1 **Metabolic engineering for the production of polyunsaturated fatty acids by**

2 **oleaginous fungus *Mortierella alpina* 1S-4**

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4 Running Title: Microbial production of polyunsaturated fatty acids

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1　　Researches related with the application of functional lipids such as

2　polyunsaturated fatty acids (PUFAs) have been conducted in various fields with a

3　view to health and dietary requirements.　Novel rich sources other than known

4　natural sources such as plant seeds and fish oils are required for increasing

5　demands of PUFAs.　The filamentous fungus *Mortierella alpina* 1S-4 produces

6　triacylglycerols rich in arachidonic acid, i.e., ones reaching 20 g/l in concentration

7　and containing 30-70% arachidonic acid as total fatty acids.　Various mutants

8　derived from *M. alpina* 1S-4 have led to the production of oils containing various

9　PUFAs.　Molecular breeding of *M. alpina* strains by means of manipulation of the

10　genes involved in PUFA biosynthesis facilitates improvement of PUFA productivity

11　and elucidation of the functions of their enzymes.　This review describes practical

12　PUFA production through mutant breeding, functional analyses of the genes of the

13　enzymes involved in PUFA biosynthesis, and recent advances in unique PUFA

14　production through molecular breeding.

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16　[**Key words:** *Mortierella alpina*; Polyunsaturated fatty acid; Arachidonic acid (AA);

17　Eicosapentaenoic acid (EPA); Molecular breeding; Fatty acid desaturase]

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1   Polyunsaturated fatty acids (PUFAs) contain more than one double bond, and some

2   20-carbon (C20) PUFAs play important roles not only as structural components of

3   membrane phospholipids but also as precursors of eicosanoids, signaling molecules

4   including prostaglandins, thromboxanes, and leukotrienes, that are essential for all

5   mammals.   Especially, arachidonic acid (AA; 20:4n-6), a representative n-6 PUFA, is

6   the most abundant C20 PUFA in humans, and not only exhibits various regulation

7   effects and physiological activities but also plays important roles in infant nutrition (1,2).

8   Eicosapentaenoic acid (EPA; 20:5n-3), a representative n-3 PUFA, is beneficial in the

9   treatment of cardiovascular diseases (3), and decreases platelet aggregation and blood

10   pressure (4).   The distinct functions of the two families make the ratio in the diet of n-6

11   and n-3 PUFAs important in inflammatory responses and cardiovascular health.   The

12   most readily available lipid sources relatively rich in C20 PUFAs, none of which are

13   found in plants, are fish oils, animal tissues, and algal cells.   Transgenic plants with

14   some exogenous desaturase genes have been reported to produce n-3 and n-6 PUFAs (5).

15   However, these transgenic sources are unsuitable for practical purposes from the

16   viewpoint of genetically modified organisms.   The term "Single Cell Oils" is used for

17   unique oils produced by microorganisms that compete with plant-seed oils and fish oils

18   (6).   Some yeasts and molds are known as microorganisms that accumulate high levels

19   of triacylglycerols.   A lipid content in excess of 40% (w/w) is not exceptional, and

20   values of 70% and even 80% have been reported (7).   Single Cell Oils having different

21   fatty acid compositions from plant-seed oils and fish oils are valuable for human life.

22   On screening of the microorganisms accumulating C20 PUFAs, a filamentous fungus,

23   *Mortierella alpina* 1S-4, was isolated as a suitable source for the AA production; it was

24   able to produce EPA through the n-3 PUFA biosynthetic pathway, while AA through the

3

1   n-6 PUFA biosynthetic pathway (8-10).   In this strain, most PUFAs are present in

2   triacylglycerols as storage oils, while some are present in phospholipids as structural

3   components of membranes.

4   Although success in this area over the last 25 years has generated much interest in the

5   development of microbial fermentation processes, manipulation of the lipid

6   compositions of microorganisms requires new biotechnological strategies to obtain high

7   yields of the desired PUFAs.   This article reviews recent progress in the breeding of

8   commercially important arachidonic acid-producing *M. alpina* strains, particularly

9   approaches to creating desaturase and elongase mutants with unique pathways for PUFA

10   biosynthesis involving conventional chemical mutagenesis and modern molecular

11   genetics.

