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

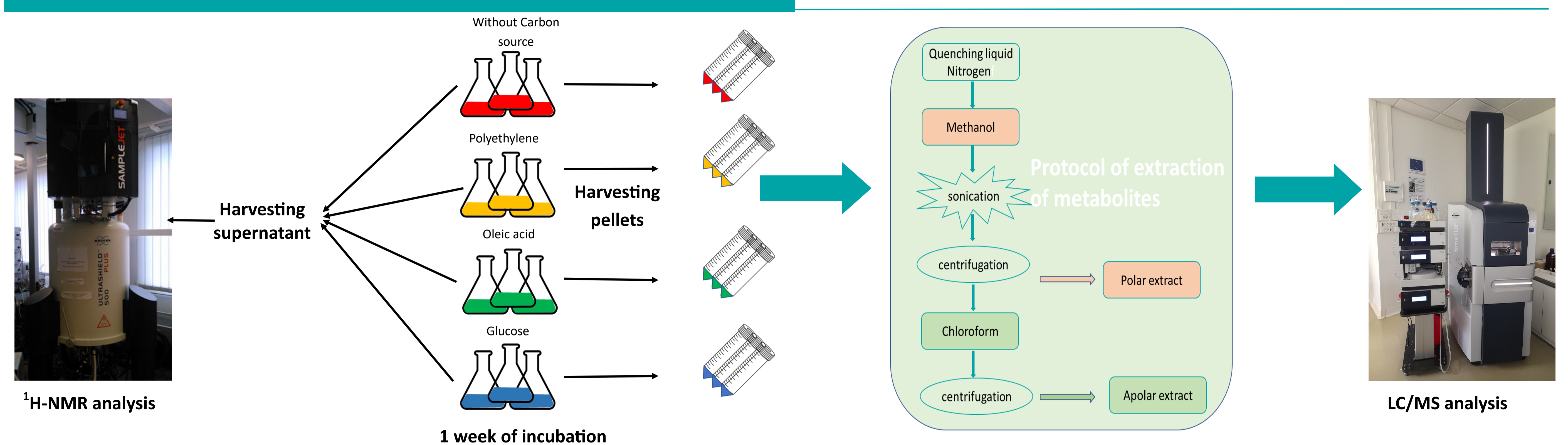
Background

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

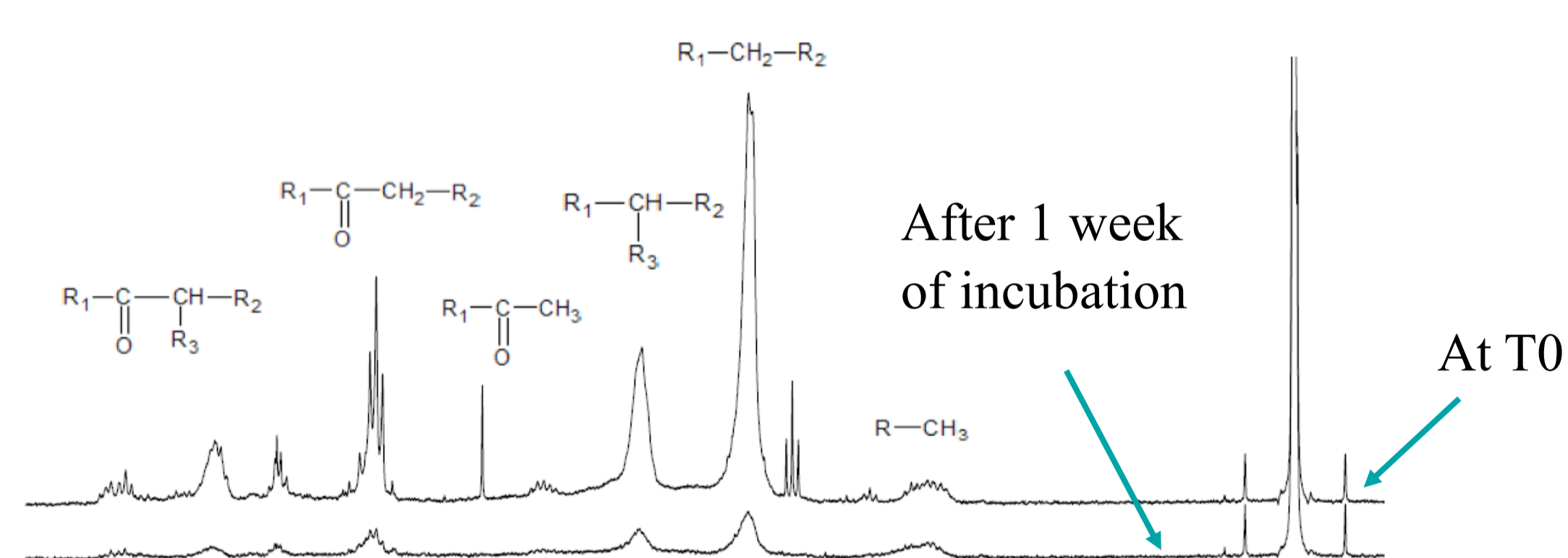
Did the bacteria able to degradate Polyethylene ?



