Camelina, a Swiss knife for plant lipid biotechnology

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Abstract – Camelina has emerged in the last decade as a multipurpose crop plant particularly suitable for engineering new lipids for diverse uses, including feed, biofuel and green chemistry. The rebirth of this ancient crop was based on several intrinsic favorable characteristics: robust agronomic qualities, attractive oil profile, genetic proximity with the model plant Arabidopsis, ease of genetic transformation by floral dip. The need to increase both the production and diversity of plant oils, while improving the sustainability of agricultural systems, has been the driving forces behind the ever-increasing investment in camelina research. Worldwide interest in engineering camelina has led to the development of a remarkable pipeline that allows the rapid production and phenotyping of new lines; it includes specific tools, such as databases, collections of natural accessions, methods of genetic transformation and lipid analysis. Implementation of numerous metabolic pathways in camelina for the production of novel lipids has highlighted the potential as well as the versatility of this new "old" oilseed crop that is well on the way to becoming an ideal plant chassis for lipid synthetic biology.

Keywords: Lipid metabolism / oilseed / omega-3 / biofuels

1 Introduction

Over the past decade, worldwide production and distribution of plant oilseeds and their products have undergone remarkable expansion; the area devoted to growing oilseeds has expanded by 19%, while production has increased by 34% since 2005 (source USDA, 2016). The plant oil market is driven by the demand for higher yield and more sustainable production of the main crops (palm, soybean, rapeseed and sunflower), but also by the need for increased crop diversification. This increased demand will require oilseed crops to be adapted to more diversified markets, in particular to provide sources of novel feedstock sources for the petroleum-based chemical industry. However, traditional oilseed crops suffer from several disadvantages that have limited their use in diversifying oil production. Each oilseed crop has relatively low genetic diversity, and the length of plant growth cycles impedes the potential to create new varieties by conventional breeding. Furthermore, for many oilseed crops, genetic engineering is a
difficult and lengthy process. Finally, potential problems must be faced concerning how large-scale cultivation of oilseed crops for industrial purposes, such as the production of novel lipids, will coexist with the continued cultivation of the same oilseed crop for human consumption. The last decade has seen the emergence of camelina (*Camelina sativa* (L.) Crantz) as an alternative species for diversifying oilseed production. Combining camelina’s very attractive agronomic traits with its unprecedented ease for genetic engineering, makes it an ideal plant chassis for biotechnology applications, in particular synthetic biology strategies (Napier et al., 2014; Vollmann and Eynck, 2015; Bansal and Durrett, 2016; Haslam et al., 2016). Also, since it remains a very minor crop in terms of human oil consumption, organizing co-existence should be easier than with the major oilseed food crops, such as rapeseed, soybean, or sunflower.

2 Camelina, the rebirth of an old crop

Camelina, also known as false flax, is an oilseed crop in the *Brassicaceae* family, and is closely related to well known wild species, including the intensively studied model species *Arabidopsis thaliana* and the widespread weed *Capsella bursapastoris*, shepherd’s purse (Al-Shelbazi et al., 2006). Under favorable conditions, camelina crops yield >2 t/ha, but lower yields (1.2 to 2.2 t/ha) are observed under conditions of limiting nutrients or water (Crowley and Frohlich, 1998; Gehringer et al., 2006). The history of camelina as a crop is quite unusual, with an ancient history interrupted by a lengthy period of neglect, followed by a renaissance of interest over the past decade. Camelina is thought to have been first domesticated in the steppes of southeastern Europe or southwestern Asia, and the earliest archeological traces of camelina cultivation date to the Neolithic (Toulemonde, 2010). Within the presumed region of domestication, Ukraine and adjacent parts of Russia are still a major center of camelina genetic diversity (Ghamkar et al., 2010). Over the millennia following its domestication, camelina was widely grown in northern Europe, but starting at the end of the 19th century it was gradually replaced by higher yielding crops such as rapeseed. Nonetheless, during the 20th century, camelina continued to be cultivated on a small scale, essentially for production of oil for human consumption. Because of this century of neglect, camelina has undergone relatively little improvement by plant breeders, and thus the currently grown cultivars can be considered to be quite primitive, and should benefit greatly from the combined efforts of plant breeding and advanced techniques of modern biotechnology as described below.

