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#### **Publisher's version / Version de l'éditeur:**

<https://doi.org/10.1111/pbi.13937>

*Plant Biotechnology Journal*, 21, 1, pp. 8-10, 2022-09-28

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## Brief Communication

Stepwise metabolic engineering of docosatrienoic acid – an  $\omega$ 3 very long-chain polyunsaturated fatty acid with potential health benefits in *Brassica carinata*Dauenpen Meesapyodsuk<sup>1</sup>, Kaiwen Sun<sup>2</sup>, Rong Zhou<sup>3</sup>, Ken Thoms<sup>4</sup> and Xiao Qiu<sup>1,2,\*</sup> <sup>1</sup>National Research Council Canada, Saskatoon, Canada<sup>2</sup>Department of Food & Bioproduct Sciences, University of Saskatchewan, Saskatoon, Canada<sup>3</sup>Saskatoon Research and Development Centre, AAFC, Saskatoon, Canada<sup>4</sup>Saskatchewan Structural Science Centre, University of Saskatchewan, Saskatoon, Canada

Received 20 July 2022;

revised 29 August 2022;

accepted 24 September 2022.

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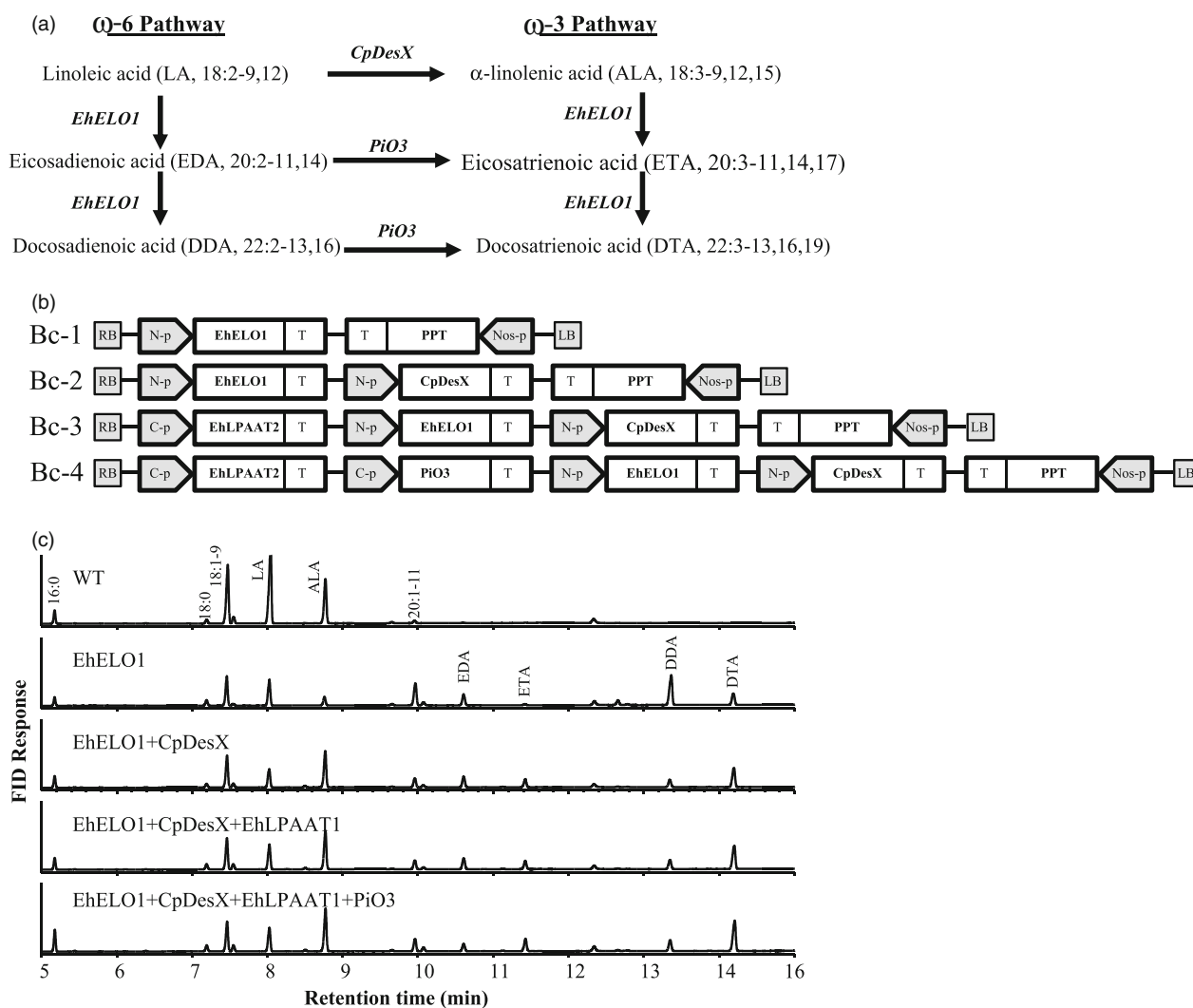
**Keywords:** very long-chain polyunsaturated fatty acid, docosatrienoic acid, metabolic engineering, *Brassica carinata*.