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13   **VARIOUS KINDS OF PUFAs IN *M. alpina* 1S-4**

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15   **Isolation of mutants producing PUFAs through different biosynthetic pathways**

16   Various mutants defective in desaturase (Δ9, Δ12, Δ6, Δ5 and ω3) or elongase

17   (MALCE1) activities, or with enhanced desaturase activities (Δ6 and Δ5) have been

18   derived   from   *M.   alpina*   1S-4   by   treating   the   parental   spores   with

19   *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine   (11).   In   addition,   a

20   diacylglycerol-accumulating mutant and several lipid-excretive ones have been obtained

21   by the same method.   They are valuable not only as producers of useful PUFAs (novel

22   or already existing) but also for providing valuable information on PUFA biosynthesis

23   in this fungus (12).   The main features of these mutants are summarized in Table 1.

24   Δ9 Desaturase-defective mutants accumulate stearic acid (18:0) as the main fatty acid

1   (up to 40%) in the mycelial oil (13).   Δ12 Desaturase-defective mutants accumulate

2   high levels of n-9 PUFAs, such as Mead acid (MA; 20:3n-9) that are not detected in the

3   wild strain because of a complete deficiency of Δ12 desaturation (Fig. 1A).   One of

4   these mutants, JT-180, yields a large amount of MA (2.6 g /L, 49% in oil) on

5   commercial production due to its enhanced Δ5 and Δ6 desaturase activities, not

6   including n-6 and n-3 PUFAs (14). Double mutants defective in both Δ12 and Δ5

7   desaturase activities accumulate n-9 eicosadienoic acid (20:2n-9) as a final product of

8   n-9 PUFAs in large quantities (15). Δ6 Desaturase-defective mutants accumulate

9   linoleic acid (18:2n-6) as the main fatty acid (up to 32%) in the mycelial oil (16).

10   These mutants are characterized by the accumulation of n-6 eicosadienoic acid

11   (20:2n-6) and nonmethylene-interrupted n-6 eicosatrienoic acid (20:3n-6Δ5)

12   synthesized from linoleic acid, as shown in Fig. 1B.   Δ5 Desaturase-defective mutants

13   exhibit a high dihomo-γ-linolenic acid (DGLA; 20:3n-6) level (4.1 g/L, 42% in oil) and

14   a reduced concentration (<1%) of AA (17).   One of these mutants, S14, is used for the

15   commercial production of DGLA. ω3 Desaturase-defective mutants are unable to

16   synthesize n-3 PUFAs at temperatures below 20°C (18), although the wild strain

17   accumulates n-3 PUFAs such as EPA below that temperature.   Therefore, these

18   ω3-desaturase defective mutants are superior to the wild strain for lipid production with

19   a relatively high content of AA.   The fatty acid profile of elongase (EL1 for the

20   conversion of palmitic acid, 16:0, to 18:0)-defective mutants is characterized by high

21   levels of 16:0 and palmitoleic acid (16:1n-7), with small amounts of various kinds of

22   n-7 and n-4 PUFAs, as shown in Fig. 1c, which are not detected in the wild strain.   The

23   total content of these PUFAs in the oil reaches about 30%.   In a similar manner, n-1

24   PUFAs can be produced from n-1 hexadecenoic acid (16:1n-1) or 1-hexadecene added

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1   to the medium (see Fig. 1C).   Triacylglycerols produced by *M. alpina* 1S-4 account for

2   90% of the total lipids, whereas diacylglycerol-accumulating mutant KY1 derived from

3   the wild strain accumulates 30% diacylglycerols in the total lipids.   Lipid-excretive

4   mutant V6 shows the same lipid productivity and fatty acid composition as the wild

5   strain, and excretes 10-40% of the total lipids into the medium during submerged

6   cultivation.   Many lipid particles containing triacylglycerols are observed on the

7   surface of V6 mycelia cultivated on a solid medium.   V6 is assumed to excrete

8   accumulated lipids out of its mycelia due to its insufficient cell wall structure caused by

9   mutations in the metabolic pathways for cell wall synthesis.

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11   **Characterization of enzyme genes involved in PUFA biosynthetic pathways**   The

12   genes encoding the fatty acid desaturases and elongases involved in C20 PUFA

13   biosynthesis in *M. alpina* 1S-4 and its mutant strains were characterized, as described

14   below.   These nucleotide sequence information revealed mutation sites of the enzymes

15   in the representative mutants as described above (see Table 1).

