ISGC 2019
May 13th - 17th

N°998 / PC
TOPIC(s) : Biomass conversion / Homogenous, heterogenous and biocatalysis

FUNGAL OXIDO-REDUCTASE MODELS: ENZYMOLOGY, STRUCTURAL DATA AND SYNERGY FOR BIOTECHNOLOGICAL APPLICATIONS

AUTHORS

Sona GARAJOVA / INRA BBF, 163 AV LUMINY, MARSEILLE
Eric RECORD / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Craig B. FAULDS / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Anne LOMASCOLO / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
David NAVARRO / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Kelly BIAGGINI / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Sana RAOUCHE / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Dehbia CHENA / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Théo DUPONT / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Mariam RIFI / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Barbara FIFANI / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Laura MUNOZ DUARTE / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Annick DOAN / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Emmanuel BERTRAND / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Mariam RIFI / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Benjamin TATTIER / AIX-MARSEILLE UNIVERSITÉ, INRA, BIODIVERSITÉ ET BIOTECHNOLOGIE FONGIQUES, 163 AV LUMINY, MARSEILLE
Corresponding author : Giuliano SCIARA / giuliano.sciara@inra.fr

PURPOSE OF THE ABSTRACT

The fungal kingdom, with its extraordinary intra and inter-specific diversity, is undoubtedly the least known, both at the fundamental level and at the level of potential applications. Fungi are major players in the decomposition of plant biomass and the enzyme sets they have developed during their evolution reflect this diversity which is the result of their encounters with the different plant matrices they use for their growth. This diversity, related to fungal strains and their enzymes, is an outstanding source of innovation in a number of areas.

Over the past 20 years, the BBF Unit (https://www6.paca.inra.fr/umrbcf) has developed a unique expertise in the discovery and exploitation of fungi and their enzymes for lignocellulosic biomass biotransformation, and in particular for modification of aromatic compounds including lignins. BBF hosts the CIRM-CF collection of filamentous fungi involved in the degradation of wood (https://www6.inra.fr/cirm_eng/Filamentous-Fungi), including species from temperate and tropical biotopes and polluted agro-food sites. This collection is a unique tool for exploring fungal functional biodiversity and for developing applications in various areas of biotechnology, including pretreatment and saccharification of woody biomass in biorefinery and delignification processes.

In this poster, we will present various examples of oxido-reductases from the analysis fungal genomes that we characterized in order to find new enzymes and synergies, and to gain new structural insights. The main objective is to improve the general knowledge of the various enzymes involved in degradation or modification of aromatic compounds or lignins, and potential applications for the industry.

FIGURES

FIGURE 1

FIGURE 2

KEYWORDS
filamentous fungi | oxido-reductases | lignin | biotechnologies

BIBLIOGRAPHY

[1] Mathieu Y. et al. Appl. Environ.Microbiol. 2016, 82:2411-23.

[2] Piumi F. et al. Appl. Microbiol. Biotechnol. 2014, 98:10105-18.

[3] Levasseur A. et al. BMC Genomics, 2014, 15:486.