

Bacteria/fungi Interactions (BFI): a way to awake secondary metabolite gene clusters

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IMPACT Biomolécules



Bacteria/fungi interactions: a way to awake secondary metabolite gene clusters

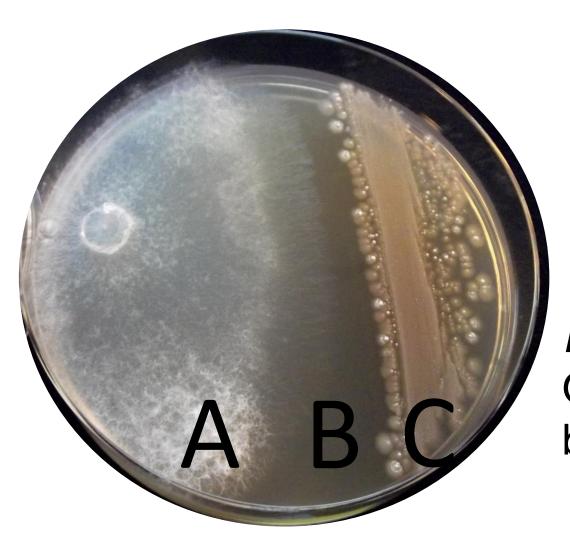


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Introduction

- > The emergence of new multiresistant bacteria is nowadays a public health issue.
- > The discovery of new antibiotics became crucial to overcome this problem.
- > Bacteria (mostly actinomycetes like Streptomyces) and fungi are a major sources of antibiotics.
- > However many gene clusters encoding for secondary metabolites production remain not expressed in lab conditions.
- > Co-cultures, that mimic the interactions occurring in nature that induce production of specialized metabolites, is a way to activate these silent gene clusters.
- > Objectives of this work are:
 - > To awake these silent gene clusters through co-cultures between microorganisms.
 - To characterize the induced metabolites.
 - > To decipher the basis of the interactions leading to secondary metabolite biosynthesis.

Methods



> 144 co-cultures between 8 Streptomyces and 9 fungal strains were performed on two media.

> The antibiosis activities of the ethyl acetate extracts of single cultures (A and C in fig1) and of their interaction zones (B in fig 1) are then tested and compared against indicator microorganisms (E. coli, Bacillus, yeast)

Figure 1: Example of a co-culture between a Streptomyces and a fungus

On MA medium, a fungus (A) and a Streptomyces (C) are incubated at the same time. The zone (B) represents the interaction zone between the two microorganisms.

Results

1) All the tested Streptomyces exhibited direct antifungal capacities during the co-cultures (1 to 9 out of 9 fungi were inhibited depending of Streptomyces strains) and gave interaction zones (B in fig1).

2) 12 out of 144 interaction zones showed an induced activity in 3) A differential metabolite production was observed comparaison to single cultures.

