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Expanding the docosahexaenoic acid food web for sustainable production: engineering lower plant pathways into higher plants

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Abstract

- **Background** Algae are becoming an increasingly important component of land plant metabolic engineering projects. Land plants and algae have similar enough genetics to allow relatively straightforward gene transfer and they also share enough metabolic similarities that algal enzymes often function in a plant cell environment. Understanding metabolic systems in algae can provide insights into homologous systems in land plants. As examples, algal models are currently being used by several groups to better understand starch and lipid metabolism and catabolism, fields which have relevance in land plants. Importantly, land plants and algae also have enough metabolic divergence that algal genes can often provide new metabolic traits to plants. Furthermore, many algal genomes have now been sequenced, with many more in progress, and this easy access to genome-wide information has revealed that algal genomes are often relatively simple when compared with plants.
- Scope One example of the importance of algal, and in particular microalgal, resources to land plant research is the metabolic engineering of long-chain polyunsaturated fatty acids into oilseed crops which typically uses microalgal genes to extend existing natural plant biosynthetic pathways. This review describes both recent progress and remaining challenges in this field.

Long-chain vs. short-chain polyunsaturated fatty acids

Long-chain polyunsaturated fatty acids (LC-PUFA) have a carbon backbone of at least 20 carbons in length and contain multiple double-bond desaturations. Long-chain polyunsaturated fatty acids can be grouped into either an omega-3 (ω 3) or ω 6 category based on the position of the first double bond from the methyl, or ω , fatty acid terminus. Fatty acid nomenclature can be used to succinctly refer to fatty acids and, as an example,

18:4 $^{\Delta 6,9,12,15}$ refers to the short-chain stearidonic acid which contains only 18 carbons and four double bonds, or desaturations, at the 6, 9, 12 and 15 carbon positions from the carboxyl, or Δ , terminus (Fig. 1). Long-chain polyunsaturated fatty acids have critical roles in human health and development, with studies indicating that deficiencies in these fatty acids can increase the risk or severity of cardiovascular disease (von Schacky 2006), inflammatory diseases and rheumatoid arthritis (Kremer *et al.* 1995; Simopoulos 2002; Nagel *et al.* 2003), hypertension (Ueshima *et al.* 2007) and

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Fig. 1 ω 3 long-chain (>C20) polyunsaturated fatty acids and their predominant natural sources. *Some Boraginaceae such as *Echium* plantagineum contain SDA, although this species is not generally recognized as an oilseed crop species.

neuropsychiatric disorders such as depression or dementia (Freeman et al. 2006; Parker et al. 2006; Schaefer et al. 2006). Recently, the human fatty acid receptor GPR120 was characterized as being an ω 3-specific receptor with strong anti-inflammatory and insulinsensitizing effects (Oh et al. 2010). Humans have limited ability to synthesize LC-PUFA, with infants in particular requiring the majority of these fatty acids through the diet. This is particularly the case with the ω 3 LC-PUFA eicosapentaenoic acid (EPA), docosapentaenoic acid (DPA) and docosahexaenoic acid (DHA) and the $\omega 6$ LC-PUFA arachidonic acid (ARA), with studies indicating positive effects on infant cognitive development after ARA and DHA supplementation (Birch et al. 2000). As a result many infant formulae now contain LC-PUFA, although it is worth noting that ARA supplementation for adults is, in many cases, often considered to be of lesser value since the ω 6 LC-PUFA tend to be pro-inflammatory in nature and counteract the strong anti-inflammatory effects of ω 3 LC-PUFA.

Just as there are differences in physiological effect between ω 3 and ω 6 LC-PUFA (i.e. anti- vs. pro-inflammatory, respectively), it is important to note that there are significant differences arising from intake of long-chain vs. short-chain (SC) ω 3 PUFA. Alphalinolenic acid (ALA) is a common ω 3 SC-PUFA found in seed oils of flax/linseed, canola/rapeseed, soybean and walnut. Stearidonic acid (SDA), another ω 3 SC-PUFA, is less common in plant oils, with the predominant natural plant dietary sources being echium and borage. Human studies along with livestock and aquafeeding trials have demonstrated that SDA in particular can be converted, in part, to the LC-PUFA EPA and, to a lesser extent, DPA (James *et al.* 2003; Tocher *et al.* 2006;

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Harris et al. 2008). Thus, although the direct health benefits of ω 3 SC-PUFA are relatively limited when compared with LC-PUFA, they are viewed by some as a surrogate for dietary EPA supplementation (Whelan 2009) due to this *in vivo* conversion and transgenic SDA crops are under development.