Over the past decade, there has been a remarkable increase in scientific interest in camelina, as shown by the increase in the numbers of publications with “camelina” in the title (Fig. 1), but this increase was driven by several quite different potential end uses. The high levels of omega-3 lipids in camelina oil are perceived as beneficial for human health (Zubr, 1997; Eidhinh et al., 2003; Abramović and Abram, 2005) and the high levels of tocopherols, including vitamin E, make camelina oil more stable to oxidation than other high omega-3 oils such as linseed oil (Abramović et al., 2007; Hrastar et al., 2009). A further attractive feature is that the residual meal after pressing can be used for animal feed (Peiretti and Meineri, 2007; Pilgeram et al., 2007; Aziza et al., 2010; Bell et al., 2010). In addition to current food uses, there are several micro-niches for camelina oil in cosmetics, soaps, lubricants, etc. (Bonjean and Le Goffic, 1999; Pilgeram et al., 2007). Nevertheless, the intense recent activity in the USA and Canada regarding camelina has been driven primarily by camelina oil’s potential as a low input source of biofuel (Fröhlich and Rice, 2005), with a particularly favorable greenhouse-gas lifecycle assessment (Shomnad et al., 2010; Chen et al., 2015; Keshavarz-Afsah et al., 2015). As shown in Figure 1, this led to a sharp increase in the areas planted in camelina from 2005 to 2007 in Montana, but this was followed by a decline to levels even below the 2005 value, due to unexpectedly poor yields and the inability to compete with petroleum-based fuels (McLaren and Sun, 2015). The current situation of low petroleum prices suggests that growing camelina for biofuel is unlikely to be economically viable in the near future, but that other uses, and particularly redesigning camelina oils to produce a variety of products including novel industrial feedstocks is a more realistic objective, and this will be the primary focus of this review.

3 Camelina is more than its oil

The increased interest in camelina oil occurred in parallel with increased interest in the crop because of its fundamental agronomic characteristics. Often cited as well adapted to growing on marginal soils, in fact camelina is remarkable adapted to a wide range of temperate climatic conditions, growing well in the semi-arid regions of western North America (Guy et al., 2014) and also in the distinctly humid environment of Ireland (Crowley and Fröhlich, 1998). It has been described as a low-input crop, requiring little or no fertilization, and since it appears at present to be resistant to many pests and pathogens that affect other Brassicaceae neither insecticides nor fungicides are routinely used on camelina
(Seguin-Swartz et al.; Canadian Food Inspection Agency (CFIA), 2014; Vollmann and Eynck, 2015). Furthermore, the camelina life cycle is quite short; if planted in the spring, it can be harvested approximately three months later. Although spring-sown camelina is more widely grown, cultivars adapted to sowing in the fall to be harvested in the spring have also been developed (Bonjean and Le Goffic, 1999). Camelina’s short lifecycle opens particularly interesting possibilities for double cropping. For instance, in the northern US corn belt, winter camelina harvested in the spring can be followed immediately by soybean (Gesch et al., 2014), and winter wheat can be followed by spring camelina in the more arid Northern Great Plains. For northern Europe a fall-sown cereal crop could be followed by camelina sown in the spring (Groeneveld and Klein, 2014). These potential double-cropping systems could be followed by camelina sown in the spring (Groeneveld et al., 2013; Martin et al., 2015). Since it was shown that camelina can be genetically transformed with ease by floral dip, using protocols similar to those used for arabidopsis (Lu and Kang, 2008), camelina has become an essential proving ground for seed oil modification (Fig. 2). A remarkably simple pipeline for testing oil modification strategies includes the following steps: (1) gene discovery; (2) construction of transgenes in a vector with a fluorescent protein marker gene (DsRed or GFP); (3) transformation by floral dip or vacuum infiltration; (4) screening T1 seeds for DsRed or GFP fluorescence, screening for changes in lipid profile and/or yield in T1 or T2 seeds, using a newly developed micropress. The overall process from transgene conception to preliminary screening of seed lipids in T2 seeds can be carried out in less than a year. Final validation of the introduced trait must, however, be carried out in the field.