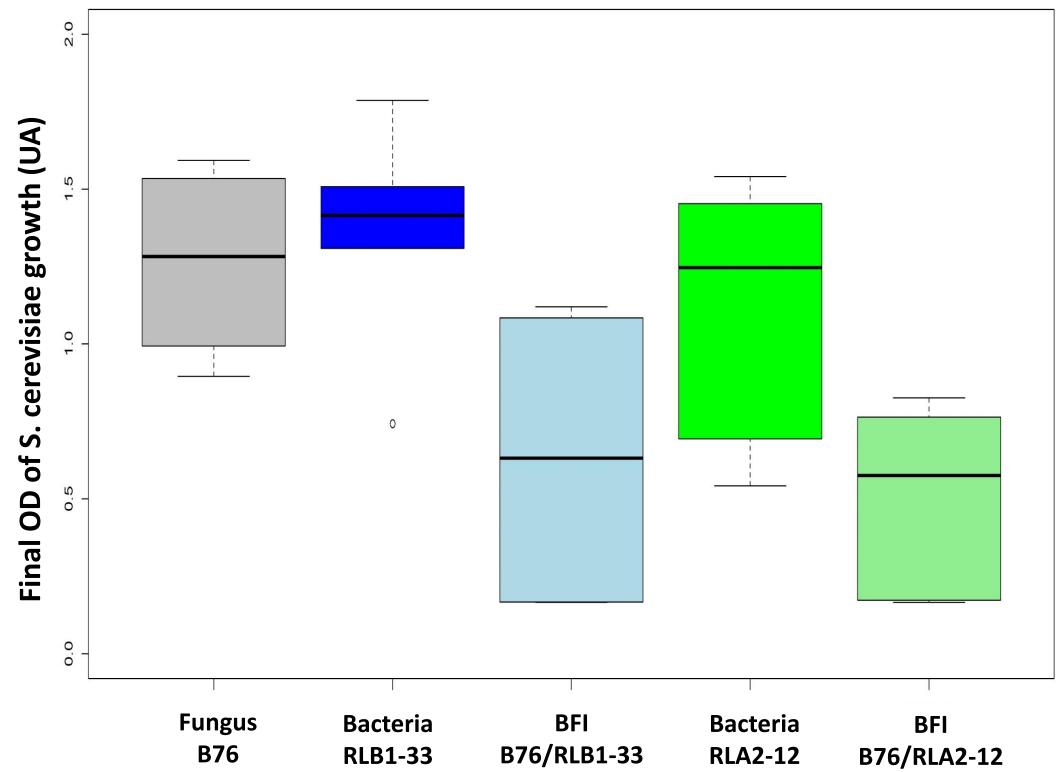


Figure 2: Example of enhanced inhibitory activities in co-culture interaction zones compared to single cultures

Yeast growth was measured by spectrophotometry in media supplemented with extracts from single strain cultures of the fungus B76 (grey), the bacteria RLB1-33 (blue) or RLA2-12 (green). Comparaisons with the interaction zone extracts of the fungus/bacteria co-cultures B76/RLB1-33 (lightblue) and B76/RLA2-12 (lightgreen) showed greater inhibitory activities.

4) HPLC chromatograms of single and co-cultures indicated the presence of new metabolites

Figure 4: Chromatograms of single and co-cultures between the fungus B76 and the Streptomyces sp. RLA2-12

The chromatograms were recorded at 254 nm with MeOH(+ 0,1% acid formic)/Water(+ 0,1% acid formic) gradient. The orange chromatogram represents the metabolite profile of Streptomyces RLA2-12. The blue chromatogram represents the metabolite profile of the fungus B76. The grey chromatogram represents the metabolite profile of interaction zone. Interaction between the fungus B76 and Streptomyces RLA2-12 could induce the production of 3 new metabolites (green circles)

between single and co-cultures.

