Asistencia a cursos/seminarios/workshops relacionados con la temática del Proyecto AGROALNEXT_2022

Lugar	Convention Centre Dublin
Fecha	2-5 marzo 2025
Lugar	Dublín, Irlanda
Proyecto:	BioValRice
Código proyecto	AGROALNEXT_2022/035
Grupo de investigación	FungalFact, CSIC, iata, Excelencia Severo Ochoa, BioTech AgriFood

INFORME DE LA ACTIVIDAD:

Durante los días 2-5 de marzo, Sandra Garrigues y Paloma Manzanares asistieron a la 17th European Conference on Fungal Genetics (ECFG), donde presentaron en un póster los resultados del proyecto BioValRice (AGROALNEXT_2022/035) de cuyo equipo investigador forma parte.

Harnessing filamentous fungi for enzyme cocktail production through rice bran bioprocessing

Ana M. Yélamos, Jose F. Marcos, Paloma Manzanares, Sandra Garrigues

Evidencia de la actividad:

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Financiado por la Unión Europea NextGenerationEU
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ECFG17 DUBLIN · IRELAND 2025

Harnessing filamentous fungi for enzyme cocktail production through rice bran bioprocessing

CSIC · iata

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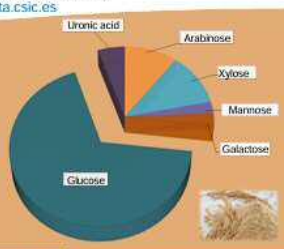
INTRODUCTION

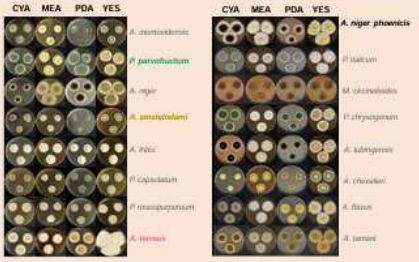
The substantial amounts of waste generated by the food industry pose a significant global challenge. Consequently, the **valorization of agri-food waste** has aroused considerable interest. Rice, one of the most cultivated and consumed crops globally, generates several by-products during milling, such as **rice bran**. Rice bran is mainly composed of **cellulose** and **xylan** and has limited commercial value. **Filamentous fungi** are proficient in degrading complex molecules and producing substantial amounts of metabolites, organic compounds and enzymes of industrial interest. In this context, the present study explores the potential of filamentous fungi to degrade and utilize rice bran and **produce enzyme cocktails of industrial interest**, contributing to its valorization and sustainable utilization.



RESULTS

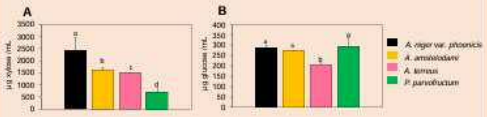
1 Strain isolation

A total of **16 filamentous fungi** were isolated from rice bran. The molecular identification determined three main genera: *Aspergillus*, *Penicillium* and *Mucor*. The protein profile of these strains cultured in rice bran-containing minimal medium was characterized by the bicinchoninic acid (BCA) method. Total protein quantification after 4 days of incubation revealed four strains with the highest protein production: ***A. niger* var. *phoenicis* RT3** (2.17 mg/mL), *Aspergillus terreus* AM39 (1.64 mg/mL), ***Penicillium parvofructum* AM8** (1.64 mg/mL) and *Aspergillus amstelodami* AM13 (1.38 mg/mL).



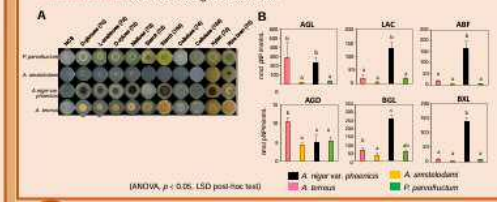
2 Xylanolytic and cellulolytic enzyme activities

The xylanase activity (A) in the supernatants of the four tested fungi grown in rice bran-containing medium was higher than the cellulase activity (B), quantified by the dinitrosalicylic acid (DNS) method. ***A. niger* var. *phoenicis*** had the highest xylanolytic activity. ***A. niger* var. *phoenicis***, *A. amstelodami* and *P. parvofructum* showed the highest cellulolytic activity.



