Morphological studies in the era of molecular biology based taxonomy

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In the last two decades, mycologists have heavily relied upon genomics and proteomics to progress fungal taxonomy. Morphological studies have frequently been neglected and used as supplementary evidence in taxa definition and creation. More recently, however, the use of polyphasic taxonomy has been adopted by many mycologists and several monographic studies have used morphological, ecological and physiological data to complement molecular biology and proteomic studies with the aim to provide an integrated taxonomy of a given fungal group.

Polyphasic taxonomy is a term coined a few decades ago to define a classification system making use of all information available on a given group of organisms. Accordingly, polyphasic taxonomy uses ecological, morphological and physiological characters, and combines them with biochemical and molecular data to generate a comprehensive characterisation of the taxonomic group studied. As such, polyphasic taxonomy is a multifactorial approach that aims at analysing all data at the same time and to provide a complete taxonomic picture of the taxa studied.

In this approach, morphology plays a major role, because genetic differences should somehow be reflected in phenotypic differentiations of metabolic profiles and morphological characters. In addition, morphology is often the only reliable means to start taxonomic studies in mycology because of the lack of enough material for phylogenetic studies.

Ideally, phylogenetic studies should be carried out under consideration of morphological grouping. A reliable phylogenetic analysis should be based on the study of a fair number of samples, using material from geographic distinct origins, studying preferentially two or more gene regions, and evaluating the resulting phylogeny in the lights of available morphological and ecological data.

Using selected taxa in the genus *Rosellinia* as a model, I shall highlight the problems linked to the taxonomic study of a poorly known genus, for which only few species have been collected in large amounts and very scant information is available on its phylogeny. Using the *Rosellinia necatrix* section as an example, I shall discuss how a morphological framework is a needed prerequisite for a sound phylogenetic study of a fungal taxon.

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What fungal endophytes tell us about plant and human fungal pathogens

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As many other scientists, mycologists are usually highly selective and specialised in their research. They deal either with plant inhabiting or animal dwelling fungi, rarely with both and almost never do they try to analyse commonalities and differences between the two groups. Yet both share several common traits that help to understand mycological phenomena in general.

Endophytes have been defined as organisms that inhabit plant tissues; they mainly live as symptomless symbionts in the plant organs but they may become pathogens under selected ecological conditions. Some appear to be obligate, while many others may be opportunistic symbionts. Pathogenicity has been shown to be linked to a number of factors, among them the production of quite specific enzymes or resistance proteins. Studies have shown that all plant species so far investigated host specific and unspecific endophyte taxa.

Among animal inhabiting fungi, some, such as several dermatophytes, are known to be obligate symbionts, yet opportunistic commensals often become feared pathogens when the host is immunocompromised or weakened. As for fungal plant pathogens, pathogenicity factors include specialised enzymes, oxidative stress resistance mechanisms, and toxin production. Recent studies have indicated that the animal mycobiome includes many different fungal taxa, with no animal species so far investigated not being colonised by fungi.

Using mainly a beech endophyte (*Discula umbrinella*) and a human commensal (*Candida albicans*) as models, I shall try to describe commonalities and differences between fungal endophytes and human pathogens. Further, I shall discuss how activities with plant and soil inhabiting fungi may impact the development of human and animal mycota. Finally, I shall outline how mycological research would benefit from a more integrated approach that would promote discussion and dialogue between human and plant mycology researchers.

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