

Untargeted metabolomics approach to study polymers biodegradation by Rhodococcus Rhodochrous using LC-HRMS

Binta Diémé, Marie Lagrée, Martin Leremboure, Mounir Traïkia, Cyril C. Jousse, Anne-Marie Delort, Boris Eyheraguibel

▶ To cite this version:

Binta Diémé, Marie Lagrée, Martin Leremboure, Mounir Traïkia, Cyril C. Jousse, et al.. Untargeted metabolomics approach to study polymers biodegradation by Rhodococcus Rhodochrous using LC-HRMS. 3ième rencontre du GDR Polymères & Océans, Jun 2022, Brest, France. hal-03879263

HAL Id: hal-03879263 https://hal.science/hal-03879263v1

Submitted on 30 Nov 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Untargeted metabolomics approach to study polymers biodegradation by *Rhodococcus Rhodochrous* using LC-HRMS



Binta Diémé¹, Marie Lagrée¹, Martin Leremboure², Mounir Traïkia^{1,2}, Cyril Jousse^{1,2}, Anne Marie Delort^{1,2}, Boris Eyheraguibel²

¹ Université Clermont-Auvergne, Unité de Nutrition Humaine, UMR 1019, Plateforme d'Exploration du Métabolisme, Clermont-Ferrand, France

² Université Clermont-Auvergne, Institut de Chimie, UMR6296, Clermont-Ferrand, France



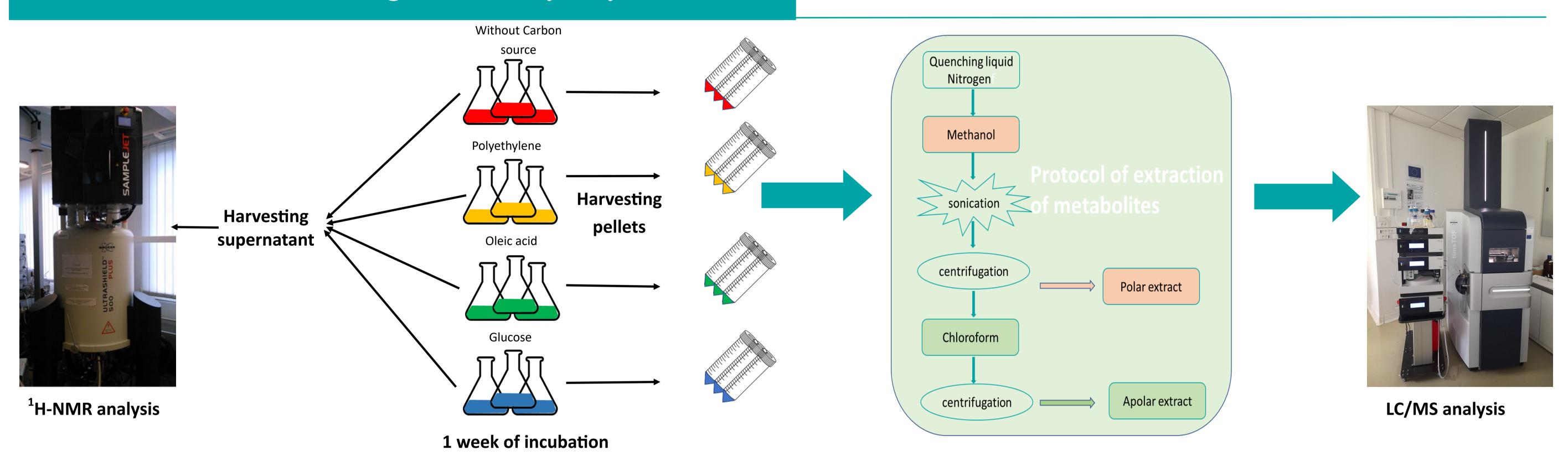
Background

Many environmental studies have identified contaminations of marine, soil, freshwater and atmospheric ecosystems by (micro) plastics. Some studies have highlighted microorganism enable of using plastics polymers as a carbon source. However, the metabolic pathways involved in polymer biodegradation are largely unknown. In order to evaluate these processes, we used a metabolomics approach.

A bacterial strain *Rhodococcus Rhodochrous* was grown with or without different carbon sources: glucose (GLU) or oleic acid (OA) or polyethylene (PE) or no carbon source (Minimum Medium, MM).

Objective: highlight the metabolic pathways involved in the biodegradation of PE

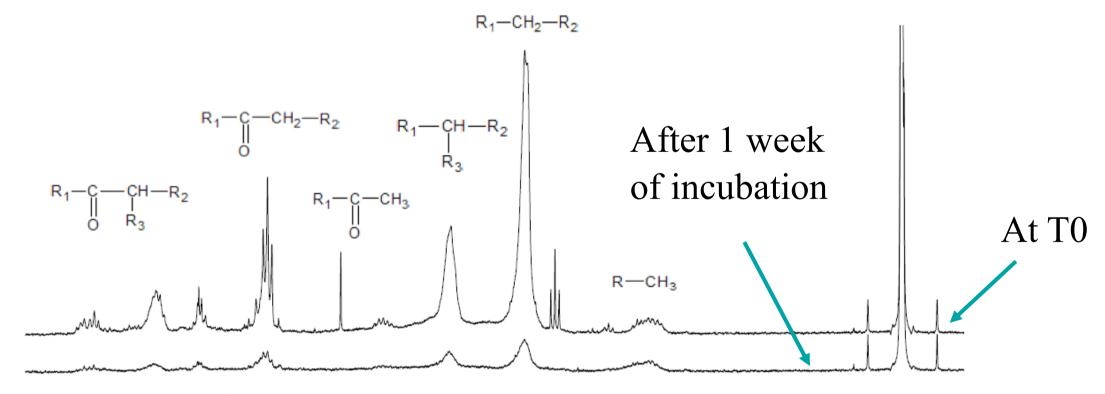
Did the bacteria able to degradate Polyethylene?