It is clear, however, that direct intake of ω 3 LC-PUFA results in the greatest health benefits (James et al. 2003; Burdge and Calder 2005; Wang et al. 2006). Furthermore, the conversion of ω3 SC-PUFA including SDA to DHA has not been observed in either humans or aquaculture species to any significant degree (James et al. 2003; Tocher et al. 2006; Harris et al. 2008). Docosahexaenoic acid fills specific physiological (e.g. Mori et al. 1999) and structural roles (such as a neural and retinal component) that cannot be replaced by EPA or other LC-PUFA, and ensuring adequate dietary intake of DHA is therefore required. Consumer awareness of the health benefits of ω 3 LC-PUFA is growing (due in part to the efforts of organizations such as the Omega-3 Centre (www.omega-3centre.com) and GOED (www.goedomega3.com)), and there is an increasing demand for these fatty acids which will be difficult for current sources to meet in a sustainable manner.

Current and future sources of ω 3 LC-PUFA

The main source of ω 3 LC-PUFA is wild-harvest marine fish stocks and these, unfortunately, are widely recognized to be in decline. One widely cited paper describes the amount of large predatory fish in the oceans as being at only 10 % of pre-industrial times (Myers and Worm 2003), although this figure has been disputed. One of the authors claimed in a later publication that the state of the oceans and the effect of this on fish stocks was such that 'all commercial fish and seafood may collapse' by 2048 (Worm et al. 2006). This view is hardly unanimous either (see Hölker et al. (2007), Wilberg and Miller (2007) and Jaenike (2007) for comment), but efforts are now under way to rebuild fisheries and to improve their sustainability. Regardless, fisheries alone are unlikely to meet the growing demand for ω 3 LC-PUFA and alternative sources of these fatty acids must be found. Aquaculture cannot meet the demand since fish themselves do not produce LC-PUFA but, like humans, accumulate LC-PUFA through their diet. In fact, the aquaculture industry itself contributes enormously to demand for LC-PUFA, with \sim 90 % of global fish oil production being used in aquafeeds. Logically, the major producers of ω 3 LC-PUFA, microalgae, would be a good target for increased production and, indeed, commercial microalgal sources of w3 LC-PUFA are available. Microbial production tends to supply relatively niche applications such as infant formulae and nutraceuticals due to high production costs and is unlikely to scale up adequately for large-volume applications.

Oilseed crops, with their production capacity and relatively low cost, would be an excellent and sustainable source of ω 3 LC-PUFA. For example, several calculations have recently been performed to examine global consumer needs for these oils and using a daily 500 mg requirement, as is recommended by national health bodies, a global population reaching 8 billion by 2025, and assuming fish contain 0.2–3.5 g of ω 3 LC-PUFA per 100 g of oil, it was estimated that the current global fish harvest (93 Mt per annum) will fall well short of this requirement. On the other hand, \sim 2.5 million hectares of an oilseed crop (about 2% of total world acreage under cultivation to major oilseed crops) containing 10-15 % DHA and EPA in its oil could replace all the fish oil currently being used globally. Oilseed crop plants do not naturally synthesize these fatty acids, meaning that a metabolic engineering solution would be required before this potential source could become a reality. An oilseed crop with ω 3 LC-PUFA production capability would provide an excellent alternative to high-volume, environmentally sensitive marine-based oils. Such an oil could be used in many applications: (i) as an ingredient for aquaculture feeds to provide aquaculture species with ω 3 LC-PUFA both for their own developmental requirements and to meet consumer demands for ω 3 LC-PUFA content in fish; (ii) as an animal feed to produce ω 3 LC-PUFA-enriched meat, eggs and milk; (iii) as a food (e.g. bread or milk) supplement in an oxidation-protected form; (iv) directly, as a nutraceutical supplement similar to the way in which fish oil capsules are currently used. As an additional benefit, an oilseed

source would be vegetarian and thus satisfy a requirement for an important sector of the global market.

