

Bioprospecting of fungi from the Borneo rain forest regarding their bioactive properties

Nadine Hochenegger^a, Robert L. Mach^a, Irina S. Druzhinina^b, Astrid R. Mach-Aigner^a,
Christian Derntl^a

^aInstitute of Chemical, Environmental and Bioscience Engineering, TU Wien, Vienna,
Austria

^bCollege of Resources and Environmental Sciences, Nanjing Agricultural University,
China

Antibiotic-resistant bacterial pathogens have become a major problem of modern medicine. Hence, we need new possibilities to handle those pathogens. The history of medicine taught us that nature provides us with tools to fight pathogenic germs but fungi are still an underutilized source of bioactive substances. In this study, we investigate tropical fungal strains on their capability to produce secondary metabolites (SM) which can potentially be used as antibiotic against bacterial or fungal pathogens. The strains derive from different locations in and around nests of the “exploding ants” *Colobopsis explodens* of the Borneo rain forest. The ant-fungus mutualism between these ants and their surrounding fungi can be a promising source of antibiotic substances. Thus, we focused on the production of SM of fungal strains found in proximity to these ants, which was triggered by biotic and abiotic stress conditions. Further, confrontational assays against other fungi or bacteria were used to induce the secretion of defensive SM. In order to test the fungal strains on their ability to produce bioactive SM, extractions from different cultivation media after incubation with those strains were performed. In the course of several bioactivity assays, the antimicrobial effect of the extracts was investigated on different model organisms representing different types of microorganisms (e.g. *Escherichia coli* for gram-negative bacteria, *Trichoderma reesei* for filamentous fungi). In further consequence, the most promising extracts were tested against common antibiotic-resistant strains. Additionally, the potential of adaptation and preservation was ascertained by co-cultivation of the strains and also whole genomes of fungi were sequenced and the phenotypes under different conditions were determined.