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Characterization of a trifunctional fatty acid desaturase from oleaginous filamentous fungus *Mortierella alpina* 1S-4 using a yeast expression system

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A ω3-fatty acid desaturase gene (maw3) which is involved in biosynthesis of
n-3 polyunsaturated fatty acids (PUFAs) was previously isolated from Mortierella
alpina 1S-4. In this report, we investigated the products of MAW3 catalyzing
reaction with endogenous and exogenous fatty acids in the yeast transformant.
Two unusual fatty acids de novo synthesized in the yeast transformant expressing
maw3 gene were identified as n-4 hexadecadienoic acid (16:2\textsuperscript{9cis,12cis}) and n-1
hexadecatrienoic acid (16:3\textsuperscript{9cis,12cis,15}) by GC-MS and \textsuperscript{1}H-NMR analyses. In
addition to the desaturation activity at the ω3-position for 18- and 20-carbon
PUFAs, MAW3 in the yeast transformant inserted a double bond at Δ12-position of
denogenous palmitoleic acid (16:1\textsuperscript{9cis}) and further at Δ15-position of the resulting
16:2\textsuperscript{9cis,12cis} to result in the formation of 16:3\textsuperscript{9cis,12cis,15} leading to a bifunctional
Δ12/Δ15-desaturase for 16-carbon fatty acids. Moreover, we evaluated the
activity of MAW3 in the yeast transformant under different temperatures. The
MAW3 did not have desaturation activities in M. alpina 1S-4 at 28°C but it had in
the yeast transformant for various fatty acids. The MAW3 was demonstrated to
be a trifunctional Δ12/Δ15/ω3-desaturase, exhibiting Δ12-desaturation for 16:1\textsuperscript{9cis},
Δ15-desaturation for 16- and 18-carbon fatty acids that had a preexisting
cis-double bond at Δ12 position, and ω3-desaturation for 20-carbon fatty acids
having that at Δ14-position. It is the first report that the fatty acid desaturase
(MAW3) is shown to have Δ12- and Δ15-desaturation activities for a 16-carbon
fatty acid, in addition to its major function, ω3-desaturation activity.
Biosynthetic pathways of fatty acids have been determined in many species by identification of their genes encoding fatty acid desaturases (1-4). An oleaginous filamentous fungus, Mortierella alpina 1S-4, has been shown to contain Δ5-, Δ6-, Δ9-, Δ12-, and ω3-fatty acid desaturases and four kinds of elongases involved in polyunsaturated fatty acids (PUFAs) biosynthesis (5). In M. alpina 1S-4, Δ5-, Δ6-, Δ9-, and Δ12-desaturases exhibit their desaturation activity at a cultural temperature of 28°C, whereas ω3-fatty acid desaturase exhibits its activity only below a cultural temperature of 20°C.

*M. alpina* 1S-4 is capable of producing triacylglycerols rich in arachidonic acid (ARA; 20:4\textit{cis},8\textit{cis},11\textit{cis},14\textit{cis}) with the amount ranging of 3-20 g/L of culture broth and 30-70% in the total fatty acid composition. On the other hand, this fungus accumulates a small amount of eicosapentaenoic acid (EPA; 20:5\textit{cis},8\textit{cis},11\textit{cis},14\textit{cis},17\textit{cis}) with 0.3 g/L of culture broth and 10% in total fatty acids below a cultural temperature of 20°C (5). We had previously reported isolation of the gene (*maw3*) encoding an ω3-desaturase, involved in biosynthesis of n-3 PUFAs, from *M. alpina* 1S-4, and have confirmed that the gene product (MAW3) converts n-6 PUFAs into n-3 PUFAs (6). MAW3 possesses three histidine rich-cluster motifs containing eight histidine residues that are proposed to form an active-site domain and two hydrophobic
membrane-spanning regions in its deduced amino acid sequence (6,7). Similar to Δ12- and ω3-desaturases found in other organisms, MAW3 has no cytochrome b5 motif in its structure (6,8,9). Overexpression of maw3 gene in M. alpina 1S-4 through Agrobacterium tumefaciens-mediated transformation led to an increase in EPA production contributing to 40% of total fatty acid content (10).