An important issue in the choice of camelina as a model crop for genetic engineering is its ability to cross with wild relatives. Some understanding of the potential for gene flow from genetically modified (GM) crops to wild relatives is necessary for authorization for GM crop field releases, and the ability to use wild relatives as a source of potentially valuable genes is obviously of great interest for classic plant breeding. For both reasons, the resurgence of interest in camelina has included re-examination of its ability to cross with wild relatives. Among the wild Camelina species, only C. microcarpa and C. alyssum are widespread, and with both, fertile hybrids with cultivated camelina can be obtained (Seguin-Swartz et al., 2013). These two species thus represent possible sources of genes of interest for future improvement of cultivated camelina. Since both are only occasionally observed in agricultural contexts, preventing pollen-mediated gene flow from GM camelina to C. microcarpa and C. alyssum in field trials should be easy to assure, as described by the Canadian Food Inspection Agency (CFIA 2012). In contrast to the relative rarity of the wild Camelina species, both Arabidopsis thaliana and Capsella bursa-pastoris are extremely abundant in agricultural environments, and occur in the margins of camelina fields (Tepfer, unpublished). Although both species flower primarily much earlier than camelina, they continue to flower throughout the summer, and are visited by the same potential pollinators (honeybees, bumblebees, syrphid flies (Groeneveld and Klein, 2014). In order to evaluate the potential for gene flow from camelina to these two wild relatives, crosses were made in the greenhouse (Julié-Galau et al., 2014; Martin et al., 2015). No F1 progeny seeds could be obtained with Arabidopsis, and with Capsella, very few F1 seeds were obtained, and the resulting F1 plants proved to be entirely male- and female-sterile (Julié-Galau et al., 2014; Martin et al., 2015). These results suggest that the likelihood of introgression of camelina transgenes in populations of Arabidopsis thaliana and Capsella bursa-pastoris is extremely low indeed.

5 Improving Camelina oil yield

Although, as described above, camelina has many attractive agronomic features, its relatively low oil yield compared
to rapeseed is a real limitation to its agroindustrial use. Improving camelina oil yield is thus a priority for development of the crop for any large-scale uses.

One strategy for increasing yield would be to improve the efficiency of photosynthetic carbon fixation. CO$_2$ fixation by Rubisco is limited by its oxygenase activity, initiating a photorespiration cycle leading to glycolate synthesis. Dalal et al. (2015) showed that expression in camelina of three *E. coli* enzymes that constitute a photorespiratory bypass led to a marked increase in vegetative biomass and also increased seed yield by 57 to 73%. Although oil yield per seed was not changed, expression of the photorespiratory bypass should be reflected in important gains in yield/ha in the field (Dalal et al., 2015). Similarly, the expression of arabidopsis purple acid phosphatase AtPAP2 modified carbon assimilation and distribution from photosynthesis and led to higher seed yields (Zhang et al., 2012). Increased photosynthesis efficiency associated with an increased seed mass and oil yield per plant was also achieved through the overexpression of the group III heterotrimeric Gy-protein AGG3 (Roy Choudhury et al., 2014).

A second strategy to improve oil yield is to globally enhance the levels of metabolic enzymes involved in triacylglycerol (TAG) synthesis by overexpression of specific transcription factors. WRINKLED1 (WR11) was shown to be an essential transcription factor for TAG synthesis in many species, and its overexpression led to 10–30% increase in seed oil content in arabidopsis, rapeseed and even maize (Cernac and Benning, 2004; Baud et al., 2007; Liu et al., 2010; Pouvreau et al., 2011; Wu et al., 2014). Overexpression of arabidopsis AtWR11 in camelina seeds led to an increase in seed weight and seed size, and as expected, to 8–31% increase in seed oil content (An and Suh, 2015). Although camelina already has three copies of endogenous *WRI1*, it is remarkable that significant yield gain could be achieved by overexpression of an orthologous gene.

