

MYCODIVERSITY, HOLISM AND EVOLUTION

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Mycodiversity (Fungal Biodiversity) is the theme of this meeting. Why is it important? What is the basis of mycodiversity? And, how did it evolve? To answer these questions, we need to take a HOLISTIC view in which the entire gamut of fungal interactions with biota and with the biome are the key to unravelling the mysteries of fungal evolution and diversity and must be understood and analysed thoroughly. The origin of fungal biodiversity is linked to the evolution of fungal behaviour, fungal interactions, fungal metabolism, besides fungal structure and ultrastructure, fungal cell wall composition, fungal reproduction, fungal life cycles and fungal genetics. The speaker will focus on these and other facets of fungus diversification such as host- and substrate-specificity, autoecism and heteroecism, host specialization, geographical distribution and the concept of races, biotypes and formae speciales. The recognition of many taxonomic and biological or ecological groups which have emerged from critical studies of fungi using refined and sophisticated approaches and techniques, and the discovery of new taxa such as, for example, the anaerobic rumen chytrids, offers insights into the evolution of mycodiversity in space and time in which co-evolution is now considered to have played a major role. We therefore need a holistic approach in understanding mycodiversity and conserving it on a global scale. The speaker will discuss these concepts with a broad spectrum of suitable examples representing a variety of fungal behaviour and fungal interactions.

REVITALIZATION OF TAXONOMY IN THE NEW MILENIUM: A BUSINESS PLAN

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The majority of the world population and biodiversity are in the developing world. Ninety four percent of taxonomists belong to developed world. The withdrawal of the former free taxonomic services by the developed world institutions like CAB-IMI, ATCC, ITCC, CBS etc. has created a lot of hue and cry and a vacuum developed. This has resulted in a decline in quarantine services and an identifiable increase in hardship to various scientists in the developing countries. In the first Rio conference in 1993 a survey of sixty taxonomists in 23 countries highlights a committed professional services which is under resourced and frustrated many taxonomists who thought it is routine service. Since taxonomists are not good salesman hence the people have not recognised its economic value if not on financial terms. Taxonomy is the science of identifying organisms. It is a service for which few people recognise the value and for which few people are willing to pay. In view of the above we have to develop a business plan by highlighting the biological and economic importance and benefits of taxonomy by using specific and dramatic examples. In the world now we have 316 bacteriologists, 926 mycologists but only 19 entomopathogenic nematodes specialists. We have to explore the new records by doing customized search of the world origin and then there databases can be put on websites and make the contribution to Global taxonomy as we are having only 16% information of the biodiversity of Developing world.

A REVOLUTION IN *VERTICILLIUM* SYSTEMATICS

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In recent years, some unnatural and unwieldy anamorph genera are being disentangled into more natural entities, which should ideally be correlated with well-defined teleomorph genera. Morphological features are reevaluated in the light of phylogenetic DNA analyses. Work on *Verticillium* exemplifies this trend. It has been known for years that *Verticillium* comprises anamorphs of Phyllachorales (including the type species and some well-known plant pathogens), Hypocreales and Clavicipitaceae.

Verticillium section *Prostrata* W. Gams was introduced in 1971 for the latter group of anamorphs. Sequences of ITS showed that even this section is heterogeneous (3), a finding confirmed by sequences of large and small subunits of rDNA (2). Consequently, four genera are now distinguished as follows (1): *Lecanicillium* comprising the largest cluster (so far 17 named species), which is closely related to *Cordyceps* sensu stricto, but also to teleomorphs of *Torrubiella*. The same phylogenetic cluster comprises species of *Beauveria* and *Paecilomyces*, rendering *Lecanicillium* paraphyletic. The most important species are *L. lecanii*, its widespread close relative *L. muscarum*, and *L. psalliotae*. A sister clade of four species with solitary phialides is comprised in *Simplicillium*. A distinct cluster comprises endoparasites of nematodes with apically adhesive conidia (together with the entomogenous *Cordyceps gunnii*) and these are comprised in *Haptocillium* (7 species). Parasites of eggs and cysts of nematodes, formerly often called *Diheterospora*, are comprised in *Pochonia* (8 species). In this group a new teleomorph, *Cordyceps chlamydospora*, is described.

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More papers in press in *Nova Hedwigia*

AN INTEGRATED REVISION OF *POCHONIA*
(*DIHETEROSPORA*); NEMATOPHAGOUS HYPHOMYCETES
FORMERLY CLASSIFIED IN *VERTICILLIUM*

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Taxonomy of the genus *Verticillium* s. l. is investigated and revised by using morphological and molecular approaches and by examining a large number of strains from various geographical origins. As a result, four distinct clades were established, each relating to specific host groups. One of the clades comprises the species of *Pochonia* (*Diheterospora*) and these species are parasitic mainly on cyst nematodes, but also occur on slug eggs. All these species produce dictyochlamydospores with different frequencies and relative position to the agar surface. The distinctness of *P. chlamydosporia* from *P. suchlasporia*, each with two varieties, is confirmed. The genus *Rotiferophthora* being a sister group of *Pochonia* is found distinct. Eight anamorph taxa are defined and keyed out, including two new species, *P. microbactrospora* and *P. rubescens*. A teleomorph, *Cordyceps chlamydosporia*, was discovered for the type species *P. chlamydosporia*. The parasite of rust fungi, *Verticillium epiphytum*, and a fungicolous species with conspicuous intercalary chlamydospores, *V. incurvum*, were studied for comparison. *Verticillium epiphytum* is close to but falls outside *Pochonia*; *V. incurvum* is found to be unrelated to the Clavicipitaceae.

THE IMPORTANCE OF A MOLECULAR PHYLOGENETIC APPROACH IN THE STUDY OF THE INSECT CLAVICIPITACEAE

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The Clavicipitaceae are a unique family of the fungal kingdom and molecular phylogenetics is beginning to clarify its relationship to the Hypocreales. Whereas most fungi have evolved with plants, the Clavicipitaceae is a family dominated by invertebrate pathogens. This is not unique: the Laboulbeniales is wholly dependent on insects. The Clavicipitaceae, however, contain pathogens of invertebrates and of plants. While it is logical to presume that these invertebrate pathogens might have evolved from a plant-pathogenic Clavicipitaceae the opposite is proving true from recent molecular phylogenetic studies. Plant pathogenic genera (e.g. *Claviceps*, *Balanisia* and *Epichloë*) appear to derive from *Cordyceps* - which is ancestral in the family. Invertebrate pathogens (e.g. *Torrubiella* and *Hypocrella*) also seem to be recently derived from *Cordyceps*. Evidence for this is present in the more restricted host ranges of *Torrubiella* (mostly spiders and Homoptera) and *Hypocrella* (Homoptera). Also, both genera have fewer species (ca. 60 *Torrubiella*; ca. 35 *Hypocrella*). Insect Clavicipitaceae are increasingly the subject of screening work in novel metabolite discovery. With the advent of molecular phylogenetics I expect the future will allow the tracking of the evolution and loss of metabolites. But especially, the Clavicipitaceae offer rewarding challenges as a fungal family where plant-pathogenic genera have derived from invertebrate-pathogenic genera rather than the other more usual way round. Work with plant endophytic Clavicipitaceae shows that many provide an anti-feeding capability for their host plants. This raises the question of whether this capability derived recently from the plant pathogen or whether it is a carry-over from an ancestral insect pathogen. Again, molecular phylogenetics combined with novel metabolite discovery programmes may help to answer such questions in the future.

CORDYCEPS UNILATERALIS IN THAILAND: AN EXAMPLE OF 'HIDDEN SPECIES'

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The genus *Cordyceps* contains *ca.* 300 described species plus at least the same number of synonyms. Many more species await description. In surveys of natural forest in Thailand a species was identified from ants attached to the underside of leaves as *Cordyceps unilateralis*. However, our re-assessment of the collections (especially recent collections) indicates that *Cordyceps unilateralis* in Thailand consists of three related species. Previously, only one other species on ants had been reported with overall morphology similar to *Cordyceps unilateralis* - namely *Cordyceps formicivora*. This was rejected for much of the twentieth century as a synonym of *Cordyceps unilateralis* and was treated so in our original identifications. Comparison of descriptions of '*Cordyceps unilateralis*' from around the world suggest that other workers have also described as *Cordyceps unilateralis* specimens that might be better named as *Cordyceps formicivora*. Material from Thailand clearly separates into species with hyaline ascospores (comparable with typical *Cordyceps unilateralis*) and ones with pigmented (yellow-brown) ascospores (comparable with typical *Cordyceps formicivora*). Significantly, the ascospore sizes reported for Thai material and from published records cover a broad range (90 – 160+ μ m) suggesting more than one species. These species are especially significant to understanding the phylogenetic relationships of the genus *Cordyceps*. Petch erected the genus *Ophiocordyceps* (based on *Cordyceps blattae* but including *Cordyceps unilateralis*) to accommodate species that produce whole, stout ascospores. This was later reduced to the level of a sub-genus. Now we have evidence suggesting that *Cordyceps unilateralis* is a whole-ascospored ancestor of the problematic *Neocordyceps* clade (which have ascospores that typically separate into 64 part-spores).

A REVISION OF *BIONECTRIA* (BIONECTRIACEAE, HYPOCREALES, ASCOMYCETES) WITH ANAMORPHS IN *CLONOSTACHYS*

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The genus *Bionectria* is reviewed based on morphological characters and sequence analyses of the rDNA (ITS1-5.8S-ITS2, and partial LSU) and partial β -tubulin gene. Forty-four holomorphic or anamorphic species are distinguished. They grow as saprotrophs on dead plant material or in soil, as necrotrophic mycoparasites on a wide taxonomic range of fungi, or, rarely, as parasites on oomycetes, myxomycetes, ticks, nematodes, and molluscs. Their ecological characters, such as common occurrence in soils, saprotrophism, and unspecific invasive necrotrophism, reveal *Bionectria* taxa as potential biocontrol agents, some of which are already used against fungal plant pathogens. The teleomorphs of *Bionectria* are morphologically diverse. Based on stromatal morphology, stroma perithecium wall interface, perithecial wall anatomy, and habit of the perithecia on the natural substratum, as well as ascospore ornamentation and septation, six subgenera are newly distinguished. The anamorphs of *Bionectria* are classified in *Clonostachys*, including taxa formerly classified in genera like *Verticillium*, *Gliocladium*, *Sesquicillium*, *Spicaria*, *Dendrodochium*, or as *Myrothecium*. Anamorphic characters such as penicillate, often dimorphic conidiophores, conidia held in imbricate chains (often collapsing to slimy masses), sometimes formation of sporodochia or intercalary phialides, and somewhat curved conidia with a laterally displaced hilum are considered more significant than teleomorphic features for the characterization of *Bionectria/Clonostachys* as a clade of naturally related species. For species delimitation in pure culture, conidiophore dimorphism, the branching pattern within the different types of conidiophores, and the tendency to sporodochium formation are emphasized and illustrated, while the pigmentation of the conidial masses (e.g. greenish versus pale orange) is in some cases not significant at species level. The morphologically delimited species are supported by DNA sequence characters, mainly of the introns of the β -tubulin gene that possibly will play a major part in future identification strategies.

Asian International Mycological Congress, 17-20 Sept. 2001, Karaj, Iran

***ACREMONIUM LACTUCUM* SP. NOV., THE CAUSAL AGENT OF
LEAF BROWN SPOT OF LETTUCE, *LACTUCA SATIVA***

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Acremonium lactucum sp. nov. is described and illustrated. It was isolated from yellowish-brown spot lesions on the lower leaves of lettuce (*Lactuca sativa*) in Taiwan. *A. lactucum* is characterized by forming cylindrical two-celled, hyaline, smooth-walled conidia in slimy heads. The vegetative hyphae are thin-walled, appressed to slightly cottony, pale orange to orange. The phialides are orthotropic, simple or occasionally branched. The hyaline chlamydospores are globose to oval, single cell, abundant, terminal or intercalary. Its pathogenicity and host range are studied and discussed in detail. (Poster 1)

ISOLATION OF *PAECILOMYCES FARINOSUS* FROM *EURYGASTER INTEGRICEPS* IN IRAN

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In 1999, a fungus was isolated from *Eurygaster integriceps* (from Isfahan and Varamin regions) and *Coccinella septempunctata* (from Varamin region). Its characteristics were as follows:

Colonies on potato dextrose agar (Difco) grew moderately slow at 24°C, with a diameter about 15-25 mm during 7 days and 25-40 mm at 14 days and its spores scattered around Petri dish and grew randomly. The shape of the colony was funicular, usually white or occasionally very pale yellow or rarely very pale pink. The color of these colonies from the other side of the Petri plate was creamy (yellowish-white) or yellowish-brown or rarely yellowish-orange. Conidiophores, with several stages of branching ended with phialides, which was flask shape from single to pericillate heads in whorls, and 5-16 µm long and 1-2.5 µm width at the broadest parts. The conidia of isolates were ellipsoidal and their sizes were 2.4-4 × 1.8-2.8 µm (from Isfahan region, Sunn pest), 2.1-3.9 × 1.8-2.5 µm (from Varamin region, Sunn pest), 2.3-4 × 1.9-2.8 µm (from Varamin region, Ladybird). (Poster 2)

Asian International Mycological Congress, 17-20 Sept. 2001, Karaj, Iran

IDENTIFICATION OF FUSARIA ASSOCIATED WITH ROOT AND BASAL ROT OF ONION IN ESFAHAN

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Root and basal rot is one of the important fungal diseases in onion fields in Isfahan where *Fusarium* species are the serious ones. The root-rot disease becomes manifest in young seedlings and at any subsequent time in the growth period of the host. Affected roots turn cream, shrivel and then die. As the plant grows new roots, they in turn eventually become diseased and functionless. The leaves of affected plants die back rapidly from the tip. If the procedure continues throughout the growing season, the affected plants reduced food supply results in the formation of mere scallions or small bulbs. Isolation and growing cultures for identification were with consistent and proper preparation of cultures on WA, PDA, SNA, CLA, Nash & Snyder and SA (Soil Agar). 129 obtained isolates were identified by using morphological characters and various keys. All isolates were categorized in 10 species including *Fusarium oxysporum*, *F. solani*, *F. proliferatum*, *F. culmorum*, *F. subglutinans*, *F. sambucinum*, *F. equiseii*, *F. acuminatum*, *F. semitectum* and *F. graminearum*. Distribution and disease severity results indicated that *F. oxysporum* was the most prevalent followed by *F. solani*, and *F. proliferatum* was the most aggressive. The test for percent onion seeds decay revealed that the highest was of *F. proliferatum* with 71.2 percent followed by *F. oxysporum*, *F. solani* and *F. culmorum* with 60.6, 60 and 55.2 percent, respectively.

ISOZYME POLYMORPHISM AND PROTEIN PROFILE IN IRANIAN STRAINS OF *FUSARIUM OXYSPORUM*

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Fusarium oxysporum is a soil-borne fungus that constitutes a group of variants including non-pathogenic, formae speciales and races that can not be differentiated solely based on morphological parameters. This study was undertaken to investigate genetic diversity among *F. oxysporum* strains using biochemical markers. SDS-PAGE as well as native PAGE were used in analyzing the relationships among *F. oxysporum* strains. A total of 13 isolates of *F. oxysporum* f. sp. *melonis* (FOM) from Iran, USA and France, 9 isolates of seven formae speciales from Iran and one isolate of *F. o. f. sp. niveum* from USA were compared based on isozyme and total soluble protein patterns. In this study, isolates of Iranian FOM from races 1 and 1,2 (belonging to one VCG group), three isolates of USA FOM from races 2 and 0 and two isolates of FOM from France were selected. Isozyme analysis of alkaline phosphatase (ALP), catalase (CAT), esterase (EST), malate dehydrogenase (MDH), xanthine dehydrogenase (XDH) and superoxide dismutase (SOD) revealed polymorphism among 21 enzyme systems being examined and determined 22 electrophoretic phenotypes among *F. oxysporum* isolates. At least ten putative loci for these six enzymes were detected and they were all polymorphic. The highest degree of genetic diversity was observed by CAT, EST and XDH loci. Twenty-two isolates were grouped into five distinct subgroups by UPGMA analysis at the similarity index of 20%. Ninety-one percent of the isolates including FOM isolates from Iran and USA, FOM isolates from France with one isolate pathogenic on pepper from Iran and isolates of five formae speciales from Iran were grouped in three subgroups, respectively. Isozyme polymorphism in formae speciales was highly correlated with VCGs and geographical origins and to a lesser extent with races. SDS-PAGE analysis showed some variations among isolates of FOM with different geographical origins. This study suggests that isozyme analysis could be a useful tool for identifying genetic diversity within *F. oxysporum* f. sp. *melonis*. (Poster 3)

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DIVERSITY IN IRANIAN *Pyricularia grisea* POPULATIONS BASED ON REP-PCR GENOMIC FINGERPRINTING

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The population structure of *Pyricularia grisea*, the rice blast pathogen was analyzed using rep-PCR DNA fingerprinting with two outwardly directed primer sequences from *Pot2* (a repetitive element found in the fungal genome) in Gilan and Mazandaran, two major rice growing provinces of Iran. The frequency and distribution of particular haplotypes within *Pot2* delimited lineages has not been examined in Iran. A total of 221 monoconidial isolates of the pathogen were collected from 12 cultivars in 22 cities during 1997-2000. Total DNA was extracted and long PCR conditions, including increased extension time (10 min) and higher pH (9.2) were used to amplify sequences lying between *Pot2* elements. It generated variable length fragments ranging from 550 bp to longer than 5 kb. Each isolate was subjected to DNA fingerprinting, and both the *Pot2* lineage (isolates with $\geq 70\%$ band similarity) and haplotype frequencies were determined. Based on phenetic analysis six distinct *Pot2* fingerprint lineages were detected (designated A, B, C, D, E and F). Among 221 isolates 12, 2, 2, 4, 3, and 18 haplotypes (isolates which had DNA fingerprints which differed by 1 to 30%) were identified within lineages A, B, C, D, E, and F, respectively. The lineage F made the largest fingerprint group with 62% of the 221 isolates. It was distributed throughout sampling sites and all rice cultivars where isolates were recovered. The lineage A, second fingerprint group with 28% of total isolates was mostly distributed in west part of sampling sites. There was a relation between lineage A and some susceptible local cultivars. However, these data indicated a low-level genetic diversity in rice blast pathogen population in Iran relative to several other populations in other countries. There was a selection effect of cultivars on some lineages so that some cultivars were effective in excluding of certain lineages.

PHYLOGENETIC STRUCTURE OF THE GENUS *LEVEILLULA* INFERRED FROM INTERNAL TRANSCRIBED SPACERS RIBOSOMAL DNA SEQUENCES

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The nucleotide sequences of the nuclear ribosomal DNA, including ITS1, ITS2 and the 5.8S rDNA were determined for 54 specimens representing 13 *Leveillula* species. Whole-cell DNA was isolated from cleistothecia or mycelia using Chelex method. Some 600 nucleotide sequences of the ITS regions was amplified twice by PCR using nested primer set, ITS1, ITS5 and P3. Direct sequencing of PCR product was done in an Applied Biosystems 373A sequencer. Phylogenetic analyses revealed that *Leveillula* species formed six clades and three basal taxa. The taxonomic positions of several species that are well characterized by morphology of conidia, especially primary conidia, are supported by the present molecular analyses. Twenty-six collections of *Leveillula taurica* recovered from 14 different plant families formed a distinct clade with *L. chrozophorae*, *L. duriaei* and *L. elaeagni*, and showed high homology in the ITS regions. Five isolates of *L. taurica* recovered from the Asteraceae, Balsaminaceae, Fabaceae and Campanulaceae showed high sequence diversity, in contrast with other *L. taurica* specimens, and clustered separately or with other taxa. Three *Leveillula* isolates from Asteraceae occupied a basal position in our phylogenetic trees. These results suggest that *Leveillula* species have colonized some host plant families such as Asteraceae several times during evolution or alternatively the composites are associated with an early evolution of *Leveillula* followed by host expansion from the Asteraceae to other plant families. Possibility of monophyly of *L. taurica* s. l. significantly rejected by Kishino-Hasegawa and Templeton tests indicating that *L. taurica* s. l. is a complicated species.