Fatty acid desaturases are known to have five specificities: chemoselectivity (desaturation or hydroxylation), regioselectivity (double bond position), stereoselectivity (cis or trans), chain length specificity, and acyl carrier specificity (acyl-CoA, acyl-lipid, or acyl-ACP substrate) (11). Three types of regioselectivities have been defined (11). The Δx-desaturases such as Δ9-desaturases insert a first double bond at x carbon atom position away from the carboxyl end. On the other hand, the ωy-desaturases such as ω3-desaturases insert a double bond at position y from the methyl end. The v + z-desaturases require a preexisting double bond as a mark (v) and catalyze the formation of a new double bond z carbon atoms further along the acyl chain, either toward the methyl end (i.e. Δ12-desaturase) or toward the carboxyl end (i.e. Δ6-desaturase). The aforementioned types of regioselectivity are explained for bifunctional fungal Δ12/ω3-desaturases from Fusarium moniliforme (12) and Aspergillus nidulans (13). These bifunctional enzymes desaturate oleic acid (OA;
$18:1^{9\text{cis}}$ at $\Delta12$-position to form linoleic acid (LA; $18:2^{9\text{cis},12\text{cis}}$) and further at the $\Delta15$-position to form $\alpha$-linolenic acid (ALA; $18:3^{9\text{cis},12\text{cis},15\text{cis}}$). Additionally, these desaturases also convert $n$-6 PUFAs: LA, $\gamma$-linolenic acid (GLA; $18:3^{6\text{cis},9\text{cis},12\text{cis}}$), dihomo-$\gamma$-linolenic acid (DGLA; $20:3^{8\text{cis},11\text{cis},14\text{cis}}$), and ARA to their corresponding $n$-3 PUFAs with preference of the 18-carbon PUFAs. Other bifunctional $\Delta12/\Delta15$-desaturases that catalyze the synthesis of unusual $n$-1 hexadecatrienoic acid (16:3$^{9\text{cis},12\text{cis},15\text{cis}}$) have been reported in the free-living soil protozoon *Acanthamoeba castellanii* (14), phytopathogenic fungus *Claviceps purpurea* (15), basidiomycete *Coprinus cinereus* (16), and nematode *Caenorhabditis elegans* (17).

In this study, we attempted to characterize the MAW3 using the yeast *Saccharomyces cerevisiae* expression system. Two unusual fatty acids synthesized *de novo* in *maw3*-expressing yeast transformant were identified by GC-MS and NMR. The MAW3 in yeast transformant inserted a double bond at $\Delta12$-position and further at $\Delta15$-position for endogenous 16-carbon fatty acids as well as at $\omega3$-position of exogenous 18- and 20-carbon PUFAs. The *M. alpina* 1S-4 $\omega3$-desaturase was found to be a trifunctional $\Delta12/\Delta15/\omega3$-desaturase that mainly acts as $\Delta15$- and $\omega3$-desaturase, and as a $\Delta12$-desaturase for 18- and 20-carbon PUFAs in addition to 16-carbon fatty acids. The finding is different from other bifunctional desaturases so far reported...
1 (12-17).

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MATERIALS AND METHODS

Strains, plasmid, growth media, and culture conditions  The maw3 gene from M. alpina 1S-4 (18) was registered in the DDBJ database under the accession number AB182163 (6). S. cerevisiae EH1315 (α trp1) was used as the recipient strain in transformation experiments (19). Plasmid pYE22m, used as a shuttle vector, carried the ampicillin resistance gene (for selection in Escherichia coli) and TRP1 (for tryptophan prototrophy selection in S. cerevisiae EH1315), with an expression of a target gene controlled under the glyceraldehyde-3-phosphate dehydrogenase (GAP) promoter and the GAP terminator from S. cerevisiae.

