



Preliminary agenda: Special Interest Group for the IMC 11, (scheduled for Wednesday July 18 and Friday July 20, each 19:30-21:00)

Day 1: Taxonomy and biodiversity (July 18)

Pedro W. Crous (WFBI), Chair

Introductory remarks/presentation of the project 5 min

Jennifer Luangsa-ard (BIOTEC)

Unravelling cryptic species in Cordycipitaceae with isarioid morphs 20 min

Xuewei Wang (WFBI)

Re-evaluation of the genera in the Chaetomiaceae 12 min

Sarunyou Wongkanoun (BIOTEC)

Daldinia sp. nov., from a community forest in Northern Thailand 12 min

Umpawa Pinruan (BIOTEC)

Productivity of edible *Amanita* at Phusing Agricultural Development Center, Sisaket, Thailand 12 min

Suchada Mongkolsamrit (BIOTEC)

Diversity and novel species of entomopathogenic fungi in a conservation area: Banphao Thai community forest, Thailand 12 min

Liu Fang, Pedro W. Crous et al. (WFBI)

Resolving fungi related to Amphisphaeriaceae 12 min

General discussion 5 min

The speakers are being asked to allocate 3 minutes for questions.



Day 2: Studies on secondary metabolites (July 20)

Marc Stadler (HZI) Chair

Introductory remarks, presentation of the project 5 min

Zeljka Rupcic, Kathrin Wittstein et al. (HZI)

Neuroprotective metabolites from *Hericium* species 15 min

Eric Kuhnert (HZI/Leibniz University Hannover)

The secondary metabolome of *Hypoxylon rickii* 15 min

Sara R. Noumeur (Univ. Batna, Algeria/HZI)

Phylogeny and chemical diversity of *Preussia similis* 15 min

Benjarong Thongbai, Birthe Sandargo et al. (HZI)

Novel bioactive metabolites from *Hohenbuehelia grisea* and other
Thai Basidiomycota15 min

Wilawan Kuephadungphan (BIOTEC/HZI)

Species-specific distribution pattern of secondary metabolites in the
spider parasitic ascomycetes *Gibellula*, *Hevansia* and related genera15 min

General Discussion and conclusions 10 min

The speakers are being asked to allocate 3 minutes for questions.

For most contributions, a poster will be presented concurrently in the regular programme,
so there will be another opportunity to discuss with the speakers.

Acronyms:

BIOTEC: National Center for Genetic Engineering and Biotechnology, Pathum Thani,
Thailand.

HZI: Helmholtz-Centre for Infection Research, Braunschweig, Germany.

WFBI: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.

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research and innovation program (RISE) under the Marie Skłodowska-Curie grant agreement No
645701, Project acronym "GoMyTri".

Submission 212

Unravelling cryptic species in Cordycipitaceae with isarioid morphs

Type: Poster Submission

Level: Ecology

Authors: J. Luangsa-Ard¹, S. Mongkolsamrit¹, W. Noisripoom¹, D. Thanakitpipattana¹, T. Wutikhun², J. Spatafora³; ¹Microbe Interaction and Ecology Laboratory, Biodiversity and Biotechnological Resource Research Unit, National Center for Genetic Engineering and Biotechnology (BIOTEC), Pathum Thani/Thailand, ²Nano Characterization Laboratory (NCL), NANOTEC, Pathum Thani/Thailand, ³Department of Botany and Plant Pathology, Oregon State University, Corvallis/United States of America

