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Review

Unsaturated fatty acid: Metabolism, synthesis and gene regulation

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In both plants and animals, unsaturated fatty acids are considered to be essential membrane components. Also they play key roles in many cellular events. The synthesis and metabolism of unsaturated fatty acid are very complex processes, involving a variety of enzymes and regulated pathways. Most recently, research has focused on identifying genes modulating unsaturated fatty acids and studying the metabolism and synthesis at both transcriptional and post-translational levels. The key enzymes and regulated pathways involved in either the metabolism or the synthesis of fatty acid have been identified.

Key words: Unsaturated fatty, oleic acid, synthesis, gene regulation.

INTRODUCTION

Over the past 10,000 years with the development of agriculture, changes began to take place in the food supply. But it was especially during the last 100 - 150 years that nutritional changes have led to an increase in saturated fats from grain-fed cattle, an increase in trans-fatty acids from the hydrogenation of vegetable oils and an enormous increase in n - 6 fatty acids (about 30 g/day) due to the production of oils from vegetable seeds such as corn, safflower and cotton. From a biochemical point of view the fatty acids have attracted the greatest interest recently. Most of the dietary fatty acids are derived from meats, oils and dairy products, giving rise to a large intake of saturated as well as monounsaturated fatty acids and relatively modest amount of polyenes. Saturated fats and cholesterol represent the most established risk factor in our diets, whereas monoenes and PUFA probably are the most important lipids that would provide beneficial effects if the dietary intake is increased.

Chemically, unsaturated fatty acids belong to the class of simple lipids, as they are fatty acids with one or more double bonds in cis configuration. There are 3 main families of unsaturated fatty acids: 18:1, 18:2 and 18:3. These fatty acids family are not convertible and have very different biochemical roles. The lipid requirement of all mammals is met by their dietary intake or by de novo synthesis of fatty acids. The (n - 3) and (n - 6) poly-unsaturated fatty acids (linolenate and linoleate, respectively) are essential fatty acids that cannot be synthesized by mammals and therefore must be obtained from dietary sources.

Oleic acid is one of the major MUFA of membrane glycerolipids in both plants and animals. It is also an important component of the plant oil. Vegetables are the main sources of 18:1, 18:2 and 18:3 fatty acids. The most important n – 6 fatty acid, LA, is found in large amounts in western diets in corn oil, safflower oil, sunflower oil and soybean oil (Adam, 1989). Because of its oxidation stability, delicious flavor and wholesome characteristics, thus increasing oil content and improving the fatty acid composition in the seed oil are important breeding goals for Oil Crops.

This review will focus on the most recent reports of the unsaturated fatty acids about the metabolism and synthesis at both transcriptional and post-translational levels, as well as finding the key enzymes and regulated pathways involved in either metabolism or synthesis of fatty acid in plant.

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Abbreviations: S-ACP-DES, Stearoyl-ACP-desaturase; **FA,** fatty acid; **PUFA,** polyunsaturated fatty acids; 18:0, stearic acid; **MUFA**: monounsaturated fatty acids; 18:1, oleic acid.

SYNTHESIS AND METABOLISM OF UNSATURATED FATTY ACIDS IN PLANT

In higher plants, PUFAs are synthesized through both prokaryotic (chloroplast) and eukaryotic (ER) pathways (Roughan et al., 1980; Browse et al., 1986). The synthesis of <18C fatty acids in the cell matrix, NADPH as essential for hydrogen donor, mainly from pentose phosphate way. The desaturated and carbon chain extended of fatty acids <18C completed through the lipid acyl connected to the lipid membrane phospholipids, need NADPH and O_2. These have proved to occur in eukaryotic cells, phospholipid is the carrier for lipid acyl desaturated, phosphatidylcholine, phosphatidylethanolamine, phosphatidyl, and inositol are the substrates. The desaturated and carbon chain extended of fatty acids under different enzyme.

In plants, 18:1 formation is catalyzed by the soluble stearoyl acyl carrier protein desaturase (S-ACP-DES). The members of S-ACP-DES are specific for particular substrate chain length and introduce double bond between specific carbon atoms. Since S-ACP-DES are the only plant enzymes which catalyze conversion of 18:0 to 18:1 in plants (Shanklin and Somerville, 1991). 18:1 can either enters glycerolipid synthesis via the prokaryotic pathway in the chloroplasts or is exported out of plastids as CoA thioesters to enter the eukaryotic glycerolipid synthesis pathway.

