

ITS sequence heterogeneity of *Xylaria* species and some other Xylariaceous genera

N. Suwannasai¹, S. Rodtong¹, S. Thienhirun² and A.J.S. Whalley³

¹School of Microbiology, Institute of Sciences, Suranaree University of Technology, Nakhon Ratchasima 30000, Thailand

²Forest Management and Forest Products Research Office, Royal Forest Department, Chatuchak, Bangkok 10900, Thailand

³School of Biomolecular Sciences, Liverpool John Moores University, Liverpool, L3 3AF, UK

Xylaria was the first described genus of the family Xylariaceae and it is a large and relatively well-known fungus group in most countries in the world. There are also other well-known genera such as *Biscogniauxia*, *Camillea*, *Daldinia*, and *Hypoxylon*. They occur on wood, leaves, seeds, dung, and soil or in a few cases are associated with insects. Some species are weak phytopathogens and many *Xylaria* species have been reported as endophytes living inside healthy plant tissue without apparent damage to the host. Recently, endophytes have been widely investigated because of their ability to produce new or interesting secondary metabolites some of which have proved to be bioactive. The conventional taxonomic studies of *Xylaria* have been based on morphological and cultural characteristics but have in some cases included their metabolite profiles. The major problems concern the high morphological variation among *Xylaria* species depending on stages of development and localities of collection, and the lack of teleomorph stage in the culture. Therefore, the molecular taxonomic study was undertaken overcome these problems. Nucleotide sequences of ITS1, 5.8S, and ITS2 rDNA of 48 *Xylaria* isolates as well as some other Xylariaceous genera obtained from different collection locations were analyzed. Alignments of the *Xylaria* species sequences exhibited the greatest variation in the ITS regions. The 5.8S sequence gave approximately 99% similarity for all isolates tested but ITS sequence comparison results supported a monophyletic group in this genus, which is separated from the genera *Biscogniauxia*, *Camillea*, *Daldinia*, and *Hypoxylon*. The sequences proved to be valuable for the taxonomic investigation of fungi such as *Xylaria* with their high morphological variation. In addition, a database of this molecular data would be useful for the designation of specific primers and for the development of species specific probes for the detection of *Xylaria* in environmental situations.