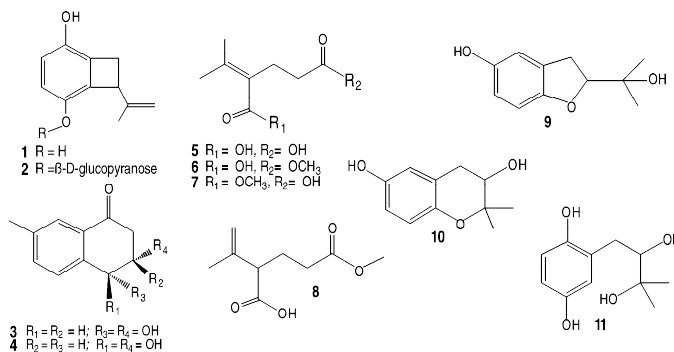


**B141 New antioxidant hydroquinone derivatives from the algicolous marine fungus *Acremonium* sp.**A. Abdel-Lateff<sup>a</sup>, G.M. König<sup>a</sup>, K. Fisch<sup>a</sup>, U. Höller<sup>a</sup>, P.G. Jones<sup>b</sup> and A.D. Wright<sup>a</sup><sup>a</sup> Institute for Pharmaceutical Biology, University of Bonn, Nussallee 6, 53115 Bonn, Germany. <sup>b</sup> Institute for Inorganic and Analytical Chemistry, Technical University of Braunschweig, Hagenring 30, 38106 Braunschweig, Germany.

A marine fungal isolate, identified as *Acremonium* sp., was mass cultivated and found to produce two novel hydroquinone derivatives **1-2**. Compound **1** and its glucoside **2** possess a most unusual ring system. The new natural products **3-4**, were obtained as a 1:0.8 mixture. **5** was isolated for the first time as a natural product and its structure proven by x-ray analysis. In addition to these compounds an inseparable mixture of three new isomeric compounds (**6-8**) was also obtained. Isolated together with the new compounds were three known hydroquinone derivatives **9-11**. Compounds **1**, and **9-11** were found to have significant DPPH radical scavenging effects and are also able to inhibit peroxidation of linolenic acid (TBARS assay).

**B142 The influence of antibacterial substances from marine fungi on the protein synthesis pattern of *Bacillus subtilis***J. Bandow<sup>a</sup>, U. Sender<sup>a, b</sup>, U. Lindequist<sup>b</sup> and M. Hecker<sup>a</sup><sup>a</sup> Institute of Microbiology and <sup>b</sup> Institute of Pharmacy, Ernst-Moritz-Arndt University of Greifswald, 17487 Greifswald, Germany.

As a part of an ongoing program designed to investigate marine fungi of the northern hemisphere for new antibacterial compounds we isolated ascocochitine and the related new structure ascocochital from a strain of the ascomycete *Kirschsteiniethelia maritima* (1). The compounds inhibit the growth of *B. subtilis* with a minimal inhibitory concentration of 0.1  $\mu$ g/ml and 0.5  $\mu$ g/ml resp. To identify their target in the bacterial cells we investigated their influence on the protein synthesis pattern in *Bacillus subtilis* using proteom analysis. The signature of many cytoplasmic proteins of *B. subtilis* could be analysed during the last years (2).

Changes in the protein synthesis rate were investigated by pulse-labeling experiments with L-[35S] methionine. Crude protein extracts of cells pulse-labeled at different time points after treatment with ascocochitine or ascocochital were separated on 2D gels. To identify newly synthesized or strongly induced proteins, dual-channel imaging (3,4) was used.

The incorporation of L-[35S] methionine added 60 min after test compound for 5 min was reduced by both compounds. The dual images showed that the synthesis pattern of cytoplasmic proteins in the pH range of 4 to 7 was significantly changed. The most dramatic effect was a strong induction of chaperones and stress-inducible proteases indicating that the test compounds cause protein stress in bacterial cells.

**References:** 1. Kusnick, C. et al. (2002) Pharmazie, in press. 2. Büttner, K. et al. (2001) Electrophoresis 22: 2908. 3. Bernhard, J. et al. (1999) Electrophoresis 20: 2225. 4. Delta2D Software (DECODON GmbH Greifswald).