

## **OPHIOSTOMA GENOMICS**

Louis Bernier

Centre d'étude de la forêt (CEF), Université Laval, Québec (QC) Canada G1K 7P4.

[Louis.Bernier@rsvs.ulaval.ca](mailto:Louis.Bernier@rsvs.ulaval.ca).

Several complementary approaches are currently available for genome-wide studies of fungi. Here, we review how these approaches are being used for exploring and understanding the structural and functional genomics of *Ophiostoma* species. Separation of whole chromosomes by pulsed-field gel electrophoresis (PFGE) is providing information of the gross characteristics and plasticity of the nuclear genome of members of the *O. piceae* complex. Mendelian analysis of polymorphic loci in F<sub>1</sub> progeny from an *O. novo-ulmi* x *O. ulmi* interspecific cross, coupled with PFGE data, has allowed the construction of a genetic map for the Dutch Elm disease pathogens. The map currently harbours over 200 coding and non-coding loci, distributed over 10 linkage groups representing seven chromosomes, and is expanding as new markers become available. A growing proportion of these markers are being provided by ongoing functional genomic studies. The latter include the construction and analysis of Expressed Sequence Tag (EST) libraries for various developmental stages of *Ophiostoma*, such as filamentous and yeast phases, asexual and sexual reproduction, substrate utilization, and pathogenicity. Bioinformatic analyses have so far allowed the identification of *Ophiostoma* ESTs that have high homology with genes with known functions in other organisms, ESTs with homology with genes whose function is still unknown and ESTs that may be unique to Ophiostomatoid fungi. The development of transformation systems for *Ophiostoma* species makes it possible to verify the phenotype of mutants in which genes of interest have been either inactivated or over-expressed. Furthermore, the availability of thousands of ESTs provides the opportunity for large-scale analysis of gene expression by either DNA microarrays or serial analysis of gene expression (SAGE and Super-SAGE). By combining the above approaches (and others), we will gain unprecedented knowledge of the genetic determinants of fitness in both pathogenic and saprophytic *Ophiostoma* species.