M. alpina 1S-4 strain was cultured in GY medium (containing 20 g/L of glucose, 10 g/L of yeast extract, pH 6.0) for 5 days at 28°C. Yeast strains were cultured in a yeast synthetic complete medium (SC medium; containing 20 g/L of glucose, 5 g/L of ammonium sulfate, 1.7 g/L of yeast nitrogen base without amino acids and ammonium sulfate, 60 mg/L of isoleucine, 60 mg/L of leucine, 60 mg/L of phenylalanine, 50 mg/L of threonine, 40 mg/L of lysine, 30 mg/L of tyrosine, 20 mg/L of adenine, 20 mg/L of arginine, 20 mg/L of uracil, 20 mg/L of histidine, and 10 mg/L of methionine) for 2 days at 15°C (or at 28°C).

maw3 expression in yeast  The full-length maw3 cDNA was amplified by PCR in
a total reaction volume of 50 μl sample containing < 0.2 μg of plasmid pYMAW3 (6) as template DNA, 0.5 μl of *PrimeSTAR HS* DNA polymerase (Takara Bio, Shiga, Japan), 10 μl of 5 × *PrimeSTAR* buffer (Mg²⁺ plus), 200 μM of each dNTP and 200 pM of each primer: ω3-1F (5’-ATGGCCCCCCCTCACGTTGTCGACGAACA-3’) containing an ATG start site (underline) and ω3-3R (5’-TTAATGCTTGTAAAAACACTACATCTCC-3’) containing a TAA stop site (underline). PCR amplification was performed as follows: initial denaturation at 94°C for 2 min, followed by 25 cycles of 98°C for 10 sec, 55°C for 15 sec, and 72°C for 2 min. The resultant 1212-bp PCR fragment was digested with *EcoRI* and treated with DNA Blunting Kit (Takara Bio) for blunt-end ligation into the yeast expression vector pYE22m to result in the construction of a plasmid, designated as pYE22MAW3, which was further transformed into the *S. cerevisiae* EH1315 strain by means of the lithium acetate-mediated transformation protocol (20). Transformants was selected for tryptophan (Trp) auxotrophy on SC (-Trp) medium.

The transformants were grown at 28°C or 15°C with shaking for 48 h in SC medium. To test for the substrate specificities of MAW3 in yeast, various free fatty acids (FFAs) were added to the culture broth at 0.1 mM concentration after 24 h of cultivation. The yeast transformant with an empty vector was used as the control.
Fatty acid analysis  Total fatty acid compositions of the yeast transformants were analyzed as described by Sakuradani et al. (6). Yeast cells after cultivation were harvested by centrifugation and dried at 120°C for 1.5 h. The dried cells were directly transmethylated with 10% methanolic HCl at 55°C for 1.5 h. The resultant fatty acid methyl esters (FAMEs) were extracted with n-hexane, concentrated and analyzed by gas chromatography (GC; Shimadzu, Kyoto, Japan). The conversion rate of substrate into the product was calculated as the enzymatic activity of the desaturase [conversion rate (%)] = 100 × product/(product + substrate)].

Total lipids were extracted from wet yeast cells using water/chloroform/methanol (2/2.5/2.5, v/v/v) according to the Bligh-Dyer method (21). The extracted lipids were saponified to obtain their FFAs using 0.5 N KOH in 90% MeOH. The unidentified FFAs were separated by HPLC with a LC-20A system (Shimadzu). A Develosil C30-UG-5 column (4.6 × 250 mm, Nomura chemical, Aichi, Japan) was used for FFA separation by HPLC with 80% (v/v) acetonitrile aqueous solution as a mobile phase at a flow rate of 1.0 ml/min. The column oven temperature was maintained at 35°C, and the absorbance was measured by UV/VIS detector at 205 nm. The mixture of FFAs separated by HPLC were transmethylated with methanol/benzene/1% diazomethane.
(4/6/1, v/v/v) for 30 min at room temperature for preparation of FAMEs. Through the Discovery Ag-Ion SPE column (SUPELCO, Bellefonte, PA, USA), most of FAMEs in the UK2 fraction except for the UK2 were removed with acetone and the UK2 was eluted with acetonitrile. The 4,4-Dimethyloxazoline (DMOX) derivatives of the UK1 and UK2 obtained through the HPLC purification was prepared and analyzed by GC-MS as described by Yu et al. (22). A GC-MS QP2010 (Shimadzu) with GC-2010 gas chromatograph was used for MS analysis. The SPB\textsuperscript{TM-1} column (0.25 mm I.D. × 30 m, SUPELCO) was used for separation of DMOX derivatives. Initial column temperature was set at 180°C and was raised to 300°C later at a rate of 5°C/min. The apparatus provides the electron impact mode at 70 eV with a source temperature of 250°C. The injection temperature was 250°C. The \textsuperscript{1}H-NMR and DQF-COSY experiments were performed with a Bruker Advance 500 (500 MHz). Samples were dissolved in chloroform-\textit{d} (Sigma, St. Louis, MO, USA). Chemical shifts were assigned relative to the solvent signal.