A third strategy for improving seed oil content is to specifically target metabolic bottlenecks in TAG biosynthesis. Fatty acids produced by plastids are shuffled between phospholipid and TAG pools (Chapman and Ohlrogge, 2012). While phospholipids like phosphatidylcholine (PC) are essential for fatty acid desaturation, they represent an important pool of acyl chains not available for TAG production. Phospholipases A (PLA) are able to hydrolyse PC to lysophosphatidylcholine, releasing a free acyl chain available for TAG synthesis. Constitutive overexpression of several *PLA* genes in arabidopsis and camelina led to a significant increase in seed oil content, but at the expense of important developmental alterations (Li et al., 2013, 2015). Similar effects on seed oil content, albeit more modest and variable, were obtained by seed-specific overexpression of arabidopsis *PLAIIIΔ* but without impacting overall plant growth, stressing the importance of targeting the desired metabolic modifications uniquely to the seed during
the maturation phase, while avoiding expression elsewhere and at other phases of the plant growth cycle (Li et al., 2015).

Although this has not yet been described, combining strategies that will increase seed yield with those that increase the proportion of oil in the seeds should make a major contribution to enhancing the economic viability of growing camelina.

6 Improving camelina oil composition for food and feed

The high levels of alpha-linolenic acid (C18:3, ALA) in camelina oil provide an ideal plant chassis for the synthesis of omega-3 long chain polyunsaturated fatty acids (LC-PUFAs) like eicosapentaenoic acid (C20:5, EPA) or docosahexaenoic acid (C22:6, DHA). Omega-3 LC-PUFAs are central dietary recommendations for fetal development and adult cardiovascular and cognitive health. The main dietary source of LC-PUFAs is oil-rich fish, such as Atlantic salmon. Since fish do not synthesize LC-PUFAs efficiently, farmed fish are fed with fish meals and fish oil enriched in LC-PUFA extracted from wild-caught fish. A more sustainable solution would be to replace fish oil by vegetable oil enriched in omega-3 LC-PUFA. Land plants do not synthesize polyunsaturated fatty acids longer than 18 carbons and with more than 3 double bonds. Transformation of ALA (C18:3) into EPA (C20:5) and DHA (C22:6) requires successive fatty acyl desaturation and elongation steps. The efficiency of this metabolic conversion is impeded by the substrate dichotomy paradigm. Indeed, fatty acid elongation in higher plants relies on the acyl-CoA pool, while desaturation takes place principally on phosphatidylcholine, implying that successful synthesis of LC-PUFA requires continuous shuffling of acyl chains between the two acyl pools, acyl-CoA and phospholipids. Substrate dichotomy was thus proposed to be one of the main metabolic bottlenecks in LC-PUFA synthesis (Domergue et al., 2005a; Napier, 2007). A major breakthrough was the discovery that the acyl-CoA dependent Δ6 desaturase of the microalga *Otracococcus tauri* could convert ALA to stearidonic acid (C18:4, SDA) (Domergue et al., 2005b; Sayanova et al., 2012). The expression of the acyl-CoA dependent Δ6 desaturase in combination with Δ6 elongase and C20 Δ5 desaturase increased the accumulation of C20 intermediates of LC-PUFA biosynthesis in yeast and arabidopsis, demonstrating the potential for reducing substrate dichotomy (Sayanova et al., 2012). Endogenous levels of the LC-PUFA substrate, ALA, has a clear effect on Δ6 desaturase activity, since camelina expressing Δ6 desaturase accumulated three times more SDA (C18:4) than arabidopsis, which synthesizes lower levels of ALA (Sayanova et al., 2012). The complete expression of five enzymes of the LC-PUFA pathway including Δ12 desaturase, Δ15 desaturase, Δ9 elongase, Δ8 desaturase, Δ5 desaturase, for respectively the synthesis of linoleic acid (C18:2), ALA, eicosatrienoic acid (C20:3), eicosatetraenoic acid (ETA) and EPA, allowed efficient EPA synthesis in arabidopsis and camelina (Ruiz-Lopez et al., 2015). Camelina again proved to be a better host, with about 8% EPA accumulated in seeds compared to 3.6% for arabidopsis. An iterative approach of LC-PUFA enzyme combinations allowed respectively a four- and a ten-fold improvement in EPA and DHA accumulation in arabidopsis seeds (Ruiz-Lopez et al., 2013). Finally, the best constructs were validated in camelina, yielding LC-PUFA levels comparable to those found in fish, with 31% EPA and 14% DHA+12% EPA for the best EPA and DHA lines (Ruiz-Lopez et al., 2014). Similar results were obtained by optimizing the expression of the Δ6 desaturase in multiple gene stacking combinations (Petrie et al., 2014). The high potential of these lines to accumulate LC-PUFA in oil was confirmed in field trials (Usher, 2015). Three lessons can be learned from this success story. It is necessary to: (i) identify metabolic bottlenecks in the metabolic pathway (substrate dichotomy) (ii) systematically test all the possible enzyme combinations and (iii) choose an optimized plant host with the highest substrate availability (ALA). While arabidopsis and yeast have been valuable tools for identifying the appropriate enzymes, camelina was essential, not only for its oil profile, but also the ease of its genetic transformation, which facilitated the screening of a large number of transformants. Furthermore, EPA-enriched camelina oil was shown to be a suitable substitute for fish oil in aquaculture (Betancor et al., 2015a,b). These results suggest that LC-PUFA-enriched camelina oil could also represent an interesting alternative source for LC-PUFA in human nutrition. This is reinforced by results obtained using mice fed an EPA-enriched camelina oil diet, which was found to be as efficient as fish oil for providing EPA, thus opening the way to human feeding trials (Tejera et al., 2016).