PHYLOGENETIC ANALYSIS OF THE IRANIAN POWDERY MILDEW FUNGI USING NUCLEOTIDE SEQUENCES OF THE 28S RIBOSOMAL DNA

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The nucleotide sequences of the 28S nuclear rDNA were determined for 27 powdery mildew taxa to infer the phylogenetic relationships for these fungi. Whole-cell DNA was isolated from cleistothecia or mycelia using Chelex method. Some 650 nucleotide sequences of the 5' end of the 28S rDNA was amplified twice by PCR using nested primer set, PM3, TW14 and NLP2. Direct sequencing of PCR product was done in an Applied Biosystems 373A sequencer. The results showed that powdery mildew taxa are divided to five groups, which were distinguish by their morphology. Members of *Erysiphe* section *Erysiphe*, *Microsphaera* and *Uncinula* clustered together. *E. sect. Galeopsidis* and *E. sect. Golovinomyces* separated from the *E. sect. Erysiphe* and made Euoidium without fibrosin bodies group. *Leveillula* and *Phyllactinia* showed close evolutionary relationship and clustered together. The genera including *Cystotheca*, *Podosphaera*, and *Sawadaea* formed a monophyletic group in 98% bootstrap replications. These fungi are well characterized by the presence of fibrosin bodies in the conidia. *Blumeria graminis*, which is characterized by some unique morphological characters clustered with fibrosin body lineage with a low bootstrap values. This result showed that *B. graminis* is not closely related to *Erysiphe* species. The nucleotide divergence for the genera ranged from 0.50 to 14.10%. The lowest nucleotide divergence was found between *Microsphaera* and *E. Sect. Erysiphe* species (0.50-4.50%). *Podosphaera* and *Sphaerotheca* showed a low level of divergence too (2.30-2.60%), which suggests a close relationship between these two genera. (Poster 4)

ORBILIACEOUS NEMATODE-TRAPPING FUNGI: A NEW GENERIC CONCEPT

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Perfect states are unknown for the majority of orbiliaceous nematode-trapping fungi. There are several genus concepts for these anamorphic fungi, which are similar because authors preferentially used the morphology of conidia and conidiophores for delimitation. The mode and morphology of the trapping device, however, was only considered for species delimitation. A new generic concept is proposed with the mode of trapping device as main morphological feature for generic delimitation. This concept corresponds well with molecular (rDNA sequences: 18S, ITS I, II), ecological, physiological, and biological features. Four genera are proposed: *Arthrobotrys* Corda em. forming adhesive networks, *Drechlerella* Subram. em. forming constricting rings, *Dactylellina* M. Morelet em. forming stalked adhesive knobs, and *Gamsyella* Scholler, Hagedorn & Rubner gen. nov. producing adhesive columns and unstalked knobs.

SOME INTERESTING RHYTISMATACEOUS FUNGI IN ASIA

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Rhytismataceous fungi were said to conjure up a picture of a north temperate and boreal group, but simultaneously, it was suggested that the numerous exceptions exist and undermine this generalization. To determine whether non-random patterns exist at all, the necessity to take a close look at the host range and mycogeography of individual members was emphasized (Pirozynski, Weresub, 1979: 101). Some observations on rhytismataceous fungi found in the Russian Far East support the existence of peculiar patterns of distribution. There are species [*Colpoma deusta* Sherwood, *Lirula abietis-concoloris* (Mayr) Darker, *Lophodermium uncinatum* Darker] that possess an amphipacific area and occur along western coasts of North America and northern Asia. Other species (*Lophodermium pini-pumilae* Sawada, *L. pini-sibiricae* C. L. Hou et S. Q. Liu) are only known from Asian countries (China, Japan, Siberian and far-eastern Russia). There is even such a rare case of 'endemic' species as *Colpoma betulae* (Fr.) Lar. N. Vassiljeva that was described by Fries (1823) from Kamchatka Peninsular and found again only in 1981 in the same region. *Colpoma* specimens were also collected on *Lonicera* and *Pentaphylloides* in Kamchatka and Magadan regions, while there are no records of such fungi on these host plants in the literature. Some species are known to be very widely distributed in the northern hemisphere but can display interesting geographic peculiarities. For example, *Rhytisma acerinum* (Pers.) Fr. was said to infect many *Acer* spp., but the diversity of maples in the Russian Far East host only *R. punctatum* (Pers.) Fr. Very characteristic stromata of *R. umbonatum* (Hoppe) Rabenh. (cf. IMI Descr. No. 1340) were found in arctic and subarctic conditions of Magadan and Kamchatka regions, while *R. salicinum* (Pers.) Fr. occurs in areas with milder climate. (Poster 5)

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SPORE SIZE VARIATION OF *GORGONICEPS* KARST. (DISCOMYCETES) FROM THE RUSSIAN FAR EAST

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The genus *Gorgoniceps* includes a group of inoperculate Discomycetes (Leotiaceae) with small and smooth apothecia and more or less filiform multiseptate ascospores. This genus includes 6 (Hawksworth *et al.*, 1995) or 7 (Seaver, 1949) species. They are widespread, especially in temperate zones (Europe, Russian Far East, North America). Similar to other genera of the Leotiaceae the species of *Gorgoniceps* are divided into groups in accordance with spore size. Species of *Gorgoniceps* are similar to those of *Vibrissea* and *Apostemidium* (Vibrissaceae) having large and septate ascospores. Several ranges of variation of spore size in the genus *Gorgoniceps* are observed, namely 12-15 μm (*G. ontariensis*), 30-35 μm (*G. iowensis*), 35-50 μm (*G. punilloni*, *G. confluens* and *G. montonensis*), more than 50 μm (*G. aridula* and *G. jamaicensis*). In addition, species of *Gorgoniceps* can be divided in accordance with the types of substrata. They occur on wood, cones and needles of pine-trees or deciduous trees or herbaceous stems (palms, bamboo). This character allows separating species with the same ascospore size.

There is a gap in the series of ranges of spore length between 15 and 30 μm , but, actually, this gap covers two ranges found in two species that may be described as new ones. One of them has spore length 15-24(25) μm and occurs on bark of *Betula tauschii* (VLA D-312, VLA D-311), while the second one has spore length 24-30 (32) μm and occurs on decaying wood of pine-trees (VLA D-314).

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As an International Mycological Congress, 17-22 Sep., 2001, Karaj, Iran

TOWARD A BETTER CIRCUMSCRIPTION OF *TREMATOSPHERIA* (DOTHIDEALES)

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The circumscription of *Trematosphaeria* is amended through comprehensive studies of several relevant genera, including *Astrosphaeriella*, *Lophiostoma* and *Melanomma*. *Trematosphaeria pertusa*, the type species of this genus, was reexamined. Characters, such as clypeate ascoma, clavate ascus and warted ascospore, are introduced to apply to the classification. They are remarkably correlated and consistent in the species assigned to this taxon. With the advent of the explicit taxonomic criteria, combinations of name are made to conform the new definition. Accordingly 12 species are hitherto considered appropriate in *Trematosphaeria*. The segregation among its similar genera are, therefore, readily distinguishable. *Astrosphaeriella* is separated by the flattened base of ascoma, *Lophiostoma* by the characteristic sporal sheath, and *Melanomma* by the smooth spore and non-clypeate ascoma. Taxonomic value of compressed ostiole, which used to define *Lophiostoma*, is reappraised, as it is often encountered in species grouped under *Trematosphaeria*. Septation of spore is various and is another feature that is not given much weight in this treatment. In the light of the sound circumscription, more species will be added to *Trematosphaeria* as more specimens are examined. (Poster 6)

SOME NEW PHYTOPARASITIC FORMS OF HYPHOMYCETE GENUS *STENELLA* ASSOCIATED WITH FOLIAR SPOTS FROM INDIA

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Stenella is also one of the important segregates of *Cercospora* complex. Earlier there was some confusion over this genus, and it was occasionally mistaken with *Cladosporium*, *Cercospora*, *Mycovellosiella* and *Ramichloridium*. However, Deighton and Muller clearly defined the distinct generic limits of *Stenella*. Deighton recognized the close similarities of *Stenella* with the aforesaid genera, particularly *Mycovellosiella*, and he has defined diagnostic characteristics of *Stenella* so as to distinguish it. These efforts established this genus beyond ambiguity. Now, it is a well-established genus with more than 125 species. Most of them are parasite and some are saprophyte, which are mainly confined to tropical to subtropical regions. The genus *Stenella* is an important cercosporoid genus, which creates severe leaf-spot diseases, ranging from discoloration to necrosis of the leaf tissues. These fungi affect a large number of plants and produce some diseases of crops and horticultural plants such as leaf spots of *Alcasia* sp., *Crotalaria* sp., Coffee, *Citrus*, *Eugenia*, *Aegle*, *Prunus* and *Bougainvillea*, etc. In this connection, this paper provides description and illustration of two new species of *Stenella* viz., *Stenella cordiae* and *S. grewiae*, occurring on living leaves of *Cordia crenata* (Boraginaceae) and *Grewia asiatica* (Tiliaceae), respectively. These species have been compared with their allied or similar taxa. The scrap-mounts have been prepared to observe these materials, under different magnifications of compound microscope.

IDENTIFICATION OF *PENICILLIUM* SPECIES IN SHIRAZ AREA

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During 2000, *Penicillium* species were collected from Shiraz vicinity, including Badjgah (15km north of Shiraz) and Pars dairy factory (25km north of Shiraz). Samples were isolated from contaminated culture media, rotted plant materials and cheese. Hyphal tip isolates were grown on Czapek yeast extract agar (CYA), malt extract agar (MEA) and 25% glycerol nitrate agar (G25N), and examined after seven days incubation. Nitrogen or sugar consumption and indole production were also tested whenever necessary using creatine sucrose neutral agar (CSN) medium and Ehrlich reagent, respectively. Based on morphological and physiological criteria the following species were identified: *P. chrysogenum*, *P. citrinum*, *P. griseofulvum** and *P. waksmanii** (all from cheese), *P. aurantiogriseum**, *P. expansum* (from both cheese and contaminated media), *P. brevicompactum*, *P. crustosum**, *P. miczynskii** and *P. viridicatum* (from contaminated media), *P. italicum* (from citrus fruit) and *P. digitatum* (from kumquat fruit, in market, originated from northern Iran). The *Penicillium* species with asterisk are new to Iran flora. (Poster 7)

POSSIBLE EVOLUTION OF PEDICILLATE TELIOSPORED RUST FUNGI

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Rust Fungi are known to possess either sessile or pedicillate teliospores. Generally it is believed that pedicillate teliospored rusts have evolved from sessile teliospored rusts. During a study of the genus *Melampsora* the author came across several teliospores being formed in older uredinia. The possible evolutionary significance of these teliospores is going to be presented. Specimens of *Melampsora* on different host plants were obtained from various International Herbaria viz., B, BERN, C, DAOM, DAVFP, E, FH, G, HBG, HClO, IMI, K, L, LE, LEV, LPS, PAD, PAV, PC, PDP, S, STE (U), UPS. Spore scrapings were mounted in lactophenol or lactophenol with cotton blue. Both free hand and microtome sections were made. The processing and embedding of the microtome sections was done as per the procedure described by Johansen (1940). The teliospores of the genus *Melampsora* are single-celled, sessile and produced in sub-epidermal or sub-cuticular non-erumpent single-layered rusts. But during the course of the present investigation in some species they were found deep inside the cortex or deep inside the mesophyll tissue. In some species instead of single layered telial crust either two or three layered telial crusts were observed. Interestingly in several specimens the teliospores were found coming in older uredinia. These teliospores have shown lot of variation in their shape. Based on their shape they were somewhat similar to the teliospores of *Puccinia*, *Uromyces*, *Diorchidium*, *Gymnoconia* etc. It is a generally accepted theory that the pedicillate teliospored rusts have evolved from sessile teliospored rusts. The present study has shown that the teliospores which were produced in older uredinia were resembled those of several pedicillate teliospored rusts. Since normally the teliospores of the genus *Melampsora* are subepidermal/subcuticular and non-erumpent. They never get an opportunity to take different shapes. But once exposed these teliospores are taking different shapes. So the author is of the opinion that in all probability the genus, *Melampsora* during the course of evolution might have given rise to pedicillate rusts.

CONNECTING TELEOMORPHS AND ANAMORPHS OF SELECTED GRASS RUSTS USING ITS SEQUENCE ANALYSES

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The majority of rust fungi (Uredinales) on grasses (Poaceae) are heteroecious or are assumed to be heteroecious. Grasses are the telial hosts harboring spore stages II and III and species from other families (e.g. Ranunculaceae, Boraginaceae, Berberidaceae) serve as aecial hosts (with spore stages 0 and I). For about 73% of the grass rust species the aecial host is not known so far. Often, grass rust species have several aecial host species, which may belong to different genera or even different families. On the other hand, one host species may harbor spore stages 0 and I of different rust species. Considering this host diversity and the lack of sufficient morphological characters it is difficult to connect anamorph and teleomorph, especially when infection experiments cannot be carried out. To obtain additional data on anamorph-teleomorph connections within grass rust fungi we sequenced and compared the internal transcribed spacer region (ITS1, 5.8S gene, ITS2) of selected herbarium specimens. These were i.) aecia of the form genus *Aecidium* which could not be assigned to a certain species but all of which were assumed to be part of the life cycle of grass rust fungi, and ii.) stages II and III of known species which were used as a reference. Further references were obtained from GenBank and our own databank. The following new anamorph-teleomorph connections could be found: Aecia on *Clematis orientalis*, *Berberis* sp. and *Cerinthe minor* are conspecific with *P. wolgensis*, *P. brachypodii* s.l., and *P. recondita* s.str., respectively. The aecial host of *P. wolgensis* was unknown so far and for the first time it could be shown that *C. minor* harbors *P. recondita* s.str. Aecia on *Thalictrum* spp. belong to *P. persistens* s.l. and an aecium on *Zygophyllum* sp. turned out to be distantly related to *P. sorghi*. (Poster 8)

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PHYLOGENETIC ANALYSIS OF *Puccinia graminis* S. L., BASED ON ITS SEQUENCES

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To study the phylogenetic relationships within the black stem rust complex (*Puccinia graminis* Pers. s.l.), ITS1, 5.8S and ITS2 sequence data of 20 herbarium specimens from Asia (Iran), North America (USA) and Europe (Germany), were evaluated. The length of the ITS region including the primer region ranged from 686 to 701 bp. Alignment of the sequences showed that the 5.8S gene was highly conserved, whereas ITS1 and ITS2 exhibited polymorphisms due to base substitution, insertion or deletion of nucleotides. Using neighbor-joining analysis the phylogram yielded three major clades. The first clade consisted of *P. graminis* isolates on wheat (*Triticum aestivum*) and various grasses from Iran, the second one isolates on *T. aestivum* from the USA, on *Secale cereale* from Germany and on *Elymus* and *Eremopyrum* species from Iran and only isolate on *Avena* sp. from Iran, formed the third clade. In the second analysis, sequences of six different *P. graminis formae speciales* from different continents obtained from GenBank were included (alignable data were the last 42 bp of ITS1, and all of the 5.8S and ITS2 sequences). This second phylogram yielded the same three major groups two of which were supported by high bootstrap values. The molecular data do not support common taxonomical concepts based on urediniospore morphology. Also, related host plants do not mirror relations within the rust complex. The genetic and morphological diversity of isolates from Iran is clearly higher in comparison to isolates from other geographical areas evaluated for this study. This high level of variation supports the theory that the ancestral *P. graminis* developed in Iran and that this area is one of the primary gene centers of the black stem rust. (Poster 9)

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MOLECULAR PHYLOGENETIC RELATIONSHIPS AMONG SELECTED CEREAL AND GRASS RUSTS BASED ON ANALYSIS OF NUCLEAR ITS SEQUENCES

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Ribosomal internal transcribed spacers (ITS1, 5.8S rRNA gene and ITS2) were PCR-amplified and sequenced from herbarium specimens of different graminicolous *Puccinia* species. These sequences were aligned with the profile mode of Clustal X. Phylogenetic analyses were performed using the neighbor-joining (NJ) algorithm with the Draw N-J Tree option of Clustal X. Phylogenetic analysis based on the ITS sequence data indicated that *Puccinia hordei sensu lato* is a complex species. We recognized three taxa within this complex species: *P. hordei sensu stricto* on *Hordeum vulgare*; *P. holcina* on *Lolium temulentum*, *Lophochloa phleoides* and *Trisetum flavescens*; and *P. sp.* on *Taeniatherum asperum*. In the *P. recondita* species complex we also recognized different taxa as follows: *P. recondita* s.s. on *Secale segetale* and *Elymus* sp.; *P. bromina* on *Bromus* spp.; *P. persistens* ssp. *triticina* (wheat leaf rust) on *Triticum aestivum* and *Aegilops tauschii*; and *P. persistens* ssp. *agropyri* on *Elymus hispidus*. Our phylogenetic analysis showed *P. recondita* s.s. is more closely related to *P. hordei* s.l., than to *P. persistens*. ITS sequences of leaf rust from *Triticum aestivum* and leaf rust on *Aegilops tauschii* were identical, which supports the idea that leaf rust collections from wheat could infect *Aegilops* species. On the basis of this analysis, variation also was observed among specimens of *P. striiformis* from wheat, *Dactylis glomerata* and *Poa pratensis*. This result agrees with a previous study on isozyme phenotypes of yellow rust from these hosts. The taxonomic implication of these results is that populations of *P. striiformis* on the above-mentioned hosts should be considered as different taxa at least at the infraspecific level. (Poster 16)

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GERMINATION OF SPORES OF *MICROBOTRYUM* SPECIMENS OBTAINED FROM HERBARIA

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Certain smut fungi on dicots, which were originally placed in the genus *Ustilago*, turned out to be very much different from *Ustilago* species on monocots with respect to ontogenetical, ultrastructural, biochemical and molecular features. Most of them were transferred to a different genus, *Microbotryum*. However, there is not only a difference at the genus level. Indeed, *Microbotryum* is more closely related to rust fungi (Uredinales) than to "true" smut fungi. For this reason Bauer et al. (Can. J. Bot. 75, 1997) placed rust fungi and *Microbotryum*-related taxa (Microbotryales), in one common class, the Urediniomycetes. Most other smut taxa including *Ustilago* spp. on monocots were placed in a separate class, the Ustilaginomycetes. Whereas the germination of spores of many Ustilaginomycetes and Uredinales species has been studied in detail by taxonomists, plant pathologists, and ecologists, there is little information available on the germination of *Microbotryum* species. We studied the germination of species restricted to Polygonaceae from Germany. Since most species are endangered or at least rare in central Europe (see Foitzik, O. Schriftenr. Vegetationsk. 28, 1996 and Scholler, Regensb. Myk. Schr. 6, 1996) the main objective of this study was to find out if spores of endangered species from herbarium specimens can still germinate and whether species, if necessary, can be revitalized. Spores were put on water agar plates under constant light and temperature conditions. The germination rate was obtained after 13 d. In addition we examined the correlation between the germination rate and the age of the spores and chemicals often used for preservation of specimens in herbaria. (Poster 11)

