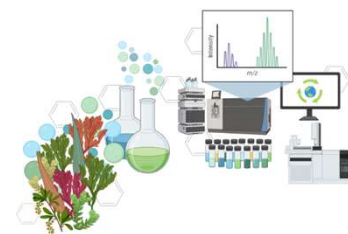


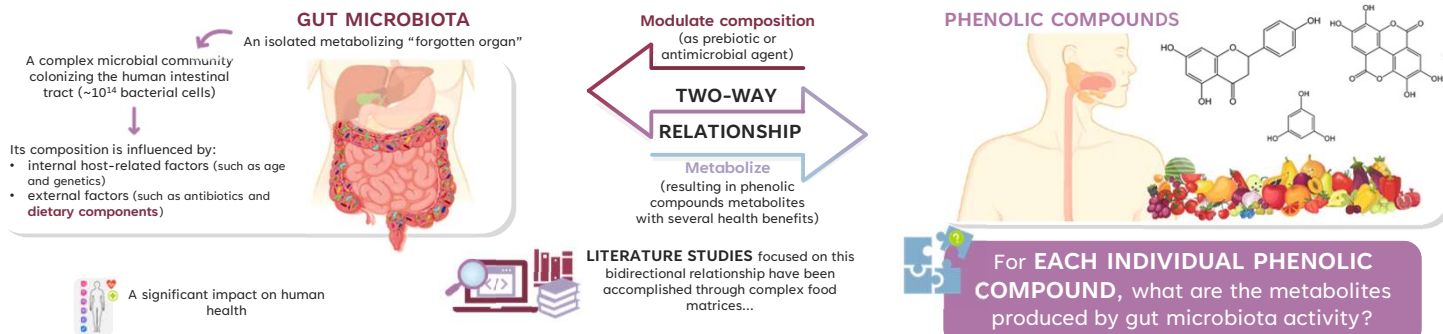
# Exploring the role of human gut microbiota in the phenolic compound's metabolism: An *in vitro* approach

País ACS<sup>1\*</sup>, Ribeiro TB<sup>2</sup>, Coscueta ER<sup>2</sup>, Pintado MM<sup>2</sup>, Silvestre AJD<sup>1</sup>, Santos SAO<sup>1</sup>

<sup>1</sup>CICECO-Aveiro Institute of Materials, Chemistry Department, University of Aveiro, 3810-193 Aveiro, Portugal; <sup>2</sup>Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina - Laboratório Associado, Escola Superior de Biotecnologia, Rua Diogo Botelho 1327, 4169-005 Porto, Portugal \*a.c.s.p@ua.pt