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

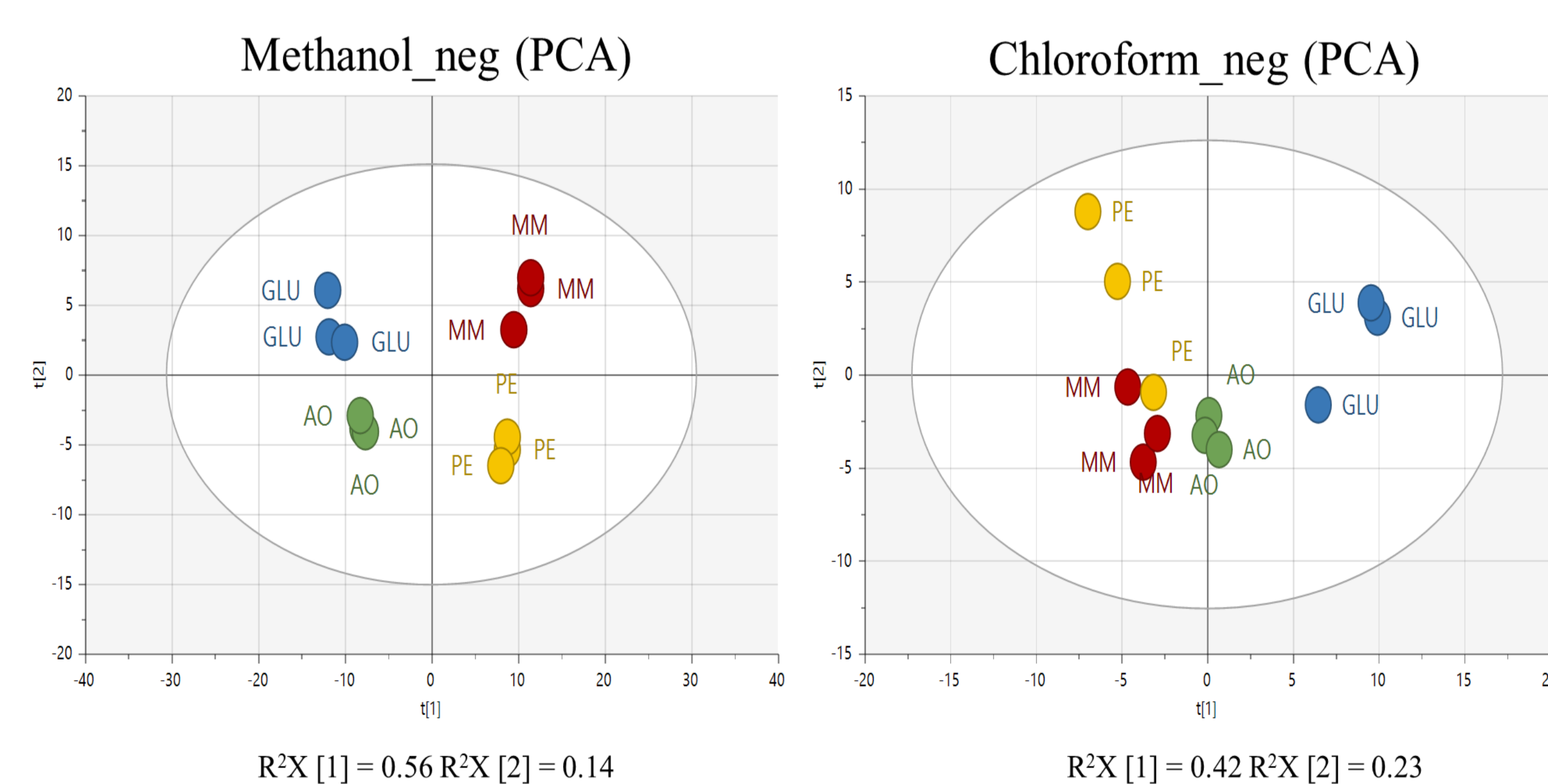


Analysis by ¹H-NMR of supernatants of *Rhodococcus Rhodochrous* incubated with polymers of PE