A REVISION OF THE SMUT FUNGI OF IRAN

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In the present study, previously reported smut fungi of Iran are reviewed. For this purpose all specimens preserved in the fungus section of Herbarium Ministerii Iranici Agriculturae "IRAN" as well as newly collected ones were studied. Moreover, all taxonomic and/or floristic papers so far published for smut fungi of Iran were considered. Important characteristics such as: host-plant(s), symptoms (sorus), spore morphology (attachment, size, shape, colour, wall structure, ornamentation and sheath), immature spores, sterile cells and spore germination were used for the identification of each specimen. The results showed that 76 species of smut fungi belonging to 13 genera exist in Iran i.e. *Anthracoidea* (2 spp.), *Entyloma* (10 spp.), *Farysia* (1 sp.), *Microbotryum* (2 spp.), *Moesziomyces* (1 sp.), *Neovossia* (1 sp.), *Sorosporium* (1 sp.), *Sporisorium* (1 sp.), *Urocystis* (17 spp.), *Ustilago* (18 spp), and *Vankya* (3 spp.). All the genera and their species were described and their host-plant(s) and geographical distribution in Iran were also mentioned. In most cases two figures (one macroscopic and one microscopic) were drawn. (Poster 12)

DIFFERENTIATION OF ISOLATES OF *NEOVossia INDICA* BY RAPD-PCR AND CLUSTERING BASED ON TELIOSPORE MORPHOLOGY

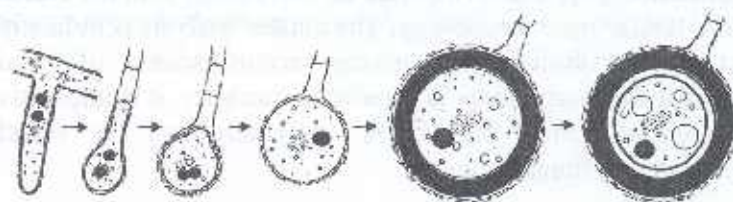
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Karnal bunt or partial bunt of wheat, caused by *Neovossia indica* (= *Tilletia indica*) was first reported from India and then from Mexico, USA, Nepal, Pakistan, Afghanistan, Iraq and Iran. In the present investigation teliospore morphology of twenty isolates of *N. indica* from different geographical regions of India was studied by light and scanning electron microscopy. The data subjected to ANOVA showed significant difference at 1% level among the isolates. UPGMA analysis divided the isolates into two major clusters. Eleven isolates were also subjected to random amplified polymorphic DNA analysis (RAPD) after monosporidial production using 34 random Operon primers. UPGMA clustering of these divided the isolates into two major clusters. This clustering had no correlation with the clustering based on teliospore morphology. The cluster analysis is indicative of the fact that variability exists among various isolates of *N. indica*. Since teliospore morphology is a variable character, it is imperative to use approaches involving DNA polymorphism for searching variability among fungal isolates.

TELIOSPOROGENESIS OF *TILLETIA INDICA*

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Teliosporogenesis of *Tilletia indica* Mitra was studied *in vitro* and *in situ* by light, fluorescent and scanning electron microscopy. During the teliosporogenesis, teliospore initials were formed in apical position in a lateral right-angle outgrowth of sporogenous hyphae. The dikaryotic plasma was concentrated in apical portions of the hypha. Fusion of nuclei occurred during the early enlargement of teliospore initial. The swelling, pyriform to spherical protoplast of the teliospore initial was delimited from the empty part of the sporogenous hypha by a sheath, which was hyaline as seen by LM, and empty part of the hypha may form appendages. Underneath the sheath, the exosporium with ornamental surface, and the smooth endosporium was deposited as seen in mature teliospores. (Poster 13)



Schematic illustration of teliospore development of *Tilletia indica*. The haploid nuclei of dikaryotic sporogenous cells fuse and form diploid nuclei during the early enlargement of teliospore initial.

GENETIC VARIATION IN IRANIAN ISOLATES OF *RHIZOCTONIA SOLANI* ANASTOMOSIS GROUP I BASED ON ISOZYME ANALYSIS AND SOLUBLE MYCELIAL PROTEIN PATTERN

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Rhizoctonia solani is a destructive pathogen with almost unlimited host range. The *R. solani* species complex includes several divergent groups on the basis of anastomosis reaction. In this study, genetic diversity among 22 isolates of *R. solani* AG1 (AG1-IA and AG1-IB subgroups) collected from Mazandaran province, Iran, was determined based on isozyme analysis and total soluble protein profile. Isozyme analysis and protein patterns were performed using non-denaturing and denaturing-PAGE, respectively. A total of 15 enzyme systems were tested, among which 6 including alkaline phosphatase (ALP), esterase (EST), lactate dehydrogenase (LDH), mannitol dehydrogenase (MADH), octanol dehydrogenase (ODH) and superoxide dismutase (SOD) generated distinct and reproducible results. The soluble protein patterns were almost similar among *R. solani* isolates examined. A total of 64 electrophoretic phenotypes were detected for all 6 enzymes used. All 16 presumed loci for these enzymes were polymorphic. Average heterozygosity percentages for the putative loci of ALP, EST, LDH, MADH, ODH and SOD were 59, 52, 58, 79, 75 and 68, respectively. Based on cluster analysis and similarity matrix, fungal isolates were divided into two genetically distant groups of I and II. These groups are in agreement with the previously reported AG1-IA and AG1-IB subgroups in AG1. Group I represented all isolates belonging to AG1-IA subgroup, whereas group II represented all isolates belonging to AG1-IB subgroup. Results from isozyme analysis indicate that the anastomosis subgrouping concept within anastomosis groups is genetically based. (Poster 14)

FLORA OF VIETNAM AND SOME NEWLY FOUND TAXA

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According to the data published from the author's studies since 1963 up today and of others since 1890, there are actually about 2000 species of Fungi *sensu lato* known from Vietnam. They are: Oomycota with 28 species, Myxomycota with 24 species, Chytridiomycota with 1 species, Zygomycota with 15 species, Ascomycota with 181 species, Mitosporic Fungi with 711 species and Basidiomycota with 1039 species (Ustomycetes with 8 species, Teliomycetes with 51 species and Basidiomycetes with 980 species). In the last two years about 250 new taxa for the checklist of Fungi flora Vietnam's were found. About 10 new taxa for science were demonstrated, namely: *Polyporus ciliatus* Fr.: Fr. var. *tropicus* var. nov., *Amanita excelsa* (Fr.) Betillon var. *nigroannulata* var. nov., *Flagelloscypha asiatica* sp. nov., *Lactarius sanguifluus* Fr. var. *asiaticus* var. nov., *Boletus queletii* Schulz. ssp. *aurantiacus* ssp. nov., *Xerocomus langbianensis* sp. nov., *Geastrum fimbriatum* Fr. var. *melanocyclum* var. nov., *Ganoderma spongium* sp. nov., *Pleurotus baolocnensis* sp. nov. Their main morphological characteristics and ecological habitats were also demonstrated. Especially the characteristics of macrofungal flora of Vietnam were demonstrated and compared with the central European mycoflora. Some ecological groups, such as lignicolous, terricolous, saprophytic, parasitic, symbiotic fungi are discussed exactly. Phalloid fungi, luminescent fungi, "fungus garden", edible fungi, fungi of pharmaceutical and other applied use are also reported.

BIODIVERSITY OF FUNGI OF THE WESTERN GHATS, INDIA, AND THEIR BIOPROSPECTIVE POTENTIAL

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The 'Western Ghats' is an extensive range of hills in south-western India, running nearly parallel to the coastline, between 8-22.5°N and 72.5-76.5°E, extending south for about 1600 km from river Tapti to Kanyakumari. The ghats (= hills) are steep along the western escarpment and gently slope in the eastern side, the average elevation of the hills being 1220 m. The Western Ghats receive southwest monsoon rain from June to September, the annual rainfall on the western side ranges from 300 to 550 mm. Mean annual temperature is 28°C to 31°C and the temperature seldom falls below 15°C. Mean annual relative humidity is above 70-80%. Under these warm and humid conditions, luxurious wet-evergreen and semi-deciduous forests flourish on the windward western side of the escarpments (Pascal, 1989). Survey of the fungi of the forests of Western Ghats has been commenced in the 1970s but the 'richness' of the mycota of the region was largely unknown, at best, partially documented (Subramanian, 1987; Subramanian & Bhat, 1987; Bhat & Kendrick, 1993). Systematic collection, isolation and analyses of the fungi and their habitats during the last 2-3 decades revealed that the forests of the Western Ghats are storehouses of not only rare, new and unusual microfungi but also of mycota of biotechnological creativity. The 'creativity index' was worked out based on results obtained from studies on litter and aquatic fungi of the region.

SUCCESSION OF MICROFUNGI ON TROPICAL LEAF LITTER: DOES C:N RATIO INFLUENCE THE RATE OF COLONIZATION AND THE FATE OF COLONIZERS

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The occurrence of saprobic microfungi on leaf litter of two plant species, i.e. *Careya arborea* Roxb. (Barringtoniaceae: Dicot) and *Dendrocalamus strictus* Nees (Poaceae: Monocot), subjected to 'nylon-bag incubation' method at their natural habitat, was evaluated at monthly intervals for a period of 9 months, from Sept. 2000 to May 2001. To begin with, the nylon bags contained freshly fallen leaf litter bundled together. The incubated bags were recovered from the site regularly on the 30th day of every month. The fungi were isolated from the litter following 'moist-chamber incubation' and 'particle-plating' methods. The mycoflora was analysed against the prevailing environmental conditions at the time of collection of samples and grade of decomposition of leaf litter. In all, 95 species of microfungi consisting of ascomycetes and mitosporic fungi were isolated from litter of two plant species. Besides several unidentified, many new and interesting taxa were encountered. Some of the fungi were specific to the substrate irrespective of the season and stage of litter decay whereas others were observed at a particular stage of decomposition. The most common taxa were *Cylindrocladium* sp., *Dendrosporium lobatum*, *Gonytrichum* sp., *Sporidesmium* sp., *Trichoderma* sp. The sequential appearance of fungi on litter and their succession with reference to climatic conditions was analysed. Hayes (1973) pointed out that plant litter has basic implications for the cycling of C and N and for supply of macro- and micro-nutrient elements to green plants. The carbon and nitrogen content of the leaf litter was analysed before 'moist-chamber incubation' and 'particle-plating' and the correlation coefficient with colonizing fungi was calculated. This approach greatly assisted in understanding whether the ratio of carbon to nitrogen influences the rate of colonization and the fate of colonizers.

DIVERSITY AND HOST PREFERENCE OF LEAF ENDOPHYTIC FUNGI IN THE IWOKRAMA FOREST RESERVE, GUYANA

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Endophytic fungi were isolated from living symptomless leaves of 12 tree species from two locations in the Iwokrama Forest Reserve, Guyana. Sixty-four fungal morphotaxa were characterized from 2492 cultures, which were derived from a total of 2520 sample units. Species of *Colletotrichum*, *Nodulisporium*, *Pestalotiopsis* and *Phomopsis* were most frequently isolated. Colonization was greater in samples from the midrib than in those from laminar tissue, and slightly greater at the tip of the lamina compared with the base of the leaf.

A number of studies have led to suggestions that endophytic fungi are hyperdiverse in tropical regions, and one of the main arguments cited in support of these hypotheses is host specificity combined with the high level of diversity of tropical plants. Our study has shown that there is little or no evidence of host specificity among the fungi isolated, based on morphological identification and colony characterization, and statistical analysis of the data sets obtained. We are currently using AFLP and ISSR-PCR molecular fingerprinting techniques for strain sets of *Colletotrichum* and *Pestalotiopsis* taxa in order to establish whether host specialization is evident at a genetic rather than phenotypic level.

If host specificity of fungal endophytes is indeed low, that may suggest that tropical fungal diversity is substantially less than has been assumed to date. High tree species diversity in tropical forests has been thought to be associated with escape from natural enemies which cause disproportionately high mortality close to adult trees. The observed lack of host specificity among the leaf endophytes studied here, many of which belong to well-known pathogen groups, provides tentative support for this hypothesis.

FUNGAL INVENTORY AND BIOPROSPECTING IN THE IWOKRAMA FOREST RESERVE, GUYANA

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CABI Bioscience is assisting in a major biodiversity inventory and bioprospecting programme funded by the EU in the Iwokrama Forest Reserve, Guyana, in collaboration with the Iwokrama International Centre, Guyana, the University of Guyana, the University of the West Indies, and the Royal Botanic Gardens, Kew, UK. Iwokrama is an autonomous international research and development centre, with the aim of demonstrating financial self-sufficiency through sustainable management of forest resources placed under its direct management by the Government of Guyana. The programme will focus on fungi. Integrated investigations into interactions between fungi and plants will target endophytes of indigenous plants, saprobes of fallen leaves, and correlation between endophyte diversity and leaf secondary metabolites. Seasonality and sampling strategies will also be considered.

Bioprospecting will focus on fungal cultures produced from the inventory, extracting chemicals and screening them for biological activity. Active compounds will be isolated and investigated using analytical chemical methods. A central theme of both programmes is technology transfer to enable the project to continue after the funding ceases, with staff trained in survey, isolation, culture and screening techniques, and appropriate facilities set up within the country.

To date, personnel have been trained in isolation, culture, identification and morphospecies recognition, data management, metabolite extraction and characterization, and in various biological screening procedures. Samples from the forest were used as training material, with valuable scientific outputs in both the bioinventory and bioprospecting enterprises. A large data set of endophyte-host associations has been collected, which suggests that tropical fungal diversity may be less extensive than has frequently been assumed.

ECOLOGY OF MYXOMYCETES FROM A WINTER-COLD DESERT IN WESTERN KAZAKHSTAN

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The moist chamber culture technique was used to study myxomycetes (plasmodial slime moulds) of a winter-cold desert in the Mangyschlak Peninsula (western Kazakhstan). A rather species-poor community of 27 myxomycete taxa, two protostelids and some undifferentiated myxobacteria was found. The productivity of the cultures was higher than recorded for any other ecosystem on earth. Respective estimations led to a possible spore fallout of 2-4 spores per square centimeter after a single strong rainfall.

The rank-abundance plot of the species is described best by a log series or a geometric model. Species developed in a successive sequence that correlated well with morphological features of the fructifications. Using canonical correspondence analysis, environmental parameters recorded within substrate sampling were related to species abundance. Substratum type and pH accounted for most of the variance in species distribution. Using five environmental parameters and development time as resource states, niche breadths were calculated for the 18 most common species. Bark-inhabiting myxomycetes were found to be more specialized than those inhabiting litter. Members of the first group tend to develop rapidly into small, usually stalked sporocarps without a peridium and possess protoplasmodia or minute aphanoplasmodia. Members of the second group usually have phaneroplasmodia and develop more slowly large, usually sessile fructifications with peridia. A plot of niche overlap versus Cole index of association for the most common species revealed frequent associations among species with small proto- or aphanoplasmodia. In contrast, species with larger phaneroplasmodia seem to avoid each other.

Myxomycetes in the investigated desert behaved as rather opportunistic k-strategists, using quickly all temporally and spatially changing microhabitats. A short development time and three dormant stages make myxomycetes well suited for survival in arid regions.

SYSTEMATICS AND ECOLOGY OF MEDICALLY IMPORTANT *ACREMONIUM*

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Acremonium, mostly known as *Cephalosporium* prior to 1971, has long been known to include species causing white-grain mycetoma, post-traumatic eye infections, and superficial white onychomycosis. After the rise of immunosuppressive therapies and HIV infection in the 1980's, it was also noted as an agent of opportunistic infection. *Acremonium kiliense* and *A. strictum* have both caused disseminated infections in compromised patients, as well as peritonitis in peritoneal dialysis patients. Sequencing studies have shown *A. kiliense* and *A. strictum* are related to *A. alternatum*, the type species of *Acremonium*, and are in the family Bionectriaceae, order Hypocreales. Some other medically important *Acremonium* spp., such as *A. alabamense*, are in the family Chaetomiaceae, order Sordariales. Preliminary evidence from G.S. de Hoog based on 5.8S ribosomal sequencing suggests that *A. recifei*, a well-known agent of mycetoma, may also belong in the latter group. Many species are still of unknown taxonomic affinity. Recent investigations of *Acremonium* spp. from proven cases of onychomycosis show that *A. strictum* is the most common *Acremonium* species causing this condition, but the previously unrecorded *A. sclerotigenum* is also a significant agent. Isolates called *A. potronii* previously isolated from onychomycosis consist of a diverse group of isolates requiring molecular analysis for taxonomic clarification.

RESEARCH ON EX SITU CONSERVATION AND CULTIVATION OF LICHEN GERM PLASM RESOURCES

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The transplantation of lichens by moving substrate with lichens, cultivation of mycobionts and photobionts, and a lichen gene library for conservation of lichen diversity and exploitation of lichen resources are made. The lichens used in the experiments are as follows: *Lasallia papulosa* (Ach.) Llano, *Rhizoplaca chrysoleuca* (Sm.) Zopf, *Stereocaulon apocalypticus* Nyl., and *Umbilicaria kisovana* (Zahlbr. ex Asahina) Zahlbr. etc. The results showed that the transplantation of lichens by moving substrate with lichens is feasible for conservation of lichen diversity. The cultivation and conservation of mycobionts and photobionts, and lichen gene library as the germ plasms and genetic resources are available for storage and future use for exploitation of lichen substances.

OCCURRENCES OF MACROFUNGI AT A FOREST OF TAIWAN

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Occurrences of fruiting bodies of basidiomycetes (basidioma) in relation to environmental factors at the Gaundashi forest in Middle Taiwan were investigated. For these studies, nine experimental quarter lots were set up at the forest site. The environmental factors such as air temperature, air moisture, light penetration, soil pH-value and soil water content were tested. We found that the basidioma occurrences in the quarter lots were correlated with both soil water content and a light penetration. Basidiomata appeared primarily when the sunlight absorption was less than 25% and soil water content higher than 70%. The fungal fruiting bodies were not frequent on sloping land and coniferous forests. No mushrooms were found in burnt forest, which have high sunlight intensity and lower humus and water contents, only few wood-decaying fungi were found.

BIODIVERSITY OF AGARICALES IN IRAN

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Four hundred and six taxa of Agaricales are known in Iran. These taxa belong to 17 families, and 93 genera, most of them are widespread in northern provinces of Iran, owing to their humid climate conditions. Four hundred and six taxa belong to the following families:

Agaricaceae 35, Amanitaceae 10, Bolbitiaceae 27 Boletaceae 17 Coprinaceae 42, Cortinariaceae 39, Crepidotaceae 12, Entolomataceae 13, Hygrophoraceae 6, Hygrophoropsidaceae 1, Lentinaceae 19, Lentinellaceae 2, Paxillaceae 2, Pluteaceae 19, Russulaceae 13, Strophariaceae 32, Tricholomataceae 117.

