

## **LEPTOGRAPHIUM SPECIES: ANAMORPHS OF GROSMANNIA**

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*Leptographium* species are anamorphic fungi with erect conidiophores terminating in verticillate branches and conidiogenous cells bearing heads of slimy conidia, which enable them to be carried by bark beetles (*Coleoptera: Scolytinae*). *Leptographium* species have been recognised as anamorphs of *Ophiostoma* species for many years but recent DNA sequence comparisons have shown that they represent a monophyletic lineage. They have consequently been transferred to *Grosmannia*, which has been resurrected to accommodate this phylogenetic group. About half of the approximately 52 species recognized in *Leptographium* have been connected to a teleomorph, while the remaining species are recognized in *Grosmannia* based only on phylogenetic inference. Most *Leptographium* species cause blue-stain of lumber but a small number are serious pathogens of trees. These include the causal agents of black-stain root disease (*L. wagneri*) and Takamaka disease (*L. calophylli*). A few species are also found in the soil and very little is known regarding their biology. Most species of *Leptographium* can be recognized using well-established morphological characteristics but these characters also overlap in closely related species, making identification very difficult. Thus, DNA sequence comparisons have become essential to identify most *Leptographium* species with certainty. Recent, comparisons of sequences for multiple genes, in *Leptographium* species have clarified their phylogenetic relationships. The close relationship of most species support earlier reports that this group forms a monophyletic clade, within the larger Ophiostomatoid group. The overall topology of the multigene tree supports previous findings based on the ITS gene region. In some cases, such as *L. lundbergii*, taxonomic controversies have been resolved and species are better delineated within this group. Using additional strains and gene regions, it has become evident that the ITS gene region is not ideal for phylogenetic studies in this group. Relationships within this group are better defined using sequences of structural genes.