



*miR-2-woodex*

## Exploring the miRnome of the ligninolytic fungus *Phanerochaete chrysosporium* during wood extractive-induced stress

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### Summary —

In the context of ecosystem preservation, forest management and sustainable economic development, understanding the key factors that improve wood durability has crucial importance. The wood durability is directly related to lignin/cellulose proportion, and the accumulation of specialized metabolites, known as wood extractives, prevents the degradation by fungi. Some ligninolytic fungi are more tolerant than others likely because of both an efficient non-specific extracellular enzymatic system for degradation of complex molecules, and an advanced intracellular multistep detoxification system that neutralizes wood extractives.

Deciphering the molecular mechanisms responsible for fungal tolerance to wood extractives is crucial to develop new strategies to increase wood durability and to obtain microorganisms with efficient detoxification capacities for biotechnological applications. Some enzymes constituting the detoxification system were already identified, like the Cytochrome P450 monooxygenases or Glutathione transferases (GSTs), but the global physiological regulation is not yet well described. To assess this point, strategies for global and central regulation network characterization, as the integration of heterologous defense mechanisms, the overexpression of native stress responses or the triggering of multiple protection pathways, modified by the transcription machinery or small RNAs, like microRNAs have been developed mainly for the improvement of solvent tolerance in microorganisms.

MicroRNA-like small RNAs (miRNAs) were identified in fungi as central regulators, involved in development and stress responses. My integration project in the Stress response and redox regulation team of the UMR "Interactions Arbres-Microorganismes" is about the characterization of miRNA variations and functions in ligninolytic fungi during wood extractive-induced stress. The one-year project will support the first step of the project, the miRnome sequencing, and will allow to describe what miRNAs are present in *Phanerochaete chrysosporium* and if specific variations are observed after exposition to wood extractives. The results will open an overview of the gene regulatory network controlled by miRNAs in ligninolytic fungi.