This study is based on the national project of Collection and Identification of the Fungi of Iran. All the taxa belonging to the above-mentioned families are preserved in the Herbarium of Plant Pests and Diseases Research Institute (Iran's Ministry of Agriculture Jihad), Mycology Section. (*Poster 15*)

THE EDIBLE FUNGI (BASIDIOMYCOTA) OF IRAN

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The basidiomycete flora of northern Iran is really rich and the diversity is very significant. Although there are numerous species of mushrooms grown wildly in the northern forests and over hilly areas of that region, none of them has so far been cultivated under controlled conditions. The most popular edible mushrooms, which are common among the natives, are *Pleurotus eryngii* and *P. eryngii* var. *nebrodensis*. They grow on umbellifer roots, and are harvested during the season and sent to the market. The said species are abundant and widespread in central, southern and western provinces. *P. cornucopiae*, *P. ostreatus*, *P. pulmonarius* are likewise widespread in northern provinces of Iran. Regarding the cultivated mushrooms, white button (*Agaricus bisporus*) has been intensified in Iran nowadays and there is a flourishing market for it. Underneath you will find a list of those mushrooms in the flora of Iran which are edible, and all of them are uncultivated: (The likelihood for their cultivation in future is not remote) *Agrocybe dura*, *Flammulina velutipes*, *Pleurotus cornucopiae*, *P. calyptratus*, *P. eryngii*, *P. eryngii* var. *nebrodensis*, *P. pulmonarius*, *Volvariella bombycina*, *Hypsizygus ulmarius*, *Cantharellus cibarius*, *Craterellus cornucopioides*, *Fistulina hepatica*, *Auricularia auricula-judae*, *Ganoderma lucidum*, *Laetiporus sulphureus*, *Polyporus squamosus*, *Agaricus arvensis*, *A. augustus*, *A. bisporus*, *A. bitorquis*, *A. langei*, *A. silvicola*, *Leucoagaricus badhamii*, *L. leucothites*, *Coprinus comatus*, *Macrolepiota excoriata*, *M. procera*, *M. puellaris*, *M. rhacodes*, *Lepiota americana*. Mycelia of *A. dura*, *C. comatus*, *F. velutipes*, *H. ulmarius*, *L. leucothites*, *P. cornucopiae*, *P. eryngii*, *P. ostreatus*, *P. pulmonarius* are preserved under monokaryon, dikaryon and tissue culture on PDA slopes at 9°C in culture collection, Mycology Section, P. P. D. R. I. (Poster 16)

IDENTIFICATION OF *ARMILLARIA* BIOLOGICAL SPECIES IN IRAN

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Thirty-four isolates of *Armillaria* were collected from a variety of hosts in fruit and forest regions in Iran. From basidiocarps, 3-4 monosporous cultures were obtained and then all haploid and diploid cultures paired in all of the possible cases in "haploid-haploid" and "diploid-haploid" pairs. Mating compatibility was determined after 25-35 days on the basis of differences in morphology of haploid colonies ranging from white, with aerial mycelium (fluffy) to brownish, without aerial mycelium (crustose). Six compatible groups named Iran Inter-Sterile Groups (IISG) were identified. IISG1 with only one isolate, IISG2 with seventeen isolates, IISG3 with eight isolates, IISG4 with only one isolate, IISG5 with two isolates and IISG6 with five isolates. Representative haploid and diploid isolates from Iran inter-sterile groups of *Armillaria* (IISG) were paired with European and Japanese haploid testers. Six intersterile groups were authenticated as *Armillaria mellea*, *A. cepistipes*, *A. gallica*, *A. borealis*, *Armillaria* sp. (IISG5) and *Armillaria* sp. (IISG6). However two groups (IISG5 and IISG6) were not compatible with any of tester species. (Poster 17)

NOTES ON *TRANZSCHIELIA DISCOLOR* OCCURRED IN GOLESTAN PROVINCE, IRAN

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In summer of 2000 some diseased leaves of plum (*Prunus domestica* L.) collected from Kalaleh of Golestan province in North east of Iran, with pale yellow and dark spots on the lower surface. Microscopic slides prepared from these spots in polyvinyl alcohol-lactic-glycerol (PVLG) mounting medium. Two types of spores released from these spots were studied with bright-field microscope (BFM) showed disease the causal agent is *Tranzschelia discolor* (Fuckel) Tranzschel and Litv. with the following characters:

Urediniospores single, with pale yellow to yellow colour, ellipsoid oblong-ellipsoidal, $(18-4) 26 (-32.2) \times (11.5) 16 (-18.4) \mu\text{m}$ (L×W), spore wall thicker in an apex and dull rough or about two third echinulate surface. Capitate paraphyses also were present with these spores. Teliospores two-celled, divided by a horizontal septum into 2 cells unequal in colour and shape. The basal cells with yellow to orange brown colour, oblong or ovate oblong shape, $(11.5-) 16.9 (-23) \times (13.8-) 16.3 (-20.7) \mu\text{m}$ and dull rough to few verrucous surface. The apical cells, with subellipsoid to subhexagonal shape, $(13.8-) 17.4 (-23) \times (16.1-) 20 (-23) \mu\text{m}$, pale orange to orange brown colour and coarsely verrucose surface. Teliospores borne singly on hyaline to pale yellow, $(4.6-) 6.2 (-6.9) \mu\text{m}$, thick pedicels, those adhere basely in groups. This fungus has world-wide distribution. (Poster 18)

THE MEROSPORANGIFEROUS FUNGI FROM TAIWAN

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During an investigation of merosporangiferous Zygomycetes in Taiwan, eight species of the family Piptocephalidaceae (Zoopagales) were isolated. Two of these species belong to the genus *Piptocephalis*. They are *Piptocephalis cylindrospora* and *P. sphaerica*. Six species belong to the genus *Syncephalis*. They are *Syncephalis depressa*, *S. nana*, *S. obconica*, *S. parvula*, *S. sphaerica* and *S. ventricosa*. All species represent new records to Taiwan. Previously none of the genus *Piptocephalis* were described and only two members of *Syncephalis* were reported from Taiwan. These eight species were all isolated from soil in northern Taiwan, mainly mountain area. The differences in morphological characters between these species and closely related taxa, together with their host range are reported.

THE MYCOFLORA OF HOT SPRING SOIL OF NORTHERN TAIWAN

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An investigation on the mycoflora, particularly of thermophilic and thermotolerant fungi inhabiting sulfurous hot spring soils of northern Taiwan resulted 12 taxa, viz. *Aspergillus fumigatus* var. *fumigatus* (66.85%), *A. fumigatus* var. 1 with green colony (7.86%), *A. fumigatus* var. 2 with brown colony (4.81%), *A. niger* (1.14%), unidentified *Aspergillus* sp. (0.045%), *Papulospora thermophila* (2.72%), *Chrysospora* sp. (0.18%), *Scytalidium thermophilum* (0.045%), *Sporotrichum* sp. (0.045%), *Mycelia Sterilia* sp. 1 (white colony) (6.63%), *Mycelia Sterilia* sp. 2 (yellow colony) (5.27%) and *Mycelia Sterilia* sp. 3 (gray colony) (4.405%), in total, 2,202 colonies were isolated from three sampling sites, i.e. site 1 (hot springhead), site 2 (2 m from site 1) and site 3 (4m from site 1) fungal colonies isolated as well as species richness in three sites were as follows: 32.92% in 9 taxa from site 1, 37.87% in 11 taxa from site 2, and 29.21% in 8 taxa from site 3, respectively. The dominant species was *A. fumigatus* var. *fumigatus* that was isolated year around from three sampling sites. *A. fumigatus* var. 1 (green) appeared from August to December in contrast, *A. fumigatus* var. 2 (brown) was isolated only in February and April. Within the sampling range of presence of ecotypes in *A. fumigatus* complex, *Chrysospora* sp. and *Sporotrichum* treatment but *Aspergillus* sp. and *Scytalidium thermophilum* were isolated only from the soils pre-treated with hot water for 30 min at 60°C. That the similarity index of fungal community between hot-water treatment and no treatment was 73%, indicating that investigation of both situations is relevant.

BIODIVERSITY OF SOIL FUNGI FROM THE SAKHALIN ISLAND (RUSSIAN FAR EAST)

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More than 160 fungal species, belonging to 60 genera have been isolated as result of mycological analysis of soil samples from native meadows, coniferous, coniferous-broad-leaved and broad-leaved forests, alpestrine and other associations. Mycobiota specificity of soil formed under the influence of forest and meadow plants associations have been discovered. A great deal of *Penicillium* isolates (70-80%) is characteristic of forest soils. Here, the most frequent species are *Penicillium spinulosum*, *P. canescens*, *P. decumbens*. The number of *Penicillium* isolates decreases to 60-70% in meadow soils. *Penicillium simplicissimum*, *P. ochro-chloron*, *P. jensenii* play the leading part here. *Aspergillus* is represented in forest soils by *A. amstelodami*, *A. nidulans*, *A. flavus*, *A. ochraceus*, *A. candidus* and by *A. ustus*, *A. terreus*, *A. janus*, *A. foetidus*, *A. sydowii* in meadow soils. Other hyphomycetous fungi which often occur in forest soils are *Cylindrocarpon destructans*, *Myrothecium roridum*, *Oidiodendron flavum*, *Trichoderma koningii*, *Paecilomyces carneus*. Meadow soils are different from forest soils in the considerable numbers of *Fusarium* and *Gliocladium* species. List of Zygomycetes of forest soils includes 17 species, belonging to 5 genera: *Mucor*, *Mortierella*, *Rhizopus*, *Cunninghamella*, *Circinella*. Among them, *Mucor ramannianus* and *Mortierella isabellina* are predominant. The diversity of ascomycetous fungi in forest soils is restricted to 7 species: *Chaetomium elatum*, *Ch. globosum*, *Ch. crispatum*, *Gymnoascus reesii*, *Trichosphaeria pilosa*, *Sordaria fimicola*, *Podospora minuta*. Soil mycobiota of mountain tundra have been characterized by the prevailing of dematiaceous hyphomycetous fungal species. (Poster 19)

FLORISTIC RESEARCH ON MITOSPORIC FUNGI IN KARAJ AREA

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Karaj area is situated 30 kilometers west of Tehran. From the north, this area is limited to south slope of Alborz mountain range and from the south, it covers the steppe and salty areas. Because of topographic variations, Karaj has a wide floral range and consequently, a diverse mycoflora. In order to identify mitosporic fungi, specimens were collected from several parts of this area during 1999-2000. In addition herbarium specimens (deposited in the herbarium of Plant Pests & Diseases Research Institute-IRAN and the herbarium of College of Agriculture, University of Tehran, Karaj) were examined. Hand-sectioned specimens were stained and observed under a light microscope. In this study, following species were identified: 1. *Diplosporonema delastreii* (Delacr.) Petrak, on *Silene latifolia* Poir. subsp. *persicum*, Kandavan, alt. ca. 2500m. 7 Jul. 1997, GH. A. Hedjaroude. 2. *Piggotia ulmi* (Grev.) Keissler, on *Ulmus* sp., Jurab, alt. ca. 1550m. 11 Jul. 1997, GH. A. Hedjaroude. 3. *Sporonema phacidioides* Desm., on *Medicago sativa* L. Gachsar, alt. ca. 2100m. 29 Jun. 1999, GH. A. Hedjaroude. 4. *Marssonina kriegleriana* (Bres.) P. Magn., on *Salix* sp., Shahrestanak, alt. ca. 1700m. 21 Aug. 1996, M. Abbasi. 5. *Septoria bornmulleri* Syd., on *Nepeta* sp., Khor, alt. ca. 1800m. 19 May 1997, M. Abbasi. 6. *Septoria convolvuli* Desm. on *Convolvulus arvensis* L., Azadbar, alt. ca. 2450m. 7 Jul. 1997, GH. A. Hedjaroude. 7. *Sporonema* cf. *punciforme* Schuepp, on *Galium coronatum* Sibth. et Sm., Azadbar, alt. ca. 2340 m. 6 Aug. 1996, M. Abbasi. (Poster 20)

A SURVEY ON SOIL *PYTHIUM* SPECIES IN FARS PROVINCE OF IRAN

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During 2000-2001, soil *Pythium* species were studied in Fars province. Soil samples were collected from various parts of the province (Abadeh, Bajgah, Beyza, Borazjan, Darab, Estahban, Fasa, Khafir, Sepidan, Shiraz, Moharlo, and Zarghan). Isolates were recovered from soil by baiting. Species were identified based on morphological characters of sexual and asexual organs, growth rate at different temperatures, and colony morphology on various media. From 270 isolates of *Pythium* recovered, 12 species and two groups were identified as: *P. aphanidermatum**, *P. aquatile*, *P. deliense*, *P. diclinum*, *P. echinulatum*, *P. inflatum*, *P. okanoganense*, *P. oliganderum*, *P. orthogonon*, *P. ostracodes*, *P. rostratum*, *P. vexans*, *Pythium* Group "G"*, and *Pythium* Group "HS"* (species with asterisk were predominant). *P. aquatile*, *P. echinulatum*, *P. inflatum*, *P. okanoganense*, *P. orthogonon*, *P. ostracodes*, and *P. rostratum* are new for Iran flora. (Poster 21)

Asian International Mycological Congress, 17-20 Sept. 2001, Karaj, Iran

MORPHOLOGICAL DIVERSITY IN POPULATION OF *PYTHIUM* *ARRHENOMANES*

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Two hundred and forty isolates of *Pythium arrhenomanes* Drechsler obtained from root rots of maize in different regions of France were cultured on water agar and kept for 5-7 days at 25°C. Formation of oospores, lobulate sporangia, and hyphal swellings were studied in the isolates. It was resulted that 22% of isolates were not able to produce oospores in Petri dishes. Lobulate sporangia were formed only in 31% of isolates, but when the pieces of water agar were transferred in solution of soil at the rate of 5 g/l all of them produced the lobulate sporangia. All isolates showed to be capable of producing compact, spacious and intermediate hyphal swellings, at 26, 51 and 33%, respectively. It can be concluded that *P. arrhenomanes* is composed of homothallic and heterothallic individuals that are able to form the hyphal swellings and the lobulate sporangia. Based on the type of hyphal swellings they can be arranged in three groups: compact, spacious and intermediate. However, between pathogenicity and virulence of different groups on maize seedlings significant difference was not found. (Poster 22)

AGRICULTURAL POLICY AND THE EXPANSION OF THE GREENHOUSE PRODUCTION SYSTEM IN THE SULTANATE OF OMAN: ADDRESSING THE PRIORITY PLANT PATHOLOGY ISSUES

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The Sultanate of Oman is expanding greenhouse production for horticultural crops including tomatoes, sweet peppers and cucumbers. This raises important issues of efficient use of resources, especially water and pesticides. Current pesticide use is largely based on prophylactic treatments, there is little information on economic thresholds for pesticides, on pathogen distribution, on resistance to economically important diseases. A multidisciplinary programme has been established to evaluate aspects of disease control using basic, applied and adaptive research methodologies. Surveys involving 140 greenhouses during 5 growing seasons have been conducted for foliar and soil diseases. This has supplied information on extent of losses, seasonality and economic impact on growers. Current farmer practice is being evaluated under experimental conditions, especially method of cultivation and frequency of irrigation. Economic thresholds are being established for principal disease problems, together with an assessment of the optimal spray regime for economically efficient disease control. Basic research has targeted popular cucumber varieties to assess resistance levels under Omani conditions, epidemiological research is modeling the distribution of pathogens in relation to the distribution of roots in soil. New techniques, such as CT and NMR scanning will enable models of root growth and development, pathogen activity and water availability to be constructed for a non-destructive assessment of the effectiveness of crop management techniques. The programme will utilize the extensive network of Ministry of Agriculture extension personnel to ensure rapid uptake of research outputs.

Asian International Mycological Congress, 17-20 Sept. 2001, Karachi, Iran

DIVERSITY AND PERPETUATION OF *FUSARIUM OXYSPORUM* F. SP. *MELONIS* IN IRAN

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Fusarium oxysporum Schlecht: Fr. f. sp. *melonis* (Leach & Currence) Snyder & Hansen causes economic loss in some parts of Iran. The fungus is a host-specific and infects different varieties of *Cucumis melo* L. The optimum temperature for pathogenicity is lower than for vegetative growth in the laboratory. The pathogen has been reported from various parts of Iran including Fars, Isfahan, Markazi and Khorasan provinces. Two distinct races of the fungus namely race 1 and race 1,2y have been found in the country. Race 1 is prevalent in Markazi and Khorasan while race 1,2y in Fars and Isfahan provinces. All isolates of the pathogen obtained from various locations in Iran belonging to race 1 and race 1,2y were found to be vegetative compatibility group (VCG) 0134. Isozyme analysis of *Fusarium oxysporum* f. sp. *melonis* from Iran have shown genetic similarity among races obtained from different geographical regions, which justify more to VCGs rather than races. Although the pathogen is host specific but under natural conditions may colonize roots of various agricultural crops such as potato and alfalfa and also several weed species including *Glycyrrhiza glabra* and *Alhaji persusarum* common perennial plants distributed in virgin and cultivated soils. There are several genetic sources of *C. melo* from Iran or other countries resistant to race 1 but none were found for race 1,2y.

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PHYSIOLOGY OF HOST-PARASITE RELATIONSHIP IN LEAF SPOT DISEASE OF SORGHUM CAUSED BY *DRECHSLERA* SP.

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Sorghum (*S. vulgare*) is grown in many regions of Sultanate of Oman mainly as fodder crop for animals. It has been reported to be severely infected with *Drechslera* sp. causing leaf spot disease. The physiological changes in sorghum leaves inoculated with *Drechslera* sp. were investigated through five recognizable stages of disease development. Small irregular necrotic spots with yellowish margin appeared three days after inoculation, enlarged and coalesced at later stages of disease development. Healthy and infected leaves were quantitatively analysed for number of constituents. Total chlorophyll, and chlorophyll a & b contents decreased significantly with the progress of infection. The level of reducing and total sugars increased, while non-reducing sugars decreased to a marked extent with the development of disease. The concentration of total phenolics showed similar trend of increase as the disease progressed. However, orthodihydroxy phenols increased sharply three days after inoculation and decreased thereafter, but the concentration was higher in all stages of disease development compared to that of healthy leaves. Considering the present results it may be concluded that *Drechslera* sp. pathogenesis interferes with various physiological and biochemical mechanisms of the host.

SOME EPIDEMIOLOGICAL ASPECTS OF TAKE-ALL IN FARS PROVINCE OF IRAN

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Take-all of wheat caused by *Gaeumannomyces graminis* var. *tritici* (Ggt) is a newly recorded disease of irrigated wheat fields in Fars province. In a survey conducted during 1999-00, the presence of the fungus was confirmed in 55 out of 320 wheat fields inspected. Most of the fields are located in semi arid and temperate areas, where 150000 ha of wheat are sown annually and about 50% of total wheat is produced in these regions. The disease cycle begins when the fungus shows its effect in late February-early March (tillering stage). Uneven growth can be seen in plant population through mid May-early June (ear emergence), and finally large patches of white heads developed prior to ripening depending on environmental conditions. The fungus was restricted to the roots in these areas and rarely attacks the stem base except in soils with silty clay texture with high moisture content. Radial growth rate of seven selected Ggt isolates were determined by daily measurement on PDA. All of tested isolates showed similar growth responses to temperature, with an optimum of 25°C, maximum near 30°C, and minimum near 10°C. No growth occurred at 35°C. This is an important attribute of take-all fungus and was correlated with its activity throughout the growing season. No perithecium was found in infected straw in infected fields, but was readily produced in the laboratory when infected roots incubated at 15-17°C in a naturally lighted growth room for 3-5 weeks. Therefore the ascospores probably have no role in disease epidemiology in this area, however the fungus was isolated from buried wheat root pieces preserved from the previous crop and found to be infective. This may serve as primary inoculum for subsequent cereal crop.

