

MYCOGEOGRAPHY, ECOLOGY AND TAXONOMY OF *FUSARIUM*

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A thorough understanding of the taxonomy of *Fusarium*, accurate morphological identification of species, and where appropriate, confirmation of identification by molecular methods are essential prerequisites for rigorous mycogeographical and ecological studies. These crucial linkages will be illustrated mainly by reference to mycogeographical studies of *Fusarium* species in Australian grassland soils, and as endophytes in tropical grasses. Australia, a large island continent is ideally suited to such studies as it has a wide range of bioclimatic regions, including tropical, arid, temperate and alpine regions. Grasslands are present in all bioclimatic regions allowing transect studies in similar ecosystems across regions. The distribution of many species is restricted to particular climatic regions. Other species such as *F. equiseti*, *F. oxysporum*, and *F. solani* appear to be cosmopolitan. However, it is possible that these morphological species are a complex of cryptic species, each with its own distribution pattern. This is a challenging area for further research. Newly recognised species have been isolated during each of the mycogeographical studies, an indication of the degree of diversity in *Fusarium* that remains to be discovered worldwide. Ecological studies have contributed to an understanding of how climate affects the distribution of species in grassland soils. Furthermore the Bioclim[®] climatic model has been used to predict distribution patterns of *Fusarium* in grassland and cropping ecosystems in Australia. Studies on *Fusarium* species associated with tropical grass stems have revealed the presence of many new species. They have also shown that some important pathogens such as *F. thapsinum* can be isolated from grasses remote from cropping areas. The implications of these findings will be discussed.

THE *FUSARIUM* TRANSPOSABLE ELEMENTS: A FABULOUS STORY

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Fusarium oxysporum has been highly productive in the characterization of active transposable elements (TEs). All eukaryotic types described are found including an extraordinary prevalence of members of the *Tc1/mariner/pogo* superfamily. An exhaustive analysis of their representation, diversification, and chromosomal distribution performed using the recently available genome sequence (BROAD Institute) provides evidence that this species has been subjected to invasion and proliferation of active TEs. TE-mediated changes, associated to transposition and recombination, provide a broad range variation, including an unexpected high number of genome rearrangements. Different processes involved in TE dynamics within a genome (silencing mechanisms, horizontal transfer) have been documented, providing a major challenge to our vision of the *Fusarium* genome. Presently in the *Fusarium* world, functional and comparative genomics are underway. Large-scale mutagenesis projects based on different transposon systems have been developed in various species and genes involved in pathogenicity, mycotoxin production and sexual cycle have been tagged. These tools and technologies have an enormous potential to develop powerful genomic tools for *Fusarium* species. In addition, comparative genomics using the available sequences of four *Fusarium* species (asexual, selfing and outcrossing) offer a stunning opportunity to understand the evolutionary history of these genomes in terms of impact of TEs on genome structure, stability and expression and to define the role of sexuality to the success of TEs proliferation.