RESULTS

Functional analysis of the maw3 gene product in the yeast transformant

To
characterize the maw3 gene product from M. alpina 1S-4 by using a yeast expression system, the yeast transformant with pYE22MAW3 containing the maw3 cDNA was obtained. The yeast transformants were grown in SC medium, and their total fatty acid compositions were analyzed by GC (Fig. 1A and 1B). The maw3-expressing yeast transformant accumulated two unusual fatty acids, named UK1 and UK2 respectively, which were not detected in the control strain. The UK1 was expected to be 16:2\(^{9\text{cis},12\text{cis}}\), because the retention time of the UK1 was consistent with that of an authentic standard (Fig. 1C).

Each FFA of UK1 and UK2 was purified by HPLC equipped with a Develosil C30-UG-5 column, followed by the further purification through Discovery Ag-Ion SPE column for UK2. The positions of the double bonds in UK1 and UK2 were determined by GC-MS analysis of their DMOX derivatives (Fig. 2). MS analysis of UK1 and UK2 DMOX derivatives in Fig. 2 revealed molecular ions of \(m/z\) 305 and 303, and the gaps of 26 atomic mass unit (amu) between \(m/z\) 196 and 222, and \(m/z\) 236 and 262, indicating double bond at the \(\Delta 9\)- and \(\Delta 12\)-positions in their structures, respectively. The gap of 41 amu between \(m/z\) 262 and 303 in the mass spectrum of UK2 (Fig. 2B) suggested a double bond at the \(\Delta 14\)- or \(\Delta 15\)-position. To determine a position of a double bond at methyl terminal of UK2 completely, the FAME of UK2 showing 95%
purity on GC chromatogram was applied for $^1$H-NMR analysis (Fig. 3) and DQF-COSY analysis (FIGURE S1). $^1$H-NMR $\delta_H$ (CDCl$_3$) spectral data of UK2: 5.82 (1H, $tt$, -CH$_2$-CH=CH$_2$, H-15), 5.38 (4H, $m$, -CH$_2$-CH=CH-, H-9, H-10, H-12, H-13), 5.02 (2H, $d$, $J_1$ = 10.1, 17.0 Hz, -CH$_2$-CH=CH$_2$, H-16), 3.67 (3H, $s$, -C(=O)-O-C$_3$H$_3$), 2.83 (2H, $dd$, $J_2$ = 6.07, 6.07 Hz, =CH-CH=, H-14), 2.79 (2H, $dd$, $J_3$ = 6.07, 6.07 Hz, =CH-CH=), 2.79 (2H, $dd$, $J_4$ = 7.33, 7.41 Hz, -CH$_2$-CH$_2$-CH-, H-8), 1.679 (2H, $tt$, $J_5$ = 7.28 Hz, -C(=O)-CH$_2$-CH$_2$-, H-2), 2.05 (2H, $dt$, $J_6$ = 6.78, 6.78 Hz, -CH$_2$-CH$_2$-CH-, H-3), and 1.31 (8H, $m$, -CH$_2$-CH$_2$-CH-, H-4, H-5, H-6, H-7). The absorption peaks at $\delta$ 5.82 (-CH$_2$-CH=CH$_2$, H-15) and 5.02 (-CH$_2$-CH=CH$_2$, H-16) in Fig. 3 revealed a double bond at the $\Delta$15-position in the structure of UK2. From these analyses, UK1 and UK2 were identified as 16:2$^{9cisc12cis}$ and 16:3$^{9cis,12cis,15}$, respectively.