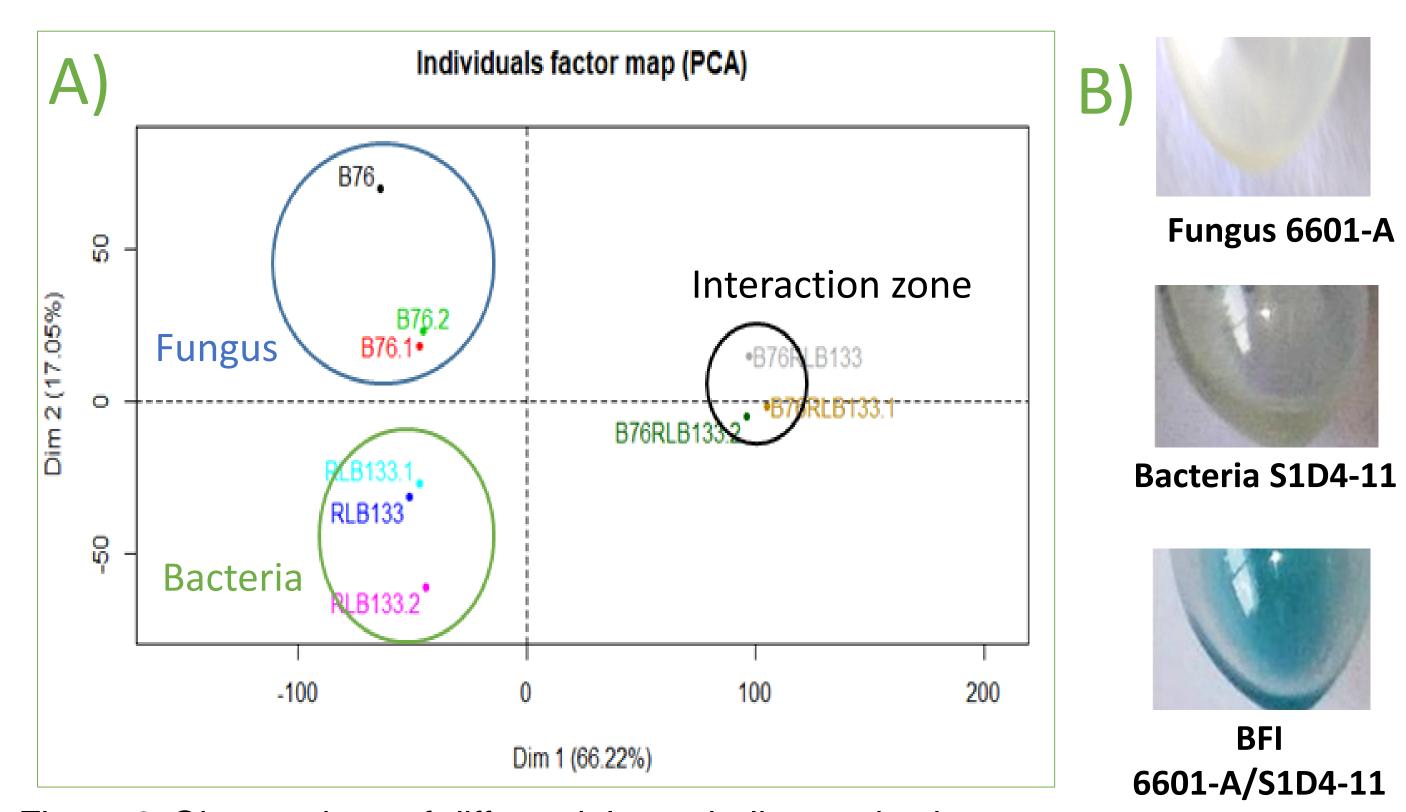
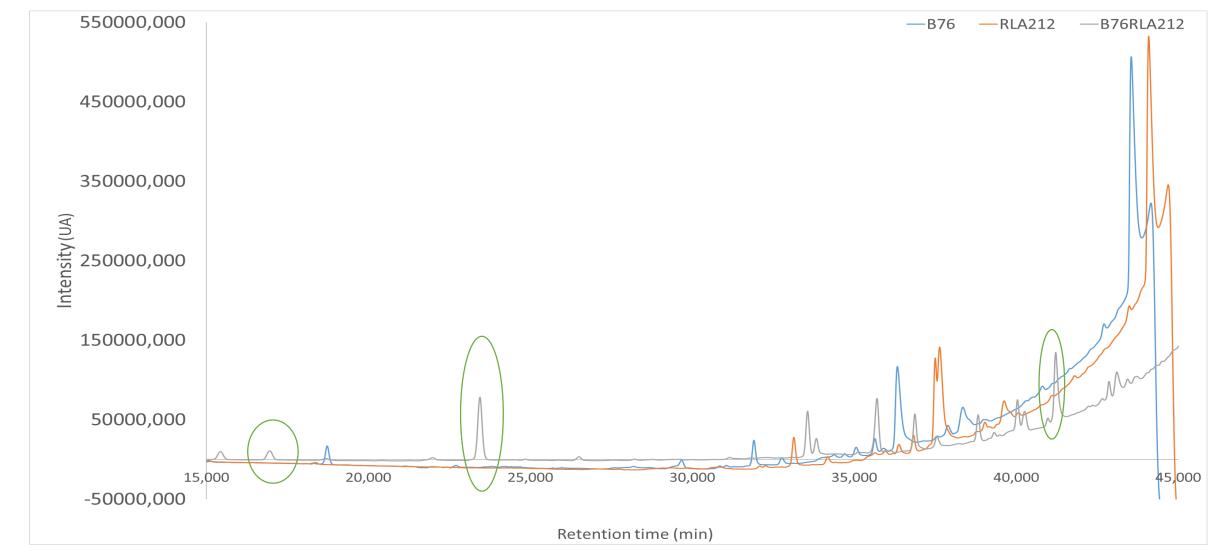


Figure 3: Observations of differential metabolite production A) The global metabolite production of single cultures of the fungus B76 and of the bacterium RLB1-33 are statistically different from their interaction zones (PCA analysis). B) A blue pigment is present in the interaction zone of the co-culture between the fungus 6601-A and the bacterium S1D4-11, but not the single cultures, indicating a difference in metabolite production.



Conclusion/Perspectives

- > The screening method of the interaction is set up.
- In some cases, co-cultures showed an enhancement of the inhibitory activity that can rely on new metabolite production.
- > Further experiments:
 - To extend the screening to others couples and indicator strains (multiresistant and phytopathogenic microorganisms).
 - To identify and to characterize the induced metabolites (new peaks on chromatograms) and their biosynthetic pathways.
 - To decipher the molecular mechanisms involved during the interactions



