O1. PRODUCTION OF CURCUMIN FROM FERULIC ACID BY AN ENGINEERED *SACCHAROMYCES CEREVISIAE*

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Curcumin is a secondary metabolite produced in the rhizome of *Curcuma longa* that represents the most active and studied naturally-derived curcuminoid product. Studies have confirmed its biological and therapeutic effects in several diseases being the anticancer activity the most documented. Since curcumin is synthetized in low amounts, its heterologous production could represent a rapid and easy method to obtain large amounts of this bioactive compound. Curcumin has already been produced in engineered *Escherichia coli* although with low yields. However, the curcumin biosynthetic pathway has never been engineered in *Saccharomyces cerevisiae*. As a eukaryotic organism, it presents unique advantages over *E. coli* that facilitate the expression of plant derived genes. This work aimed to design an artificial biosynthetic pathway for the production of curcumin by *S. cerevisiae*. The principal enzymes involved in the artificial pathway are: 4-coumarate-CoA ligase (4CL) and the type III polyketide synthases (PKSs). In *C. longa* there are two types of PKSs - diketide-CoA (DCS) and curcumin synthase (CURS) - that catalyse different reactions. Curcuminoid synthase (CUS) from Oryza sativa is also a PKS able of catalysing the "one-pot" synthesis of curcuminoids in *E. coli*. Herein, we intended to produce curcumin using ferulic acid as precursor. For that purpose, shuttle vectors with enzymes from different organisms were constructed and transformed in *S. cerevisiae* CENPK2-1C. The vectors carry 4CL from *Arabidopsis thaliana* or *Lithospermum erythrorhizon*, and DCS and CURS or CUS. DCS and CURS were codon-optimized for *S. cerevisiae*. In addition, CRISPR-Cas9 method was used to knockout a gene from *S. cerevisiae* that codifies ferulic acid decarboxylase that is responsible for the ferulic acid decarboxylation as a detoxification process. The engineered strains are currently being tested for curcumin production.