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GLECHOMA HEDERACEA AND PUCCINIA GLECHOMATIS IN NORTH AMERICA: A COMPARATIVE EPIDEMIOLOGICAL STUDY

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Glechoma hederacea (Ground-ivy, Lamiaceae) and its microcyclic rust parasite, *Puccinia glechomatis* are natives to Eurasia, but were introduced to North America. Whereas the host is known already from the beginning of the 19th century, *P. glechomatis* was reported for the first time in North America in 1998 (Scholler, M., Plant Dis. 84: 371, 2000). To reconstruct the spread of both the host and the rust, and to make future estimates, we evaluated literature, databanks and herbarium records to obtain host data. Rust data were obtained indirectly by checking for rust infections on 1600 *G. hederacea* specimens from herbaria. Records from field studies were considered as well. Data were evaluated with the computer program ArcView. Preliminary results show that both, host and rust were probably introduced twice independently, first at the East Coast and later at the West Coast. Both species were found for the first time in Pennsylvania (USA). Whereas *G. hederacea* was first recorded in the 1920s, *P. glechomatis* was probably introduced at the beginning of the 1990s. The rust is spreading about 80 km/year. This is about twice as fast as the spread of the host. There is no record of the rusts appearance in Canada so far; the rust seem to spread only south- and westward. (Poster 23)

DISTRIBUTION PATTERN AND ECOLOGICAL CHARACTERISTICS OF SNOW MOLD FUNGI IN ASIA

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Fungi of several taxonomic groups grow under a covering of snow. Snow mold fungi are psychrophilic fungal pathogens that infect winter cereals grown countries in the Northern hemisphere. Among these snow molds, *Typhula ishikariensis* S. Imai has evolved several infraspecific taxa adapted to different winter climates. *T. ishikariensis* has been classified into two biological species based on mating experiment. We reported that frost resistance of mycelia and sclerotia were one of the important factors for geographical distribution of *T. ishikariensis*. Many papers of snow mold fungi in Japan, European part of Russia, Nordic countries and North America were reported. However, there are a few reports of snow mold fungi in West Siberia, China and Central Asia. During 1998-2001, we observed snow mold fungi in Siberia and Russian Far East. We collected many sclerotia of various snow mold fungi (*T. incarnata*, *T. ishikariensis*, *S. borealis* and *S. nivalis*) from Siberia (Ekaterinburg, Novosibirsk and Irkutsk) and Russian Far East (Vladivostok and Sakhalin Is.). Snow mold fungi were widely distributed in snowfall area in Asia (exclude the steppes). Some isolates of *T. ishikariensis* from Siberia showed irregular growth at 10°C on PDA. Similar characteristics were obtained in isolates from the Arctic (Northern Norway, Spitsbergen Is. and West Greenland). These results indicate that some Siberian isolates may had the same genetic background with isolates from the Arctic. (Poster 24)

A NEW REPORT OF *CERATOCYCTIS RADICICOLA* TO CAUSE LEMON FRUIT ROT IN IRAN

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This study was conducted to identify the causal agent associated with lemon fruit rot. In August 2000, lemon (*Citrus limon*) fruit rot was observed in Kahnouj region, Iran. Brown rot on fruit rind progressed entirely leading to complete fruit decay following the harvest. *Ceratocystis radicicola* was isolated from symptomatic fruit tissues. This is considered the first report of *C. radicicola* being able to induce disease symptoms on lemon fruit in the world. Infected tissues were cut in small pieces in distilled water and a drop of suspension was streaked out on PDA or NA medium. After a few days, fungal isolates were purified by single spore dilution. Colonies vary from light grey to black in color with dispersed growth. Conidia ovate to ovoid, with a flattened base, mostly $14-22.5 \times 10-17.5 \mu\text{m}$, borne singly on short hyphae. Phialoconidia hyaline, $7.5-18.5 \times 2.5-6.5 \mu\text{m}$, cylindrical, catenate. The pathogenicity test was accomplished by injection of phialoconidia under lemon fruit rind. Alternatively, pathogenicity test was carried out on seedlings and fruits of date. After two days of inoculation, lemon fruit rot was observed. In advanced disease stage, a complete fruit decay occurred and the tissues were colonized by conidia. The fungus was pathogenic on date palm. *C. radicicola* was reisolated from inoculated tissues. *C. radicicola* has previously been reported on date palm in both Iran and the USA. Its pathogenicity on lemon is an unusual record. Because of its severity and wide host range on lemon cultivars, disease occurrence must be taken seriously. (Poster 25)

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ISOLATION OF *BOTRYOSPHERIA DOTHIDEA* FROM ALMOND TREES IN BONAB (EAST AZARBAIJAN)

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In summer 2000 a disease on almond seedling and mature trees with decline and band canker was observed in Bonab (West Azerbaijan province of Iran.). The disease symptoms consisted of gum exudation on band canker with brown discoloration of infected areas. This canker is unusual because unlike other cankers it extends around the branch or trunk instead of longitudinally along the affected part. Fungus kills the bark and cambium layers and the affected area become sunken and frequently girdles the limb. Causal agent on infected tissues was characterized on stroma and perithecia morphology. Stroma pulvinate, black; perithecia sunken in stroma, globose, ostiolate, with short neck, crumpled through host tissues. Asci clavate, $85-122 \times 18-22 \mu\text{m}$ and with numerous filiform paraphyses. Ascospore fusoid and 1-celled, $20-23 \times 6-8 \mu\text{m}$. Based on the above criteria the fungus was identified as *Botryosphaeria dothidea*. This is the first report of the fungus on almond in Iran. (Poster 26)

RELATIVE IMPORTANCE OF *SCLEROTINIA SCLEROTIORUM*, THE CAUSAL ORGANISM OF STEM-ROT OF CHICKPEA AND THEIR PATHOGENIC VARIABILITY IN EGYPT

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Chickpea (*Cicer arietinum* L.) is one of cool season food legumes in Egypt. More than 50 pathogens have been reported from different parts of the world, and only a few of them have the potential to devastate the crop. Sclerotinia stem rot (*Sclerotinia sclerotiorum* [Lib] de Bary) is one of the most important pathogens which causes damage to aerial plant parts. Eight isolates of *S. sclerotiorum* isolated from chickpea in different governorates were tested to determine their pathogenic variability on fifteen chickpea entries. Results indicate that the fungus was found in all inspected chickpea fields, and percentage of infection varied between governorates, it was high in Gaharbia and Beheria followed by Beni-Suief and Assuit and low in Kafer El-Sheikh. From the survey of diseased chickpea plants, the causal pathogen of stem-rot was in high frequency level compared with the other isolated fungi as 58.1%. Pathogenicity test of isolates showed different pathogenic variability on cultivar Giza 88 and disease severity varied from 2% to 93.3%. Results show significant interaction between isolates $\times$ entries. Isolate no. 8 show avirulent reaction to all entries except one or/and two entries pre or/and post emergence damping off, while isolates 1, 2, 4, 5, 7 showed virulent reaction with some entries till to the end of experiment. On the other hand, mycelial compatibility groups (MCGs) test among isolates showed incompatible reaction between some of the confronting paired isolates, therefore, they belong to different MCGs, while some isolates were compatible, belonging to the same MCG. (Poster 27)

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POSSIBLE EFFECTS OF CLOVER ROOT EXUDATES ON FUSARIUM FOOT-ROT OF WHEAT

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It is well known that root exudates are involved in microbial inhibition or stimulation of the growth of plants. A better understanding of the nature of exudates may provide better means to biological control of certain soil-borne pathogens. The aim of this study was to determine the chemical characteristics of clover root exudates especially as they relate to wheat stem-base pathogen promotion/inhibition. Since the results from field experiments represented the inhibitory effects of wheat-clover intercrops on the incidence of *Fusarium* foot-rot of wheat, a series of experiments were devised in order to examine in greater detail the role of clover in reducing the incidence of cereal diseases. Surface sterilised clover seeds of cultivars Donna, Menna, Alice, Grassland HUIA, Milkanova, and Aberystwyth-S184, were germinated aseptically and the root exudates were collected according to El-Hamalawi & Erwin (1986). For preparing the *F. avenaceum* conidia a procedure similar to that used by Zeider & Hill (1988) was used.

The results indicated that exudates from some of the clover cultivars had promoting effects on *Fusarium* spore germination; in the case of cvs Donna and Aberystwyth S184 the difference relative to distilled water was significant ($P < 0.05$). From root exudates of cultivar Donna four more amino acids were detected which were not found in cultivar Milkanova. The results from subsequent testing showed the individual effects of the amino acids, those found only in Donna, indicate that the amino acid content of the root exudate could be responsible for a stimulatory effects on the germination of *Fusarium avenaceum* conidia. Further biological investigations are discussed for definitive proof of the involvement of these compounds as inhibitory factors on development of wheat fusarium foot-rot. (Poster 28)

INHIBITION OF ROT PATHOGENIC FUNGAL GROWTH BY CERTAIN PLANT EXTRACTS: AN *IN VITRO* TEST

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The effect of twenty-three water extracts from plant sources were individually tested *in vitro* on growth of *Sclerotinia sclerotiorum*, *Sclerotium rolfsii*, *Fusarium solani* and *Rhizoctonia solani*. The extracts were obtained by dissolving the dry film of the evaporated cold ethanol filtrate of the soaked plant material. Each test solution was prepared in a concentration equivalent to 20% of the dry weight and was kept under freezing in test tubes in 100 ml aliquots. The extracts were mixed each separately with the growth media before fungal inoculation in ratio of 1:3 v/v in a replication of 10 Petri plates for each fungus under test. The plants were incubated at temperatures ranged from 18-25°C for a period of 7 to 21 days until maximum linear growth was reached in the control untreated plates of each fungus. The effects of plant extracts under test were evaluated by measuring the average of linear growth of each fungus compared with the control. Three of the tested plant extracts caused total elimination of the growth of the four fungi under test. Seven of them reduced the average linear growth of 90 mm measured separately for each control of the four fungi to an average ranged between 2 up to 60 mm in *Sclerotinia sclerotiorum*, *Sclerotium rolfsii*, *F. solani* and *R. solani*. The effects of the rest tested plant extract samples, i.e. thirteen; were completely negative. The result suggested that the extracts of some of the plants under test are of value to be considered as sources of natural compounds of fungicidal action. (Poster 29)

NON-CEREAL GRASS SPECIES AS NEW HOSTS FOR *GAEUMANNOMYCES GRAMINIS* VAR. *TRITICI* IN IRAN

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A number of common grass weeds such as *Secale cereale* L., *Lolium rigidum* Gand., *Alopecurus myosuroides* Huds., *Avena fatua* L., *Hordeum murinum* L., *Bromus tectorum* L., *Phalaris minor* Retz., and *Hordeum spontaneum* C. Koch, showing root blackening, vascular discoloration and stunting, were collected from several irrigated wheat fields with take-all patches in Fars province. For isolation, grass roots were cultured on PDA. After 2-3 days at 25°C, from the majority of the root pieces a fungus with typical colony characteristics of *Gaeumannomyces graminis* was isolated. Pathogenicity of the fungal isolates from grasses on wheat plants using a test-tube technique (Yeates *et al.*, 1986) in a germinator at 15-17°C caused seedling death within 3-4 weeks. Based on pathogenicity on wheat seedling, morphology of the hyphopodium and ascospore length of all the fungal isolates from grasses were identified as *Gaeumannomyces graminis* (Sacc.) Arx & Olivier var. *tritici* J. Walker (Ggt). A pot experiment was conducted to test the virulence of Ggt isolates on eight grass species. Weed seeds were sown in plastic pots containing a mixture of virgin soil and sand inoculated with sterilized wheat seeds precolonized with Ggt (0.5g/Kg soil). Control pots received uninfected sterilized wheat seeds. Each treatment replicated three times in a completely randomized design. The pots were placed in glasshouse (22-28°C). After four months roots were washed free of soil and cultured on PDA. The same fungus was reisolated. The rate of reisolation varied from 7-100%. In addition plant height and weight were measured. The root system of each plant was assessed for disease severity using four infection categories: Healthy, Slight (less than 25% of the root system infected), Moderate (25-75%), and Severe (more than 75%). In these pot experiments *Secale cereale* and *Lolium rigidum* showed marked resistance to Ggt, while *Alopecurus myosuroides*, *Avena fatua* escaped with less than 25% of the root system infected. On the other hand, *Hordeum murinum*, *Bromus tectorum*, and *Phalaris minor* were moderately infected. *Hordeum spontaneum* was severely infected and the plant weight was significantly reduced. This investigation revealed that saprophytic or parasitic survival of Ggt inoculum on grass roots could play an important role in carry-over of infection to subsequent cereal crops. (Poster 30)

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GREY MOULD OF CUCUMBER IN PLASTIC TUNNELS IN MAZANDARAN

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Grey mould of cucumber was observed in plastic tunnels in Sari during a surveying in March 1999. The symptoms of the disease appeared as brown greyish mass of fungus colonies over the surface of cucumber fruits. *Botrytis* fungus was also consistently isolated from diseased fruit. The disease colonises the dead or wounded tissues of foliage and stem due to pruning or any damage during harvest times. The fungus had grayish colonies on PDA and covered the entire medium surface in less than one week at 25°C. Koch's postulates were completed with one isolate of the fungus. Based on morphological and cultural characteristics the causal fungus was identified *Botrytis* sp. This is the first report of this disease in Mazandaran province. (Poster 31)

OCCURRENCE OF *SCLEROTINIA* STEM ROT OF RAPESEED IN MAZANDARN

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Stem rot of rapeseed was observed in May 1996 at Baye-Kola Research Station of Mazandaran, Iran. The symptoms of the disease appeared as bleached stem and shredding. Sclerotia were formed on infected tissues. The *Sclerotinia* fungus was also consistently isolated from diseased stems. Koch's postulates were completed by one isolate of the fungus. The fungus had white to grey colonies on PDA and covered all of the media surfaces during one week at 21°C. Sclerotia were rounded to elongated and measured 2 to 20 mm on PDA. Microconidia with olive color were formed in 4-week-old cultures. Apothecia were formed on the surface of the sclerotia on soil surface as cupulate, stipitate and had brown color. Asci matured in the apothecia. Ascospores (8 per ascus) were hyaline, single cell and elongated. Based on personal information by L. Kohn (1979), the causal fungus was identified as *Sclerotinia sclerotiorum* (Lib.) DeBary. This is the first report of this fungus on rapeseed in Mazandaran. (Poster 32)

ANTAGONISTIC ACTIVITY OF FUNGI ISOLATED FROM THE SEMI ARID SOIL IN UZBEKISTAN

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Biological control of plant diseases using nonpathogenic fungi has received increasing attention. The objectives of this study were: to isolate a large number of fungi from the soil under cotton, to screen these isolates for their *in vitro* antagonism against soil-borne plant-pathogenic *Fusarium* species. Soil samples were from cotton fields of Surhandarya region. 743 strains of *Trichoderma*, *Aspergillus* and *Penicillium* were isolated and screened for antagonistic activity. Plant-pathogenic fungi of *Fusarium solani* f. *argillaceum*, *F. javanicum*, *F. moniliforme*, *F. moniliforme* f. *lactis* and *F. moniliforme* f. *subglutinans* were used for study. Antifungal activity was measured as the width of the zone of growth inhibition between the fungus and the organism tested. One hundred and thirty six isolates were strong antagonists to the plant-pathogenic species of *Fusarium*. Isolates of *Aspergillus ochraceoroseus*, *Trichoderma lignorum*, *Penicillium notatum*, *A. terreus* and *A. ustus* showed more antagonistic activity among all isolates (24-33%). The highest inhibitory effect against *Fusarium* was found in *Trichoderma lignorum* 158. Others e.g. of *Penicillium* and *Aspergillus* showed lower antagonistic activity. This study shows that some non-pathogenic fungi may be useful in protecting agricultural plants against damping off *Fusarium* pathogens. The most highly protective isolates need to be further studied to optimize conditions for their establishment and antifungal activity.

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BIOLOGICAL CONTROL OF WHITE MOLD IN SOME VEGETABLE CROPS TESTS AT SEEDLING GROWTH STAGES

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Preliminary experiments were carried out to test the biocontrol action of the fungus *Coniothyrium minitans* against *Sclerotinia sclerotiorum* causing white mold disease in some vegetables, i.e. cantaloupe, cucumber, celery, chicory, lettuce, parsley and tomato. The test was conducted in soil previously contaminated with a *Sclerotinia* isolate. The biocontrol agent was added as solution and incorporated into the soil at seeding, in the seedling trays and in pots. In plastic boxes, the contaminated soil was incorporated with the biocontrol agent solution, 70 days before seeding. In comparison to plants grown in clean soil, the fungus *Coniothyrium minitans* remarkably reduced the percentage of infection caused by *Sclerotinia sclerotiorum*. In treated plants the infection ranged from the least of 5.5% in tomato to the highest of 40% in celery in 7-day-old seedlings grown in the seedling trays in the lab. In untreated plants, these values were 60% and 90% in celery and parsley, respectively. In 14-day-old potted plants, the least recorded infestation in lettuce of 56% was reduced to 15% under the treatment; while the highest one of 90% was decreased to 25% in parsley. In 14-day-old plants grown in plastic boxes under lab conditions; where the bioagent in solution was incorporated 70 days before seeding, the infection ranged from the least of 16% in parsley to the highest of 34% on chicory. In untreated plants the corresponding values were 46% and 98% in cucumber and parsley, respectively. The results are discussed in respect to international observation obtained on the subject.

EFFECT OF BIOCIDES COMPOUND, BIOFLY (*BEAUVERIA BASSIANA* VUILLEMIN) ON *TETRANYCHUS URTICAE* KOCH

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The efficiency of biocide compound, Biofly (*Beauveria bassiana* Vuillemin). With 3x10 conidia, at 100 cc/100 l., of water on different egg stages and adult females of *Tetranychus urticae* Koch and the biological aspects of *T. urticae* were studied. Also, the effect of Biofly against *T. urticae* on apple trees in Qualubia Governorate was conducted.

The obtained results showed that the effect of this compound against egg stages was higher than the adult females of *T. urticae*. Moreover, treating 3-day-old eggs was the most effective. The biological aspects of *T. urticae* when treated one-day-old eggs with Biofly indicated that the average number of deposited eggs per female decreased to 95.9%. Moreover, it caused 90% mortality during immature stages. Under field condition, the average reduction in population density of *T. urticae* was 71.06% after the fourth application with *B. bassiana*. Biofly can be used in the integrated control programmes to control *T. urticae*.

CELL WALL LYTIC ENZYMES PRODUCED BY *TRICHODERMA* SPP.

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The cell walls of basidiomycetes and ascomycetes contain chitin and laminarin (β -1,3 glucan) but no cellulose. Oomycetes contain β -1,3 glucans and cellulose, and relatively small amount of chitin (less than 1%, as in *Pythium*) or no chitin (as in *Phytophthora*). Selected *Trichoderma* isolates were grown on SMCS medium containing 1% chitin or FCW (fungal cell wall). The amount of N-acetyl-D-glucosamine (NAG) released by 1 ml of supernatant was determined from the standard curve and specific activity is expressed as λ moles of NAG per mg chitin or FCW per hour. Amount of glucose released was measured according to Nelson (1944). Specific activity is expressed in λ mole of glucose released/mg laminarin/hour. Cellulase activity in *Trichoderma* culture filtrates was determined by growing the disk of 5 mm diameter of *Trichoderma* isolates in 100 ml flask containing 1% cellulose powder. Exoglucanase (C1) activity is expressed in λ mole of glucose released/mg CMC/hour. Endoglucanase (Cx) activity is expressed in λ mole of glucose released/mg cellulose/hour. All tested isolates of *Trichoderma* spp. released N-acetyl-D-glucosamine from colloidal chitin. Isolate EM15 produced the highest amount of chitinase (0.017) from colloidal chitin, while EM64 showed the highest chitinase activity on FCW. Isolate WT5 and EM15 with 0.333 λ mole glucose/mg/h each, showed the highest amount Cx activity. WT8 showed the maximum C1 activity 0.044.