ω3 LC-PUFA biosynthesis

Biosynthesis of LC-PUFA occurs by either aerobic or anaerobic pathways in nature, with the latter found predominantly in some marine bacteria (e.g. Vibrio and Shewanella) and protists (e.g. Schizochytrium and Thraustochytrium). Anaerobic synthesis of LC-PUFA is performed by polyketide synthase (PKS) pathways which are cyclical in nature, with multi-enzyme complexes iteratively performing a series of desaturations and 2-carbon elongations using malonyl-CoA and acetyl-CoA as the source of the carbon units. The complex nature of the PKS pathway and the requirement for associate genes has to date resulted in this being a challenging pathway to introduce into plants. The aerobic pathway, on the other hand, consists of a series of distinct desaturation and elongation steps with the genes coding for each of the enzymes having been isolated and characterized. This review focuses on metabolic engineering of plants by the aerobic pathway, although it is worth noting that considerable progress has been made in understanding and engineering the PKS pathways (Metz et al. 2001, 2006, 2009; Lippmeier et al. 2009).

Aerobic production of LC-PUFA (Fig. 2) can be thought, in the context of plant metabolic engineering, to commence with the native plant fatty acid oleic acid. This fatty acid is first Δ 12-desaturated to produce linolenic acid (LA), which is in turn ω 3-desaturated to produce ALA. Linolenic acid and ALA are the respective substrates for the ω 6 and ω 3 LC-PUFA pathways, with the first committed step in both pathways being a $\Delta 6$ -desaturation to produce either γ -linoleic acid (GLA) (ω 6) or SDA (ω 3). All the fatty acids up to this point can be found naturally in angiosperms, although GLA and SDA are relatively rare and efforts have been made to engineer these SC-PUFA into oilseed species (see below). The C18 fatty acids GLA and SDA are then $\Delta 6$ -elongated to the longchain (\geq C20) fatty acids di-homo- γ -linoleic acid (DGLA) and eicosatetraenoic acid (ETA), respectively. This elongation (and the others described in this review) consists of four consecutive enzymatic steps (condensation, ketoreduction, dehydration and enoyl reduction), although the transgenic introduction of the condensing enzyme or 'elongase' is sufficient to confer specificity to the entire elongation with the other elongation reaction components being supplied by the host organism. The products of the $\Delta 6$ -elongation, DGLA and ETA, are then $\Delta 5$ -desaturated to ARA and EPA, respectively. Arachidonic acid marks the end of the traditionally

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represented ω 6 LC-PUFA pathway, although ARA can be Δ 5-elongated to docosatetraenoic acid which can finally be Δ 4-desaturated to DPA ω 6. Similarly, EPA can be



Fig. 2 Long-chain polyunsaturated fatty acid biosynthesis pathways in lower plants, including algae (ω 6 and ω 3), marine bacteria and protists (PKS). Enzymes are referred to as either 'E' for elongase (e.g. $\Delta 9E$ is $\Delta 9$ -elongase) or 'D' for desaturase (e.g. $\Delta 6D$ is $\Delta 6$ -desaturase) and belong to the aerobic pathway for LC-PUFA synthesis. A generalized scheme for the processive synthesis of LC-PUFA by the anaerobic PKS pathway is also shown. In this system acetyl-CoA undergoes several rounds of sequential reactions (ketosynthase, keto-reductase, dehydratase and enoyl reductase) that result in repeated elongations by two carbons per cycle of a fatty acyl chain esterified to an acyl carrier protein. Names and abbreviations for the $\omega 3$ fatty acids are provided in Fig. 1 and $\omega 6$ fatty acids are $18:2^{\Delta 9,12}$, LA; $18:3^{\Delta 6,9,12}$, GLA; 20:3^{Δ 8,11,14}, DGLA; 20:4^{Δ 5,8,11,14}, ARA. The Δ 9-elongated fatty acids are $20:2^{\Delta 11,14}$, EDA and $20:3^{\Delta 11,14,17}$, ETRA.

