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Título:

Enhancing curcuminoid production using E. coli engineered strains

Autores:

Couto MÁRCIA, Rodrigues JOANA, Rodrigues LÍGIA

Centro de Trabajo:

Centre of Biological Engineering, University of Minho

Email:

marciacouto93@gmail.com

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Comunicación:

Curcuminoids are natural secondary metabolites from the herb *Curcuma longa*. Their beneficial properties, mainly as anti-cancer agents, have been exhaustively reported but the therapeutic effect of curcumin is limited by its fast systemic elimination along with poor bioavailability. Besides, curcumin extraction from plants is very expensive and it is hard to synthesize chemically. For these reasons, the use of microorganisms to produce these remarkable compounds on large scale and with greater yields constitutes an interesting approach. In the SYNBIOBACTER project, the aim of producing curcumin from ferulic acid using an engineered *Escherichia coli* was achieved adding three enzymatic steps using plant genes (4-coumarate-CoA ligase (4CL) from *Arabidopsis thaliana*; diketide-CoA synthase (DCS) and curcumin synthase 1 (CURS1) from *C. longa*). The present work aims to improve curcumin production from ferulic acid by optimizing the production medium and other operational conditions. Previously, we used a standard two-step fermentation strategy (LB + M9 minimal media) to overcome the metabolic burden associated with protein overexpression and poor growth observed in minimal medium. Although feasible at the laboratory scale, the biomass separation is much more difficult, laborious and expensive in large scale fermentations. Therefore, we intend to develop a single medium formulation more suitable for the production of curcuminoids. MOPS minimal medium, TB and also LB and M9 are being evaluated. Furthermore, previously we studied *in silico* which gene deletions would enhance the curcumin production by the metabolic engineered *E. coli*. Using a recombineering approach, we are implementing those gene knockouts to construct several *E. coli* mutants ( $\Delta$ gnd;  $\Delta$ fumA,fumB,fumC;  $\Delta$ fumA,fumB,fumC,ccmA;  $\Delta$ fumA,fumB,fumC,ccmA,argO) that will produce curcumin from ferulic acid. The curcuminoids production by these *E. coli* mutants is being evaluated.