Abstract

Isaria Pers. is one of the oldest asexually typified genera of invertebrate fungal pathogens, with its species characterized by the formation of branched synnemata, that give rise to flask-shaped phialides produced in whorls. The phialides tend to possess swollen bases that narrow abruptly forming a distinct neck. Conidia are one-celled, hyaline, smooth, subglobose to subcylindrical and are produced in divergent chains. Aspects of this morphology are shared with other genera, resulting in a turbulent taxonomic history. With *Isaria* being polyphyletic throughout Cordycipitaceae and rejected in favor of *Cordyceps*, there is a need to identify the taxonomic placement of isarioid species collected in Thailand. We collected isarioid morphs of invertebrate-pathogenic fungi and other *Cordyceps* and *Torrubiella* species infecting coleopterans, lepidopterans and spiders. Sexually reproductive species that produce isarioid morphs in culture and a *Torrubiella* sp. on a spider, were also included in this study. The purposes of these investigations are to re-examine the taxonomic position of these specimens and to describe new taxa to accommodate the phylogenetic diversity of isarioid fungi. Phylogenetic analyses based on a combined dataset comprising ITS and 28S rDNA, partial sequences of translation elongation factor 1- α gene (*TEF1*) and the genes for RNA polymerase II largest (*RPB1*) and second largest (*RPB2*) subunits were used to clarify their relationships within Cordycipitaceae. A new genus and eight new species, all with isarioid phialides, are described in Cordycipitaceae from Thailand. The new genus, *Samsoniella*, is segregated from *Akanthomyces* based on morphological and molecular evidence. *Samsoniella* differs from *Akanthomyces* in producing orange cylindrical to clavate stromata with superficial perithecia and orange conidiophores with isarioid phialides and white to cream conidia. A new combination for CBS 240.32 and CBS 262.58, originally identified as *Paecilomyces farinosus* (*Isaria farinosa*) and *Penicillium alboaurantium*, respectively, is made in *Samsoniella*. Two new species, *Samsoniella aurantia* and *S. inthanonensis* are described from lepidopteran larvae. Two new species in *Cordyceps*, *C. blackwelliae* and *C. lepidopterorum*, are also found on coleopteran and lepidopteran larvae. Both species produce isarioid morphs with globose phialides and attenuated long necks and white mycelium in culture. We have established sexual-aseexual link of *Cordyceps javanica* (= *Isaria javanica*) on lepidopteran larvae. Four new species described in *Akanthomyces* are pathogenic to spiders or unidentified insect larvae. *Akanthomyces kanyawimiae*, *A. sulphureus*, *A. thailandicus* and *A. walte rgamsii* were found on spiders with some strains of *A. kanyawimiae* also found on unidentified insect larvae. These four species of *Akanthomyces* are found on the underside of leaves and produce white to cream white powdery conidia, while *S. aurantia* and *S. inthanonensis* were found in the leaf litter and produce bright orange stromata and synnemata with white conidia. Another new combination, *Akanthomyces ryukyuensis* is also proposed. Our results from molecular phylogenetic analyses strongly support these new species in *Cordyceps*, *Akanthomyces*, and in a new genus *Samsoniella* in Cordycipitaceae.

Submission 664

Re-evaluation of the genera in the Chaetomiaceae

Type: Poster Submission

Level: Evolution

Authors: X.-W. Wang¹, F.-Y. Bai¹, R.A. Samson², P. Crous³, J. Houbraken²; ¹State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing/China, ²Applied and Industrial Mycology, Westerdijk Fungal Biodiversity Institute, Utrecht/Netherlands, ³Phytopathology research, Westerdijk Fungal Biodiversity Institute, Utrecht/Netherlands

Abstract

The Chaetomiaceae (Ascomycota) are well known for their cellulolytic activity and the production of various biologically active secondary metabolites that have great potential in agriculture, medicine and industry. On the other hand, many species are also able to grow in the indoor environment, causing adverse health effects, or are reported as causal agents of fungal infections in humans. Most genera occurring in Chaetomiaceae have not been revised based on molecular data. In this study, genera of Chaetomiaceae are re-evaluated on the basis of morphology and a four-locus DNA phylogeny. The asexual genera *Botryotrichum*, *Humicola* and *Trichocladium* are redefined to include species that reproduce sexually, and *Chaetomium longicolleum* is shown to represent the sexual morph of *Staphylotrichum*. Furthermore, most of the other known genera in Chaetomiaceae are re-circumscribed. The present study is a first attempt to establish an inclusive modern classification of the Chaetomiaceae composed of monophyletic genera.

