

THE GLOBAL SPREAD OF DUTCH ELM DISEASE: LESSONS IN BIOSECURITY AND PATHOGEN EVOLUTION. C. Brasier.

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The appearance of the invasive Dutch elm disease pathogens, *Ophiostoma ulmi* and *Ophiostoma novo-ulmi*, between 1920 and 2000 has resulted in the death of the majority of mature elms across Eurasia and North America: one of the major ecological disasters of the 20th century. The use of ecological and molecular genetics to study *O. ulmi* and *O. novo-ulmi* populations has revealed a remarkable picture of their spread and continuing evolution. At the macro level, it has revealed the previously unnoticed arrival of a new, behaviourally different DED pathogen species and the rapid replacement of one species by another. At the micro level it has revealed a series of unique interspecies hybridisation and lateral gene transfer events, including the first demonstration of selective transfer of mating type and vegetative compatibility genes between species; and inter-specific transfer of deleterious fungal viruses. These developments have, in turn, highlighted major scientific weaknesses in current international biosecurity (plant health) protocols, including: (1) evidence that many (perhaps most) dangerous plant pathogens are not on current plant health schedules; (2) the need for modern, population-based definitions of pathogen taxa in the schedules; (3) the risk that rapid evolution and adaptation of invasive fungal pathogens may occur following their introduction. These issues will be discussed.

TOOLS FOR EXPLORING THE DIVERSITY AND DISTRIBUTION OF PHYTOPHTHORAS IN NATURAL ECOSYSTEMS.

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Molecular analysis continues to revolutionise the study of many plant pathogens and *Phytophthora* is no exception. Sequencing of the rDNA internal transcribed spacer (ITS) regions remains a valuable first step in the identification of isolates. Such sequence data also provides insights into the evolutionary history and speciation processes amongst *Phytophthora* species and provides the foundations for practical assays for detection and diagnosis. The GenBank database of ITS sequences provides a valuable resource used worldwide and this dataset will be reviewed. With increasing challenges from *Phytophthora* species damaging natural ecosystems comes a need to understand the origins, ecology and diversity of *Phytophthora* in natural habitats. Again ITS-based assay systems are proving valuable and recent developments will be presented. There are however, occasions when ITS-based systems are not appropriate and a finer scale of resolution is needed. An overview of the development and potential of such methods for phylogeographic analysis will be presented.