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 Δ 5-elongated to DPA (DPA ω 3) which is then Δ 4-desaturated to produce DHA. This ' Δ 6' pathway is the most commonly found aerobic pathway, although the alternative ' Δ 8' pathway also exists. In this pathway, LA and ALA are Δ 9-elongated to eicosadienoic acid (EDA) and eicosatrienoic acid (ETRA), respectively, which are then Δ 8-desaturated to DGLA and ETA (Fig. 2). At this point, the Δ 6 and Δ 8 pathways merge and subsequent desaturations and elongations continue as described above.

Long-chain polyunsaturated fatty acid metabolic engineering

It is surprising to some people that fish and other marine species, the predominant source of ω 3 LC-PUFA oils in the human diet, are not the source of the genes used in LC-PUFA metabolic engineering applications. Rather, the genes come from microalgae (that fish and other marine species consume), fungi and protists. As already mentioned, genes coding for each step in the LC-PUFA pathways have been isolated and characterized, and several groups have been expressing these in land plants to modify the fatty acid profiles of the plant oil (Fig. 3, Table 1). There are several technical or scientific challenges that must be met before oilseed crops can be engineered to accumulate adequate levels of LC-PUFA. These challenges are mainly focused on increasing the conversion of the native plant fatty acid substrates through to the LC-PUFA of interest with as few intermediate fatty acids as possible. In theory, this simply requires the use of transgenic enzymes which have high conversion efficiencies. In practice,



Fig. 3 Some notable LC-PUFA engineering results discussed in this review. See Table 1 for details of genes used in these studies. Format adapted from Venegas-Calerón et al. (2010).

Publication	Pathway	Host species	Genes
Qi et al. (2004)	Δ9	Arabidopsis thaliana leaf	Isochrysis galbana Δ9-elongase* Euglena gracilis Δ8-desaturase* Mortierella alpina Δ5-desaturase
Abbadi <i>et al.</i> (2004)	Δ6	Linum usitatissimum seed	· Phaeodactylum tricornutum Δ6-desaturase* Physcomitrella patens Δ6-elongase Phaeodactylum tricornutum Δ5-desaturase*
Robert <i>et al</i> . (2005)	Δ6	Arabidopsis thaliana seed	Danio rerio ∆5/6-desaturase Caenorhabditis elegans ∆6-elongase Pavlova salina ∆5-elongase* Pavlova salina ∆4-desaturase*
Kinney <i>et al</i> . (2004)	Δ6	Glycine max seed	Arabidopsis thaliana Δ 15-desaturase Saprolegnia diclina Δ 17-desaturase Mortierella alpina Δ 6-desaturase Mortierella alpina Δ 6-elongase Mortierella alpina Δ 5-desaturase
Kinney <i>et al</i> . (2004)	Δ6	Glycine max somatic embryo	As above plus: Pavlova sp. ∆5-elongase* Schizochytrium ∆4-desaturase*
Wu et al. (2005)	Δ6	Brassica juncea seed	Calendula officinalis Δ 12-desatuase Phytophthora infestans ω 3-desaturase Thraustochytrium sp. LPCAT* Pythium irregulare Δ 6-desaturase Thraustochytrium sp. C18 elongase* Thraustochytrium sp. Δ 5-desaturase* Oncorhynchus mykiss C18/C20 elongase Thraustochytrium sp. Δ 4-desaturase*
Cheng <i>et al</i> . (2010)	Δ6	Brassica carinata seed	Pythium irregulare Δ 6-desaturase Thraustochytrium sp. C18 elongase* Thraustochytrium sp. Δ 5-desaturase* Calendula officinalis Δ 12-desatuase Phytophthora infestans ω 3-desaturase
Petrie <i>et al</i> . (2010a)	Δ6	Arabidopsis thaliana seed	Micromonas pusilla ∆6-desaturase* Pyramimonas cordata ∆6-elongase* Pavlova salina ∆5-desaturase* Pyramimonas cordata ∆5-elongase* Pavlova salina ∆4-desaturase*
Petrie <i>et al</i> . (2010b)	Δ9	Nicotiana benthamiana leaf	Pavlova salina: Δ9-elongase* Δ8-desaturase* Δ5-desaturase* Δ5-elongase* Δ4-desaturase*

Table 1 The genes used in the studies described in Fig. 3. *Denotes an algal gene source.