STUDY ON INTERACTION BETWEEN *TRICHODERMA* SPECIES AND *SCLEROTINIA MINOR* AND *S. SCLEROTIUM* CAUSAL AGENTS OF SCLEROTINIA STEM ROT OF SUNFLOWER IN KILOY AND UROMIEH REGIONS

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Crown and root rot of sunflower (*S. minor* and *S. sclerotiorum*) is one of the most important diseases of sunflower. Chemical control of this disease is very difficult, because the causal agent is a soil-born pathogen, therefore biological control is the best method. In this investigation interaction between 9 isolates of *Trichoderma* (6 isolates of *T. harzianum*, 2 isolates of *T. viride* and 1 isolate of *T. virens*) and *S. minor* and *S. sclerotiorum* were studied. Microscopic studies showed that hyphal contact, coiling and penetrating *Trichoderma* isolates within hyphae of the pathogen was not observed, but the lysis and deformation of hyphal tip of pathogen was observed. In dual culture, the mycelial growth of *S. minor* and *S. sclerotiorum* were suppressed upon contact the competitor hyphae of all isolates, then parasite growth continued over the host mycelium and some of the isolates inhibited the formation of sclerotia of *S. minor* and *S. sclerotiorum*. Study on volatile metabolites showed that *T. harzianum* (J1) was the most effective, which inhibited mycelial growth of the pathogen by 90.42 % and 77.77%, respectively. Study on culture filtrates were used in three concentrations (10, 20 and 30%) showed that *T. harzianum* (J6) was more effective and inhibited mycelial growth of the pathogen by 86.47% and 78.88%, respectively at 30% concentration. Study on colonization ability of the isolates on 14-day-old culture of pathogen showed that all isolates were grown over the sclerotia of the pathogen, but some of them were only able to sporulate and autolysing the sclerotia of *S. minor* and *S. sclerotiorum*.

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BIOLOGICAL CONTROL OF *ARMILLARIA MELLEAE* THE CAUSAL AGENT OF ROOT AND BUT ROT USING *TRICHODERMA* SPECIES

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Root and butt rot caused by species of *Armillaria* is one of the most serious diseases of fruit and forest trees in Iran. In this study, antagonistic effects of *Trichoderma* in biocontrol of *Armillaria* were investigated. *Armillaria mellea* was isolated from infected roots and butts and identified with pairing tests method. *Trichoderma* was recovered from rhizomorphs and around soil of infected roots. *Trichoderma* species identified were: *Trichoderma virens* (9 isolates) and *T. harzianum* (3 isolates). In dual culture tests, which *Trichoderma* isolates cultured 16 days after growing *Armillaria* on MEA, indicated that all isolates of *Trichoderma* inhibited growth of *Armillaria*. All isolates of *Trichoderma* colonized *Armillaria* colonies in 5-7 days. Volatile compounds of *Trichoderma* isolates, inhibited *Armillaria* growth and rhizomorph formation. Mechanisms of biocontrol, investigated by light and scanning electron microscopy (SEM) included penetration of *Trichoderma* hyphae in rhizomorphs, colonization of rhizomorphs with *Trichoderma* mycelium, colonization of apex meristem center and apical buds of rhizomorphs, sporulation of *Trichoderma* in outer and inner surface of rhizomorphs, degeneration of rhizomorph tissue, and discharge of rhizomorph content.

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ULTRASTRUCTURE AND INTERACTION BETWEEN THE MYCOPARASITE *PYTHIUM OLIGANDRUM* AND *PYTHIUM ULTIMUM*

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Pythium oligandrum Drechsler, in comparison with other mycoparasitic Oomycetes, is aggressive and destructive with a wide host range, including genera in the Ascomycetes, Basidiomycetes and Oomycetes. Parasitism of *P. ultimum* oospores in dual culture in various media (PDA, CMA and Soyf) and in soil was consistently observed by light microscope. It was found that PDA was most suitable to support parasitism. When *P. oligandrum* was cultured in soil the percentage of oospores parasitized was less than on nutrient agar significantly higher than in a single culture of *P. oligandrum*. *P. ultimum* oospores appeared deformed, with partial disruption of spore walls and the appearance of granulated cytoplasm after contact with the mycoparasite. Electron micrographs revealed that parasitized oospores were attacked by an aggressive mycelial network of *P. oligandrum* and were invaded via dual culture with *P. oligandrum* showed signs of erosion, indicating the possible action of the mycoparasites enzymes upon them (B-1,3 glucanase, protease and lipase). In interaction culture *P. oligandrum* produced more oospores at the contact sites in the hyphal interaction zone. *P. oligandrum* produced club-shaped appressoria at the tips of short branch according to scanning electron micrographs.

Asian International Mycological Congress, 17-20 Sept. 2001, Karaj, Iran

EFFECT OF SEVERAL ANTAGONISTIC BACTERIA ON *PHYTOPHTHORA SOJAE*

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This study was conducted to evaluate antagonistic effects of a total of 158 bacterial isolates collected from soybean rhizosphere against *Phytophthora sojae*, the causal agent of damping off using the dual culture method. Fifty-seven strains were identified as Gram positive, 74 isolates as fluorescent pseudomonads and two isolates as Gram negative. Among these bacteria, a total of 99 strains that caused growth inhibition zone of 3 mm or more against *P. sojae* and a non-antagonistic control isolate (B-40) were chosen for greenhouse studies to control damping off. Each experiment was conducted in a factorial design with two factors representing soil and seed treatments. Results revealed that isolates B-3, B-80, B-12, B-43, B-51, B-63 and B-64 using either application method displayed effects similar to or higher than Ridomil fungicide in reducing the disease percentage. In soil treatment method, isolates B-3 and B-43 caused 70.84% reduction in damping off whereas B-63 and B-51 had 58.34%. Isolates B-12, B-80 and B-64 exhibited 66.67, 54.17 and 50% decline in disease development, respectively. In seed treatment method, isolates B-43, B-51 and B-63 reduced damping off by 50%, respectively; whereas B-3, B-12, B-64 caused 62.5, 58.34 and 37.5% decrease in disease occurrence. B-80 isolate caused 45.84% reduction in damping off. Application method had different effects on disease suppression. B-3 and B-12 isolates applied as soil treatment had a significantly higher disease control compared to seed treatment. B-43, B-63, B-51, B-80 and B-64 strains produced similar effects in reducing damping off regardless of the application method used. Bacteriological tests identified B-3, B-12, and B-80 as *Bacillus* spp., whereas B-43, B-51, B-63 and B-64 were fluorescent *Pseudomonas* spp.

THE FUNGUS *HIRSUTELLA THOMPSONII* VAR. *SYNNEMATOSA*
FISHER, BIOLOGICAL CONTROL AGENT OF THE RED MITE,
TETRANYCHIUS URTICAE KOCH

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A laboratory study was conducted to determine the effect of the pathogenic fungus, *Hirsutella thompsonii* var. *synnematos* on different stages of the two-spotted spider mite, *Tetranychus urticae* Koch. The fungus was grown on Sabouraud dextrose agar + yeast extract (SDAY). Spray, dipping and contact methods were applied to infect adult females of the two-spotted spider mite. The spray method was also applied to inoculate eggs, larvae, nymphs and adult females of the mites. The contact method was found as the most effective for the infection of mites, followed by the spray and dipping methods. Much mortality of mites was obtained at 30C, which seemed to be favourable for this pathogenic fungus species to give high mortality, followed by 25 C, while 20C showed the least suitable temperature. Egg hatching was not affected by the fungal infection, while all moving stages of the red spider mite were found to be sensitive to the fungal infection. (Poster 33)

ISOLATION OF FUNGAL ANTAGONISTS OF *VERTICILLIUM DAHLIAE* CAUSAL AGENT OF COTTON WILT FROM GOLESTAN COTTON FIELDS SOIL AND INVESTIGATION OF THEIR ANTAGONISTIC EFFECTS IN *IN VITRO* CONDITION

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In Khordad 1378 (June-July 1999) soil samples were collected from 79 cotton fields in Golestan province. Based on standard isolation procedures 20 different fungal isolates were isolated from soil samples. Antagonistic effect of fungal isolates against *V. dahliae* was investigated in Petri dishes using dual culture method. Results showed that 12 isolates reduced the growth of *V. dahliae*. Of the remaining isolates, five increased the growth of *V. dahliae* and the other three showed no effect. Antagonistic fungal isolates belonged to *Trichoderma harzianum* (two isolates), *Talaromyces flavus* (three isolates), *Aspergillus* spp. (three isolates), *Fusarium* spp. (three isolates) and *Verticillium* sp. (one isolate). The range of antagonistic effects (percent inhibition of *V. dahliae* colony growth) for the above fungi was 11.1-77.7, 11.1-55.5, 17.7-48.8, 4.4-33.3 and 4.4, respectively. In microscopic studies the lysis of *V. dahliae* hyphae and size reduction of its microsclerotia were observed following the hyphal penetration of *T. harzianum*, *Aspergillus* spp., *T. flavus*, and *Fusarium* spp. The antagonistic isolate of *Verticillium* sp. showed only hyphal penetration against *V. dahliae*. (Poster 34)

STUDYING BIOLOGICAL CONTROL OF WHEAT SCAB IN MAZANDARAN

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Scab of wheat caused by *Fusarium graminearum* (F. g.) (the most dominant species in the region), is one of the most important diseases of wheat in Mazandaran province. Planting resistant/tolerant cultivars is the best method to prevent yield losses. As resistant materials are rare and chemical control is very difficult, biological control with the use of effective antagonists are a component of a suitable integrated management strategy. In this study effects of *Pseudomonas aeruginosa* (Bayehkola-1), *Bacillus subtilis* (Bayehkola-4), *Trichoderma harzianum* (Bayehkola-1) and *T. viride* (Gharakheil-4) were evaluated against F. g. The isolates were able to prevent the growth of F. g. on PDA, by using dot and double culture methods for the bacteria and fungi, respectively. *Trichoderma* isolates could colonize the pathogen. Volatile metabolites of the isolates also reduced the growth rate of F. g. For disease control, suspension of bacterial cells and fungal conidia and also Rovral T-S fungicide were sprayed on Falat cultivar (susceptible wheat) which had been planted in pods, at booting and flowering stages in greenhouse in 2000-2001 growing season. Two days after the second spraying with antagonists/chemicals, artificial inoculation was made by spraying the plant with suspension of F. g. macroconidia and repeating the sprays every other day for a total of 5 times. The experimental design was a randomized complete design (RCD) with 3 replications. Records were taken 3 weeks after the last treatment when the control plants were fully diseased. The results showed all treatments were equally effective in reducing the disease severity. There was no significant difference at 1% level, between the effect of the fungicide and the antagonists in reducing infection and in increasing the thousand kernel weight of wheat. (Poster 35)

BIOLOGICAL CONTROL OF TAKE-ALL OF WHEAT BY *PHIALOPHORA* SP. (LOBED HYPHOPODIA) UNDER CONTROLLED ENVIRONMENTAL CONDITIONS

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Isolates of *Phialophora* sp. with lobed hyphopodia (T58, & T201) originally isolated from roots of grass ley in Fars province of Iran were tested for their ability to control *Gaeumannomyces graminis* var. *tritici* (Ggt) on wheat in a test tube assay. In a preliminary experiment inoculation of wheat by these isolates resulted in vascular discoloration of the lateral roots but not the main axis. The early stages of infection of wheat by *Phialophora* sp. resemble those by Ggt but the weaker pathogen usually penetrate as far as few cell layer of the cortex of wheat seminal root. In order to test the ability of T58 and T201 to suppress Ggt a combination of precolonized wheat straw of T58, and T201 (avirulent) and Ggt (virulent) isolates were placed in a test tube containing sterilised sand in an inoculum ratio of 5:1, respectively. The top layer being the avirulent and the bottom layer the pathogen. When wheat roots grow through the top layer, the roots became colonized by the avirulent fungus. The distal portions of the roots were infected by the pathogen in the bottom layer, but the disease lesions did not progress toward the crown. Wheat seeds were sown in the test tubes and incubated in a growth room at 15 ± 2 C with alternating light of 16 hr. Ggt was used in the control test tubes alone. After four weeks disease evaluation was made by measuring number of blackened lesion on roots, % root infected, length of the crown blackened and plant weight and height. Disease rating of the treatments inoculated with *Phialophora* sp. (lobed hyphopodia) were significantly ($p=0.05$) less than Ggt treatment alone indicating the non-pathogenic nature of the isolates T58 & T201. Crown blackening was only observed in Ggt inoculated treatments. It is concluded that the avirulent isolates were able to restrict the growth of the mycelium by localized host responses. Further tests are required to assess the potential performance of these isolates as biocontrol agents to control take-all under field conditions. (Poster 36)

STUDY ON INTERACTION BETWEEN *TRICHODERMA* SPECIES AND *SCLEROTINIA MINOR* AND *S. SCLEROTIORUM* CAUSAL AGENT OF SCLEROTINIA STEM ROT OF SUNFLOWER IN KHOY AND UROMIEH REGIONS

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Crown and root rot of sunflower (*S. minor* and *S. sclerotiorum*) is one of the most important diseases of sunflower. Chemical control of this disease is very difficult, because the causal agent is a soil-born pathogen, therefore biological control is the best method. In this investigation interaction between 9 isolates of *Trichoderma* (6 isolates of *T. harzianum*, 2 isolates of *T. viride* and 1 isolate of *T. virens*) and *S. minor* and *S. sclerotiorum* were studied. Microscopic studies showed that hyphal contact, coiling and penetration of *Trichoderma* isolates within hyphae of the pathogen was not observed, but the lysis and deformation of hyphal tip of pathogen was observed. In dual culture, the mycelial growth of *S. minor* and *S. sclerotiorum* were suppressed upon contact with the competitor's hyphae of all isolates, then parasite's growth continued over the host mycelium and then some of the isolates inhibited the formation of sclerotia of *S. minor* and *S. sclerotiorum*. Study on volatile metabolites showed that *T. harzianum* (J1) among all isolates was the most effective one, which inhibited mycelial growth of the pathogen by 90.42 % and 77.77%, respectively. Study on culture filtrates that were studied in three concentrations (10, 20 and 30%) showed that *T. harzianum* (J6) was more effective and inhibited mycelial growth of the pathogen by 86.47% and 78.88%, respectively at 30% concentration. Study on colonization ability of isolates on 14-day-old culture of pathogen showed that all isolates were grown over the sclerotia of pathogen, but some of them only were able to sporulate and autolysing the sclerotia of *S. minor* and *S. sclerotiorum*. (Poster 37)

BIOLOGICAL CONTROL OF *SCLEROTINIA* STEM ROT (*S. MINOR* AND *S. SCLEROTIUM*) OF SUNFLOWER USING *TRICHODERMA* SPECIES

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On the basis of laboratory experimental result (*in vitro*), three isolates namely *T. harzianum* (J1), *T. harzianum* (J6) and *T. virens* were selected for greenhouse studies. Biocontrol efficacy of these isolates and the combination of *T. harzianum* (J1) and *T. virens* on rotten crown and root of sunflower were attempted in series of experiments using three methods; incorporation of spore suspension into the soil (10^7 spore/g soil), incorporation of spore suspension with substrate into the soil (10^7 spore/g compost) and impregnating of sunflower seeds with spore suspension (10^7 spore/ml). Experimental data were analyzed by Randomized Complete Block Design (RCBD) and means separated by Duncan's multiple range test. Glasshouse experiments (*in vivo*) showed that application of the combination of *T. harzianum* (J1) and *T. virens* using incorporation of spore suspension with substrate into the soil (10^7 spore/g compost) all of the treatments was the most effective and prevented the crown and root rot of sunflower caused by *S. minor* and *S. sclerotiorum* by 50% and 41.66%, respectively. Consequently, the results indicated that the second method of antagonist application was the most effective in biocontrol of crown and root rot of sunflower caused by *S. minor* and *S. sclerotiorum*. (Poster 38)

BIOLOGICAL CONTROL OF AFLATOXINS, OCHRATOXINA
AND FUMANISIN B₁ PRODUCTION BY *TRICHODERMA*
HARZIANUM

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The effect of *Trichoderma harzianum* (as a biological agent) on aflatoxins, ochratoxin A (OA) and/or fumonisin B₁ (FB₁) production by *Aspergillus parasiticus*, *A. ochraceus* and/or *Fusarium moniliforme* was studied. *T. harzianum* was inoculated at the same time or one week after *A. parasiticus* or *A. ochraceus* inoculation on corn. The results indicate that the reduction of aflatoxin or ochratoxin A production by *T. harzianum* on corn was 73.48 and 93.31%, respectively. While the reduction of toxin with combination of cultures was 80.54 and 97.2%, in the same order. After one week incubation of *A. parasiticus* or *A. ochraceus*, the reduction of aflatoxin and ochratoxin A was 9.78 and 44.57% by *T. harzianum*, while they were 45.49 and 91.09% in the combination of both *A. parasiticus* and *A. ochraceus* inoculated in the same time. The data also showed that the inhibition production of aflatoxin and fumonisin B₁ by *T. harzianum* was 46.85 and 91.41%, respectively, while reduction of toxins with the combination of cultures were 87.44 and 98.04% in the same order. Incubation was found to reduce toxin production by 22.41 and 33.23%, respectively, while the reduction was 46.51 and 91.41% in the combination of both *A. parasiticus* and *A. ochraceus* incubated in the same time. In conclusion, *T. harzianum* was effective as a biological agent to control aflatoxins and/or ochratoxin production on corn. (Poster 39)

EFFECT OF *FUSARIUM SOLANI* AND *F. OXYSPORUM* ON POPULATION OF *PRATYLENCHUS VULNUS* IN ACER SEEDLINGS

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There are some reports that show the effect of *Fusarium* on the population of plant parasitic nematodes. In the present study nematodes and fungi have been isolated from seedlings of *Acer velutinum* in forest nurseries. The nematodes were propagated on carrot disc culture and about 40 nematode specimens per 100cc soil were added to each pot. This study has been conducted in randomised complete block with four replications and six treatments. The result showed a highly significant difference ($p=0.01$) between different treatments. In treatments with nematodes and fungi together, the population of nematodes were decreased (compared with the nematodes alone). Population of extracted nematodes from the root tissues in treatments of nematodes, nematodes + *Fusarium solani*, nematodes + *F. oxysporum* were 1266, 737 and 22 nematodes/gram and from the soil were 11.2, 9.4 and 6.2 nematodes/gram, respectively. (Poster 40)

A STUDY OF THE AERIAL MYCOFLORA OF MAURITIUS IN RELATION TO ALLERGY AND ASTHMA

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In the past 100 years changes have occurred in the outdoor environment and indoors, which have contributed to increased prevalence of allergy and asthma. Several studies have been conducted in various countries (Verma *et al.*, 1995 from India; Li & Hau, 1997, Taiwan; Takatori *et al.*, 1994, Japan; Xia, 1992, China; Bachman *et al.*, 1995, U.S.A. and others). This is creating greater awareness of the need, in the management of such problems, to seek additional causes of allergy and asthma, and in particular the precise identity of allergy-causing fungi and the actual mechanisms of these allergic reactions.

