Influence of Phosphatidylethanolamine Metabolism on Triacylglycerol Synthesis

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Triacylglycerol (TAG) synthesis in the yeast is accomplished by the acyltransferases Dga1p, Lro1p, Are1p and Are2p. Dga1p, Are1p and Are2p catalyze TAG synthesis from diacylglycerol (DAG) in an acyl-CoA dependent reaction. In contrast, Lro1p uses phospholipids as acyldonors with some preference for phosphatidylethanolamine (PE). In this study, we addressed the question whether the PE level in the yeast has an impact on TAG synthesis. The main enzyme which contributes to PE formation is phosphatidylserine decarboxylase 1 (Psd1p) localized to the inner mitochondrial membrane. Besides this major site of synthesis, PE can also be formed by Psd2p in the Golgi/vacuolar compartment, the acyltransferase Ale1p in the mitochondria associated membrane and the CDP-ethanolamine branch of the Kennedy pathway. The contribution of these pathways to TAG synthesis was tested in various deletion strains bearing defects in PE metabolism, namely, *psd1Δ*, *psd2Δ*, *psd1Δpsd2Δ*, *ale1Δ* and *cki1Δdpl1Δeki1Δ* under stringent conditions by using minimal lactate media supplemented with ethanolamine. Our data show that TAG synthesis is linked to PE metabolism, but rather through the CDP-ethanolamine pathway than through *PSD*s.

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