16   The three $\Delta9$ desaturase homologues (designated as $\Delta9$-1, $\Delta9$-2, and $\omega9$) in *M. alpina*

17   1S-4 has a cytochrome b_5-like domain linked to its carboxyl terminus, as also seen for

18   the yeast $\Delta9$ desaturase (19).   *Mortierella* $\Delta9$-1 exhibits 45% and 34% amino acid

19   sequence similarity with those of *Saccharomyces cerevisiae* and rat, suggesting that the

20   *Mortierella* $\Delta9$-1 is a membrane-bound protein using acyl-CoA as substrates.   Both

21     $\Delta9$-1 and $\Delta9$-2 desaturate 18:0 to oleic acid (18:1n-9), whereas $\omega9$ desaturates a very

22   long saturated fatty acid (26:0) to the corresponding monounsaturated fatty acid

23   (26:1n-9) (20).   Although the *Δ9-2* gene is not transcribed in the wild strain, the *Δ9-2*

24   gene is transcribed and its derivative enzyme exhibits $\Delta9$ desaturation activities in $\Delta9$

1   desaturation-defective mutants which have a mutation site in its *Δ9-1* gene.

2   *Mortierella* Δ5 and Δ6 desaturases have a cytochrome b_5-like domain linked to its

3   N-terminus.   The two Δ6 desaturase homologues (designated as Δ6-1 and Δ6-2) are in

4   the wild strain, in which the *Δ6-1* gene is transcribed much more highly (2- to17-fold)

5   than the *Δ6-2* one (21).   *Mortierella* Δ12 and ω3 genes lacking a region encoding a

6   cytochrome b_5-like domain were cloned and characterized by means of heterologous

7   gene expression systems.   The gene expression analysis in yeast revealed that

8   *Mortierella* ω3 desaturase converts n-6 PUFAs to n-3 PUFAs with carbon 18 and 20

9   chain lengths, especially *Mortierella* ω3 desaturase could effectively convert AA into

10   EPA (22).

11   *M. alpina* 1S-4 possesses 4 kinds of genes encoding fatty acid elongases (MALCE1,

12   MALCE2, GLELO, and MAELO) involved in long chain saturated fatty acid or PUFA

13   biosynthetic pathways.   MALCE1 and MALCE2 belong to Δ9 elongases which

14   efficiently perform elongation of 16:1n-7, 18:2n-6, and 18:3n-3.   Furthermore,

15   MALCE1 plays an important role in the elongation of 16:0 to 18:0 in *M. alpina* 1S-4

16   (23).   GLELO is a Δ6 elongase which plays a critical role in the elongation of both

17   C18 n-3 and C18 n-6 PUFAs to the corresponding C20 PUFAs (24).   The enzyme

18   encoded by the *maelo* gene was demonstrated to be involved in the biosynthesis of

19   saturated fatty acids (20:0, 22:0, and24:0) in *M. alpina* 1S-4 (25).

20

21   **GENETIC MANIPULATION OF *M. alpina* STRAINS FOR PUFA**

22   **PRODUCTION**

23

24   **Development of a transformation system for *M. alpina* strains**   A transformation

system for *M. alpina* 1S-4 has been developed with *M. alpina* uracil auxotrophs and a complementary gene as selective marker (26). *M. alpina* uracil auxotrophs were isolated by spontaneous mutation on a solid medium containing 5-fluoroorotic acid, of which 0.5 mg/ml inhibited the growth of the wild strain completely, with the addition of a little uracil. The uracil auxotrophs were proved each to have a point mutation in the *ura5* gene encoding orotidine-5'-monophospate decarboxylase. These uracil auxotrophs, used in the transformation as hosts, were confirmed to exhibit the same lipid productivity, AA productivity, growth speed, and spore formation capacity as the wild strain.

Transformation with spores of *M. alpina* 1S-4 and a vector containing the *M. alpina* 1S-4 *ura5* gene as a marker has been performed through microprojectile bombardment (27), while other methods frequently used for transformation, such as ones involving protoplasting, lithium acetate, and electroporation, did not give satisfactory results, because of the difficulty of effective protoplast formation by the use of general and commercial lytic enzymes, such as chitinase, chitosanase, and glucanase, for cell walls. Transformants were obtained at a transformation frequency of 0.4 transformants/μg of vector DNA. Southern blot analysis revealed that most of the integrated plasmids in the stable transformants were present as several copies at ribosomal DNA (rDNA) positions and/or random positions in the chromosomal DNA.

An *Agrobacterium tumefaciens*-mediated transformation system for *M. alpina* 1S-4 has been developed (28), in which the *ura5* gene is used as a selectable marker under the control of the homologous histone H4.1 promoter in the transfer-DNA region. The frequency of transformation reached more than 400 transformants/10^8 spores. Southern blot analysis revealed that most of the integrated transfer-DNA appeared as a

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1   single copy at a random position in the chromosomal DNA.

