

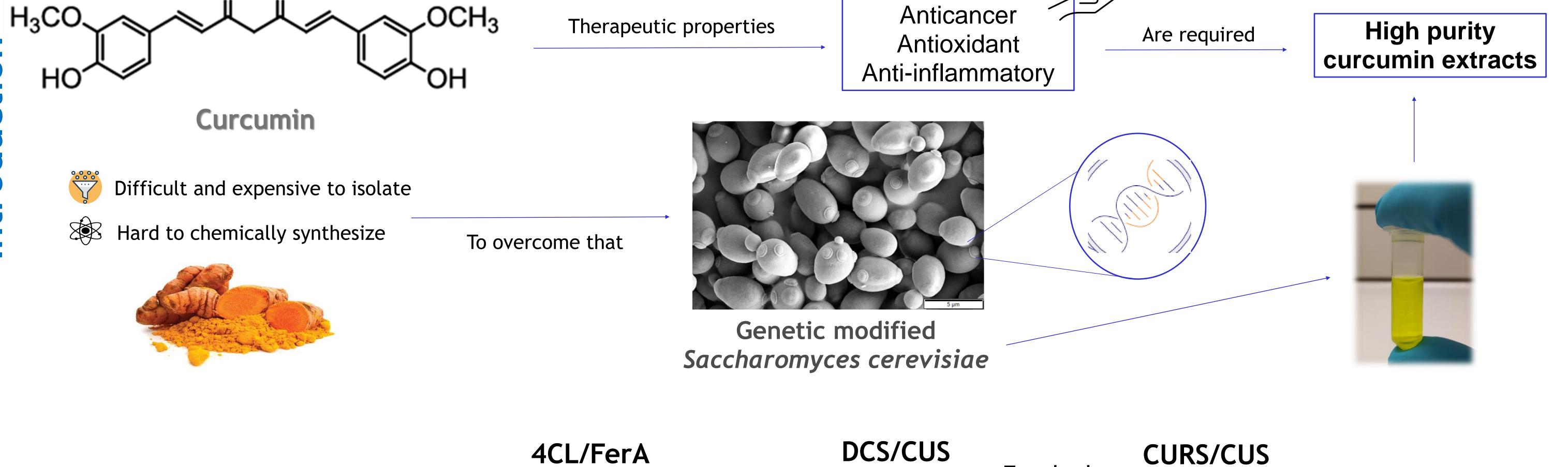
Metabolic engineering of curcumin production in Saccharomyces cerevisiae

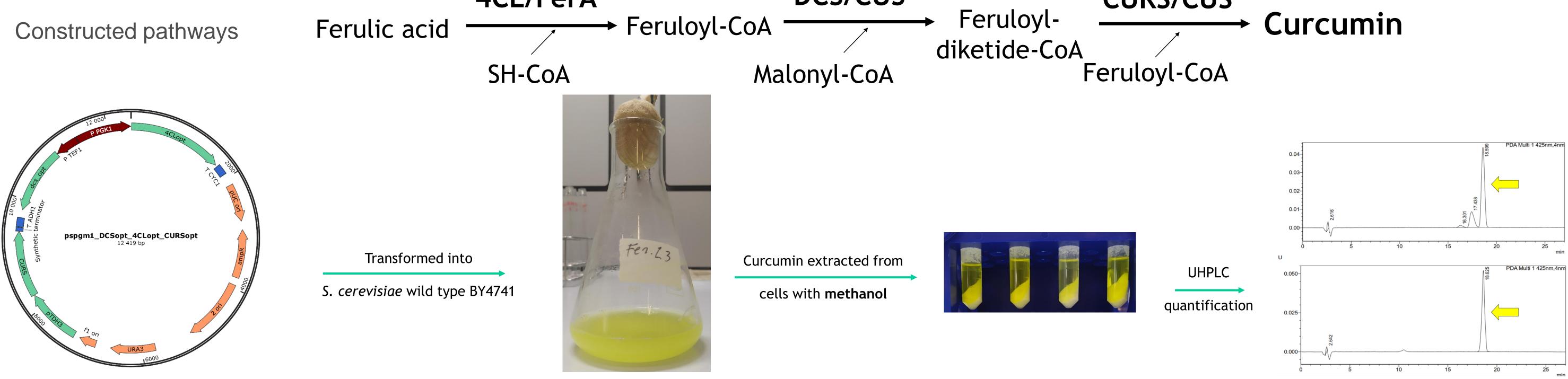
João Rainha, Joana Rodrigues, Lígia Rodrigues

CEB - Centre of Biological Engineering, University of Minho, Braga, Portugal

E-mail: joao.rainha@ceb.uminho.pt

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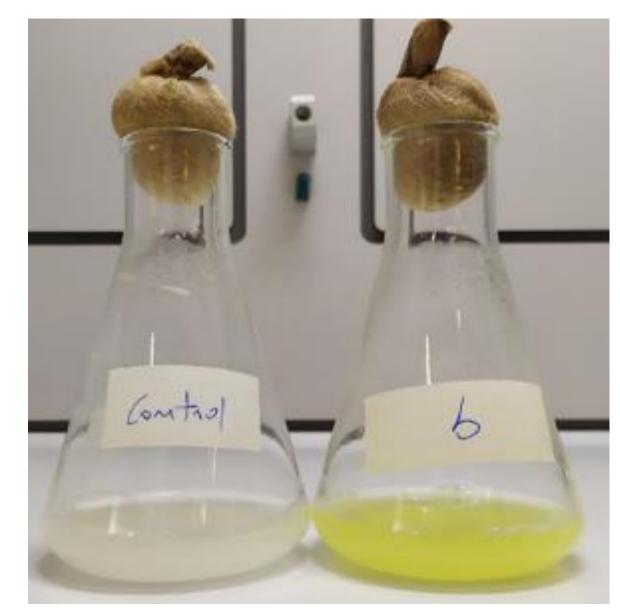