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the conversion efficiencies of LC-PUFA biosynthesis enzymes are not only affected by actual enzyme activity but also by factors such as substrate dichotomy, the requirement of some enzymes to use substrates from certain metabolic pools.

The biosynthesis of ω 3 LC-PUFA in land plants was first reported in 2004 with publications describing the introduction of both the $\Delta 8$ and $\Delta 6$ pathways. Qi et al. (2004) demonstrated the production of 3 % EPA and 6.6 % ARA in Arabidopsis thaliana leaf tissue by a $\Delta 8$ pathway consisting of the Isochrysis galbana Δ 9-elongase, Euglena gracilis Δ 8-desaturase and Mortierella alpina Δ 5-desaturase with constitutive 35S promoters. This study demonstrated that production of LC-PUFA in land plants was possible, albeit in leaf tissue. Shortly after, Abbadi et al. (2004) published the production of LC-PUFA in the seeds of tobacco and linseed by the $\Delta 6$ pathway. In this pathway, SDA (11.4%) and GLA (16.8%) were produced in linseed, although these fatty acids were not effectively Δ 6-elongated with only 0.8 % EPA and 1.0 % ARA being produced. These studies were important proofs of concept that the production of ω 3 LC-PUFA in land plants was possible.

ω6 vs. ω3 biosynthesis

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These two 2004 publications also showed the complication of parallel ω 6 and ω 3 pathways in which an individual gene generally functions in both branches (Fig. 2). Using the $\Delta 6$ pathway as an example, the $\Delta 6$ -desaturase is the first committed step of both ω 6 and ω 3 LC-PUFA production and can desaturate both LA and ALA. The Δ 6-desaturation of LA to produce GLA, however, effectively reduces the production of ALA since LA is also the substrate for Δ 15-desaturase activity, which produces ALA. One seemingly obvious solution is to increase the production of ALA by introducing more efficient Δ 15-desaturase activity, but the success of this approach can be limited by the fact that competition for LA remains between the Δ 15- and Δ 6-desaturases. This can be overcome by introducing a more broadly functioning ω 3-desaturase that not only converts LA to ALA by $\Delta 15$ -desaturation but can also convert the $\omega 6$ fatty acids GLA, DGLA and ARA to their ω 3 counterparts. Another approach is to reduce or remove the competition for LA experienced by the Δ 15-desaturase by using a $\Delta 6$ -desaturase that favours ALA as a substrate. A patent describing LC-PUFA synthesis in soybean somatic embryos (Kinney et al. 2004) contained an example of the first approach of including an ω 3-desaturase gene that could convert ω 6 products to their ω 3 counterparts. In this work, a Δ 6 pathway coupled to a strong $\Delta 17$ -desaturase resulted in the production of nearly 20 % EPA with very little ARA accumulation due to the ω 3-desaturase activity of the Δ 17-desaturase. Wu *et al.* (2005) also included a Δ 17-desaturase in their Δ 6 pathway and this, combined with a lysophosphatidyl acyltransferase (LPAT) which was included as a way of increasing incorporation of novel fatty acids, resulted in the accumulation of up to 15 % EPA in *Brassica juncea* seeds. Similar results were obtained by Cheng *et al.* (2010) who engineered *Brassica carinata* with a Δ 6 pathway including an ω 3-desaturase and accumulated in excess of 20 % EPA in seed.