As shown in Table 1, the fatty acid composition of the maw3-expressing yeast transformant was different from that of the control strain. The 16:2$^{9cisc12cis}$ and 16:3$^{9cis,12cis,15}$ comprised 0.8% and 4.0% of the total fatty acid content, respectively, which were not detected in the control strain. The percentage of 16:1$^{9cis}$ was decreased slightly in the yeast transformant, compared to that in the control strain. Neither LA nor ALA was detected in both yeast strains, suggesting that MAW3 in the transformant prefers a 16-carbon fatty acid like 16:1$^{9cis}$ to an 18-carbon fatty acid like OA.
Catalytic properties of MAW3 gene product analyzed in the transformant

To investigate the substrate preference of MAW3, the yeast transformants were grown in SC medium containing 0.1 mM of exogenous FFA substrates such as 16:2\(^{9\text{cis},12\text{cis}}\), 18:1\(^{9\text{cis}}\) (OA), crepenyiacid (9cis-octadecen-12-ynoic acid; 18:1\(^{9\text{cis},12\text{yn}}\)), 18:2\(^{9\text{cis},12\text{cis}}\), 12\(^{9\text{cis}}\), 3\(^{18\text{cis}}\), 19\(^{cis}\) (OA), crepenyiacid (9cis-octadecen-12-ynoic acid; 18:1\(^{9\text{cis},12\text{yn}}\)), 4\(^{18\text{cis}}\), 12\(^{9\text{cis}}\) isomers (18:2\(^{9\text{cis},12\text{cis}}\), 18:2\(^{9\text{cis},12\text{yn}}\), 18:2\(^{9\text{trans},12\text{cis}}\), and 18:2\(^{10\text{trans},12\text{cis}}\)), 18:3\(^{6\text{cis},9\text{cis},12\text{cis}}\) (GLA), 20:2\(^{9\text{cis},12\text{cis}}\), 20:3\(^{8\text{cis},11\text{cis},14\text{cis}}\) (DGLA), and 20:4\(^{5\text{cis},8\text{cis},11\text{cis},14\text{cis}}\) (ARA). Conversions of the substrates by the maw3-expressing yeast transformant were carried out during cultivation at 15°C or 28°C (Table 2). *M. alpina* 1S-4 has no \(\omega3\)-desaturation activity at 28°C cultivation, whereas the yeast transformant exhibited the activity for the substrates even at 28°C. The MAW3 in the yeast transformant desaturated the following PUFAs: 16:2\(^{9\text{cis},12\text{cis}}\), 18:2\(^{9\text{cis},12\text{cis}}\) (LA), 18:3\(^{6\text{cis},9\text{cis},12\text{cis}}\) (GLA), 20:3\(^{8\text{cis},11\text{cis},14\text{cis}}\) (DGLA), and 20:4\(^{5\text{cis},8\text{cis},11\text{cis},14\text{cis}}\) (ARA) to 16:3\(^{9\text{cis},12\text{cis},15\text{cis}}\), 18:3\(^{9\text{cis},12\text{cis},15\text{cis}}\) (ALA), stearidonic acid (SDA; 18:4\(^{6\text{cis},9\text{cis},12\text{cis},15\text{cis}}\)), eicosatetraenoic acid (ETA; 20:4\(^{8\text{cis},11\text{cis},14\text{cis},17\text{cis}}\)), and 20:5\(^{5\text{cis},8\text{cis},11\text{cis},14\text{cis},17\text{cis}}\) (EPA). Putative \(\Delta15\)-desaturation products of 18:2\(^{9\text{cis},12\text{yn},15\text{cis}}\) (9cis,15cis-octadecadien-12-ynoic acid), 18:3\(^{9\text{trans},12\text{cis},15\text{cis}}\), and 18:3\(^{10\text{trans},12\text{cis},15\text{cis}}\) from 18:1\(^{9\text{cis},12\text{yn}}\), 18:2\(^{9\text{trans},12\text{cis}}\), 18:2\(^{10\text{trans},12\text{cis}}\), respectively, were also observed on GC chromatograms. The \(n\)-6 PUFAs (LA, GLA, DGLA, and ARA) were more effectively
converted into n-3 PUFAs (ALA, SDA, ETA, and EPA) at a low temperature (15°C) cultivation of *M. alpina* 1S-4 than at 28°C temperature. In addition, conversion rates for 16:2\(^{9\text{cis},12\text{cis}}\) and crepencynic acid were observed at similar or higher levels at 28°C as compared to the ones at 15°C. Neither Δ15-desaturation nor ω3-desaturation products were detected for 20:2\(^{9\text{cis},12\text{cis}}\) in the yeast transformant.