Nervonic acid (C24:1n15) is a natural component of human breast milk fat, and is used in infant formula supplementation, but also in treatment of several neurological diseases, such as multiple sclerosis, adrenoleukodystrophy and Zellweger syndrome (Huai et al., 2015). This fatty acid is found in oil from several *Brassicaceae*, such as *Lunaria annua*, but the production of this species is insufficient to meet the demand. Production of nervonic acid in camelina was developed by the overexpression of *L. annua* keto acyl synthase (KCS), the first enzyme of the cyclic elongation reaction that provides fatty acid specificity of the elongase complex. To improve fatty acid elongation efficiency in camelina seeds, combinations of two elongase enzymes from arabidopsis were associated with *L. annua* keto acyl synthase (KCS), the first enzyme of the cyclic elongation reaction that provides fatty acid specificity of the elongase complex. To improve fatty acid elongation efficiency in camelina seeds, combinations of two elongase enzymes from arabidopsis were associated with LaKCS (Huai et al., 2015). Expression of LaKCS led to significant accumulation of nervonic acid in camelina seeds (up to 12% of lipids), but expression of the additional elongase genes did not improve the yield. Even if LaKCS expression allows nervonic acid synthesis, strategies could be implemented to improve its accumulation, such as: combine all four enzymes of the elongase complex rather than just two, use the elongase enzymes from camelina or *L. annua* directly, reduce the expression of endogenous KCS to minimize substrate competition by the different elongase complexes.