The alternative method of reducing $\omega 6$ products. namely to use a $\Delta 6$ -desaturase with preference for the ω3 substrate ALA, has also been demonstrated. Several examples have been reported of genes encoding such Δ6-desaturases (Sayanova et al. 2003; García-Maroto et al. 2006; Hoffmann et al. 2008; Petrie et al. 2010a), although the strength of the preference varies. For example, the primula $\Delta 6$ -desaturase isolated by Sayanova et al. (2003) essentially has ω 3 specificity with high activity on ALA but very low ω6 activity (Ruiz-López et al. 2009). The ω 3 preference observed by Hoffmann et al. (2008) and Petrie et al. (2010a) in their $\Delta 6$ -desaturases was not as strong as that seen in the primula enzyme, although the $\Delta 6$ -desaturases were from microalgal sources and seemingly able to access acyl-CoA substrate pools, as will be discussed below. Other microalgal acyl-CoA desaturases such as the Ostreococcus tauri $\Delta 6$ -desaturase (Domergue et al. 2005) did not have ω 3 preference.

Several Δ 9-elongases have now been isolated (Qi *et al.* 2002; Damude *et al.* 2008), although none has a strong ω 3 preference. Use of these genes in high-level ω 3 LC-PUFA production would therefore likely require the addition of an ω 3-desaturase. This is exemplified by the isolation and transgenic plant expression of the entire Δ 8 DHA pathway from a single algal species, *Pavlova salina* (Petrie *et al.* 2010b). In this study, a high proportion of the newly produced LC-PUFA were ω 6 despite these being almost absent in the native algal fatty acid profile, in which large amounts of ω 3 LC-PUFA are present (Zhou *et al.* 2007). Since the *P. salina* Δ 9-elongase did not have ω 3 preference, it is likely that this alga either has a strong ω 3-desaturase or a method of selectively accumulating ω 3 LC-PUFA.

Acyl-CoA pathways

Alternative approaches to building $\omega 3$ LC-PUFA pathways have been taken with several groups focusing on the construction of acyl-CoA pathways to reduce the 'pool shuffling' that can occur in transgenic LC-PUFA pathways. The LC-PUFA elongation condensing reactions occur using acyl-CoA thioester substrates (the 'acyl-CoA pool'). In contrast, the majority of desaturases now isolated are lipid-linked desaturases that generally use a phosphatidylcholine substrate (the 'acyl-PC pool'). A desaturated fatty acid must therefore be transferred between the acyl-PC and acyl-CoA pools by acyltransferase enzymes before a subsequent elongation can occur. The synthesis and accumulation of triacylalycerol in seeds are likely more complex than previously thought (Bates et al. 2009) and the requirement for acyltransfer between pathway steps presents opportunities for the novel fatty acid to be lost into pools which are, relatively, metabolically inert. This leads to a build-up of intermediate fatty acids along the biosynthetic pathway, with the eventual result being that the terminal product (e.g. DHA) does not accumulate to adequate levels. One solution to this challenge is the addition of acyltransferase enzymes which are capable of rapidly converting the newly elongated or newly desaturated fatty acids to the appropriate pool (e.g. the approach taken by Wu et al. (2005) described above in which an LPAT was included in the pathway). Unfortunately, this approach requires the addition of at least one extra gene to an already sizeable transgenic pathway. Fortunately, an alternative solution exists in the form of acyl-CoA desaturases.

The majority of desaturases are lipid linked, although there are published examples of enzymes which are able to function on acyl-CoA thioesters (Kajikawa et al. 2004; Domergue et al. 2005; Hoffmann et al. 2008; Petrie et al. 2010a) and several of these have been used in DHA pathways. Using such acyl-CoA desaturases means that elongation and desaturation can occur in the same metabolic pool, and thus avoid the efficiency and accumulation losses associated with the 'pool shuffling' described above. Acyl-CoA LC-PUFA pathways can often be characterized by high elongation efficiency. Petrie et al. (2010a), for instance, described a large increase in $\Delta 6$ -elongation efficiency when the Δ 6-elongase substrate, SDA, was produced by an acyl-CoA Δ 6-desaturase when compared with SDA produced by an acyl-PC Δ 6-desaturase. Similarly, Hoffmann et al. (2008) were able to construct an acyl-CoA pathway with efficient elongation, although the amounts of LC-PUFA produced were very low.