The Δ12-desaturation catalyzed by MAW3 was observed only for 16:1\(^{9\text{cis}}\), and not for 18:1\(^{9\text{cis}}\) and 18:2\(^{6\text{cis},9\text{cis}}\). The high conversion rate with more than 60% was shown for 16:2\(^{9\text{cis},12\text{cis}}\) to 16:3\(^{9\text{cis},12\text{cis},15}\) by Δ15-desaturation of MAW3 in the yeast transformant. Furthermore, the ω3-desaturation of MAW3 was observed for 18- and 20-carbon PUFAs having a preexisting 12cis-double bond or 12-triple bond and a preexisting 14cis-double bond, respectively.

**DISCUSSION**

The fungus *M. alpina* 1S-4 not only produces a great number of n-6 PUFAs rich in ARA, but also accumulates n-3 PUFAs such as EPA below a cultural temperature of 20°C (23). The n-3 PUFAs in *M. alpina* 1S-4 *in vivo* are expected to be synthesized from n-6 PUFAs through ω3-desaturation. The *maw3* gene was previously isolated
and characterized as to its function of $n$-6 PUFAs conversion to $n$-3 PUFAs in *M. alpina* 1S-4 (6).

In this study, the *maw3*-expressing yeast transformant was found to accumulate two newly synthesized fatty acids, $16:2^{9 cis, 12 cis}$ and $16:3^{9 cis, 12 cis, 15}$. Thus far, we had no idea that the MAW3 had $\Delta 12$-deaturase activity as an alternative function. The accumulation of $16:2^{9 cis, 12 cis}$ and $16:3^{9 cis, 12 cis, 15}$ suggested that the yeast transformant had both $\Delta 12$-desaturation activity with a conversion rate of 10.2% (calculated as $100 \times \frac{[16:2 + 16:3]}{[16:1 + 16:2 + 16:3]}$) for endogenous $16:1^{9 cis}$, and $\Delta 15$-desaturation one at $\omega 1$-position, not $\omega 3$, with a conversion rate of 83.0% (calculated as $100 \times \frac{[16:3]}{[16:2 + 16:3]}$) for the resultant $16:2^{9 cis, 12 cis}$. Once the $16:2^{9 cis, 12 cis}$ was formed from $16:1^{9 cis}$ by $\Delta 12$-desaturation, $16:2^{9 cis, 12 cis}$ was demonstrated to be rapidly converted to $16:3^{9 cis, 12 cis, 15}$.

The analysis of substrate specificities (Table 2) showed that the MAW3 not only had $\omega 3$-desaturation activity for 18- and 20-carbon PUFAs, but also demonstrated bifunctional $\Delta 12/\Delta 15$-desaturation activities for 16-carbon fatty acids. The $\Delta 12$, $\Delta 15$, or $\omega 3$-desaturation activity of MAW3 requires a preexisting double bond at $\Delta 9$, $\Delta 12$, or $\omega 6$-position, respectively. Hence, MAW3 is classified as $v + 3$ desaturase ($v$ indicating the position of the preexisting double bond) which inserted a new double bond.
bond 3 carbon atoms further along the acyl chain toward the methyl end.