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Submission 311

Daldinia sp. nov, from a community forest in Northern Thailand

Type: Poster Submission

Level: Ecology

Authors: [S. Wongkanoun](#)¹, P. Srikitikulchai¹, L. Went², M. Stadler², J. Luangsa-Ard¹; ¹Microbe Interaction and Ecology Laboratory, Biodiversity and Biotechnological Resource Research Unit (BBR), National Center for Genetic Engineering and Biotechnology (BIOTEC), Pathum Thani/Thailand, ²Microbial Drugs, Helmholtz Centre for Infection Research, Braunschweig/Germany

Abstract

Hypoxylaceae is one of the well-known and widely distributed families of pyrenomycetous fungi with unitunicate asci and pigmented ascospores. Our survey and collection of Xylariaceae and Hypoxylaceae in the northern part of Thailand has found many specimens and one of these may be a new species of the genus *Daldinia*. The genus *Daldinia* was described by Cesati & De Notaris in 1863 (Hypoxylaceae, Xylariales, Xylariomycetidae, Sordariomycetes, Pezizomycotina, Ascomycota). In this study *Daldinia* sp. nov was found on decaying wood from a community forest in Chiang Dao district, Chiang Mai province, northern area of Thailand. It is characterized by productions of superficial small to widely effused, pulvinate stromata, with mouse grey to pale mouse grey surface, inconspicuous perithecial mound. The perithecia are monostichous lanceolate with black drop, umbilicate ostiole, containing unitunicate cylindrical asci, unicellular ellipsoid dark brown to blackish brown ascospores, and with straight to slightly curved germ slit much less than the spore length on convex size, smooth perispore dehiscent in 10% KOH. The morphological characteristic of this fungus is very similar to that of *D. placentiformis* in the shape of stromata, but is different in KOH extraction in producing dark vinaceous pigment. However, phylogenetic analysis of the multiple loci including internal transcript spacer region (ITS), large subunit of the rDNA (LSU), second largest subunit of the RNA polymerase II (RPB2), and beta-tubulin (TUB2) shows this fungus is placed in the Hypoxylaceae and is closely related to *D. korfii*. It is clear that this fungus showed inconspicuous horizontal zones but *D. korfii* has conspicuous zones. The stromatal acetonitrile extraction contains BNT, and 2 new compounds (Cytochalasin). Critical examination of the phenotypic characters indicates that this fungus represents a new species in Thailand.

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Submission 168

Productivity of edible Amanita at Phusing Agricultural Development Center, Sisaket, Thailand

Type: Poster Submission

Level: Ecology

Authors: U. Pinruan¹, S. Somrithipol¹, S. Sommai¹, P. Khamsuntorn¹, T. Boonpratuang¹, S. Takhiankling², K. Nissa³; ¹Microbe Interaction and Ecology Laboratory, National Center for Genetic Engineering and Biotechnology (BIOTEC), Pathum Thani/Thailand, ²Forestry, Phusing Agricultural Development Center, Sisaket/Thailand, ³Royal Forest Department, Forest Research and Development Bureau, Bangkok/Thailand

Abstract

The cultivation of edible ectomycorrhizal mushrooms associated with forest trees is becoming popular in Thailand. It is currently applied to reforestation projects by forestry officials, and in agroforestry situations by farmers. However, information on the mushroom productivity and sustainability is unavailable. This study investigated and reports on the yield of edible *Amanita* and other wild edible mushrooms in a 1280m² plot at Phusing Agriculture Extension Center, Sisaket Province between 2014 and 2016. The plot was on an area mainly covered by *Dipterocarpus alatus* trees, which were planted on bare land in 2003 and were inoculated with *Amanita* during 2004–2005. In 2014 eight edible mushroom species (total weight 72.6 kg) were found in the plot. Three *Amanita* spp. (60.2 kg, 83%) were the dominant group: red *Amanita* (*Amanita* cf. *hemibapha*; 43.2 kg, 59%), yellow *Amanita* (*Amanita* cf. *hemibapha*; 15.7 kg, 22%), and white *Amanita* (*Amanita* cf. *princeps*; 1.3 kg, 2%). These *Amanita* species morphologically resemble *Amanita hemibapha*, and *A. princeps*, but molecular data based on ITS and LSU show that they are taxonomically new to science, and are currently being described. Other inferior mushrooms found in the plot were *Russula nigricans* (8.1 kg), *Termitomyces microcarpus* (2.4 kg), *Lactarius* sp. (1.5 kg), and *Russula emetica* and *Russula* sp. (less than 1 kg). In 2015, two additional mushroom species, *Russula virescens* and *Termitomyces* sp., were also found, but the total yield of the plot was stable (72.1 kg). Yellow and white *Amanita* increased their yields (40 kg, 56% and 6.3 kg, 9%) but red *Amanita* sharply decreased (2.5 kg, 3%) resulting in decline of the total *Amanita* yield (48.8 kg, 68%). In 2016, nine edible ectomycorrhizal mushrooms were found with the total yield 73.6 kg. *Russula nigricans* became the dominant species (38.4 kg, 52%) while the *Amanita* group (31.6 kg, 43%) decreased: yellow *Amanita* (25.9 kg, 35%), white *Amanita* (3.6 kg, 5%), and red *Amanita* (2.1 kg, 3%). In 2017, seven edible mushrooms were found with the total yield only 17.1 kg. Yellow *Amanita* became the dominant species (6.7 kg, 39%), red *Amanita* (4.5 kg, 26%), white *Amanita* (3.0 kg, 17%), while *Russula nigricans* decreased (0.8 kg, 5%). The presentation will show monthly yields of each mushroom species and some environmental factors throughout the last four years. Declining trend of the *Amanita* productivity, as well as possibility of rehabilitation in correlation of environmental factors, will be also discussed.

