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Extracellular proteome of the fungus *Trametes versicolor* – Insights into the development of tools for ecotoxicity assessment in soils

Nathalie CHEVIRON¹, Achref ALOUI¹, Christelle MARRAUD¹, Kevin VARANDAS¹, Didier CHEVRET² et Christian MOUGIN¹

¹UR251 Physico-chimie et Ecotoxicologie des Soils d'Agrosystèmes Contaminés, INRA, Versailles
²Plateforme PAPPSO, Unité MICALIS, INRA, Jouy en Josas



ABSTRACT

The development of relevant and sensitive tools to assess the ecotoxicity of soils contaminated by chemicals is an actual key challenge. Actual approaches are mainly based on the expression of the genetic potentialities of microbial communities, or on the measurement of the resulting enzymatic activities. Because multiple levels of regulation exist between these two endpoints, genomic studies do not reflect the functional biodiversity really expressed into the soils, and enzymatic activities measurements can be submitted to interferences, thus disturbing their interpretation. Other endpoints are studied, such as profiles of secreted proteins.

Fungal proteomics is well expanding and may provide interesting developments for our purpose. Because of the complexity of the soil ecosystem, our studies were targeted on the extracellular proteome of the basidiomycete *Trametes versicolor*, a well-known strain that can be easily inoculated into the soil. Here, our objectives were to study the proteome secreted by *Trametes* exposed to soil pollutants: an organic compound (Xylidine) or a metal (copper) in a two-step approach based on the use of pure liquid culture and spiked soil. We aimed at identifying secretion profiles specific to each pollutant.

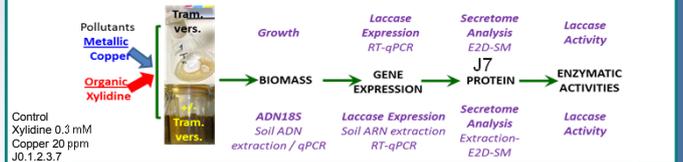
Our results obtained in liquid cultures showed global patterns of protein secretion quite similar in response to pollutants, but some differences were noticed. Protein analysis by mass spectrometry has identified 46 well separated proteins, being essentially oxidases. Among these, two laccase isoforms were specifically induced either by Xylidine or copper. By contrast, numerous spots remained unidentified. Data analysis revealed three groups of protein whose secretion was 1) stimulated by Xylidine, 2) suppressed by the pollutant, and 3) overexpressed by copper. These proteomic results are in agreement with our transcriptomic and functional responses. In spiked soils inoculated with the fungus, we revealed specific pathways in functional response to pollutants. Proteomic and transcriptomic approaches are in progress.

These preliminary results are promising and encourage us to continue our approach in soils.

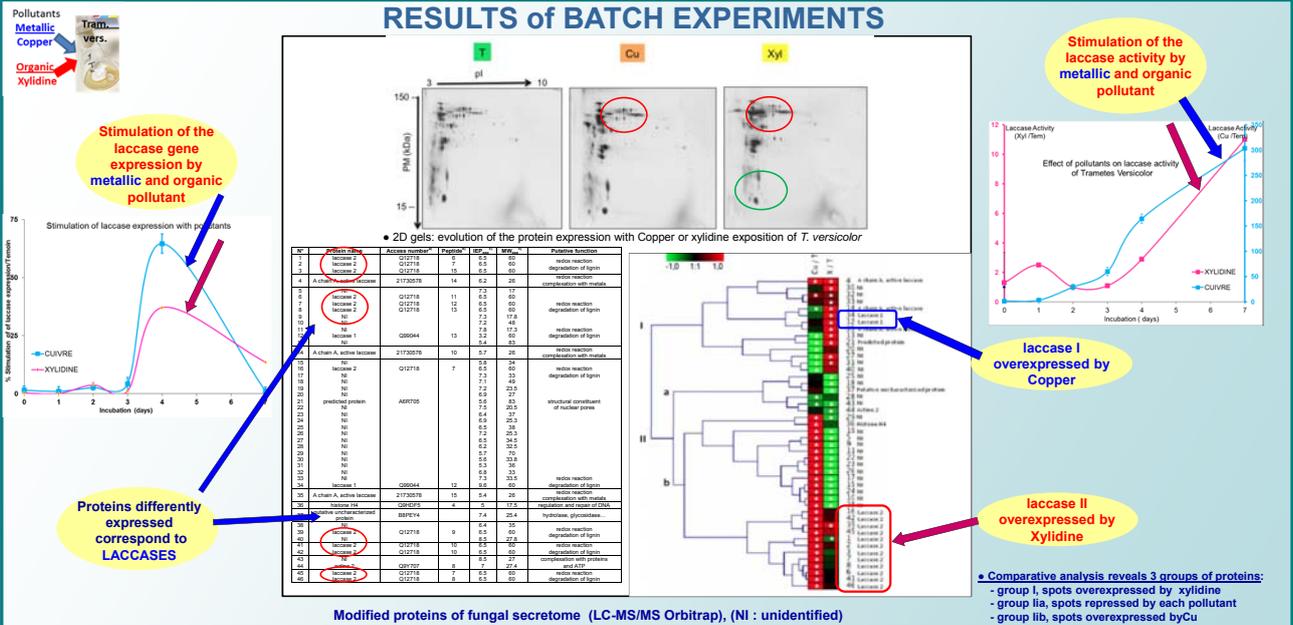
STRATEGY: 3 steps



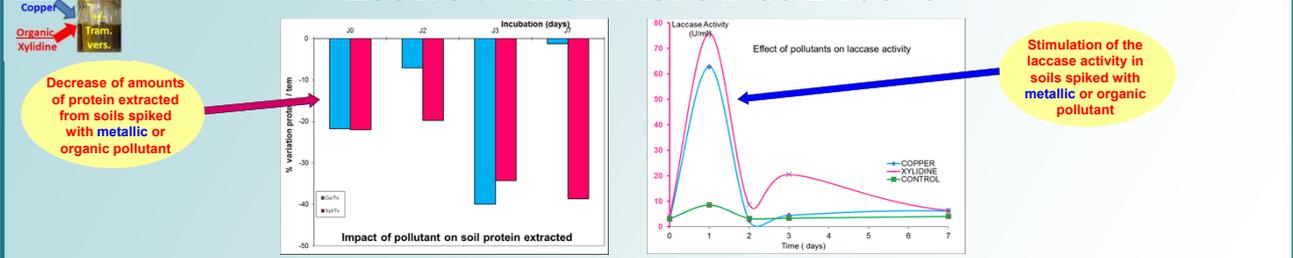
METHODOLOGY



RESULTS of BATCH EXPERIMENTS



RESULTS of INCUBATIONS in SOIL COSMS



CONCLUSIONS

- Results confirm the relevance of our approach
- Results in protein expression, synthesis and activity vary in same ways in batches and soils cosms
- The lack of information concerning sequences of fungal proteins in databases limits the use of secretion profiles as biomarkers
- It remains necessary to improve the extraction of soil proteins and RNAs

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