2   *M. alpina* 1S-4 exhibits resistance to various antibiotics used in the transformation

3   systems of filamentous fungi.   A high concentration (20 mg/ml) of Zeocin completely

4   inhibited the germination of *M. alpina* 1S-4 spores, and decreased the rate of growth of

5   fungal filaments to some extent.   *M. alpina* 1S-4 showed Zeocin resistance with

6   integration of the Zeocin-resistance gene at the rDNA locus of the genomic DNA (29).

7   On the other hand, the fungicide carboxin (100 µg/ml) was found to inhibit the hyphal

8   growth and spore germination of *M. alpina* 1S-4 completely (30).   The *sdhB* gene

9   encodes the iron-sulfur (Ip) subunit of the succinate dehydrogenase (SDH, EC 1.3.99.1)

10   complex.   The mutated *sdhB* (*CBXB*) gene, which leads to an amino acid substitution

11   (H243L, a highly conserved histidine residue within the third cysteine-rich cluster of

12   SDHB being replaced by a leucine residue), conferred carboxin resistance.   The

13   transformants obtained with the homologous *CBXB* gene from *M. alpina* 1S-4 as a

14   selective marker exhibited carboxin resistance.   The *sdhC* gene encoding a subunit of

15   the SDH complex was also isolated from *M. alpina* 1S-4.   The *sdhC* gene has been

16   reported to act as a selectable marker instead of the *sdhB* gene (31).   In the same

17   manner, a mutated *sdhC* (*CBXC*) gene was constructed to encode a modified SdhC with

18   an amino acid substitution (H83K and T86I, highly conserved histidine and threonine

19   residues within a putative SDH quinine-binding site of SDHC being replaced by lysine

20   and isoleucine ones respectively).   Transformants obtained with a *CBXC* plasmid

21   exhibited carboxin resistance, too.   These genes for Zeocin and carboxin resistance are

22   thus useful as selective markers in the transformation not only of the parental strain, *M.*

23   *alpina* 1S-4, but also of its mutants.

24

PUFA production through molecular breeding of *M. alpina* A practical transformation system for *M. alpina* 1S-4 allows overexpression and RNA interference (RNAi) of the genes involved in PUFA biosynthesis for improvement of the production of various PUFAs. The valuable *Mortierella* mutants derived by chemical mutagenesis were directly transformed with drug resistance markers, or their uracil auxotrophs were transformed with the *ura5* marker. Molecular breeding of *M. alpina* 1S-4 and its mutants led to unique fatty acid profiles and high productivities of valuable PUFAs, as summarized in Table 2.

Mutant JT-180 exhibits no activities of $\Delta 12$ desaturase and enhanced $\Delta 5$ and $\Delta 6$ desaturase activities. On overexpression of the endogenous *$\Delta 12$* gene in JT-180, it accumulated a higher amount of AA (2.0 g/l/7 d, 39% of total fatty acids), instead of MA, due to both enhanced $\Delta 5$ and $\Delta 6$ desaturation as compared to the case of the wild strain (1.2 g/l/7 d, 21%).

Expression of the gene encoding GLELO, which has been suggested to be the limiting step in AA biosynthesis (32), was successfully performed in *M. alpina* 1S-4 (33). The resulting transformants yielded more AA (3.6 g/l/10 days, 28%) than the wild strain (1.9 g/l/10 days, 19%). In addition, overexpression of the endogenous *malce1* gene in *M. alpina* 1S-4 also led to faster and higher AA accumulation (0.76 g/l/6 d, 34%) than in the wild strain 1S-4 (0.68 g/l/6 d, 28%). Overexpression of both *malce1* and *glelo* genes had significant effects on AA production by *M. alpina* 1S-4.