[Print](#)

Submission 349

Diversity and novel species of Entomopathogenic fungi in a conservation area: Banphao Thai community forest, Thailand

Type: Poster Submission

Level: Ecology

Authors: S. Mongkolsamrit¹, S. Lamlerththon², W. Noisripoom¹, K. Tasanathai¹, D.

Thanakitpipattana¹, J.J. Luangsa-Ard¹; ¹Microbe Interaction and Ecology Laboratory, Biodiversity and Biotechnological Resource Research Unit, National Center for Genetic Engineering and Biotechnology (BIOTEC), Pathum Thani/Thailand, ²Centre of Excellence in Fungal Research Faculty of Medical Science, Naresuan University, Phitsanulok/Thailand

Abstract

In Thailand, entomopathogenic fungi are one of the species diverse groups. They play an important role in the control of population of insects. Banphao Thai forest in Phitsanulok province is a community forest located in the upper central part of Thailand, and covers an area of 0.64 square kilometers. The ecosystem of Banphao Thai community forest is unique by having cassava plantations surrounded by wilderness. The diversity and molecular phylogenetic studies of entomopathogenic fungi were the objectives that have been established in a collaboration between the Centre of Excellence in Fungal Research (CEFR), Naresuan University and Microbe Interaction and Ecology laboratory, BIOTEC, Thailand. During a field study carried out from 2016 to 2017, specimens were recorded, collected, then preliminarily identified according to their morphological characteristics and then subjected to molecular phylogenetic study. The diversity and abundance of entomopathogenic fungi is high during the rainy season from May to November. A total of 393 entomopathogenic fungi belonging to six genera include *Beauveria*, *Cordyceps*, *Conoideocrella*, *Ophiocordyceps*, *Metarhizium* and *Polycephalomyces*. Their insect hosts were classified to Coleoptera (75.3%), Hemiptera (6.9%), Hymenoptera (0.3%), Isoptera (8.7%), Orthoptera (0.5%), Lepidoptera (8.4%). *Shimizuomyces* sp. growing on fruit plants were also found in the ecosystem. Interestingly, the interactions between the hyperparasitic fungus *Polycephalomyces* and their diverse hosts has been observed in this ecosystem. The novel fungal pathogen *Polycephalomyces phaothaiensis* is a parasite of coleopteran larvae which occurs in rainy season. Meanwhile *P. phaothaiensis* also plays a role as hyperparasitic fungus which infects numerous fungal hosts such as *Ophiocordyceps* sp.1 and *Ophiocordyceps* cf. *brunneipunctata*, found predominantly during the rainy season. From our investigations, we found 21 species of entomopathogenic fungi and a first record of the genus *Shimizuomyces*. *Polycephalomyces phaothaiensis* has multiple hosts and little is known about its life cycle and ecology.