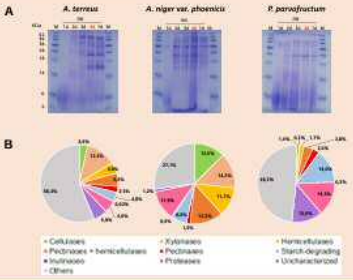
3 Specific enzymatic activities

These four fungal isolates were chosen for further characterization of growth capabilities (A) and specific enzymatic activities required for rice bran degradation using the colorimetric *p*-nitrophenol (pNP) assays (B). The α/β-D-galactosidase (AGL/LAC), α-L-arabinofuranosidase (ABF), α/β-D-glucosidase (AGD/BGL), and β-D-xylosidase (BXL) were determined in the 4-day supernatant samples. ***A. niger* var. *phoenicis* RT3** and *A. terreus* AM39 showed the highest activities.



4 Protein profile and proteomic analyses

Proteomics studies were conducted to characterize the exoproteome of *A. terreus*, ***A. niger* var. *phoenicis*** and *P. parvofructum* after 4 days (d) of growth in rice bran (RB)-containing medium (A). The identified proteins were functionally classified according to their roles primarily related to plant biomass degradation (B). In total, 745 proteins were identified in the *A. terreus* secretome, while 382 and 263 proteins were identified in *A. niger* var. *phoenicis* and *P. parvofructum* secretomes, respectively. Hemicellulases were more abundant than cellulases in all cases, and pectinases and inulinases were overall under-represented. *P. parvofructum* also revealed the production of small cysteine-containing peptides comprising a total of 4.6% of the secretome, which included two different proteins belonging to the **antifungal protein (AFP) family**: a class A AFP (protein ID A0A8H4WM31), comprising 2.1% of the secretome, and a class C AFP (ID A0A167U5W7), which accounted for 0.6%.



CONCLUSIONS

- All the species isolated exhibited xylanase and cellulase activities, with *A. niger* var. *phoenicis*, *A. amstelodami*, *A. terreus*, and *P. parvofructum* showing particularly high enzymatic potential.
- *A. niger* var. *phoenicis* exhibited the highest activities for β-D-galactosidase (LAC), α-L-arabinofuranosidase (ABF), β-D-glucosidase (BGL), β-D-xylosidase (BXL), and α-D-galactosidase (AGL), the latter being similarly high in *A. terreus*. In contrast, α-D-glucosidase (AGD) activity was generally low across all species.
- *A. niger* var. *phoenicis* showed the highest amount of hemicellulases, including xylanases (39.2% of the secretome), followed by *A. terreus* (22.7%) and *P. parvofructum* (5.8%). These results correlate with the xylanase activity of these three isolates, with *A. niger* var. *phoenicis* displaying the highest xylanase activity, followed by *A. terreus* and *P. parvofructum*.
- The results of the rice bran-induced exoproteome revealed the presence of AFP proteins produced by *P. parvofructum*, emphasizing their potential as 'green antifungals' for sustainable applications within a circular economy framework.

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ECFG17
DUBLIN · IRELAND
2025

CERTIFICATE OF ATTENDANCE

This is to certify that

Dr Paloma Manzanares

attended the 17th European Conference on Fungal Genetics (ECFG17) 2025

Convention Centre Dublin, Ireland

02 – 05 March 2025

Professor Özgür Bayram
Maynooth University, Ireland

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Y para que conste a los efectos oportunos

Firmado por MANZANARES MIR PALOMA MARIA - DNI ***9105** el día 15/04/2025 con un certificado emitido por AC Sector Público

Firma del IP1.