The $\Delta 5$ and $\Delta 6$ (Pav$\Delta 5$ and Ost$\Delta 6$) desaturases from microalgae *Pavlova salina* and *Ostreococcus lucimarinus*, respectively, have desaturation activities for acyl-CoA forms of substrates. On the other hand, the $\Delta 5$ and $\Delta 6$ desaturases from *M. alpina* make phospholipids their substrates. By gene expression of these microalgal desaturases

1 with different substrate specificities for fatty acid derivatives in *M. alpina*, higher

2 contents of PUFAs might be obtained through molecular breeding.   Overexpression of

3 the *PavΔ5* gene in the wild strain led to a high rate of AA and a quite low rate of DGLA

4 in the total fatty acids, compared with AA and DGLA rates in the wild strain.   As the

5 same manner, overexpression of the *OstΔ6* gene in the wild strain led to a total higher

6 rate of 18:3n-6, DGLA and AA in the total fatty acid than that in the wild strain

7 Overexpression of the endogenous *ω3* gene in the wild strain and S14 (Δ5

8 desaturation-defective mutant) led to higher production of EPA (0.8 g/l, 30%) as shown

9 in Fig. 2 and 20:4n-3 (1.8 g/l, 35%), which usually comprise about 10% of the total

10 fatty acids in the wild strain and S14 cultivated at low temperatures (<20°C).

11 Molecular breeding of *ω3* gene-overexpressing transformants gave only high

12 productivities of these n-3 C20 PUFAs.   Overexpression of both the elongase *PavElO*

13 (involved in the conversion of C20 to C22 PUFAs in marine microalga *Pavlova* sp.) and

14 *ω3* genes in the wild strain led to the formation of C22 PUFAs, n-6 docosatetraenoic

15 acid (22:4n-6) and n-3 docosapentaenoic acid (22:5n-3).

16 RNAi method with double strand RNA was applied to silencing gene expression in

17 *M. alpina* 1S-4 (34).   *Δ12* Gene-silenced strains accumulated n-9 octadecadienoic acid

18 (18:2n-9), 20:2n-9, and MA, which are not detected in either the control strain or

19 wild-type strain 1S-4.   The fatty acid composition of these transformants was similar

20 to that of Δ12 desaturation-defective mutants previously identified.   Thus RNAi can be

21 used to alter the types and relative amounts of fatty acids produced by commercial

22 strains of this fungus as a simple method of silencing gene expression.

23 The RNAi of the *Δ12* gene in MALCE1 activity-defective mutant M1 led to an

24 accumulation of n-7 PUFAs and a decrease in n-4 PUFAs.   This indicates that n-4

PUFAs are biosynthesized from n-7 PUFAs by Δ12 desaturation. In addition, the M1 transformant obtained on RNAi of the *maelo* gene accumulated n-4/n-7 PUFAs with a decrease in n-6 PUFAs, which suggests that MAELO is involved in the elongation not only of long chain saturated fatty acids such as 20:0 and 22:0 but also of 16:0. Such molecular breeding of *M. alpina* strains should facilitate improvement of PUFA productivity and elucidation of the functions of the enzymes involved in PUFA biosynthesis.

CONCLUSION

The studies described above summarize our results related to PUFA production by oleaginous fungus *M. alpina* 1S-4 and the elucidation of fungal lipogenesis involved in PUFA biosynthesis. *M. alpina* 1S-4 and derivative mutants are potential sources of triacylglycerols rich in various PUFAs, including n-1, n-3, n-4, n-6, n-7, and n-9 PUFAs. It is possible to control the fatty acid profiles of fungal mutants and to regulate the flow of glucose or exogenous fatty acids to obtain a desired PUFA. The recent study on *M. alpina* and its mutants have been focused on molecular engineering of the enzyme genes involved in PUFA biosynthesis and pioneered the improvement of PUFA productivity. The breeding of mutants and transgenic strains may make it possible to produce desired PUFAs effectively. Further development of an efficient gene expression system for unique heterologous genes involved in such processes as lipid synthesis, PUFA synthesis, and lipid conversion, and construction of a homologous gene disruption system for *M. alpina* 1S-4 will enable elaboration of metabolic engineering for the production of various lipids with industrial interests.