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Submission 164

Resolving fungi related to Amphisphaeriaceae

Type: Poster Submission

Level: Evolution

Authors: F. Liu¹, B. Guido², L. Cai¹, P. Crous²; ¹State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing/China, ²Phytopathology research, Westerdijk Fungal Biodiversity Institute, Utrecht/Netherlands

Abstract

Amphisphaeriaceae related fungi are endophytic, pathogenic or saprobic, and associated with a wide range of host plants. The classification of *Amphisphaeriaceae* sensu lato has undergone considerable change since its inception in 1887. Traditional classification was mainly based on morphology, such as conidiomatal morphology, conidial pigmentation, septation, and mode of conidiogenesis. Although recent molecular studies have addressed familial and generic boundaries of fungi related to *Amphisphaeriaceae*, they only included a limited number of DNA loci. Currently, two contradictory viewpoints regarding the family level classification of *Amphisphaeriaceae* and related fungi are applied, and the generic delimitation is even more controversial. The aim of the present study is to provide a natural classification for the *Amphisphaeriaceae* and its allies through multi-locus phylogenetic analyses based on LSU, ITS, *TEF*, *TUB* and *RPB2* gene loci, combined with morphological comparison. Multi-locus phylogenetic analysis of 770 isolates supported the treatment of *Bartaliniaceae*, *Discosiaceae* and *Pestalotiopsisaceae* as synonyms of *Sporocadaceae*. A total of 37 well-supported monophyletic clades in *Sporocadaceae* were recognized, representing 24 known and 13 new genera. Furthermore, typifications were proposed for the type species of six genera (*Diploceras*, *Disaeta*, *Discosia*, *Monochaetia*, *Sarcostroma* and *Truncatella*), to help stabilize the application of these names.

[Print](#)

Submission 669

Neuroprotective metabolites from *Hericium*

Type: Poster Submission

Level: Cell Biology

Authors: [Z. Rupcic](#)¹, K. Wittstein¹, M. Rascher^{1, 2}, S. Kanaki³, R. Köster², M. Stadler¹; ¹Microbial Drugs, Helmholtz Centre for Infectious research, Braunschweig/Germany, ²Cellular and molecular neurobiology, Zoological Institute, TU Braunschweig, Braunschweig/Germany, ³Department of Biotechnology, Toyama Prefectural University, Toyama/Japan

Abstract

Antibiotic resistance and neurodegenerative diseases are two major medical issues we have to face and which will become even more serious in the future. In order to cope with them and to develop improved therapies new classes of bioactive natural products with different modes of action are needed urgently. *Hericium* spp. of the phylum basidiomycota are among the most praised medicinal and edible mushrooms, and they have been known to produce secondary metabolites, such as hericenones and erinacines, which were isolated from the fruiting bodies and cultured mycelium, respectively. Many of these compounds were found to promote nerve growth factor (NGF) biosynthesis. Recently, corallocin A–C were isolated from basidiomes of the species *Hericium coralloides* and were the first members of this compound family that were found to be able to modulate both, NGF and brain-derived neurotrophic factor (BDNF) production. This prompted us to extend our studies to the metabolites from cultures of *Hericium* species, where metabolite profiles of a strain of the Lion's Mane mushroom (*Hericium erinaceus*) and a strain of the rare species, *Hericium flagellum* (synonym *H. alpestre*) were examined. Highly similar metabolites were observed in both strains, with cyathane diterpenoids being the predominant ones. Seven metabolites obtained from *H. erinaceus* and *H. flagellum* were evaluated regarding their neurotrophin inducing effects. Although none of the tested compounds showed intrinsic neurotrophic activity, erinacines A, B, C, CJ14.258 and the new derivative Z1 clearly enhanced the neurotrophin production in astrocytic cells. Moreover, for the first time we observed a promoting effect of cyathane diterpenoid derivatives on BDNF expression. As they are able to stimulate the transcription of both neurotrophins, they may act upstream on a common molecular target of both pathways or via a third independent pathway.

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Submission 1264

The secondary metabolom of Hypoxylon rickii (Hypoxylaceae)

Type: Poster Submission

Level: Applications

Authors: E. Kuhnert¹, R. Cox¹, F. Surup², M. Stadler³; ¹Institute of Organic Chemistry, Leibniz Universität Hannover, Hannover/Germany, ²Microbial Drugs Department, Helmholtz–Center for Infection Research, Braunschweig/Germany, ³Microbial Drugs, Helmholtz Centre for Infection Research, Braunschweig/Germany