Improving $\Delta 5$ -elongation

A final area of recent focus has been the Δ 5-elongation step. Although Wu *et al.* (2005) and Cheng *et al.* (2010) demonstrated significant levels of EPA production (15 and 25 %, respectively), there have, to date, been no reports of high levels of DHA production in transgenic plants. This is mostly due to low Δ 5-elongation efficiency and it has been suggested that the inclusion of enzymes with suitable acyl-transfer function (such as the acyltransferases described above) may be required to achieve adequate efficiency. Indeed, the authors of this review have previously had similar difficulty in obtaining adequate $\Delta 5$ -elongation efficiency (Robert et al. 2005), although the recent isolation of a highly efficient enzyme from the microalga Pyramimonas cordata is encouraging (Petrie et al. 2009). This enzyme functions extremely well in plants (Fig. 3) and may be an important component of a transgenic DHA biosynthesis pathway for oilseed crops. Figure 3 demonstrates the importance of careful enzyme selection when constructing transgenic pathways, with a clear increase in EPA elongation observed with the *P. cordata* Δ 5-elongase. Furthermore, Fig. 3 also demonstrates the effectiveness of using a $\Delta 6$ -desaturase with $\omega 3$ preference (i.e. extremely low $\omega 6$ fatty acid levels without using an ω 3-desaturase) and an acyl-CoA-like nature (i.e. the subsequent $\Delta 6$ -elongation is extremely efficient). The high conversion efficiency of the *P. salina* Δ 5-desaturase used in this pathway, both in terms of desaturation and provision of the $\Delta 5$ -desaturated products to the Δ 5-elongase, indicates that this enzyme may also be able to access acyl-CoA substrates although this is not yet biochemically proven. If so, this demonstrates the importance of using a pathway in which most of the desaturases are acyl-CoA-dependent for DHA synthesis. It is also worth noting that all transgenes in this pathway are from algal sources.

Long-chain polyunsaturated fatty acid production and accumulation in oilseed crops

Figure 4 describes results from a rapid transient expression system in a model plant, Nicotiana benthamiana (Wood et al. 2009; Petrie et al. 2010c). This transient expression of a DHA pathway alongside the A. thaliana DGAT1 yielded an impressive level of EPA and DHA accumulation in the leaf triglycerides. Such an oil composition, if replicated in oilseeds, would yield oils whose fatty acid profile will compare very favourably to that of a fish. Other groups rely extensively on A. thaliana, cultured soybean embryos or similar, relatively rapid, systems to test hypotheses and constructs before transforming crop species. The transition from an interesting result in a model system to a good result in an oilseed crop species is not necessarily trivial. Whilst this transition is broadly applicable to most crop metabolic engineering projects, the introduction of LC-PUFA to crops presents some specific problems. LC-PUFA, including DHA, are unusual fatty acids in a land plant context and may



Fig. 4 Docosahexaenoic acid production in plant leaf. Gas chromatography (GC) traces of fatty acid methyl esters (FAME) produced from triacylglycerol in *N. benthamiana* leaf tissue transiently expressing single-gene Cauliflower mosaic virus 35S promoter-driven binary constructs containing the P19 gene silencing suppressor, *Micromonas pusilla* $\Delta 6$ -desaturase, *P. cordata* $\Delta 6$ -elongase, *P. salina* $\Delta 5$ -desaturase, *P. cordata* $\Delta 5$ -elongase (A) or *P. salina* $\Delta 5$ -elongase (B), and the *P. salina* $\Delta 4$ -desaturase. The accumulation of EPA in the sample using the *P. salina* $\Delta 5$ -elongase demonstrates the manner in which metabolic pathways can be tailored by careful selection of a single gene in the pathway.

not necessarily be metabolized by germinating seed of oilseed crop species. The physiological impact of this would likely vary, depending on both the amount of oil present and available in the seed during germination and the proportion of LC-PUFA accumulated in the seed oil. High-oil species such as rapeseed or flaxseed naturally have a greater energy store than lower oil crops which can then be accessed during germination since these species have been selectively bred to produce oil in excess of germination requirements. The effective removal of a fraction of these 'surplus' triacylglycerols would likely have a relatively small effect on germination and seedling vigour when compared with lower oil crop species such as soybean. Similarly, it could reasonably be expected that the production of high levels of LC-PUFA in lower oil crop species could dramatically affect germination rates and seedling vigour.