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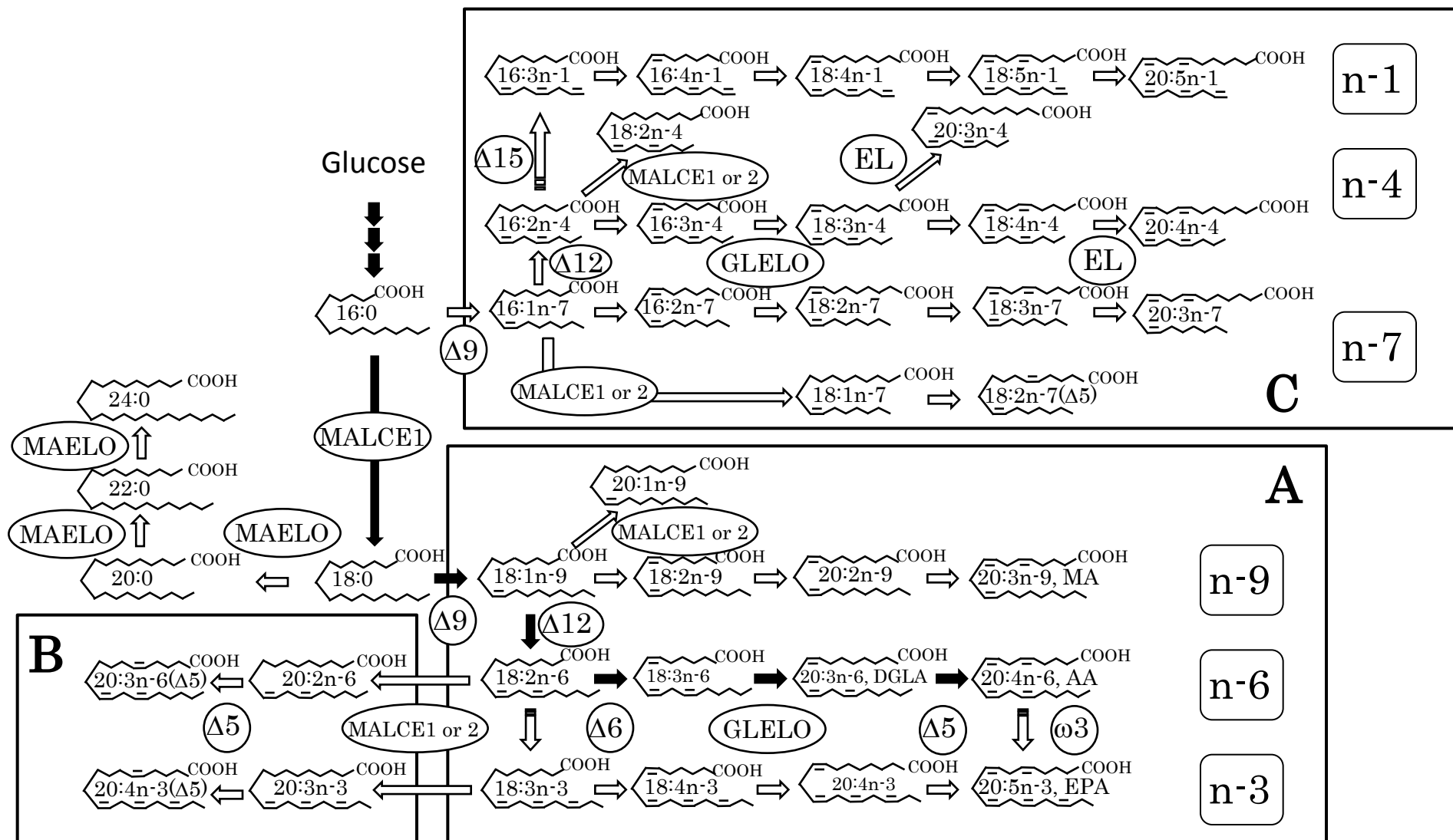
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