In nature, algae, fungi, bacteria, insects and other invertebrates have a series of desaturase (DS) and elongase (EL), and other active substances. it can be synthesis PUFAs from scratch, are the main source of these compounds.

THE KEY ENZYMES AND GENE REGULATION ON PUFA IN PLANT

The *Arabidopsis* genome carries seven S-ACP-DES like genes, including the SSI2/FAB2. The ssi2 allele encodes a S-ACP-DES of reduced function and as a result the mutant plants accumulate increased levels of 18:0 and reduced levels of 18:1 (Lightner et al., 1994; Kachroo et al., 2001). The vitamin e-deficient2 (vte2) mutant of *Arabidopsis thaliana* has reduced seed viability and impaired seedling development, both of which are associated with a massive elevation in lipid peroxidation (Sattler et al., 2004, 2006), indicating that tocopherols play an essential role as lipid-soluble antioxidants during seed dormancy and early seedling development. It has been demonstrated that LT-treated vte2 has a distinct composition of polyunsaturated fatty acids (PUFAs), lower levels of linolenic acid (18:3) and higher levels of linoleic acid (18:2) compared with the wild type. PUFA changes in LT-treated vte2 occur primarily in phospholipids due to reduced conversion of dienoic to trienoic (Hernández et al., 2008). A series of mutations affecting plastid or ER-localized fatty acid desaturases were introduced into the vte2 background and the consequences for the vte2 LT phenotypes were assessed (Maeda et al., 2006). The results showed that fad2, and to a lesser extent the fad6 mutation into the vte2 background suppressed the LT-induced vte2 phenotypes, provided biochemical and genetic evidence that plastid-synthesized tocopherols modulate ER PUFA metabolism early in the LT adaptation response of *Arabidopsis* (Hiroshi et al., 2008).

The major exported fatty acid in *Arabidopsis* is 18:1 and based on *in vitro* activity, it can be predicted that FATA determines the *in vivo* levels of 18:1 that move out from the plastid (Salas and Ohlrogge, 2002).

In plants, changes in the levels of oleic acid (18:1), results in the alteration of salicylic acid (SA) and jasmonic acid (JA)-mediated defense responses. In *Arabidopsis*, oleic acid (18:1) has been implicated to participate in SA- and JA-mediated defense pathways (Kachroo et al., 2001, 2003a, b, 2004, 2005 and 2007). This is evident in the *Arabidopsis* ssi2/fab2 mutant, which encodes a defective stearoyl-acyl carrier protein desaturase (S-ACP-DES) and consequently accumulates high levels of stearic acid (18:0) and low levels of 18:1. 18:1 levels are regulated at both transcriptional and post-translational levels.

Increases in oleic acid content can potentially be achieved by reducing the activity of oleate desaturase (oleoyl-phosphatidylcholine D12-desaturase), the enzyme which converts oleate into linoleate in the developing seed. High-oleic peanut oils produced by HpRNA-mediated gene silencing of oleate desaturase (Dongmei Yin et al, 2008).

Genetic engineering methods have been used successfully to modify the fatty acid profile of elite Australian germplasm of *Brassica napus* and *B. juncea*. Co-suppression plasmids carrying oleate desaturase genes from each species have been constructed and transferred into Australian elite breeding lines of *B. napus* and *B. juncea* using *Agrobacterium tumifaciens* plant-transformation techniques silencing of the endogenous oleate desaturase genes has resulted in substantial increases in oleic acid levels (Stoutjesdijk et al, 2000).

In 1992 and 1994 workers have cloned FAD3 (Arondel et al., 1992) and FAD2 (Okuley et al., 1994) from mutant of *A. thaliana*. Subsequently, it has been found that desaturated enzyme gene FAD6 can also introduce a second bond. In the fatty acids, Hitz et al. (1994) confirmed that the past hypothesis on the "existence of 2 substrate specific enzyme can introduce a second bond in fatty acids ". In 1993 and 1994 workers have found FAD7 (Iba et al., 1993) and FAD8 (Gibson et al., 1994) in *Arabidopsis*. Currently several other enzymes and encoding genes participating in the process of desaturation have been identified (Hugly and Somerville 1992; Maeda et al., 2006; Gueguen et al., 2000).