It will also be interesting to observe the positional distribution of LC-PUFA in the triacylglycerols constituting high LC-PUFA crop oil, especially since studies have indicated that LC-PUFA located on the *sn*-2 position are

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more stable under storage and also more bioavailable to human infants, and possibly adults, than those on the *sn*-1,3 positions (Berry 2009).

Acceptance of crop-based ω3 LC-PUFA

As with many projects in the broader field of land plant metabolic engineering, the scientific and technical hurdles around the production of LC-PUFA are only part of the challenge. The real-world delivery of a crop-based source of ω 3 LC-PUFA will inevitably require acceptance of the technology by the broader public. A genetically modified ω 3 LC-PUFA crop will have tremendous environmental sustainability credentials due to the role it will play in relieving pressure on global fish stocks. Furthermore, such a crop will have direct health benefits for the consumers and, given the increasing awareness of the importance of ω 3 LC-PUFA in the general public, these factors are likely to play an important part in increasing consumer acceptance.

Some regions have a high level of aversion to transgenic technologies due to perceived risks

(Hansen et al. 2003; Food and Agriculture Organization 2004: Cox et al. 2008a, b), although this does not appear to be the case in other countries. One study, for example, has found that 99 % of consumers in the USA were more concerned with hygiene, sanitation and food-borne illnesses than with biotechnology (IFIC 2005). Regardless, it is useful to review consumers' attitudes to transgenic ω 3 LC-PUFA in particular: Cox et al. (2008a, b, 2011) have investigated both US and Australian consumer attitudes toward ω 3 LC-PUFA and also ω 3 LC-PUFA produced from transgenic oilseeds. They found that whilst a minority had concerns about the use of transgenic technology, the majority of study participants, generally, were either ambivalent or positive about the use of transgenic ω 3 LC-PUFA oilseeds. This agrees with earlier data which also suggested that consumers are likely to accept transgenic technology where there is a direct benefit to the consumer (Hossain et al. 2003; Hossain and Onyango 2004). Interestingly, consumers tended to prefer a transgenic ω3 LC-PUFA oilseed as the preferred source of oil to be incorporated into bread, milk and supplements above oils sourced from fish and algae (Cox et al. 2011).

Conclusions and forward look

Algal genes have contributed significantly to the LC-PUFA metabolic engineering efforts described in this short review. Similarly, research towards the in planta production of carotenoids, and in particular astaxanthin, continues to require the use of genes from algal species that naturally synthesize these compounds (see Misawa (2009) for a review). In a broader context, algal model species such as Chlamvdomonas reinhardtii are now being used to better understand metabolism and catabolism in plants and plant-like species (Wijffels and Barbosa 2010). Recent focus on finding or engineering sustainable sources of biofuels has seen increased use of algal models to investigate mechanisms of lipid accumulation and starch conversion. Wang et al. (2009) and Moellering and Benning (2010) have described the formation of lipid droplets in C. reinhardtii after nitrogen starvation, with Miller et al. (2010) then describing changes in transcript abundance in these systems. It is likely that findings such as these will have relevance in land plants due to the high degree of similarity between the organisms (Hicks et al. 2001). There has been considerable effort under way by the US Department of Energy-funded Joint Genome Institute to sequence the genomes of a number of algal species. This data set is publically available at http://genome.jgi-psf.org/. Detailed analyses of algal genomes not only provide important information

for research into functional genomics, but also increase our understanding of the physiology, environmental adaptation mechanisms, morphogenesis and evolution of organisms (especially the origin of photosynthetic organisms) and their evolution into land plants.

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Conflicts of interest statement

None declared.

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