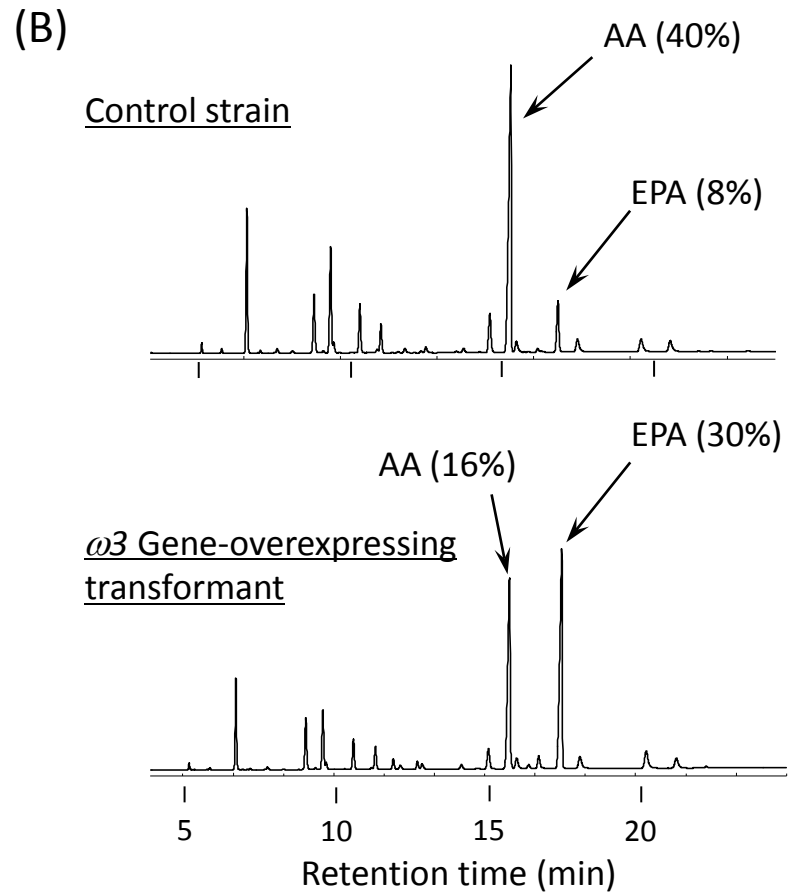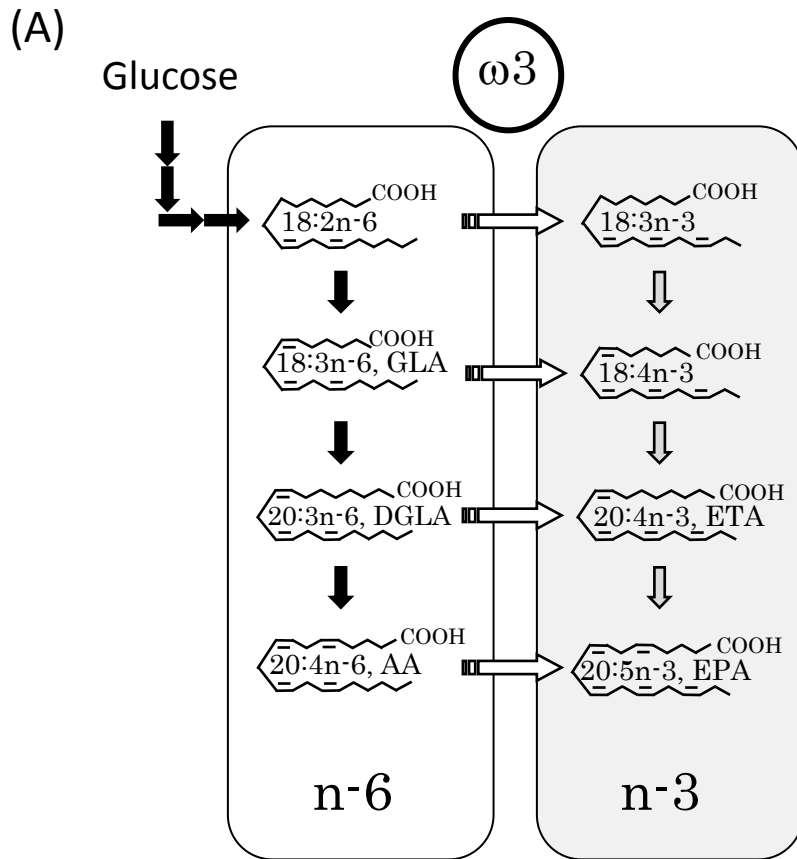
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Figure legends