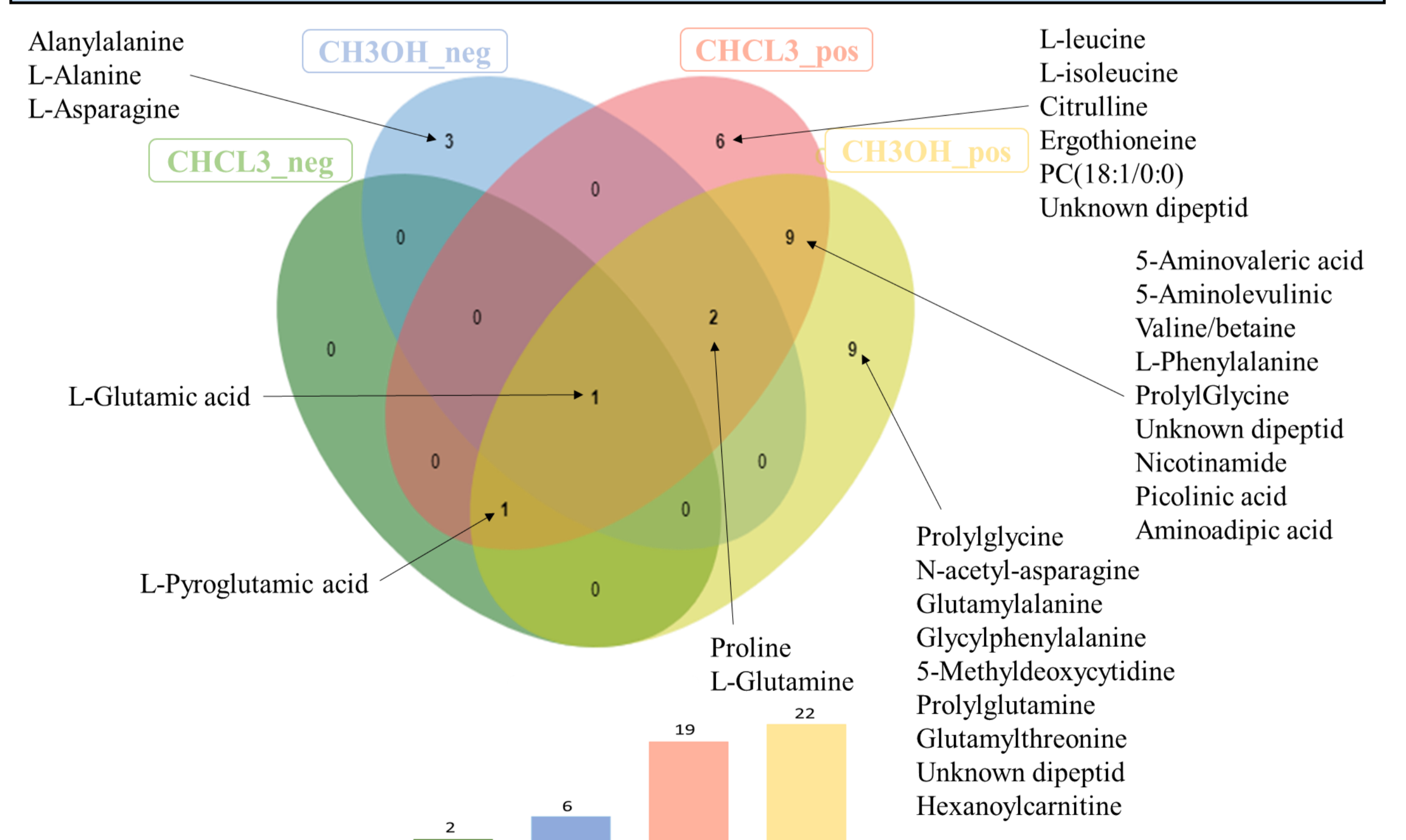
Samples	Concentrations of proteins (µg/ml)
Mean PE	81.85
Mean OA	36.57
Mean GLU	38.05

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

Statistical analysis on data from negative ionization mode



Putative annotations of metabolites with in house database



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.