

DISCOVERY, CHARACTERIZATION AND POTENTIAL MOBILITY OF DNA TRANSPOSONS IN THE DUTCH ELM DISEASE FUNGI

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The occurrence of transposable elements (TEs) in genomes is a generally accepted paradigm. We present here different techniques to recover DNA transposons, and then describe the first three TEs found in the Dutch Elm disease pathogens *Ophiostoma ulmi* and *O. novo-ulmi*. These three elements, named *OPHIO1*, *OPHIO2* and *OPHIO3*, have 42-nt long terminal inverted repeats that flank a potential transposase coding sequence, as well as "TA" dinucleotides as target site duplication. These global features, complemented by phylogenetic analyses, allowed us to ascribe the three TEs to the *Fot1-pogo* family, the most common representative in fungi. Results from Southern hybridizations suggested that the history of *OPHIO* transposons could be correlated with that of the Dutch Elm disease fungi, and that interspecific hybrids could act as genetic vectors for horizontal transmission of TEs between *O. ulmi* and *O. novo-ulmi*. Therefore, mobility of fungal transposons can be investigated from two perspectives: mobility inside the host genome or between different host strains or species. Transposon *OPHIO3*, which had an imperfect structure and displayed the signature of silencing by Repeat-Induced Point (RIP) mutation, is thought to be an ancient transposon.