FAD2 and FAD3 are ER-localized fatty acid desaturases. Thus, the fad2 and fad3 mutants have reduced PUFAs content predominantly in phospholipids, the major lipid components of extraplastidic membranes (Miquel and

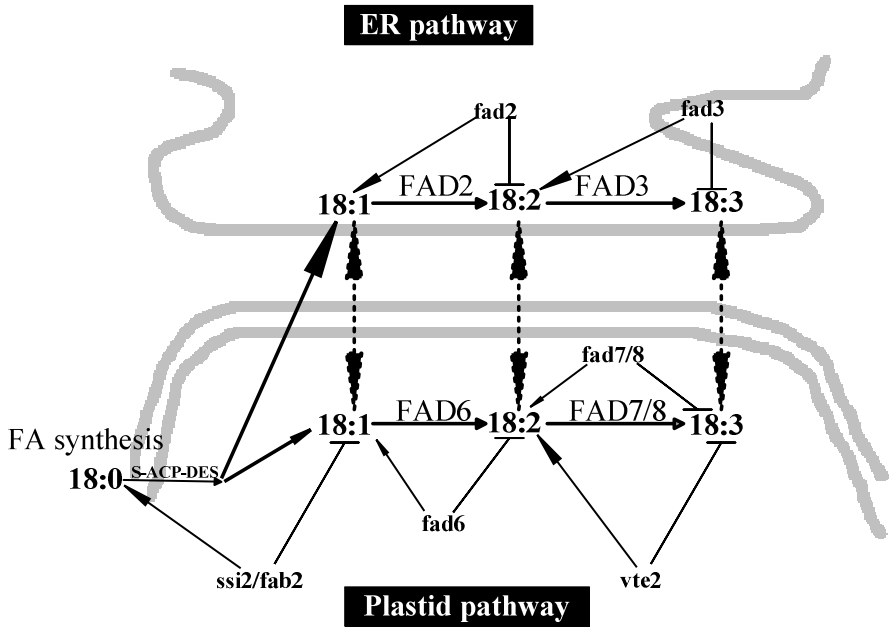

Figure 1. A diagram summarizing membrane PUFA biosynthesis in *Arabidopsis*. Black arrows indicate acyl pairs derived from the ER and plastid pathways, respectively. Dotted arrows illustrate proposed transfer of lipids between the ER and plastid. Gray arrows indicate the promotion role. T-type symbols are inhibition role. Capital letters on behalf of the key enzymes. Lowercase letters indicate mutants.

Browse, 1992; Okuley et al., 1994). Mutants of *Arabidopsis* at the fatty acid desaturarion 2 (fad2) locus are deficient in activity of the endoplasmic reticulum desaturase (Miquel and Browse, 1992). FAD6, FAD7 and FAD8 are plastid-localized fatty acid desaturases and the fad6 and fad7 fad8 mutants have reduced PUFAs predominantly in galactolipids, the major lipid components of plastidic membranes (Browse et al., 1989; Falcone et al., 1994; McConn et al., 1994). FAD2 and FAD6 convert monoenoic- to dienoic-fatty acids, whereas FAD3, FAD7 and FAD8 convert dienoic- to trienoic fatty acids (Figure 1). Thus compared with Col, the fad2 and fad6 mutants contain higher 18:1 and the fad3, fad7 and fad8 have higher 18:2 and all these genotypes have lower 18:3 (Browse et al., 1989, 1993; Miquel and Browse, 1992; Falcone et al., 1994; McConn et al., 1994; Okuley et al., 1994; Wallis and Browse, 2002). FAD2, FAD6, FAD3, FAD7 and FAD8 genes have been cloned from *Arabidopsis* (Browse et al., 1989; Arondel et al.,1992), rape (Darwin et al.,2000), olive (Hernández et al.,2008), maize (Berberich et al., 1998) tobacco (Hamada et al., 1998) and many other plants (Wharfe and Harwood, 1978; Wang et al., 2006).

CONCLUSION

In both plants and animals, unsaturated fatty acids are considered to be essential membrane components. The data reported in the past few years have confirmed the importance of unsaturated fatty acids as universal cellular regulators, which played key roles in many cellular events. The synthesis and metabolism of unsaturated fatty acid is a very complex process, involving a variety of enzymes and regulated pathways. Several genes modulating unsaturated fatty acids at both transcriptional and post-translational levels, as well as many key enzymes and regulated pathways involved in either the metabolism or the synthesis of fatty acid have been documented. This will help us to increase oil content and improve the fatty acid composition in the seed oil.

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