7 Developing new camelina oil profiles for industry

Due to its specific profile, camelina oil is already used in industrial applications. Highly unsaturated fatty acids are for instance more prone to epoxidation, which is of interest for adhesive properties (Kim et al., 2015a). Epoxidation could be followed by partial acrylation and dihydroxylation, leading to acrylic polyols, which are the source of numerous polymers...
Camelina oil metabolism could also be modified to enhance the accumulation of lipids of industrial value. Jet fuels require medium-chain fatty acid (MCFA) of 8 to 14 carbon length. Camelina plastids elongate acyl-ACP by fatty acid synthase until C16 and C18 carbon length, and the resulting acyl CoAs are then released in the cytosol by acyl thioesterases. C16:0-ACP is hydrolyzed by FatB thioesterases, while FatA is more specific to C18:0- and C18:1-ACP. Cuphea species that accumulate MCFA in their TAG have specific FatB genes (Kim et al., 2015). Expression of different Cuphea FatB genes associated with different MCFA profiles (C8, C10, C16) led to significant MCFA accumulation in camelina seeds. This effect was enhanced by the coexpression of coconut lysophosphatidic acid acyltransferase (LPAT) and the inhibition of the endogenous camelina plastidial beta-ketoacyl-ACP synthase CsKASII (Kim et al., 2015b).

A similar strategy was used to enrich camelina oil in omega-7 fatty acids, like palmitoleic acid (C16:1Δ9) and cis-vaccenic acid (C18:1Δ6). Camelina as an alternative producer of non-TAG high value products

Wax esters are neutral lipids that have higher energy density compared to TAGs, and their refinement does not produce glycerol as a side product. They could thus represent a valuable source of biodiesel. They are also used as lubricants, since they have low melting points, an excellent resistance to oxidation, and yet are biodegradable. The desert shrub jojoba is a natural source of wax esters, but since it is not adapted to high yield cultivation, particularly in temperate regions, a more efficient and sustainable approach is required. Only two enzymes are necessary for wax ester synthesis: a fatty acyl-CoA reductase (FAR) and a wax ester synthase (WS). The possibility to accumulate wax esters in seeds was validated in arbidopsis with different variants of FAR and WS from mouse or the bacterium Marinobacter aquaeolei (Lardizabal et al., 2000; Heilmann et al., 2012). A total of seven different novel enzyme combinations were tested first in arbidopsis, after which the best three were introduced into camelina (Iven et al., 2016). Similar types of wax esters were produced in arbidopsis and camelina, but the yield in camelina was half that in arbidopsis. Arbidopsis could accumulate 89–108 ng/seed (representing 43–59% neutral lipids) compared to 33–47 ng/seed (15–21%) for camelina. Since wax ester synthesis uses acyl-CoA as substrates, and thus competes directly with TAG synthesis, a possible improvement would be to favor substrate channelling toward wax ester biosynthesis instead of TAG. Recently, a relative 30% content in wax ester was achieved in camelina by the combined overexpression of jojoba FAR and WS with L. annua FAE1 and associated with FAD2 inhibition.

Acetyl-TAGs are unusual triacylglycerols in which the sn-3 position has an acetyl group instead of a fatty acyl group. This modification, which reduces viscosity and lowers the oil melting point compared to conventional TAG, is sought for lubricants, food emulsifiers and plasticizers. The main source of acetyl-TAG is the seeds of Euonymus alatus (Burnishing Bush) thanks to a specific acyltransferase (EaDAct) that transfers the acetyl group of acetyl-CoA to the sn-3 position of DAG (Durrett et al., 2010). Overexpression of EaDAct in camelina led to an average of 50% acetyl-TAG in seeds, a value that could be increased to 80% when combined with down-regulation of DAGT1 by RNAi (Liu et al., 2015a). The effect of EaDAct expression, combined or not with DGAT1 RNAi, was significantly higher in camelina transgenic lines compared to arbidopsis or soybean, confirming the particular value of camelina in oil engineering strategies. Interestingly, the high levels of acetyl-TAG accumulation in seeds did not impair seed yield, nor did it modify seed germination in several field studies (Liu et al., 2015a, b). As expected, camelina oil enriched in acetyl-TAG showed lower viscosity, a higher crystallization temperature, and higher caloric content, providing a direct alternative for biodegradable lubricants, hydraulic fluids and transformer oils. The fact that camelina acetyl-TAGs are also rich in oleic acid, and are thus less susceptible to oxidation, could open new markets in the food industry, such as for water retention on food surfaces, emulsifiers, foam stabilizers and packaging plasticizers.