Compared to other bifunctional Δ12/Δ15-desaturases [amoeba A. castellani (14); basidiomycete C. cinereus (16); nematode C. elegans (17)], MAW3 in the yeast transformant exhibited Δ12-desaturation for 16:1<sup>9cis</sup>, not 18:1<sup>9cis</sup>, and in addition to that, also exhibited Δ15-desaturation for 16:2<sup>9cis,12cis</sup> with a high conversion rate (83.0%). The previously reported bifunctional Δ12/Δ15-desaturases mainly act as a Δ12-desaturase, except for the fungal ω3-desaturases described by Damude et al. (12) and Hoffmann et al. (13), however do not possess Δ12-desaturation activity for the 16-carbon fatty acid. The ratios of ω3/ω6 fatty acids (calculated as [16:3 + 18:3]/[16:2 + 18:2]) in yeast transformant were calculated as follows: 5.0 [MAW3, described here], 21 [ω3-desaturase from F. moniliforme (12)], 0.008 [Δ12-desaturase from F. moniliforme (12)], 2.1 [ω3-desaturase from A. nidulans (13)], 0.48 [Δ12-desaturase from A. castellani (14)], 0.042 [Δ12-desaturase from C. cinereus (16)], and 0.090 [Δ12-desaturase from C. elegans (17)] respectively based on the information derived from each report. The bifunctional Δ12/Δ15-desaturases from F. moniliforme and that has a high ratio of 21, mainly work as a ω3-desaturase, which prefers the 18-carbon PUFAs as substrates and not the 16-carbon fatty acids. On the other hand, the bifunctional Δ12/Δ15-desaturase from C. purpurea (15) introduces a double bond for
both 16- and 18-carbon fatty acids, demonstrating increased activity of Δ12-desaturation
as compared to Δ15-desaturation.

On investigation of substrate specificities, the characteristic feature of MAW3
was shown to have both the Δ12/Δ15-desaturation activity for the 16-carbon fatty acids
and ω3-desaturation activity for 18- and 20-carbon PUFAs, indicating its substrate
specificities that differed from the other bifunctional Δ12/Δ15-desaturases (12-17). It
is of interest to note that, the maw3-expressing yeast transformant exhibited the
ω3-desaturation activity on cultivation at 28°C, whereas M. alpina 1S-4 had no such
ω3-desaturation activity under similar culture conditions. This may imply the
possibility of some regulation in the translation process and/or localization of MAW3 in
M. alpina 1S-4 in vivo. The localization of MAW3 might be detected in cells of M.
alpina 1S-4 by means of labeling techniques. We expect that the elucidation of the
mechanism for the difference in MAW3 activity (depending on the culture temperature)
may contribute to the accumulation of basic information on membrane-bound
desaturases and to efficient production of n-3 PUFAs by M. alpina breeding.

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Figure legends

**FIG. 1.** GC chromatograms of FAMEs prepared from total lipids of the control strain (pYE22m) (A), the *maw3*-expressing yeast transformant (pYE22MAW3) (B), and the FAMEs of $16:2^{9\text{cis},12\text{cis}}$ (C).

**FIG. 2.** Mass spectra of DMOX derivatives of (A) UK1 and (B) UK2 obtained from the yeast transformant (pYE22MAW3). The specific mass fragments of authentic $16:2^{9\text{cis},12\text{cis}}$ were $m/z$ 113, 126, 140, 154, 168, 182, 196, 208, 222, 236, 248, 262, 276, 276, 290, and 305.

**FIG. 3.** $^1$H-NMR analysis of the UK2 methyl ester.
FIG. 1. Kikukawa et al.
UK1; hexadecadienoic acid (16:2<sup>9cis,12cis</sup>)

UK2; hexadecatrienoic acid (16:3<sup>9cis,12cis,15</sup>)

FIG. 2. Kikukawa et al.
FIG. 3. Kikukawa et al.
Table 1. Fatty acid compositions of the yeast transformants

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Fatty acid composition (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Control strain (pYE22m)</td>
</tr>
<tr>
<td>16:0</td>
<td>12.4</td>
</tr>
<tr>
<td>16:1&lt;sup&gt;9cis&lt;/sup&gt;</td>
<td>45.4</td>
</tr>
<tr>
<td>16:2&lt;sup&gt;9cis, 12cis&lt;/sup&gt;</td>
<td>N.D.</td>
</tr>
<tr>
<td>16:3&lt;sup&gt;9cis, 12cis, 15&lt;/sup&gt;</td>
<td>N.D.</td>
</tr>
<tr>
<td>18:0</td>
<td>5.7</td>
</tr>
<tr>
<td>18:1&lt;sup&gt;9cis&lt;/sup&gt;</td>
<td>34.6</td>
</tr>
</tbody>
</table>

<sup>a</sup> N.D., not detected
Table 2. Conversion of various fatty acids by the *maw3*-expressing yeast transformant.  

