Inferring the infection biology of the wood decay fungus Perenniporia fraxinea through an analysis of genotypic diversity: a case study in northern Italy

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INFERRING THE INFECTION BIOLOGY OF THE
WOOD DECAY FUNGUS PERENNIPORIA FRAXINEA
THROUGH AN ANALYSIS OF GENOTYPIC DIVERSITY:
A CASE STUDY IN NORTHERN ITALY.
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Perenniporia fraxinea is a fungal pathogen causing wood decay
in roots and bole of a wide variety of broadleaf tree species. Despite
the crucial role played by P. fraxinea in wood decay processes,
little is known on how the fungus spreads from tree to tree. In
order to clarify its ways of spread, genetic variation among P. fraxinea
isolates collected from closely located trees was investigated
coupling molecular analysis with vegetative incompatibility assays.
Twenty samples were isolated from P. fraxinea fruiting bodies collected
from different standing trees in the Parco della Vernavola
(Pavia, Italy) and in several surrounding areas. All the isolates were
genotyped by using Random Amplified Microsatellites (RAMS) and
somatic incompatibility tests. Analysis through RAMS allowed to
distinguish 19 different haplotypes. Somatic incompatibility tests allowed
to detect 16 compatibility groups, thus failing to distinguish
all haplotypes identified through molecular analysis. These results
of genotyping suggest the presence of high intrapopulation diversity,
even when isolates collected from closely located trees were
compared. These findings may suggest that the spread through root
contacts is unlikely for P. fraxinea, which rather may spread through
basidiospores. In addition, a significant correlation between spatial
distribution and genetic variation was observed for the isolates collected
in the Parco della Vernavola. This is one of the first genetic
population studies on P. fraxinea aimed at uncovering its spreading
mechanisms.