Aerial fungi from different parts of Mauritius were collected and their identification to generic/specific level determined. This study was initiated in view of the increasing importance of fungi in various human disorders particularly in asthma, allergic reactions, allergic sinusitis and lung diseases.

A review of the literature and the survey conducted indicate that several genera of aerial mycoflora in Mauritius are similar to those known to cause various allergic reactions in humans elsewhere. These common genera are *Cladosporium*, *Aspergillus*, *Penicillium*, *Alternaria*, and others. Some 200 isolates were studied and the species described. This initial study will pave the way for various tests to establish the role of those species causing or implicated in allergy and asthma in children and adults in Mauritius.

THE EFFECT OF ONION EXTRACTS ON GROWTH PATTERN AND LIPASE ACTIVITY IN *MALASSEZIA FURFUR*

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The genus *Malassezia* (*Pityrosporum*) is consisted of seven related species that implicate the etiology of a diverse group of mycoses specially *Tinea versicolor*. Although several factors such as intraspecific differences in lipase activity are probably involved in predisposition to *Malassezia* infections, very little information has been documented about exact mechanism(s) involved in pathogenesis of these diseases. In this survey, the effect of onion extracts on growth pattern and lipase activity of *M. furfur* was examined. First, 10 isolates of *M. furfur* that were obtained from patients with *T. versicolor* were grown under different culture conditions. Optimal condition for growth and lipase production related to pH, temperature and incubation time were determined as 5.8, 28° C and 4 days, respectively, in Sabouraud dextrose broth. Then, the best producer of lipase strain (*M. furfur* No.132) was grown at optimal conditions in the presence of various concentrations of aqueous and oil onion extracts. Dose-dependent inhibition of fungal growth was observed for all concentrations of the aqueous onion extract with a maximum about 73%. Also, some concentrations of both types of the extracts. Aqueous onion extract contains specific compounds which inhibit fungal growth and lipase activity in *M. furfur* and thus, can be used as a therapeutic agent in treatment of *Malassezia* infection.

USING A NATIVE PAGE FOR SHOWING THE CATALYTIC ACTIVITY IN CATALASE ENZYME ISOLATED FROM *ASPERGILLUS FUMIGATUS*

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Aspergillus species are one of the most common groups of fungi in the human environment. There are more than 150 species in this genus, but the most important pathogen in human tissue is *A. fumigatus* which is an airborne mould, found world-wide in soil and decaying vegetation. *A. fumigatus* is capable of the production of a variety of toxin metabolites and enzymes including catalase. Catalase is a heme-containing enzyme which has a widespread occurrence in mammalian and non mammalian aerobic cells containing a cytochrome system. The enzyme may sometimes amount to as much as 1% of the dry weight of bacteria. In some organisms, catalase has been reported to be a virulence factor helping the organism resist the oxidative burst. Catalase from different sources have been reported with different biochemical characteristics. Bovine liver catalase has a molecular mass of 250 Kda and two classes of catalase have been detected in *Salmonella typhimurium* with apparent mol mass of 320 and 350 Kda. *A. fumigatus* catalase is important for the process of colonization and establishment of infection by this fungus. In this study catalase detected after one day in mycelium disruption and two days in culture media. This enzyme in *A. fumigatus* was shown that consist of three parts: F with MW=240 KDa, S1 with MW=320 KDa and S2 with MW=420 KDa. All these parts shown catalytic activity on 5-15% native Gradient-PAGE with ferri cyanide negative staining.

GENOPROTECTIVE PROPERTIES OF MUSHROOMS

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Aqueous extracts of the sporophores of eight mushroom species were assessed for ability to prevent H₂O₂-induced oxidative damage to cellular DNA using the single-cell gel electrophoresis ("Comet") assay. The capacity of the various mushroom-derived preparations (MDP's) to protect against DNA strand breakage was assessed using an *in vitro* assay of cultured human B-lymphocyte cells (Raji). Cells were pretreated with each individual MDP for 2 h, washed and then challenged with 10 μ M H₂O₂. Highest genoprotective effects were obtained with cold (20°C) and hot (100°C) water extracts of *Agaricus bisporus* and *Ganoderma lucidum*, respectively. No protective effects were observed with MDPs from *Flammulina velutipes*, *Auricularia auricula*, *Hypsizygus marmoreus*, *Lentinula edodes*, *Pleurotus sajor-caju* and *Volvariella volvacea*. In the case of *A. bisporus* MDP, concentrations as low as 0.5 mg/ml of tissue culture medium provided virtually complete protection against H₂O₂-induced damage to cellular DNA. This genoprotective effect is not due to cellular uptake or binding of a catalase-like activity within the MDP. Furthermore, no cytotoxic effects *per se* were seen at concentrations up to 1 mg/ml, even after 24 h exposure. Intraperitoneal administration of the *A. bisporus* MDP also protected the DNA of rat lymphocytes against H₂O₂-induced damage in an *ex vivo* assay. Research is now underway to purify and characterise the active components from *A. bisporus* and *G. lucidum* and to establish the nature of the protective mechanism(s). These findings indicate that some edible mushrooms represent a valuable source of biologically active compounds with potential for protecting cellular DNA from oxidative damage. Such materials could be incorporated into low-cost mushroom-based food supplements for lowering the risk of diseases linked with oxidative stress, and provide therapeutic treatments for offsetting the adverse effects of chemo- and radiation therapies used in the treatment of certain cancers.

PHAEOHYPHOMYCOSIS OF THE SINUSES AND CHEST BY *CLADOSPORIUM BANTIANUM*

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Fungal sinus infections are being recognized with increasing frequency. We report one case with rhinocerebral and chest phaeohyphomycosis infection caused by *Cladosporium bantianum*, in an 18-year-old man with Wegener's Granulomatosis. The diagnosis was established by histopathological appearance, direct examination, culture and computerized tomography (CT) scan. This case was successfully treated by a combination of surgery and amphotericin B. The present case of paranasal sinus mycosis due to *Cladosporium bantianum* is the first case reported in Iran. (Poster 41)

DEEP-SEATED FUNGAL DISEASES IN IMMUNOCOMPROMISED PATIENTS

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During the last two decades or so, the fungal infections have increased dramatically. Deep-seated mycoses are creating serious problems for clinicians working with certain populations of patients, such as those with cancer, the immunocompromised, and physiologically compromised. A study of deep fungal infection was carried out in the section of Medical Mycology, Pasteur Institute of IRAN from April 1994 to March 1998 (7 years) 777 samples examined for deep fungal infections. Diagnosis was established by demonstration of fungus in direct and cultural examinations. In this study fungal infection occurred in 102 men and 100 women. Sixty-eight fungal infections occurred in patients with one or more predisposing factors for disseminated fungal infections. One hundred and thirty four fungal infections occurred in normal patients. The most frequent mycotic infections were caused by *Candida* with 75.74%. In this study more frequent predisposing factors in immunocompromised hosts was hematologic malignancy, metabolic acidosis hyperglycemia and organ transplant recipients. The incidence of infections in immunocompromised patients is extremely high. It is still possible that prophylaxis is in fact early therapeutic intervention at a stage during which clinical signs of infection are still absent, indicating that immunocompromised patients with probable fungal infection should be treated very aggressively and antifungal treatment started as early as possible. (Poster 42)

ROLE OF C3, C4 COMPLEMENT IN PREVENTING THE OCCURRENCE OF CANDIDIASIS INFECTION IN PATIENTS WITH LEUKEMIA AND LYMPHOMA

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Candidiasis is a type of opportunistic fungal disease that some susceptible factors such as immunity disorders and haematological such as leukaemia and lymphoma play role in its creation, immunity and resistance of body have important role in prevention of candidiasis infection. So researching in the field of complement system in patients who due to infection by disabling disease such as leukaemia and lymphoma disease, had also affected by the infection of candidiasis.

The case group consisted of 50 candidiasis patients with lymphoblastic leukaemia and lymphoma. The control group consisted of 50 people without candidiasis. The findings obtained from this study for detection of C3, C4 complement and the mean of CH50 in patients serum, were compared with control person with no evidence of candidiasis infection. There was a significant decrease in the mean of C3 complement and CH50 in leukaemia and lymphoma patients in comparison to control group ($p < 0.05$). But there was no significant difference between the mean of C4 complement in all patients in comparison to control group ($p > 0.05$). This research shows a deficiency in the mean of C3 complement in patients with leukaemia and lymphoma. For reasons of decrease in the amount of C3 and CH50 in patients suffering from leukaemia, these had been affected by candidiasis. (*Poster 43*)

ROLE OF CELLULAR IMMUNITY IN PREVENTING THE OCCURRENCE OF CANDIDIASIS INFECTION IN PATIENTS WITH LEUKEMIA AND LYMPHOMA

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Candidiasis is an opportunistic fungal disease with several predisposing factors, such as leukaemia and lymphoma. Immune system can play a major role in prevention of candidiasis. In this study, part of the relation between cellular immunity and candidiasis in leukaemia and lymphoma patients was investigated. The case group consisted of 50 candidiasis patients with leukaemia and lymphoma. The control group consisted of 50 persons without candidiasis. Blood samples were taken from both groups. The average and type of lymphocytes were examined using the Flow cytometric method. Statistical analysis was performed by SPSS and EPI softwares, using Z and T test. The averages of T and CD4 lymphocytes were significantly ($P < 0.05$) lower in patients compared to control group. But there was no significant difference in B and CD8 lymphocytes between case and control groups. It seems that the lower counts of T and CD4 lymphocytes in case group, are the predisposing factors for candidiasis, since these lymphocytes play a major role in prevention of candidiasis. (Poster 44)

ISOLATION OF POLYFLAGELLATE RUMEN ANAEROBIC FUNGI FROM SHEEP IN IRAN

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Experiments were carried out to isolate rumen anaerobic fungi from fistulated sheep. Anaerobic technique was used to inoculate serum bottles containing of an undefined culture medium called medium C. Inoculum was a small amount of fresh rumen contents. Antibiotic solution was also used to prevent the growth of bacteria in the medium. Fungi were grown anaerobically in press sealed serum bottles at 39°C. Samples were examined by light microscope after 48 hours of incubation. Anaerobic fungi were observed at different stages of development. Motile zoospores having one or more flagellates were abundant in examined samples. Various forms of fungal sporangium variable in size with extensive rhizoidal systems were also observed. This is the first report of isolation of rumen fungi from Iran and so, further works is needed to identify different fungal genera that maybe present in the gastrointestinal of ruminant animals. However, results indicated that uniflagellate and polyflagellate anaerobic fungi are normal inhabitants of the rumen ecosystem.

EVALUATION OF THE SUSCEPTIBILITY OF DERMATOPHYTES TO GARLIC EXTRACT

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Garlic has shown to inhibit the growth of a variety of microorganisms such as bacteria, parasites, viruses and fungi. Fungi are included: *Aspergillus* spp., *Fusarium oxysporum*, *Sclerotinia sclerotiorum*, *Cryptococcus neoformans*, *Paracoccidioides brasiliensis* and some Dermatophytes included: *Microsporium audouinii*, *T. violaceum*, *T. simii* etc. In this study, we have evaluated the activity of garlic extract against Dermatophytes namely *Trichophyton mentagrophytes* var. *mentagrophytes*, *T. mentagrophytes* var. *interdigitale*, *T. rubrum*, *T. tonsurans*, *Microsporium canis*, *Microsporium gypseum*, *Epidermophyton floccosum*. Garlic was obtained from Hamadan, Iran. Dry garlic bulbs were peeled and homogenized with two parts of distilled water in a Waring blender. The homogenized garlic extract was then run through Amicon ultra-filtration system. 300xm, 100xm, 50xm, 30pm, and 10pm membrane were used. The ultra-filtrated fractions were collected as Residue (R) 300, 100, 50, 30, 10 and filtrate (F) 10. The fractions were evaluated by SDS-PAGE, using 14 percent Acrylamide gel. Serial dilutions of fraction from 1/25 up to 1/3200 were tested against each Dermatophyte. The results indicate that fraction 10 was the most effective anti-Dermatophytes. F10 has shown to inhibit the growth of *T. rubrum*, *T. tonsurans*, *Microsporium canis*, *Epidermophyton floccosum*. (Poster 45)

INTRACELLULAR ESTERASE ACTIVITY IN *CANDIDA ALBICANS* AND ITS EVALUATION AS A VIRULENCE MARKER

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Candida albicans is the most common agent of fungal diseases in human beings, often appearing as an opportunistic infection in immunocompromised individuals. Recent findings show that *C. albicans* is a contagious microorganism and in appropriate conditions, especially highly virulent strains, may cause hospital outbreaks. Therefore fast and easy identification of the virulence of *C. albicans* isolates may have much epidemiological importance. So far, many methods have been introduced to differentiate *C. albicans* strains, but none of them turns out to be capable to distinguish high and low virulent strains from each other. In the present study, using a colorimetric method, we assayed carboxylesterase activity of the *C. albicans* isolates differing in virulence against 5 synthetic substrates (1-naphthyl acetate, 2-naphthyl acetate, 1-naphthyl caprylate, 1-naphthyl laurate, 1-naphthyl palmitate), and evaluated the esterase activity as a virulence marker. All studied isolates showed enzyme activity against each of the used substrates and the mean of esterase activity of the isolates showed indirect correlation with the number of carbon of the substrate carboxylic residue (except 1-naphthyl laurate). Although there were significant quantitative and qualitative differences in esterase activity of the isolates, there was no positive or negative correlation between virulence and esterase activity against each of the 5 substrates. By dividing the isolates into two groups of highly and little virulent strains and comparing their esterase activity, no significant difference was found. It is concluded that intra-cellular esterase activity of the *C. albicans* against substrates used in this study isn't a suitable virulence marker for this pathogenic yeast. (Poster 46)

PRODUCTION OF ALPHA-AMYLASE BY MUTANT STRAIN OF *ASPERGILLUS ORYZAE*

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Alpha-amylase from *Aspergillus oryzae*, which hydrolyses α -1,4-glycosidic linkages randomly throughout the starch molecule, is a widely used industrial enzyme. In this study, u.v. light, nitrous acid and MNNG were used to mutagenize *A. oryzae* conidia, which were then cultured in the presence of 2-deoxy-D-glucose to select derepressed α -amylase mutants. As parent strain, the α -amylase producing strain of *Aspergillus oryzae* PTCC 5164, was used. Mutant colonies showing a halo zone/colony diameter (H/C ratio) larger than that of the parent strain, were selected for second step of screening. Both the saccharogenic (measured by DNS method) and amyloclastic (measured by iodine method) activities of the mutants were determined. It was showed that MNNG has produced the poorest result, in comparison with u.v. or nitrous acid. About 1.11% and 5.5% of mutants obtained by u.v. and nitrous acid, respectively, had H/C ratio bigger than 130% of the parent's. The best mutants obtained at each step, were tested again based on their enzyme activity in liquid culture, in the secondary screening step. The best strain was a result of mutagenesis by nitrous acid, which produced 6.73 times more amyloclastic and 5.13 times more saccharogenic activity than the parent strain. 2-deoxy-D-glucose showed to be a suitable anti-metabolite for isolation of α -amylase derepressed mutants.

DEVELOPMENTS IN SOLID STATE FERMENTATION

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The overall picture of solid state fermentation (SSF), once regarded as a low-technology, useful for developing countries, in contrast to submerged fermentation (SmF) as a high-tech for more developed countries, is now changing. SSF, which was introduced to industrial world by far east countries, normally was employed for production of traditional foods like Tempeh, Rac, Miso, etc., but is now being used for other area of biotechnology like bioconversion of agro-food industrial wastes, and production of a diverse range of value-added bio-products such as: enzymes, antibiotics, organic acids and many others. Apart from completely industrialised processes of composting agro-food wastes, mushroom production and cheese fermentation, the commercialised areas of using SSF are: (1) production of industrial enzymes, (2) organic acids and (3) protein enriched feeds. Although fungi are regarded as most appropriate micro-organisms for SSF processes, yeasts, actinomycetes and even eubacteria are increasingly tested for production of bioactive compounds. In this regard, production of ethanol by *Saccharomyces cerevisiae*, lipase by *Candida* sp., tetracyclines by *Streptomyces viridifaciens*, cephamycin C by *Streptomyces clavuligerus*, L-glutamic acid by *Brevibacterium* sp., xanthan gum by *Xanthomonas campestris*, biosurfactants by *Bacillus subtilis*, and bacterial endotoxin by *Bacillus thuringiensis* could be mentioned. SSF processes have their own characteristics for monitoring and controlling the fermentation course. For example sterilization, inoculation and aeration of the substrate has remained a problem, while high yield, low cost of substrate and process control and many others has made it a real competitor of SmF. In this article bioprocessing aspects of SSF and many benefits our country can receive from exploiting this technique will be discussed in more detail.

ASPERGILLUS NIGER IS A RICH SOURCE FOR PRODUCTION OF GLUCOSE OXIDASE

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The glucose oxidase (GOD) catalyzes oxidation of D-glucose to D-gluconic acid and H₂O₂. *Aspergillus niger* is one of the most important fungal sources for GOD production. The present report deals with the optimization of culture conditions for enzyme production, enzyme purification from culture broth and cell extract; characterization of the purified enzyme and comparison with standard enzymes. Seventeen samples of *Aspergillus niger* were screened for GOD activity. Samples were cultured in non-specific diagnostic medium. Then GOD overproducer samples were detected in the specific diagnostic medium and NRRL-3 strain was selected for optimization of GOD synthesis in submerged culture that was optimized with "ONE AT A TIME" method. After optimization, the specific activity reached from 0.17 to 0.22 IS/ mg protein. For production of GOD in large scale, NRRL-3 was cultured in optimized medium were used for enzyme purification. GOD was purified by a combination of ion-exchange and filtration chromatography with approximately 90-fold enrichment in specific activity and enzyme recovery of 9%. Purified enzyme had an apparent native molecular weight of 160 kD and a denatured molecular weight of 80 kD that was determined by SDS-PAGE and pH optimum of 5.6 to 5.8. It was inhibited severely by O-phthalate (10 mM) and partially by Ag²⁺, Cu²⁺, Hg²⁺, hydrazine and hydroxylamine (all at 10 mM). The Km value for glucose was 37 mM.

POSITIVE CORRELATION EXISTS BETWEEN AFLATOXIN
FORMATION AND SOME BIOCHEMICAL PARAMETERS IN
ASPERGILLUS FLAVUS AND *A. PARASITICUS*

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Aflatoxins are secondary metabolites produced by certain strains of closely related fungi *Aspergillus flavus* and *A. parasiticus*. Very little information has been documented about the exact role of fungal metabolic and detoxification pathways in aflatoxin formation. In this communication, an attempt has been made to examine the possible correlation between aflatoxin formation and certain enzymes, which are either directly or indirectly involved in aflatoxin synthesis. The presence of fatty acid synthase (FAS) and glutathione S-transferase (GST) activities has been established in the cytosolic fraction of the aflatoxigenic and non-toxigenic strains of *A. flavus* and *A. parasiticus*. Significant differences in the FAS and GST activities were observed between toxigenic and non-toxigenic strains. A positive correlation has been demonstrated between aflatoxin formation and biochemical parameters, namely FAS and GST activities. The age-related production of aflatoxin follows the same pattern as the cytosolic FAS and GST activity profiles. Activities of these two enzymes were higher in toxigenic strains than non-toxigenic ones. Significantly higher enzyme activities were associated with mycelia of toxigenic strains grown in sucrose-low salts (SLS) medium, which support aflatoxin synthesis, while the enzyme activities were low in non-supporting medium known as glucose ammonium nitrate (GAN). Neem (*Azadirachta indica*, A. juss) mediated inhibition of aflatoxin synthesis was accompanied with remarkable decrease in FAS and GST activities. The above mentioned evidences support FAS and GST induction by endogenous aflatoxins in *A. flavus* and *A. parasiticus*.