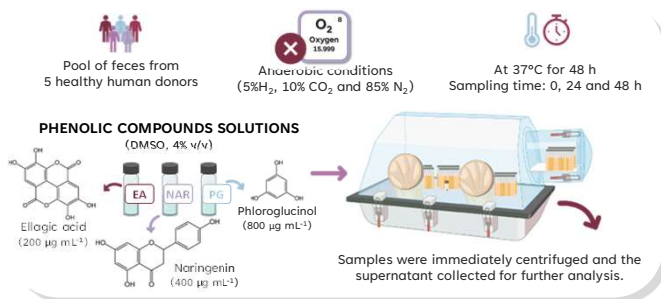


## BACKGROUND AND AIM



## METHODS

### IN VITRO FECAL FERMENTATION



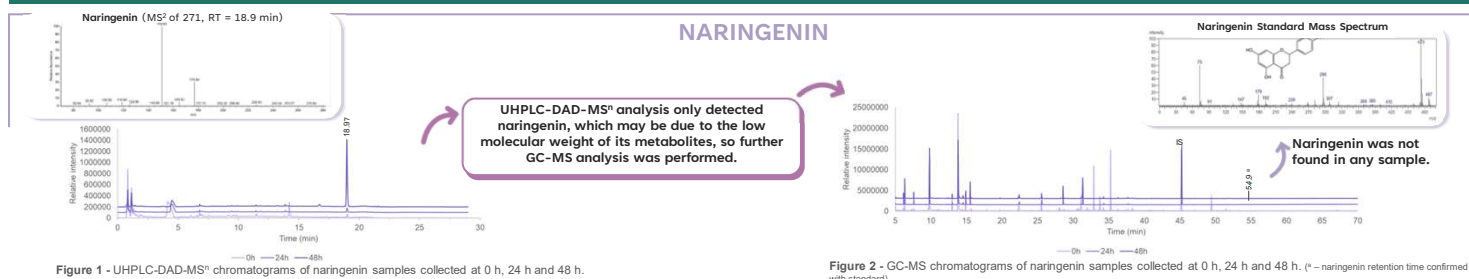
### UHPLC-DAD-MS<sup>n</sup> ANALYSIS



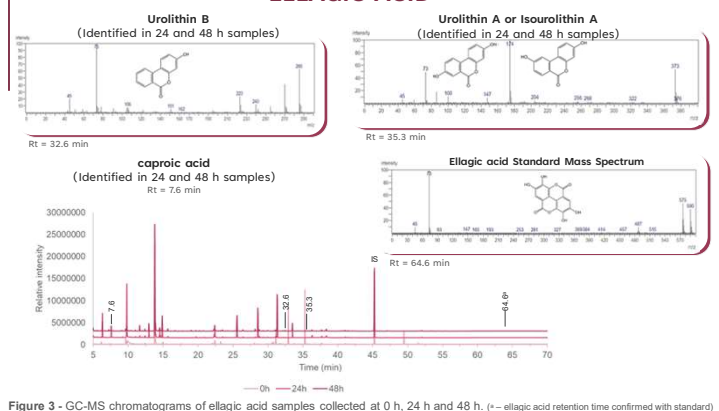
### GC-MS ANALYSIS



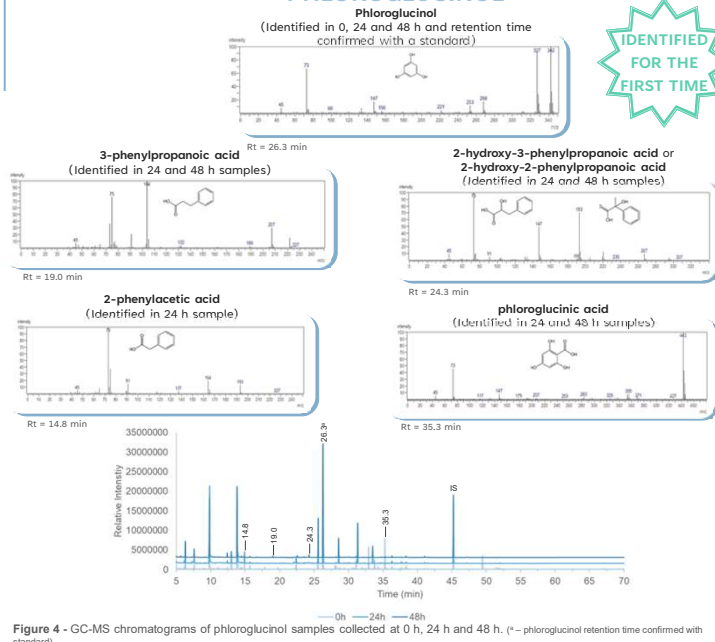
## RESULTS



### ELLAGIC ACID



### PHLOROGLUCINOL



## FINAL REMARKS

- UHPLC-DAD-MS<sup>n</sup> allowed to detect all pristine phenolic compounds, but no metabolites have been detected.
- GC-MS was successfully used to detect and identify several low molecular weight metabolites.
- Three and four compounds were identified as gut microbiota metabolites of ellagic acid and phloroglucinol respectively. Urolithin B and (iso)urolithin A were putatively identified in 24h and 48h ellagic acid samples.
- 2-Phenylacetic acid (48 h), 3-phenylpropanoic acid, 2-hydroxy-2-phenylpropanoic acid or 2-hydroxy-3-phenylpropanoic acid and phloroglucinol acid (all in 24 and 48 h samples) were putatively identified for the first time as phloroglucinol metabolites.
- The absence of naringenin gut microbiota resultant could be due to early metabolization (before 24 h) of this compound or to being below the limit of detection, which hinders analysis/identification.

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