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FUNGUS DIVERSITY AND GENETIC CHARACTERIZATION

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Abstract

The extent of Fungus diversity is reviewed, with respect to revised estimates of the numbers of plant species, and recent data on the extent of novelty in tropical forests, unexplored habitats, and numbers of orphaned, cryptic, and collected but yet undescribed species. Collections of Fungus cultures are considered to be better referred to as "genetic resource collections" rather than "culture collections" to mesh with current terminology in other groups of organisms. Finally, the special role and responsibilities of CBS, as the major centre for the conservation of Fungus genetic resources worldwide, is emphasized.

INTRODUCTION:

The issue of Fungus diversity, its extent and conservation, has attracted more attention in the last 10–15 years than in any period of history. But what implications do the recent debates have for collections of Fungus cultures, especially in the genomic age? The centenary of the Centraal bureauvoor Schimmel cultures (CBS), the Fungus Biodiversity Centre, now in Utrecht, provides an appropriate occasion to consider the emerging issues, the extent of the problems, and implications for the role of such collections [1]. Just as living organisms evolve to meet environmental challenges, so the scientific infrastructure needs to adapt. In particular, institutions must both meet the immediate needs of successive generations of scientists, and also position themselves to be able to fulfil anticipated future demands. Having been privileged to be entrusted with the management of one of the world's leading mycological centres for 14 years, through a period of major change and relocation [2-4], I am acutely aware of the need for pragmatic approaches. Here the current state of our knowledge of Fungus diversity, existing Fungus genetic resource collections, and the challenges collections face in supporting the needs of Fungus genomics and molecular biology, as well as those of conservation [5].

Soil microcosms and DNA extraction to study the Fungus community in wheat rhizosphere soil, we collected soil from a small field plot on the campus of the Universityof Utrecht located on the Uithof, Utrecht, and The Netherlands. Thisis a clay soil containing 4% organic

matter with a pH of 5.0. Samples from this soil were used for plating culturable fungiand for setting up the microcosm experiment [6-8]. The soil was airdried and sieved, and nine small pots (diameter, 10 cm) were filled.Soil was seeded with eight seeds of Triticumaestivum cv. Baldusper pot. Fluctuations in moisture content were minimized by supplyingwater daily to keep the soil moisture content at 20%. Microcosmswere incubated in a climate chamber with a light-dark regimenof 16 and 8 h at 20 and 15°C, respectively. Microcosms were sampledin duplicate on days 5 and 10. Bulk soil samples of 3g were takenfrom root-free soil. Rhizosphere soil was obtained by gently shakingthe soil from the roots, and roots with adhering soil were addedto 50-ml polypropylene tubes with 10 ml of sterile sodium phosphatebuffer (120 mM; pH 8) and 1g of gravel. Tubes were vortexes for30 s, and the buffer-soil slurry mixture was poured into a newtube, leaving the gravel and roots behind [9, 10]. Total DNA was extractedfrom the rhizosphere soil slurry by using a bead beater.One microliter of the extract was used for PCRamplification.

STATEMENT OF RESEARCH ARGUMENT:

Research on the genetic structure of Fungus populations has mushroomed, and review studies that summarize these studies are numerous. Although the number of Fungus studies has increased greatly, the most comprehensive work has focused on a small number of plant-pathogenic fungi. The majority of these fungi can be recognized easily by their fruiting bodies or disease symptoms on aboveground plant parts. It has proven more difficult to assess the genetic structure of Fungus populations that exist mainly belowground, because the distribution of individuals cannot be visualized directly and appropriate sampling procedures are less obvious and more cumbersome. Nevertheless, substantial progress has been made in interpreting the population genetic structure of some soil borne fungi. The purpose of this study is to provide an overview of the tools and techniques of Fungus population genetics.

OBJECTIVE OF THE STUDY:

- To study the Fungus strains, culture conditions, and amplification range.
- To study the Extent of Fungus Diversity.
- To study the Fungi in tropical forests.
- To study the Fungus Genetic Resource Collections.
- To study the Bioremediation-Bacterial Degradation, Fungus Degradation.

CONCLUSION:

Fungus classification is far from static, and even which organisms are actually members of Fungi is changing. For example, the group Trichomycetes describes gut inhabitants of

arthropods that share similarities with zygomycetes. Molecular phylogenetic studies have demonstrated that two of the four orders of Trichomycetes are actually members of the Mesomycetozoea protest group. Other organisms that were previously considered to be Fungi because of their heterotrophic, mold-like growth forms are now classified as stramenopiles (Oomycota, Hyphochytriomycota, and Labyrinthulomycota) or slime molds (Myxomycota, Plasmodiomycota, Dictyosteliomycota, Acrasiomycota). More interesting for mycologists are the findings that some species previously considered protozoa are actually Fungi. The most revolutionary addition to the Fungus lineage has occurred with phylogenetic evidence indicating the protist group microsporidia is closely related to Fungi–possibly derived from zygomycetes or sister to the genus *Rozella* on the earliest branch in the Fungus nation. Microsporidia are highly specialized intracellular parasites (primarily of animals) that lack mitochondria but have chitin and trehalose in their spores (similar to Fungi). All molecular studies have shown that microsporidia evolve at an extremely accelerated rate of evolution, making their placement in the Tree of Life difficult. The relationship with fungi is supported by many single and multiple gene phylogenies, but an exact placement within the fungi has not received strong support.

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