Production of oil enriched with erucic acid by *Yarrowia lipolytica*

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Plants, especially members of the genus *Brassica*, are known for biosynthesis of monounsaturated cis-13-docosenoic acid (22:1ω9) called as erucic acid (EA). The main source of this fatty acid is high-erucic-acid rapeseed oil with the EA content of 50 – 56%. Global demand for EA is still increasing mainly for its uses for industrial purposes as surfactants, lubricants, emollients etc. Such growing interest in EA applications in various fields has focused attention on the provision of alternative and suitable natural sources of this fatty acid. Oleaginous microorganisms should be considered as one of the best candidates for biotechnological production of EA provided that their fatty acid metabolic pathway will be appropriately re-designed. Of them, *Yarrowia lipolytica* is an oleaginous yeast that is widely used as excellent genetic engineering tool for production of various "tailor-made" lipids.

EA is biosynthesized in maturating plant seeds through elongase complex. The first and key initial condensation step is catalyzed by the condensing enzyme β-ketoacyl-CoA synthase (KCS). KCS in plants is harbored on FATTY ACID ELONGATION (FAE1) protein, which is encoded by *FAE1* gene. Although *FAE1* genes from different Brassicaceae species have been isolated, *FAE1* gene from field pennycress (*Thlaspi arvense*) was overexpressed in *Y. lipolytica* mutant strain possessing *fad2* deletion. This led to accumulation of almost 10% of EA in yeast cell oil. Other elongation products, namely C20:1 and C24:1, were observed as well. Moreover, percentage of intracellular C20:0, C22:0, and C24:0 fatty acids in *Y. lipolytica* increased at least two-fold in the presence of *FAE1* gene. Further analysis revealed, that EA was accumulated exclusively in triacylglycerols. *FAE1* gene was also overexpressed in Q4 strain (Δ*dga1*, Δ*dga2*, Δ*lro1*, Δ*are1*) carrying one of the acyltransferase genes (*DGA1*, *DGA2*, *LRO1*, *ARE1*). It was observed, that only Q4-*DGA1* mutant strain was able to effectively accumulate EA in the storage lipids. This indicates the strict specificity of *Y. lipolytica* DGA1 acyltransferase for erucoyl-CoA in TAG biosynthesis pathway.

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