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The lipase system of *Yarrowia lipolytica*

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Among yeast species, *Yarrowia lipolytica* is one of the highest producers of extracellular proteins (acid, neutral and alkaline proteases, acid phosphatase, ribonucleases and lipases). Lipases (triacylglycerol hydrolases) are important enzymes in fat metabolism, catalyzing the breakdown of triacylglicerols to free fatty acids and glycerol. Owing to the very low solubility of their natural substrates, this hydrolysis is catalyzed at the interfase between an insoluble substrate and the aqueous phase in which the enzyme is solubilized. This feature distinguishes them from esterases, which preferentially catalyze the hydrolysis of soluble esters in water. Lipases constitute a ubiquitous group of enzymes able to catalyze a number of different reactions, many of them of industrial interest (stereoselective hydrolysis, transesterification, etc). In the present work, we report the molecular cloning and characterization of two genes encoding lipase-like proteins from *Y. lipolytica*. The complete DNA sequence encodes for two putative proteins of 486 and 498 aminoacid. The deduced aminoacid sequences shows similarity with lipases from other fungi (*Candida cylindracea, Geothricum candidum*) sharing in common the sequence for the interfacial activation site. The lipases from *Yarrowia lipolytica* have two potential N-glycosylation sites and one possible cAMP-dependent phosphorylation site near the C terminus. The proteins do not show clear signal peptide, although it does have a C-terminal hydrophobic tail.

Disruption of one of the genes (*YlLIP1*) produces lower lipase activity in olive's oil medium when comparing to the wild type.

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