Results

¹H-NMR analysis highlighted a decrease in the amount of PE in the medium after 1 week of incubation. The amount of protein in the extracellular medium is greater in the PE condition. We presume the bacteria produce enzymes able to cut polymer chains of PE. Multivariate statistical analysis showed a separation of samples according to the conditions of culture. These results suggest differences in metabolic profiles depending on the source of carbon.

Measures of Rhodococcus Rhodochrous activities



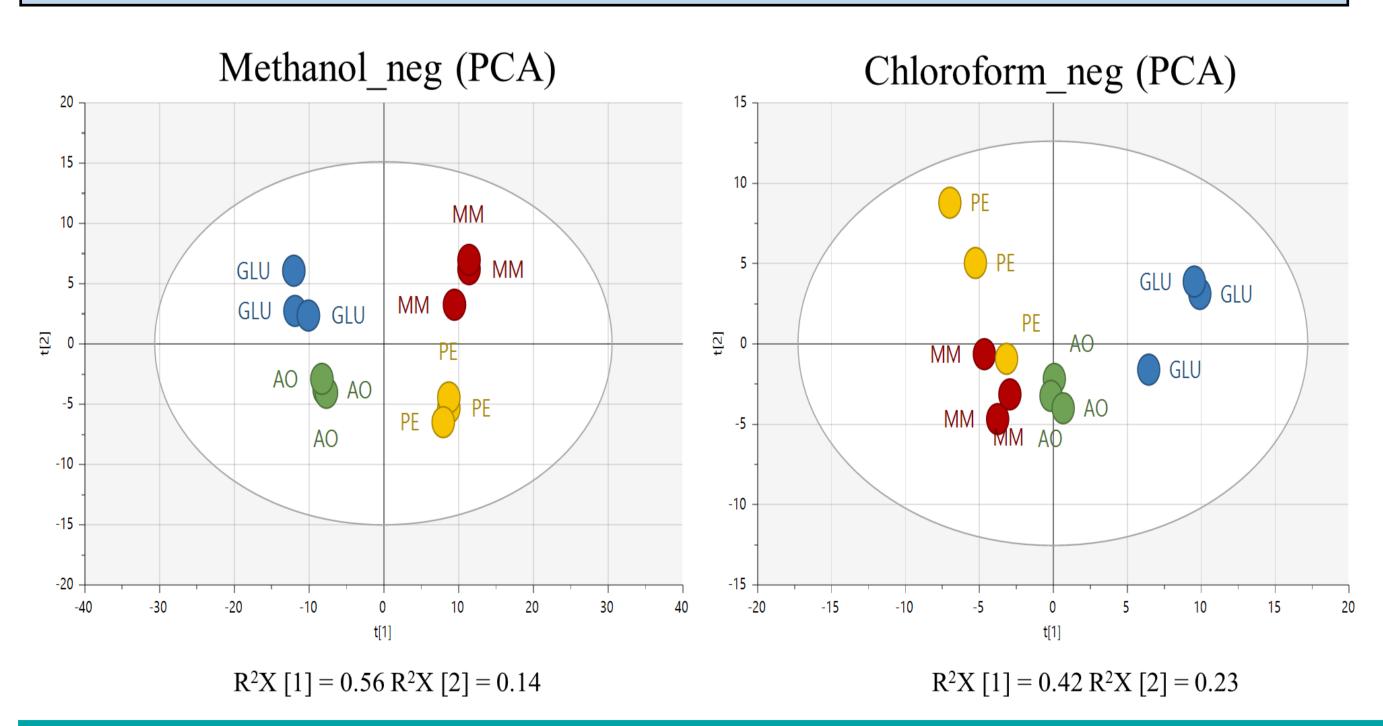
Analysis by ¹H-NMR of supernatants of *Rhodococcus Rhodochrous* incubated with polymers of PE

SamplesConcentrations of proteins (μg/ml)Mean PE81.85Mean OA36.57Mean GLU38.05

Concentrations of proteins in media after one week of incubation with PE or OA or GLU

Putative annotations of metabolites with in house database

Statistical analysis on data from negative ionization mode



L-leucine Alanylalanine CHCL3_pos CH3OH neg L-isoleucine L-Alanine Citrulline L-Asparagine Ergothioneine CHCL3_neg PC(18:1/0:0) Unknown dipeptid 5-Aminovaleric acid 5-Aminolevulinic Valine/betaine L-Phenylalanine ProlylGlycine L-Glutamic acid Unknown dipeptid Nicotinamide Picolinic acid Aminoadipic acid Prolylglycine N-acetyl-asparagine L-Pyroglutamic acid Glutamylalanine Glycylphenylalanine Proline 5-Methyldeoxycytidine L-Glutamine Prolylglutamine Glutamylthreonine Unknown dipeptid Hexanoylcarnitine

Conclusions

The different extraction protocols allowed us to detect a bigger part of the metabolome. The peaks detected are mainly more intense in the PE group compared to the other groups. The annotated peaks are mostly amino acids and dipeptides and are generally in higher amounts in the PE group compared to AO, GLU groups. This is in agreement with the other results and shows an important bacterial activity in the PE group. These metabolites are involved in the metabolism of Glutathione, the urea cycle and in many pathways of amino acids metabolism.