Very long-chain polyunsaturated fatty acids (VLCPUFAs) are essential components of cell membranes and precursors for bioactive compounds regulating important physiological processes in humans and animals. Lack or imbalance of these fatty acids can lead to various physiological problems in humans such as immunological disorders, neurological conditions and cardiovascular diseases (Bazinet and Laye, 2014). The current market and transgenic plant production of VLCPUFAs is primarily focused on two  $\omega$ 3 VLCPUFAs, docosahexaenoic acid (DHA, 22:6n-3), eicosapentaenoic acid (EPA, 20:5n-3), while other VLCPUFAs have been overlooked (Ganesh and Hettiarachchy, 2016; Napier *et al.*, 2019; Qiu *et al.*, 2020). Docosatrienoic acid (DTA, 22:3n-3) is an  $\omega$ 3 VLCPUFA with 22 carbons and three double bonds at 13, 16 and 19 positions, and was recently found to possess anti-inflammatory and antitumor properties comparable to DHA with potential nutraceutical and cosmetic uses (Chen *et al.*, 2021). Biosynthesis of DTA follows the elongation and desaturation pathways of  $\omega$ 6 and  $\omega$ 3 polyunsaturated fatty acids (PUFAs; Figure 1a). In the  $\omega$ 3 pathway,  $\alpha$ -linolenic acid (ALA, 18:3n-3) is elongated to eicosatrienoic acid (ETA, 20:3n-3) which is then elongated again to DTA (22:3n-3) by a single ELO type elongase (EhELO1) (Meesapyodsuk *et al.*, 2018). In the  $\omega$ 6 pathway, linoleic acid (LA, 18:2n-6) is elongated to eicosadienoic acid (EDA, 20:2n-6) and elongated again to docosadienoic acid (DDA, 22:2n-6) by the same elongase. In addition, LA can be desaturated to ALA by a 18C-PUFA  $\omega$ 3 desaturase (CpDesX) while EDA can also be desaturated to ETA by a VLCPUFA  $\omega$ 3 desaturase (PiO3). Both desaturated products, ALA and ETA, can then be elongated to DTA by EhELO1.

To produce DTA in oilseed crop *B. carinata*, a dedicated oilseed crop in Canada for specialty oil, four constructs were made expressing the elongase and desaturases following the biosynthetic pathway (Figure 1b). Besides the expression cassettes with genes in the biosynthetic pathway, all constructs carried a herbicide phosphinothricin resistant gene under the control of a constitutive promoter for transformant selection (Meesapyodsuk

*et al.*, 2018). The first construct (Bc-1) expresses a single elongase EhELO1 from plant *Eranthis hyemalis* that can elongate a wide range of PUFAs, which has been reported previously (Meesapyodsuk *et al.*, 2018). The second construct (Bc-2) expresses two genes encoding EhELO1 and CpDesX. CpDesX is an  $\omega$ 3 desaturase from fungus *Claviceps purpurea* with regioselectivity towards  $\omega$ 6-18C-PUFAs that can effectively convert LA to ALA (Meesapyodsuk *et al.*, 2007). The third construct (Bc-3) expresses three genes coding for EhELO1, CpDesX and EhLPAAT2. EhLPAAT2 is an endoplasmic lysophosphatidic acid acyltransferase from *E. hyemalis* that can incorporate VLCPUFAs into the sn-2 position of triacylglycerols, as *B. carinata* lacks the capacity (Meesapyodsuk *et al.*, 2021). The fourth construct (Bc-4) expresses EhELO1, CpDesX, EhLPAAT2 and PiO3. PiO3 is another  $\omega$ 3 desaturase from fungus *Pythium irregulare* that can convert  $\omega$ 6-VLCPUFAs to  $\omega$ 3-VLCPUFAs particularly for  $\omega$ 6-20C-VLCPUFAs (Cheng *et al.*, 2010). Each of these genes in the four constructs was under the control of a seed-specific promoter, *napin* or *conlinin*, and an octopine synthase (OCS) terminator.

The three new constructs were introduced into a low erucic acid breeding line through a Agrobacterium-mediated transformation approach using petioles as explants (Cheng *et al.*, 2010). Transgenic plants selected with phosphinothricin and genomic DNA PCR were grown in growth cabinets at 22 °C under a 16-h-light (120  $\mu$ Em<sup>-2</sup>/s)/8-h-dark photoperiod. Fatty acid analysis of transgenic *B. carinata* by GC-FID expressing the first construct Bc-1 with *EhELO1* alone has been reported previously (Meesapyodsuk *et al.*, 2018), producing several new VLCPUFAs such as EDA, ETA, DDA and DTA. Among them, DDA was the most abundant, followed by EDA, DTA and ETA. Transgenic *B. carinata* expressing the second construct Bc-2 with two genes *EhELO1* and *CpDesX* produced a similar fatty acid profile as Bc-1; however, the abundance of fatty acids varied significantly. Particularly, the abundance of LA and ALA was the reverse of each other in Bc-1 and Bc-2. This was due to the desaturation activity of CpDesX on LA, giving rise to ALA. The high level of ALA for elongation by EhELO1 resulted in the higher level of DTA than DDA in Bc-2 transgenic plants. Transgenic *B. carinata* expressing the third construct Bc-3 produced a similar fatty acid profile as Bc-2, but the amount of DTA was further increased, which was due to the pulling activity of EhLPAAT2 in the incorporation of VLCPUFAs into the sn-2 position of TAGs (Meesapyodsuk *et al.*, 2021). Transgenic plants expressing the four gene construct Bc-4 produced a similar fatty acid profile as Bc-3, but with a higher level of ETA than EDA due to the desaturation from EDA to ETA catalysed by PiO3. The higher level of ETA for elongation by



