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Philip D. Bates

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Understanding the control of acyl flux through the lipid metabolic network of plant oil biosynthesis

Philip D. Bates

Nina Bell Suggs Endowed Assistant Professor Department of Chemistry and Biochemistry The University of Southern Mississippi 118 College Dr. #5043 Hattiesburg, MS 39406-0001 Phone: 601-266-4199 Email: Philip.Bates@usm.edu

Corresponding Author: Philip D. Bates

Abstract

Plant oil biosynthesis involves a complex metabolic network with multiple subcellular compartments, parallel pathways, cycles, and pathways that have a dual function to produce essential membrane lipids and triacylglycerol. Modern molecular biology techniques provide tools to alter plant oil compositions through bioengineering, however with few exceptions the final composition of triacylglycerol cannot be predicted. One reason for limited success in oilseed bioengineering is the inadequate understanding of how to control the flux of fatty acids through various fatty acid modification, and triacylglycerol assembly pathways of the lipid metabolic network. This review focuses on the mechanisms of acyl flux through the lipid metabolic network, and highlights where uncertainty resides in our understanding of seed oil biosynthesis.

Highlights

- Acyl flux through phosphatidylcholine is central to plant lipid metabolism
- Plant oil biosynthesis utilizes multiple distinct diacylglycerol pools
- Genes encoding multiple acyl flux reactions are still unknown

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