FIG. 1. Pathways for the Biosynthesis of PUFAs in *M. alpina* 1S-4 and its Mutants. The n-3, n-6, and n-9 PUFAs are derived from 18:1n-9 (A), the nonmethylene-interrupted PUFAs are detected in $\Delta 6$ desaturase-defective mutants (B), and the n-1, n-4, and n-7 PUFAs are derived from 16:1n-7 (C). Black arrows show the AA biosynthetic pathway in the parental strain, *M. alpina* 1S-4. AA, arachidonic acid; ΔN, ΔN desaturase; DGLA, dihomo-γ-linolenic acid; EL, fatty acid elongase; EPA, eicosapentaenoic acid; MA, Mead acid; $\omega 3$, $\omega 3$ desaturase.

FIG. 2. Conversion of n-6 PUFAs to n-3 PUFAs by $\omega 3$ desaturase from *M. alpina* 1S-4 (A) and chromatograms of fatty acid methyl esters prepared from fungal cells. The strains were cultivated at 12˚C for 11 days.

(A)

Glucose

ω3

18:2n-6 COOH

18:3n-6, GLA COOH

20:3n-6, DGLA COOH

20:4n-6, AA COOH

n-6

18:3n-3 COOH

18:4n-3 COOH

20:4n-3, ETA COOH

20:5n-3, EPA COOH

n-3

(B)

Control strain

AA (40%)

EPA (8%)

ω3 Gene-overexpressing transformant

AA (16%)

EPA (30%)

5   10   15   20

Retention time (min)

TABLE 1. Lipid productivities of *Mortierella alpina* 1S-4 mutants

Deficient Enzyme	Mutation site	Parent strain	Mutant	Accumulation	Reference
Δ9	G265D	1S-4	T4	18:0 (40%)	13
Δ12	P166L	1S-4, Mut48[b], and M209-7[b]	JT-180	MA (2.6 g /L, 49% of total fatty acids) Enhanced activities of Δ5 and Δ6 desaturases	14
Δ12 and Δ5	P166L in (Δ12) and W301Stop (Δ5)	1S-4 and Mut48[b]	M226-9	20:2n-9 (2.2 g/L, 37%)	15
Δ6	Incorrect splicing	1S-4	Mut49	20:3n-6(Δ5) (0.48 g/L, 7%)	16
Δ5	Incorrect splicing	1S-4	S14	DGLA (4.1 g/L, 42%) and AA content (<1%)	17
ω3	W232Stop	1S-4	Y11	AA (1.5 g/L, 45%) without n-3 PUFAs	18
EL1	H154Y andT185I	1S-4	M1	16:0 (30%), 16:1n-7 (8%), and n-4/n-7 PUFAs (30%)	–
N.D. [a]	–	1S-4	KY1	Diacylglycerol (30% of total lipids)	–
N.D.	–	1S-4	V6	Lipid excretion (10-40% of total lipids)	–

[a]N.D., not determined.

[b]Mutants derived from *M. alpina* 1S-4.

TABLE 2. Molecular Breeding of *M. alpina* 1S-4 and Its Mutants for PUFA Production

Accumulated PUFA	Host[a]	Target gene[b]	Method[c]	Note
AA	JT-180	Δ12	OE	Higher AA production in JT-180 (2.0 g/l/7 days, 39% of total fatty acids) than wild strain 1S-4 (1.2 g/l/7 days, 21%)
AA	1S-4	*malce1*	OE	Higher accumulation of AA in a transformant (0.76 g/l/6 days, 34%) than wild strain 1S-4 (0.68 g/l/6 days, 28%)
AA	1S-4	*glelo*	OE	Higher AA production in a transformant (3.6 g/l/10 days, 28%) than wild strain 1S-4 (1.9 g/l/10 days, 19%)
AA	1S-4	*PavΔ5*	OE	A higher rate of AA (40%) and a lower rate of DGLA (1%) in a transformant than rates of AA (35%) and DGLA (4%) in wild strain 1S-4
AA	1S-4	*OstΔ6*	OE	A higher rate of AA (44%) in a transformant than (35%) that in wild strain 1S-4
EPA	1S-4	ω3	OE	High EPA production (0.8 g/l/11 days, 30%)
20:4n-3	S14	ω3	OE	High 20:4n-3 production (1.8 g/l/11 days, 35%)
22:4n-6, 22:5n-3	1S-4	*PavELO, ω3*	OE	Detection of small amounts of 22:4n-6 and 22:5n-3 in wild strain 1S-4
MA	1S-4	Δ12	Ri	Accumulation of n-9 PUFAs
20:3n-6(Δ5), 20:2n-6	1S-4	Δ6	Ri	Accumulation of 20:3n-6(Δ5) and 20:2n-6
16:0, 16:1n-7	1S-4	*malce1*	Ri	Accumulation of 16:0 and 16:1n-7
n-4/n-7 PUFA	M1	*maelo*	Ri	Accumulation of n-4/n-7 PUFAs and decrease of n-6 PUFAs
n-7 PUFA	M1	Δ12	Ri	Accumulation of n-7 PUFAs and decrease of n-4 PUFAs
18:0, PUFA	1S-4	*maelo*	Ri	No accumulation of 22:0 and 24:0, and small increases in 18:0 and the following n-6 PUFAs

[a]JT-180, Δ12 desaturase activity-defective mutant (see TABLE 1); M1, EL1 elongase activity-defective mutant; S14, Δ5 desaturase activity-defective mutant.

[b]The genes, except for *PavΔ5*, *OstΔ6*, and *PavELO*, were all derived from *M. alpina* 1S-4.

[c]OE, overexpression; Ri, RNAi.