**FIGURE 1** Stepwise metabolic engineering of DTA in *Brassica carinata*. (a) Biosynthetic pathway of DTA. (b) Simplified maps of the binary vectors used for *B. carinata* transformation. N-p: napin promoter; C-p: conlinin promoter; Nos-p: NOS promoter; T: ocs terminator; PPT: gene for phosphinothricin N-acetyltransferase. (c) GC analysis of T1 transgenic seeds expressing one-, two-, three- and four-gene constructs.

EhELO1 resulted in a further increase of DTA in Bc-4 (Figure 1c, Table S1). One elite line of Bc-4 transgenic plants was selected for propagation to the next generations. Fatty acid analysis of transgenic seeds from the three generations showed that the amount of DTA was slightly increased over these generations. DTA was in a range from 16% to 20% along with DDA in a range of 4%–6% over the three generations. The amount of DTA was more than three times that of DDA, accounting for 20% on average in the T3 transgenic plants (Table S2).

MALDI-TOF/MS was then utilized to profile the TAG species (Hong *et al.*, 2002) in the seeds of T3 transgenic plants of selected elite lines with a single *EhELO1* and four genes (*EhELO1*+*CpDesX*+*EhLPAAT2*+*PiO3*). Untransformed *B. carinata* produced three major fatty acids, 18:1 (oleic acid), LA and ALA where the major molecular species of TAGs were ALA/LA/18:1, LA/LA/LA, LA/LA/18:1, ALA/LA/LA and LA/18:1/18:1 according to the relative abundance. Transgenic *B. carinata* expressing EhELO1 alone produced many new TAG species such as DDA/ALA/EDA (or DTA/LA/EDA), DDA/18:1/18:1 (or 20:1/LA/20:1), DDA/LA/DDA (or DDA/18:1/DDA), and DDA/18:1/16:0 (or 20:1/LA/18:0). Those

were also among the most abundant TAG species. As compared to those in wild type, molecular weights of TAGs in the *EhELO1* transgenics were shifted up by 2 to 8 carbons, indicating one to two VLCPUFAs such as DDA, DTA and EDA were incorporated into TAGs. Transgenic *B. carinata* expressing the four genes (*EhELO1*+*CpDesX*+*EhLPAAT2*+*PiO3*) further produced many new TAG species with three VLCPUFAs such as DTA/DTA/24:3 and DTA/DTA/DDA. Among all TAG profiles produced, those TAG species with three VLCPUFAs were the most abundant, followed by those with one or two VLCPUFAs such as DTA/DDA/ALA, DTA/ALA/ETA, DTA/18:1/LA, DDA/ALA/16:0. In TAGs with one or two VLCPUFAs, the shift of the molecular weights down by 2 to 4 daltons, as compared to those in EhELO1 transgenic seeds, indicated an addition of one or two double bonds in acylated fatty acids (Figure S1).

In summary, ω3-VLCPUFA DTA possesses potential health benefits, but the source for this fatty acid does not exist in nature. This study employed a stepwise strategy to engineer the biosynthetic pathway in *B. carinata*; about 20% DTA of the total fatty acids was produced in the transgenics. No obvious

phenotypic changes such as seed germination, seedling growth and development were observed in the plants. The amount of DTA in seeds remained stable over three generations where DTA was mainly placed in TAG species with two or three VLCPUFAs. Efficient and sustainable production of DTA in the oilseed crop provides an opportunity for this fatty acid to be used in cosmetics, foods and feeds.

## Acknowledgement

We would like to thank Shengjian Ye, Nagamani Datla and Yi Chen for technical assistance in plant transformation and growth, and Dr. Robert Chapman for the initial discussion of project. This is National Research Council of Canada publication number 58317.

## Conflict of interest

The authors declare no conflict of interest.

## Author contributions

XQ and DM perceived the project and designed the experiments, DM conducted primary experiments, KS did the plant and fatty acid analysis, RZ analysed the oil content, KT did the MALDI-TOF/MS analysis of TAGs, and XQ and DM wrote the paper.

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## Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

**Figure S1** TAG molecular species in *B. carinata* transgenic seeds expressing one- and four-genes.

**Table S1** Fatty acid compositions of T1 *B. carinata* transgenic seeds expressing one-, two-, three- and four-gene constructs (weight %).

**Table S2** Fatty acid compositions and oil contents of an elite line expressing the four genes over three generations (weight %).