FUNGUS *BLAKESLEA TRISPORA*: CHARACTERISTICS AND ITS APPLICATION IN BIOTECHNOLOGY

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Developing of mycology is considered as a cause of developing of many fields such as biotechnology. Different fungi are used for producing different products such as: organic acids, alcohol, oil, vitamins, pigments, antibiotics, pharmaceutical and enzymes. One of the important fungi that are used in biotechnological processes is *Blakeslea trispora* from Choanophoraceae. It produces beta-carotene and this pigment has an important role in food industry as a colorant, antioxidant and provitamin A agent. The fungus belongs to order Zygomycetes. They live on plants and animals as parasites. *Blakeslea trispora* has two modes for reproduction: sexual and asexual. Sexual reproduction is an important stage in beta-carotene production. Both negative and positive microorganisms can be either spores or mycelia depending on their stage in fungal life cycle. During the asexual reproduction, a non-mated microorganism spore germinates into a mycelium. When the mycelium has grown to an appropriate size, it produces aerial hyphae, containing sporangia filled with spores. During the sexual reproduction, a negative microorganism interacts with a positive one to form a mated culture. It is believed that this interaction triggers signals by negative and/or positive microorganism that stimulates beta-carotene production by the mated culture. While negative microorganisms typically produce significantly more beta-carotene than positive microorganisms, the highest level of beta-carotene production generally occur when negative and positive microorganisms are physically contacting each other. Ratio of 20:1 from (-) to (+) microorganisms *B. trispora* in a suitable medium containing nitrogen and carbon sources (pH=5.5-7.5) and temperature of 22-23°C gives a high amount of beta-carotene (2.5 g/L) in 7 days.

FUNGI AND AFLATOXINS IN PISTACHIO NUTS, ANIMAL AND POULTRY FEED IN THE SULTANATE OF OMAN

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A study was carried out on fungi and aflatoxins in pistachio nuts. Ten batches of each of six different animal feeds were also surveyed. The feeds were poultry layer feed, animal feed, hay, barley, soybean and maize. Samples of pistachio nuts, animal and poultry feed, hay, barley, soybean and maize were incubated at $24 \pm 2^\circ\text{C}$ and fungi were identified. Aflatoxins were extracted from the samples by monoclonal antibody techniques (immunoaffinity columns). Aflatoxins were quantified by HPLC. Fungi were isolated from pistachio nuts with percentages as follows: *Aspergillus niger* 14.8%, *Penicillium* spp. 13.6%, *Aspergillus flavus* 9.7%, *A. nidulans* 1.6% and less than 1% for other species. Significant differences were found among the batches and brands contaminated by *A. flavus*. Aflatoxins B₁ and B₂ were found in 15 samples of the 55 samples assayed at levels ranging between 20-400 ppb.

Ten genera and 16 species were isolated from the animal and poultry feed, hay, barley, soybean and maize. These include *Alternaria alternata*, *Aspergillus flavus*, *A. nidulans*, *A. niger*, *A. ochraceus*, *A. versicolor*, *Aureobasidium pullulans*, *Drechslera hawaiiensis*, and others. The predominant species were in *Aspergillus* and *Penicillium*. Aflatoxins B₁ and B₂ were found in 33% of hay and 42% of maize at levels ranging between 60-500 ppb. No aflatoxin was found on the other animal feed. Maximum levels of aflatoxins in foods and feeds according to Omani Standards No. 703 of 1997 is 20 ppb for nuts, 10 ppb for animal feed and 20 ppb for poultry feed. These regulations need to be enforced.

EVALUATING THE EFFECTS OF VAM SPECIES ON GROWTH CHARACTERISTICS AND ROOT INFECTION OF MAIZE

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Vesicular arbuscular mycorrhiza are well known fungi having symbiotic association with crops. In this association VAM fungus helps plants in nutrient absorption, especially P in poor soils. In this study, potential benefits of some species of VAM on growth and development of corn were evaluated in three separate experiments. In the first attempt 5 treatments including species of *Glomus mosseae*, *G. geosporum*, *G. caledonium* and a native species of *G. intraradices* and also a control treatment of non-mycorrhizal plots were used in a completely randomized design. Based on the results of the first experiments, in the second experiment that conducted in greenhouse condition, *G. geosporum* was disregarded due to its ineffectiveness. In the third experiment, which was conducted at two years field conditions, 4 species of VAM were used. Results of pot culture experiments indicated that there was a difference between species in terms of plant dry matter production and root colonization. Plant diameter, height, number of open leaves, stem, tassel and ear dry weight was affected by mycorrhizal treatment. In this experiment, VAM species had significant effects on maize root infection. This value by *G. caledonium*, *G. intraradices* and *G. mosseae* were 66.67, 53.33, 46.47%, respectively. In the second pot culture experiment almost the same results derived. The greatest root infection was determined by *G. intraradices* and *G. caledonium* (91.67, 93.66%) and the lowest value obtained from *G. mosseae* (35%). In the third experiment mean results of two years showed, the effects of VAM fungus compared with control plots on total dry weight were significant. Also percent root infections were significant in both years. The mean results indicated that the percent of root infection by *G. mosseae*, *G. caledonium* and *G. intraradices* were 84.94, 82.62 and 88.46 %, respectively.

IMPACT OF FOUR *GLOMUS* SPECIES ON PHYSIOLOGICAL & BIOCHEMICAL CHANGES IN *CATHARANTHUS ROSEUS*

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Arbuscular mycorrhizal (AM) fungi are important components of the microbiota influential in transfer of nutrients from soil to plants (George *et al.*, 1995). *Catharanthus roseus* is an important medicinal plant of family Apocynaceae, cultivated on commercial scale in many parts of the world. Nearly 60 indole alkaloids including the most widely used anti-cancer drugs vincristine and vinblastine are produced by it. Initially absence of AM fungi was reported in medicinal plants possessing alkaloids. However, Ratti & Janardhanan (1995) reported AM fungal association with medicinal plants. The present study was undertaken to select the best species of *Glomus* among *G. aggregatum*, *G. fasciculatum*, *G. mosseae* and *G. intraradices* for the growth and alkaloid content of *C. roseus*. The plants were raised from the surface sterilized seeds and seedlings were inoculated separately with four different *Glomus* cultures at the time of transplanting. The control treatment had no inoculum of *Glomus* species. Phosphatase activity of the plant was estimated by the modified method of Bergmeyer (1974), while protein content was studied according to the standard method of Lowery (1951). For the estimation of crude cytokinin the method of Vreman & Corse (1975) was applied. The alkaloids were extracted by the method of Kurz & Constabel (1982) and qualitative estimation was done employing HPLC. Phosphatase activity (12.57%), chlorophyll content (114.29%), protein content of leaf (36.24%), crude cytokinin content in root (6.66%) and total alkaloid content in leaf (12.9%) were higher in *G. mosseae* inoculated plants as compared to control plants. Qualitative analysis of crude alkaloids from the leaf tissue showed that vinblastine percentage was maximum followed by catharanthine, vincristine and vindoline, respectively. Thus *G. mosseae* can be adjudged best for growth and alkaloid content of *C. roseus*.

ARBUSCULAR MYCORRHIZAL (AM) FUNGI FROM COASTAL SAND DUNE VEGETATION OF GOA-INDIA

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Arbuscular mycorrhizae (AM) may be used for rebuilding the vegetation of coastal region under threat. Prior to exploiting the reclamation potential of these organisms, it is necessary to examine their occurrence and distribution in sand dunes. The occurrence and the number of AM propagules in the rhizosphere soils of six selected saline host plant species viz., *Cyperus* sp., *Urgenia indica*, *Calotropis gigantea*, *Spinifex squarrosa*, *Cocos nucifera* and *Lantana camara* have been studied.

The results indicated that the AM propagules were observed in the rhizosphere soils of all the selected host plant species. The average spore density was found to be 327.8 spores/100g rhizosphere soil which ranged from the minimum spore density in *Lantana camara* (170 spores + 4 sporocarps/100g rhizosphere soil) to a maximum spore density observed in *Cyperus* sp. (427 spores/100g rhizosphere soil). In all, a total of 15 species of AM fungi belonging to 4 genera viz., *Glomus*, *Gigaspora*, *Acaulopsora* and *Sclerosystis* were identified from the soil samples. It is observed that species of *Glomus* dominated the rhizosphere soils of the sand dune ecosystem.

SEASONAL DYNAMICS OF ARBUSCULAR MYCORRHIZAL (AM) FUNGI IN IRON ORE MINE WASTELANDS OF GOA, INDIA

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The seasonal variation in arbuscular mycorrhizal (AM) spore population and root colonization for a selected mined area i.e. Codli, Goa, India (15.2°N Latitude & 74.8°E Longitude) was investigated during summer season (March), Monsoon season (July) and Winter season (November). Six quadrates, each with an area of 10x10 square meter were laid on the mine and eight selected host plants, common to all the six quadrates were worked out for percent infection and spore density. Arbuscular mycorrhizal (AM) fungal spores and percent infection was recorded separately for different seasons. Average spore count was maximum in summer season (289/100g rhizosphere soil) and was minimum in monsoon season (68/100g rhizosphere soil). Highest percent colonization was recorded in monsoon season (51%) and least was recorded during summer season (23%).

Arbuscular mycorrhizal (AM) fungal spores recorded from the present study belonged to five genera viz., *Acaulospora*, *Gigaspora*, *Glomus*, *Sclerocystis* and *Scutellospora*. Total of nine arbuscular mycorrhizal (AM) fungal species namely, *Acaulospora spinosa*, *Acaulospora scrobiculata*, *Glomus fasciculatum*, *Glomus macrocarpum*, *Glomus geosporum*, *Gigaspora margarita*, *Scutellospora gregaria*, *Scutellospora pellucida*, *Scutellospora reticulata* were recorded in all the three seasons. (Poster 47)

AFLATOXIN IN RICE BRAN

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When aflatoxin B₁ (AFB₁) forms in rough rice, it is confined to the aleurone layer, so it comes out completely in the bran fraction during milling, leaving the polished rice free of toxin. However, man is still at risk because rice bran is widely used as a source of cattle feed and of edible oil. It is difficult to prevent AFB₁ formation in rough rice, as *Aspergillus flavus* forms a major component of the air mycoflora of rice fields, especially during harvest and threshing. After milling, there is rapid increase in AFB₁ content of bran during storage. Poor hygiene of commercial mills often provides an additional source of contamination. So a detoxification process prior to usage is essential for rice bran. In our studies over 90% detoxification was achieved with ammonia. There was some indication that varietal differences, rather than climate or storage conditions, are a deciding factor in aflatoxin contamination of rough rice, the native varieties being more resistant than artificially bred varieties - a factor that should be considered in future breeding programmes. Financial assistance in the form of a research grant to the first author from the Ministry of Environment, Government of India, is gratefully acknowledged.

COLOSSOLACTONES, NEW TRITERPENOID METABOLITES
FROM A VIETNAMESE MUSHROOM *GANODERMA*
COLOSSUM AND THE POSITION OF *TOMOPHAGUS* IN THE
FAMILY GANODERMATACEAE DONK

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The fungal family of the Ganodermataceae Donk is represented by more than 200 species that mostly occur in subtropical and tropical regions. From medically important species, numerous terpenoid compounds have been reported. In this paper we report the structure of seven new triterpenoid metabolites, colossolactones A-G (1-7) isolated from an Indochinese species of *Ganoderma colossus sensu lato*. They display unusual carbon skeletons such as two linearly annelated seven-membered rings A and B as part of a tetracyclic terpene skeleton or a delta-lactone as C17-side chain. The structures of compounds 1-7 were settled on the basis of physico-chemical methods such as optical spectroscopy, MS and NMR. This fungus was collected on a trunk of *Delonix regia*. These characteristics are due to the description of Furtado (1965:979-984) or Ryvarden and Johansen (1980:89) as type species of *Tomophagus* group, which is considered a synonym of *Ganoderma* by modern authors such as Furtado (1965), Steyaert (1972), Ryvarden and Johansen (1980). Recent molecular and morphological studies (Moncalvo et al. 1995c; Moncalvo 1996) indicated little relationship between *G. colossus* and *G. oregonense* as well as other *Ganoderma* species and supported a generic distinction of *Tomophagus*. We accept *Tomophagus* as a distinct genus of Ganodermataceae Donk. It is easily distinguished from other *Ganoderma* spp. by being soft and light when dry, having a thick and pale context and especially containing unusual triterpenoid metabolites, which have not been found in other species of Ganodermataceae. So the genus *Tomophagus* (1965a) is nomenclaturally valid (Donk, 1960) and was proposed to replace *Dendrophagus* Murrill (1905b), which was preoccupied with *Dendrophagus* Toumey 1900. Type species: *Tomophagus colossus* (Fr.) Murr. Syn: - *Polyporus colossus* Fr; *Ganoderma colossus* (Fr.) Baker; *G. colossus* (Fr.) Torr; *G. colossus* (Fr.) Bose; *G. colossus* (Fr.) Pat; *G. colossus* (Fr.) Cunn.; *Dendrophagus colossus* (FR.) Murr.

SCREENING OF STRAINS PRODUCING *CEPHALOSPORIN C*; PRODUCTION AND EXTRACTION OF THIS ANTIBIOTIC

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Cephalosporin C (CPC) as a major precursor of semi-synthetic cephalosporin antibiotics, is produced by few strains of *Acremonium* species. Obtaining producing strains and confirming their production, as well as defining optimal production and extraction conditions were the main objectives of this study. Selective media were used for soil screening. Standard strains were obtained from DSMZ. CPC production was confirmed by biological and chromatographic methods. For production induction several kinds of media with different carbon and nitrogen sources were used. Recovery process and extraction were done by filtration of culture media, followed by absorption and column chromatography purification and a final crystallization. By soil screening, a native producing strain with similar macroscopic and morphological characteristics of obtained standard strains was isolated. CPC production in these strains was confirmed by biological and chromatographic (TLC, PC, bioautography and HPLC) methods in comparison with pure CPC standard. Native and standard strains were different in CPC production in various fermentation media. CPC is recovered and extracted from culture media with 65% purity. By obtaining producing strains, we can produce and recover CPC from fermentation media. These data can be used for large-scale production of CPC in Iran. (Poster 48)

PURIFICATION OF CELL WALL MANNOPROTEINS OBTAINED FROM *CANDIDA ALBICANS* BY AFFINITY CHROMATOGRAPHY

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Candida albicans ptcc-5027 was grown on synthetic medium "gyep" (glucose, yeast extract, peptone) at 28°C for 48h. Yeast cells were broken with "threuma in tube" (glass bead 0.5 mm + Vibrofix) method. Proteins obtained from crude extract were detected by SDS-PAGE. Then crude extract was subjected to affinity chromatography on Concanavalin-A (Con-A) bound sepharose. Most of the material bound to Con-A, was eluted with a buffer containing 0.2 M α -methyl mannoside (Sigma), the competitive inhibitor of mannan-ConA complex formation. Fractions were obtained from column (Con-A-Sepharose), were detected by SDS-PAGE. Three protein bands were detected in electrophoresis with MW about 22.5 kDa, 18.75 kDa, 16.5 kDa. (Poster 49)

SCUTELLOSPORA DIPURPURASCENS, NEW FOR THE ASIAN MYCORRHIZAL FLORA**M. Sadravi¹, E. Mohammadi Goltapch² & J. Blaszkowski³;**¹Department of Plant Protection, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran, ²Department of Plant Pathology, Tarbiat Modarres University, Tehran, Iran, ³Department of Plant Pathology, Academy of Agriculture, Szczecin, Poland

Arbuscular mycorrhizal fungi have many important roles in increasing nutrient absorption, growth and plant resistance to soil borne pathogens. In investigation arbuscular mycorrhizal fungi of Iran, from rhizosphere of some cereal crops, spores of an arbuscular mycorrhizal fungus were collected with these characters:

Spores: borne singly in soil on a bulbous cell, with pale yellow with a greenish tint to yellow brown colour, subglobose to ellipsoid shape, (120-) 177.9 (-220) × (150-) 189 (-260) µm. Structural wall with two layers, a thin hyaline outer layer and a laminate coloured layer, two Flexible Inner Wall (FIW) also were present, FIW1 had one hyaline layer usually tightly adherent to laminate layer FIW2: Two layers, L1: was hyaline, (1.1) 1.9 (-3.4) µm thick, stains a light pink in Melzer's reagent, L2: hyaline, (2.2-) 3.2 (-4.2) µm thick, stains red purple in Melzer's reagent. Germination shield: oblong, with 4-6 folds and placed on FIW 2. Auxiliary cells, which were present around mycorrhizal roots, were aggregates of cells with smooth surface, born on coiled hyaline hypha. All above evidences indicated this fungus was *Scutellospora dipurpurascens* Morton & Koske, it was present in 16% of samples and are new for wheat, barley and corn mycorrhizal flora in Iran Asia. (Poster 50)

EVALUATION OF VESICULAR-ARBUSCULAR MYCORRHIZAE (VAM) IN SAFE AND ZN DEFICIENT POTATO FIELDS IN IRAN

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VAM infection and spore number were studied in relation to the amount of Zn in soil and leaves of potatoes. Field experiments involving eight locations in Chahar Mahal and Bakhtiary province of Iran, were conducted in 2 cropping seasons. Sampled fine roots were stained with chlorazol-black-E, and root length colonized by fungal mycorrhizal symbionts was calculated. Extracted spores wet sieving and sucrose centrifugation were counted and calculated per gram soil. The proportion of infected root length and the spore number decreased markedly in soils with low Zn content while there was more Zn concentration in the leaves of plants with lower VAM infection. This indicates that while larger amounts of Zn in soils provide better condition for VAM infection, extra available phosphorus in these soils causes Zn deficiency in all leaves. (*Poster 51*)

THE PROTEIN CONTENT AND NITROGEN IN FOUR MUSHROOMS FROM IRAN

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The protein content and nitrogen of four wild mushrooms of Iran, *Terfezia clavaryi*, a giant species of puffball (Lycoperdaceae), *Agaricus silvaticus* and *Cantharellus cibarius*, were studied. The soluble proteins were assayed by Lowry method (Lowry *et al.*, 1951) and for crude protein (N*6.25) and nitrogen used Micro-Kjeldal method. Results showed 2.8, 9.2, 6.5 and 3.1% soluble proteins, 16.1, 60.5, 33.3 and 18.9% crude protein and 2.6, 9.7, 5.3 and 3.0% nitrogen for *Terfezia clavaryi*, the giant puffball, *Agaricus silvaticus* and *Cantharellus cibarius*, respectively. These results were compared with the protein content in two cultivated mushrooms, *Agaricus bisporus* and *Pleurotus ostreatus*. The soluble proteins in the two latter mushroom species were determined 7.7 and 3.8%, crude protein 35.2 and 26.9%, nitrogen 5.6 and 4.4%, respectively. As compared with the other mushrooms, the giant puffball had the highest protein and nitrogen. (Poster 52)

Reference

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Figures printed in bold face indicate the presenting authors.

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