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Comparative genomics between the invasive forest pathogen *Heterobasidion irregulare* and the native sibling species *H. annosum* provide a glimpse into their divergent adaptive evolution

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COMPARATIVE GENOMICS BETWEEN THE INVASIVE FOREST PATHOGEN *HETEROBASIDION IRREGULARE* AND THE NATIVE SIBLING SPECIES *H. ANNOSUM* PROVIDE A GLIMPSE INTO THEIR DIVERGENT ADAPTIVE EVOLUTION. F. Sillo¹, M. Garbelotto², P. Gonthier¹.

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The fungal plant pathogens *Heterobasidion irregulare* and *H. annosum* have been evolving allopatrically for 34–41 million of years. *Heterobasidion irregulare* was recently introduced from North America to Italy, within the natural range of *H. annosum*, generating hybrid swarms. Divergent adaptive evolution affecting the genomes of these pathogens is still poorly studied. Here, a comparative genomic approach was used to determine which gene groups were affected by divergent positive selection during the allopatric phase. In particular, it was tested the hypothesis that genes involved in pathogenicity are not as divergent between the two species compared to genes involved in saprobic ability and sporulation, as previously demonstrated in phenotypic observations. Results based on the whole-genome sequencing of three genotypes per species confirmed their status as sister taxa, despite a large macrosynteny was observed. Genes involved in pathogenicity appeared to be more conserved between the two species compared to genes involved in saprobic growth and sporulation. This finding provided genomic evidence that differences in fitness are more likely to be determined by these two last functions, as previously documented by *in vitro* experiments. A large fraction of genes under positive selection was described as involved in transcriptional functions and mitochondrial factors. Genes in interspecific structural variations were also found to be related to these two categories and to transposable element activity. The study has shown at the genomic level that factors related to transmission rather than those related to pathogenicity might explain the invasiveness of exotic pathogens.