YEP harbouring curcumin biosynthetic pathway

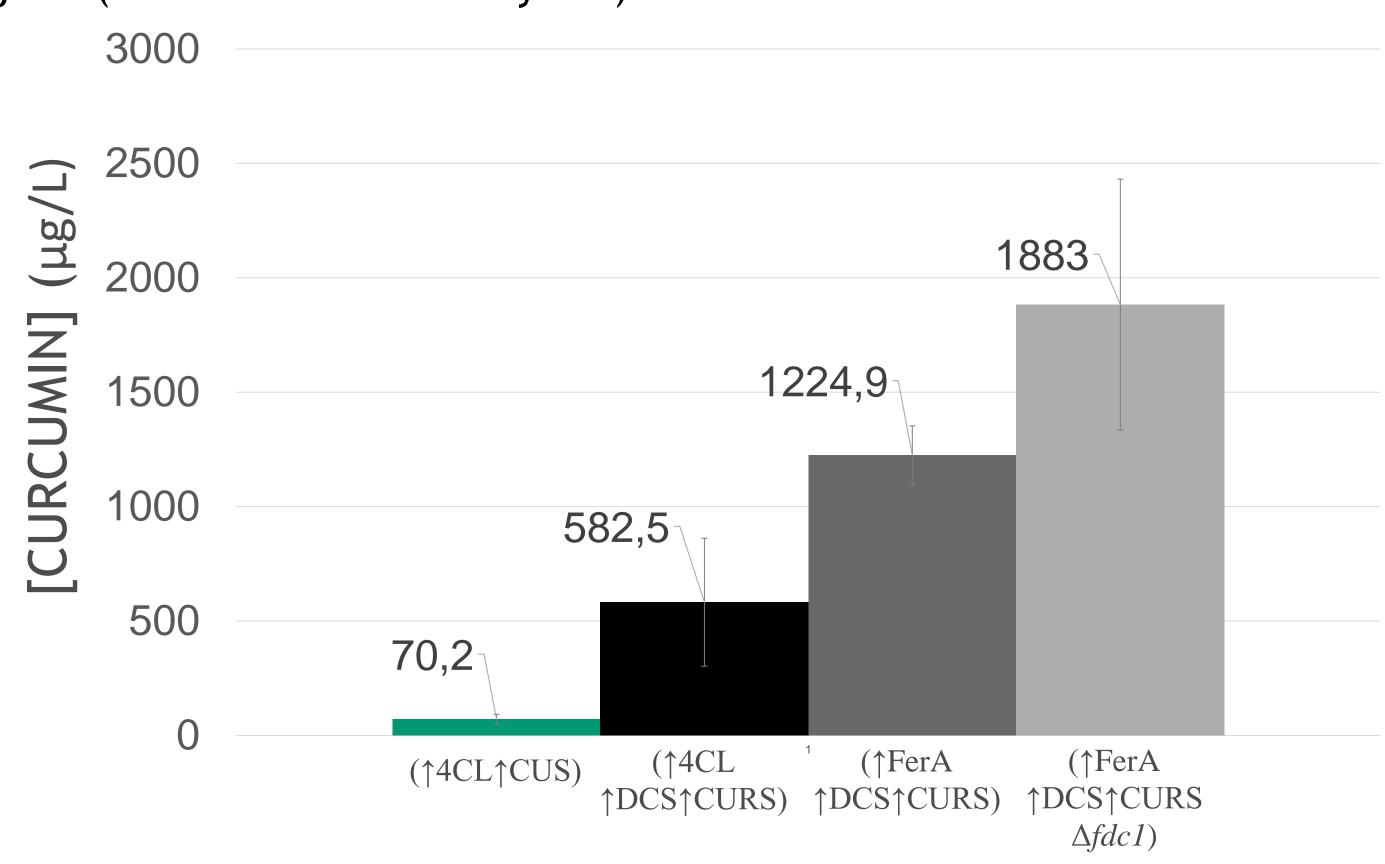
Flask cultivation of mutants w/ supplemented ferulic acid

Heterologous pathway combinations tested:

- A 4CL1 (4-coumarate-CoA ligase) from Arabidopsis thaliana and CUS (curcuminoid synthase) from Oryza sativa (capable of one-pot synthesis of curcumin from feruloyl-CoA)
- B 4CL1 from A. thaliana, DCS (diketide-CoA synthase) and CURS (curcumin synthase) from Curcuma longa
- C FerA (feruloyl-CoA synthetase) from *Pseudomonas paucimobilis*, DCS and CURS from C. longa
- D FerA from P. paucimobilis, DCS and CURS from C. longa, fdc1 (ferulic acid decarboxylase) knock-out strain



Left flask: No ferulic acid was added to the culture media; Right flask: 16 mg/L of ferulic acid were added to the media at 24 h of fermentation



- * Engineered S. cerevisiae expressing type III PKS (DCS and CURS) from C. longa produced more curcumin than when CUS from O. sativa was expressed;
- ❖ FerA from P. paucimobilis resulted in more curcumin than 4CL from A. thaliana;
- ❖ Deletion of *fdc1* improved curcumin production;

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