Improved Phylogenetic Classificationof Ascomycetous Fungi Using Partial β-Tubulin Sequences as Molecular Marker

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Ascomycota, the largest group of the second largest kingdom of eukaryotic life named fungi, has a huge significance on every biome on earth. This kingdom of life has been found closely related with the kingdom animals from an evolutionary perspective, so it is crucial to understand its ecology and diversity. Micro and macro-morphological characteristics have been the traditional ways to classify microorganisms. Since the advent of DNA amplification and automated sequencing, a revolution in microbial molecular systematic started.

Many molecular markers have been tested for distinguishing species, with especially rDNA sequences receiving huge attention. However, later studies detected some intrinsic drawbacks in rDNA sequences as molecular markers. In many cases they failed to resolve complicated species boundaries. Following this finding a search for alternative species markers began.

The primary goal of this study is to search for secondary potential molecular marker in order to resolve complicated species boundaries. The focus has been on protein coding genes especially the beta–tubulin encoding genes as this protein is universal, highly conserved and functionally essential in all eukaryotes and accumulates very few mutations, unlike rDNA sequences. The beta tubulin sequences have been used as primer of interest to assess its utility and potentiality as an alternative molecular marker in the genus *Penicillium* of the phylum Ascomycetous.

The preliminary results of this study seem to be very promising as the marker was found to be applicable for distinguishing the distinct species of the economically and medicinally important *Penicillium chrysogenum* (Antibiotic producer). In addition a clearer and resolved classification of *Penicillium spinulosum* was obtained which the previous studies based on rDNA sequences especially the internal transcribed spacer regions (ITS) failed to detect.

In the future this interesting marker will be used to classify other strains of the phylum Ascomycetous from the collections at the hosting lab in Vienna.