of Porto, Rua do Campo Alegre, 4169-007 Porto, Portugal

Cyanobacteria are a genetically diverse group of phototrophic prokaryotes. On a secondary metabolite perspective, however, filamentous and benthic forms have been the major sources of compounds isolated from these organisms. Nevertheless, unicellular, free-living, planktonic cyanobacteria also contain enzymatic machinery for secondary metabolite biosynthesis. Here, we report the production of hierridin B (**1**) by the planktonic *Cyanobium* sp. strain LEGE 06113. This strain was isolated from an intertidal sample collected at Aguda beach, northern Portugal.
Isolation of pure hierridin B was achieved by NMR-guided investigation of a non-polar vacuum liquid chromatography (VLC) fraction. The agreement of 1H NMR chemical shifts and coupling constants with the literature values for hierridin B isolated from *Phormidium ectocarpi* [1] formed the basis for dereplication. This metabolite features a 2,4,6-substituted phenol moiety with two methoxy groups and one long aliphatic chain as the substituents. Hierridin B has been previously shown to have antiplasmodial activity. Here we present the results of investigations of its bioactivity profile in other systems. In addition, *Cyanobium* genome data available in the databases was mined for genes that may be involved in the biosynthesis of hierridin B. As a fast-growing, unicellular strain, culturing of *Cyanobium* sp. LEGE 06113 presents as a convenient system to obtain this compound in relatively high amounts and further explore its activity profile.



1

[1] Papendorf O, König GM, Wright AD (1998) Phytochemistry 49(8):2383-2386.

P180: Genotype determined microcystin content in *Planktothrix* spp.

Rainer Kurmayer, and Guntram Christiansen

Institute for Limnology, Austrian Academy of Sciences, Mondsee, Austria e-mail: rainer.kurmayer@oeaw.ac.at

Microcystins (MC) are bioactive secondary metabolites produced by several cyanobacterial genera. Although MC synthesis of a specific MC-producing isolate is continuous and cannot be induced by environmental conditions it is known that individual, MC-producing isolates differ in their MC content by an order of magnitude, e.g. from 0.5–5 microgram of MC per mg dry weight[1].
The biosynthesis of MC is catalyzed by non-ribosomal peptide synthesis and several *mcy* gene clusters encoding MC synthetases have been isolated from different cyanobacterial species. Our aim is to identify factors leading to the observed differences in MC content within forty MC-producing isolates of *Planktothrix agardhiii* and *P. rubescens*.
The *mcy* gene cluster of *Planktothrix* is consisting of nine genes transcribed in a bi-directional operon [2]. The majority of the intergenic spacer regions was found invariable. Only within the largest spacer between the *mcy*E and the *mcy*G gene (274 bp) significant genetic variation due to the insertion of transposable elements (1433 bp), deletions (128 bp) was found. Further within the bi-directional promoter region (*mcy*TD), the insertion of a 1240-bp region coding for two hypothetical proteins was observed.
In relation to two reference genes (phycocyanin, RNA polymerase) a relationship between the transcript amount of individual genes of the *mcy* gene cluster and the MC content among all *Planktothrix* strains was found. The transcripts of the genes *mcy*G, H, A located downstream of the intergenic spacer region *mcy*EG were found as strongest predictor variables. Notably, the strains carrying a 128bp deletion within *mcy*EG showed a high MC content and a weaker relationship between the transcript amount and MC content.
These results show for the first time that individual *mcy* genotypes differ significantly in the *mcy* transcript amount which can explain a significant part of the variation of the MC content among isolates.

[1] Kosol, S., Schmidt, J., and Kurmayer, R. (2009): Variation in peptide net production and growth among strains of the toxic cyanobacterium *Planktothrix* spp. Eur. J. Phycol. 44:49-62; [2] Christiansen, G., Fastner, J., Erhard, M., Borner, T., and Dittmann, E. (2003) Microcystin biosynthesis in *Planktothrix*: Genes, evolution, and manipulation. J. Bacteriol. 185:564-572.