Abstract

The recently erected Hypoxylaceae comprise a rather large world-wide distributed family of ascomycetes with more than 300 accepted species. The majority of its members is associated with decaying hard wood, where they form stromatal tissue embedding one or more perethicia. It is assumed that most of the species spend part of their life inside of healthy trees as endophytes without causing any visible symptoms. With only few exceptions the Hypoxylaceae are characterized by an unusual abundancy of pigments on the surface and/or within the stromatal tissue. These pigments are traditionally extracted with a potassium hydroxide solution and the resulting color is used as a distinctive feature between species. In the last 20 years natural product researcher began to elucidate the underlying chemical structures and revealed a plethora of carbon skeletons including azaphilones (e.g. mitorubrins, multiformins, lenormandins, daldinins), cytochalasins, tetramic acids (e.g. hypoxyvermelhotins), binaphthyls and derivatives (e.g. BNT, hypoxylone, urceolone), benzo[j]fluoranthenes (e.g. hypoxylonols, daldinones, truncatone), prenylated indol derivatives (e.g. truncaquinones) or other aromatic polyketides (e.g. macrocarpones). Furthermore, cultures derived from spore isolates and endophytic mycelia were intensively screened for bioactive natural products leading to the discovery of hundreds of additional compounds. Many of them displayed interesting activity such as the topoisomerase I inhibitor hypoxyxylone, the antioxidative rickenyls, the insecticidal nodulisporic acids, the antifungal hypoxysordarin, the anti-HIV agent concentricolide or the immunosuppressive dalesconols. The production of the seemingly unlimited amount of different secondary metabolites is controlled by biosynthetic gene cluster (BGC) encoded in the genome of the producing organism. The advances in the area of genome sequencing enabled us to study the genomes of various Hypoxylaceae and identify BGC using bioinformatics and molecular tools for gene knockouts and heterologous expression systems. By comparing BGC of related species we are about to reveal conserved as well as unique biosynthetic pathways, helping to trace back the evolution of the secondary metabolom. In the past, we extensively evaluated the production capabilities of the prolific secondary metabolite producer *Hypoxylon rickii* and purified more than 30 compounds of eight structural distinct families. Together with the recently obtained genome of the species we could get an insight into the true diversity of its secondary metabolom, which is showcased in this presentation.

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Phylogeny and chemical diversity of *Preussia similis*

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The genus *Preussia* (Sporormiaceae, Pleosporales) comprises filamentous Ascomycota that live on animal dung, plant debris, soil, and wood or as endophytes. *Preussia similis* (Khan & Cain) Arenal was found to be a rich source of antifungal compounds, such as similins A and B and preussomerins. From our collection of endophytic fungi isolated from the medicinal plant *Globularia alypum* Linn. (Plantaginaceae) collected in Batna, Algeria, three isolates of *Preussia similis* were studied for their phylogenetic relationship and screened in order to search for novel biologically active secondary metabolites. Phylogenetic tree inferred from the multigenes analysis revealed that the three strains fell in one strongly supported monophyletic clade of *Preussia similis* complex. Additionally, the three strains originated from the same host plant, have been shown to generate chemical diversity in secreted secondary metabolites. In total, thirteen compounds have been isolated including six new bicyclic polyketides and one new dimer of 2-aminobenzoid acid along with known cytochalasins and xanthones. These chemical features might be considered as good chemotaxonomic markers of the genus *Preussia*.

The results of this project were published in Noumeur et al. 2017. **Preussilides a–f, bicyclic polyketides from the endophytic fungus *preussia similis* with antiproliferative activity.** *Journal of natural products*.

<https://pubs.acs.org/doi/10.1021/acs.jnatprod.7b00064>

Submission 1263

Novel bioactive metabolites from *Hohenbuehelia grisea* and other Thai Basidiomycota

Type: Poster Submission

Level: Applications

Authors: B. Sandargo¹, B. Thongbai^{1, 2}, F. Surup¹, M. Stadler³; ¹Microbial Drugs Department, Helmholtz–Center for Infection Research, Braunschweig/Germany, ²Center of Excellence in Fungal Research, and School of Science, Mae Fah Luang University, Chiang Rai/Thailand, ³Microbial Drugs, Helmholtz Centre for Infection Research, Braunschweig/Germany

Abstract

Cultures of Basidiomycota were obtained from specimens collected in the field in northern Thailand and screened for antimicrobial effects in collaboration with a worldwide leading group of experts on natural product derived drug discovery in Germany. From selected strains that showed prominent activities, several novel active compounds were isolated from mycelial cultures during the course of this study. These include new isolates belonging to the genera *Cyathus*, *Hohenbuehelia*, *Deconica*, *Gymnopus*, *Marasmius*, and *Panus*. The morphological characteristics of these mushrooms were described and molecular data (nrITS) were used to characterize the producer organisms.