8 Camelina as an alternative producer of non-TAG high value products

Camelina oil properties could also be profoundly changed by the accumulation of new lipids like acetyl-TAG. Recent work demonstrated that alkyd resins used in the coating and paint industry could also be synthesized from camelina oil and polyglycerols (Nosal et al., 2015).
Nevertheless, camelina yields were lower than those of *Crambe abyssinica* transformed with the same constructs, perhaps because that the latter naturally accumulates high levels of very long chain fatty acids (Zhu et al., 2016).

The high oil content of camelina seeds could also favor the accumulation of bioactive compounds such as terpenes, which are components of essential oils used in food additives, cosmetics, drugs, rubber and lubricants (Degenhardt et al., 2009). Terpenes also increase oil caloric value, which is an important parameter for biofuel applications, in particular for kerosene. As a proof of concept, the synthesis of the monoterpenes (4S)-limonene and the sesquiterpene (+)-delta-cadinene was investigated in camelina seed. Interestingly, these two terpenes are produced via two different pathways: the cytosolic mevalonate pathway and the plastidial 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway, respectively. Combinatorial association of the different enzymes expressed either in the cytosol or in the plastids allowed direct comparison of the most efficient pathways (Augustin et al., 2015). (4S)-limonene could only be accumulated in camelina seed via the expression of plastid-localized enzymes, while (+)-delta-cadinene was accumulated in camelina seeds expressing enzymes either in the cytosol or plastids. Interestingly, the ectopic localization of (+)-delta-cadinene biosynthetic enzymes in plastids was at least five times more efficient than that of the cytosol-localized enzymes. Globally, for both terpenes, the levels obtained were around 5–7 mg/g seed and about 22–29 mg/ml oil. The presence of terpenes in camelina oil increased its caloric value, but the ratio terpene(TAG) was still too low for biofuel applications. The use of strong seed-specific promoters could improve terpene production in camelina seeds (Borghi and Xie, 2015). Nonetheless, the minimal loss of these volatile molecules during seed development, as well as their protection from possible degradation, makes camelina seed oil a potentially interesting alternative terpene source for cosmetics and pharmacological use.

There has been much interest in poly-3-hydroxybutyrate (PHB) for use as a biosourced biodegradable replacement for petroleum-derived plastics. Most plant-based PHB has been produced in leaves, but its accumulation in seeds of arabidopsis, rapeseed, tobacco or soybean has had limited success (7% PHB in rapeseed). Camelina was used in an attempt to alleviate this limitation, and the ectopic expression of the three biosynthetic enzymes with different combinations of seed-specific promoters allowed a modest increase to 15% for the best line (Malik et al., 2015). PHB accumulation was however toxic to the embryo, with cotyledon chlorosis and weak seed vigor. The challenge to come will be to develop strategies to minimize PHB toxicity in the embryo cells in order to achieve yields compatible with industrial use.

9 Conclusions

In many studies, camelina has been shown to be an efficient host for bioengineering strategies, with higher oil yields compared to arabidopsis, rapeseed or soybean. The fact that camelina has potentially valuable agronomical characteristics should also increase its interest, not only as as a new crop, but also as a convenient translational tool for arabidopsis research results. In conclusion, current strategies for modifying oil yield or changing the endogenous lipid profile in camelina have had some real success, and can now provide market-compatible products derived from camelina seeds like omega-3 L-PUFA-enriched oil. Exciting challenges remain to improve production yield of new lipids in camelina to levels that are economically viable. New strategies are currently being implemented that couple knowledge of the intricated metabolic fluxes over time and space with synthetic biology tools in order to fine-tune lipid metabolism for specific needs.

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