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Product</th>
<th>Conversion rate (%)</th>
<th>15°C</th>
<th>28°C</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Endogenous fatty acid</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16:1(^{9\text{cis}})</td>
<td>16:2(^{9\text{cis},12\text{cis}})</td>
<td>10.2 ± 0.2</td>
<td>N.D. (^c)</td>
<td></td>
</tr>
<tr>
<td>16:2(^{9\text{cis},12\text{cis}})</td>
<td>16:3(^{9\text{cis},12\text{cis},15})</td>
<td>83.0 ± 0.5</td>
<td>N.D.</td>
<td></td>
</tr>
<tr>
<td><strong>Exogenous fatty acid</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16:2(^{9\text{cis},12\text{cis}})</td>
<td>16:3(^{9\text{cis},12\text{cis},15})</td>
<td>68.8 ± 0.6</td>
<td>60.3 ± 0.6</td>
<td></td>
</tr>
<tr>
<td>18:1(^{9\text{cis}}) (OA)</td>
<td>N.D.</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>18:1(^{9\text{cis},12\text{yn}})</td>
<td>18:2(^{9\text{cis},12\text{yn},15\text{cis}}) (^d)</td>
<td>11.0 ± 0.4</td>
<td>19.5 ± 1.5</td>
<td></td>
</tr>
<tr>
<td>18:2(^{6\text{cis},9\text{cis}})</td>
<td>N.D.</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>18:2(^{9\text{cis},12\text{cis}}) (LA)</td>
<td>18:3(^{9\text{cis},12\text{cis},15\text{cis}}) (ALA)</td>
<td>65.2 ± 0.6</td>
<td>24.4 ± 0.4</td>
<td></td>
</tr>
<tr>
<td>18:2(^{9\text{cis},11\text{trans}})</td>
<td>N.D.</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>18:2(^{9\text{trans},12\text{cis}})</td>
<td>18:3(^{9\text{trans},12\text{cis},15\text{cis}}) (^d)</td>
<td>63.8 ± 0.2</td>
<td>40.0 ± 3.7</td>
<td></td>
</tr>
<tr>
<td>18:2(^{9\text{trans},12\text{trans}})</td>
<td>N.D.</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>18:2(^{10\text{trans},12\text{cis}})</td>
<td>18:3(^{10\text{trans},12\text{cis},15\text{cis}}) (^d)</td>
<td>41.3 ± 0.2</td>
<td>18.1 ± 0.5</td>
<td></td>
</tr>
<tr>
<td></td>
<td>GLA (18:3&lt;sup&gt;5cis,9cis,12cis&lt;/sup&gt;)</td>
<td>SDA (18:4&lt;sup&gt;6cis,9cis,12cis,15cis&lt;/sup&gt;)</td>
<td>conversion rate (%)</td>
<td>EPA (20:5&lt;sup&gt;5cis,8cis,11cis,14cis,17cis&lt;/sup&gt;)</td>
</tr>
<tr>
<td>-----</td>
<td>---------------------------------</td>
<td>---------------------------------</td>
<td>------------------</td>
<td>------------------------------------------------</td>
</tr>
<tr>
<td>1</td>
<td>74.8 ± 0.1</td>
<td>32.6 ± 0.7</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>N.D.</td>
<td>N.D.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>57.7 ± 1.1</td>
<td>6.7 ± 0.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>52.5 ± 2.6</td>
<td>8.7 ± 0.7</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- All exogenous free fatty acid substrates were added at 0.1 mM. All the values are for three independent samples (mean ± SD).
- Conversion rate (%) = 100 × [product]/[product + substrate].
- N.D., not detected.
- Putative product.
FIGURE S1. DQF-COSY analysis of the UK2 methyl ester.