Hohenbuehelia grisea has been known to produce the antibiotic and anticancer–lead compound pleurotin and dihydropleurotinic acid. Recently, the discovery of a *Hohenbuehelia grisea* led to the isolation and identification of novel bioactive metabolites, by the interpretation of spectral data (HRESIMS, 2D–NMR). Our results show seven new derivatives of dihydropleurotinic acid, out of which three are novel sulfur–bearing derivatives and their decreased cytotoxicity and antimicrobial activities, compared to the other compounds, hint to a possible glutathione detoxification pathway in filamentous fungi. Additionally, a novel derivative of hydroxypleurotin featuring an exocyclic double bond as well as two compounds with a 4–membered ring scaffold have been isolated. The isolation of new derivatives of the carotane antibiotic fulvoferruginin from a *Marasmius* sp. which also prove to be cysteine–derived conjugates of fulvoferruginin, further support our hypothesis of a glutathione detoxification in filamentous fungi.

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Submission 273

Species-specific distribution pattern of secondary metabolites in spider parasitic ascomycetes *Gibellula*, *Hevansia* and related genera

Type: Poster Submission

Level: Evolution

Authors: [W. Kuephadungphan](#)¹, M. Stadler², S. Helaly², J. Luangsa-Ard³, S. Phongpaichit¹, V. Rukachaisirikul⁴, A. Macabeo², C. Daengrot⁴, P. Phainuphong⁴; ¹Microbiology, Prince of Songkla University, Songkhla/Thailand, ²Microbial Drugs, Helmholtz Centre for Infection Research, Braunschweig/Germany, ³Microbe-Interaction, National Center for Genetic Engineering and Biotechnology (BIOTEC), Pathum Thani/Thailand, ⁴Chemistry, Prince of Songkla University, Songkhla/Thailand

Abstract

Even though the pathogenic fungi associated with invertebrates are well-known for centuries and have been intensively studied for a long time, certain groups of fungi, and in particular the spider parasitic fungi have not yet received much attention. *Gibellula* and *Hevansia* are classified in the Cordycipitaceae which are known to be obligate parasites of spiders. Most of them have been investigated based solely on morphological descriptions. Over a few decades there has been an increasing interest in the study of phylogenetic relationship between them and their allies, it is nevertheless limited to specific research groups. Besides the limited molecular data, their production of secondary metabolites also remains largely unexplored. In the course of a study on invertebrate-pathogenic fungi in Thailand where is accepted to be a rich source for a diverse range of microorganisms particularly invertebrate-pathogenic fungi, more than a hundred of fungal specimens were collected from various areas and encountered in the study. To extend our understanding of the taxonomic relationship among *Gibellula*, *Hevansia* and allied genera as well as to investigate and explore their secondary metabolites, HPLC- and PCR-based techniques were employed to generate the fungal chemoprofiles and molecular data, respectively. The species identification was relied on morphological features and multigene phylogenetic analysis. Five nuclear gene regions including the internal transcribed spacer (ITS), nuclear ribosomal large subunit DNA (nrLSU), elongation factor 1 α (EF-1 α), the largest and second largest subunits of RNA polymerase II (RPB1 and RPB2), were sequenced and the phylogenetic tree was subsequently reconstructed. The fungal secondary metabolite profiles were examined using analytical HPLC coupled with diode array and mass spectrometric detection (HPLC-DAD/MS) and compared within species according to the multigene tree. Some species remarkably revealed a unique pattern of secondary metabolite production in particular *H. novoguineensis* in which all nine unprecedented secondary metabolites are specifically produced by the species. This is the first report on secondary metabolite profiling of *Gibellula* and *Hevansia* showing the species-specific distribution pattern of their secondary metabolites as well as unprecedented components that might eventually be used as powerful chemotaxonomic markers in species identification.

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