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Identification of a novel type of polyunsaturated fatty acid synthase involved in arachidonic acid biosynthesis

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ABSTRACT

Arachidonic acid (ARA) is a polyunsaturated fatty acid (PUFA) and an essential component of membrane lipids. However, the PUFA synthase required for ARA biosynthesis has not been identified in any organism. To identify the PUFA synthase producing ARA, we determined the draft genome sequence of the marine bacterium *Aureispira marina*, which produces a high level of ARA, and found a gene cluster encoding a putative PUFA synthase for ARA production. Expression of the gene cluster in *Escherichia coli* induced production of ARA, demonstrating that the gene cluster encodes a PUFA synthase required for ARA biosynthesis.

1. Introduction

Polyunsaturated fatty acids (PUFAs) such as docosahexaenoic acid [DHA, 22:6(4,7,10,13,16,19)], eicosapentaenoic acid [EPA, 20:5(5,8,11,14,17)], and arachidonic acid [ARA, 20:4(5,8,11,14)] are essential components of membrane lipids and used as biosynthetic precursors of signaling molecules [1–4]. Two major pathways are known for PUFA biosynthesis. One is the aerobic pathway, in which saturated fatty acids synthesized by fatty acid synthase are desaturated and elongated by desaturases and elongases, respectively, to PUFAs [5–7]. The other is the anaerobic pathway, in which PUFAs are anaerobically synthesized from acetyl-CoA by PUFA synthases rather than multiple desaturation and elongation reactions [8,9]. In comparison with the aerobic pathway, the anaerobic pathway has some benefits for production of PUFAs [9]. The anaerobic pathway requires fewer reducing equivalents such as NADPH and produces simple fatty acids consisting solely of a specific fatty acid such as EPA and DHA.

PUFA synthases are composed of four to five separate multidomain proteins. Each protein has one to several domains responsible for PUFA synthesis. A PUFA synthase capable of synthesizing EPA was first found in *Shewanella* sp. [8,10], and then a PUFA synthase responsible for DHA biosynthesis was identified in the marine bacterium *Moritella marina* [11]. Although bioinformatic analyses of genomic data deposited in the databases have suggested PUFA synthases that may be involved in biosynthesis of other PUFAs other than EPA and DHA [12], the PUFA synthase required for ARA biosynthesis has not been identified in any organism. Because ARA is an omega-6 PUFA different from omega-3 PUFAs such as EPA and DHA, comparing PUFA synthases that produce ARA with those that produce EPA and DHA is important to understand the mechanism of how fatty acids are elongated and double bonds are inserted during PUFA biosynthesis.

Aureispira marina is a bacterium that belongs to the phylum Bacteroides. This bacterium was isolated from a marine sponge and algae collected from the southern coastline of Thailand and produces 30–40% ARA of total fatty acids [13]. However, how this bacterium produces ARA is still uncertain.

In this study, we identified the *A. marina* draft genome sequence and found a candidate gene cluster encoding a PUFA synthase for

Abbreviations: ACP, acyl-carrier protein; ARA, arachidonic acid; AT, acyltransferase; DHA, docosahexaenoic acid; EPA, eicosapentaenoic acid; ER, enoyl-ACP reductase; GC, gas chromatography; GC–MS, GC–mass spectrometry; DH, 3-hydroxyacyl-ACP dehydratase; FAME, fatty acid methyl ester; IPTG, isopropyl β-D-1-thiogalactopyranoside; KR, 3-ketoacyl-ACP reductase; KS, 3-ketoacyl-ACP synthase; LB, Luria–Bertani; MAT, malonyl-CoA:ACP transacylase; PCR, polymerase chain reaction; ppTase, phosphopantetheinyl transferase; PUFA, polyunsaturated fatty acid; X:Y(z), fatty acid containing X carbon atoms with Y double bonds in the *cis* configuration at position Z counted from the carboxy terminus

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ARA biosynthesis. Expression of the gene cluster in *Escherichia coli* resulted in the production of ARA, demonstrating that the gene cluster is involved in ARA biosynthesis. This is the first identification of a PUFA synthase for ARA production, and the information obtained in this study will provide a clue to understanding the mechanism of how ARA is synthesized by the anaerobic pathway and catalyzed by a PUFA synthase.

2. Materials and methods

2.1. Bacterial strains

A. marina (JCM23201) was obtained from the RIKEN Bioresource Center. The *E. coli* strains BW25113 (*lacIq*, *rrnBT14*, *ΔlacZWJ16*, *hsdR514*, *ΔaraBADAH33*, *ΔrhaBADLD78*) and a derivative of BW25113 (BW25113 *ΔfadE*::FRT) were obtained from the Keio Collection [14].

2.2. Gene identification

A. marina (JCM23201) genomic DNA was extracted from cells using a Wizard Genomic DNA Extraction kit (Promega, Madison, WI, USA) according to the manufacturer's instructions.

The nucleotide sequence of the genomic DNA was determined using a 454 GS FLX sequencer [15]. In total, 609 397 reads, including up to 196 000 700 bp were obtained, which represented a 33-fold coverage of the genome. Assembly was performed using the GS de novo assembler software program 454 and Velvet ver. 0.7.63, algorithms for de novo short read assembly [16]. Finally, we obtained the *A. marina* draft genome of 5.18 Mbp distributed in 103 contigs with a GC content of 37%. A putative PUFA gene cluster was identified using the NCBI BLAST tool. A local TBLASTN search of *pfa* genes known to produce EPA and DHA was performed against the draft genome sequence. A subsequent TBLASTN search of individual domains (KS, MAT, ACP, KR, DH, and ER) was performed. An additional round of sequencing using the Sanger method was performed for gap closure. Polymerase chain reaction (PCR) products were subjected to cycle sequencing with ABI BigDye Terminator v3.1 and analyzed on a 3730XL DNA Analyzer (Applied Biosystems, Foster City, CA, USA). A domain analysis of each *pfa* gene was carried out using the Pfam database [17]. The nucleotide sequence of the region including the gene cluster was deposited in DDBJ/EMBL/GenBank nucleotide sequence databases with accession number AB980240.

2.3. Vector construction

The *A. marina pfaABCDE* gene cluster was expressed in *E. coli* (BW25113 *ΔfadE*::FRT) using three compatible vectors; pUC19 [18] for *pfaE* expression, pSTV29 (Takara Bio, Otsu, Shiga, Japan) for *pfaA* and *pfaB*, and pMW219 (Nippon Gene, Tokyo, Japan) for *pfaC* and *pfaD*. The pUC19-*Plac-pfaE*, pSTV29-*Plac-pfaAB*, and pMW219-*Plac-pfaCD* plasmids containing one or two genes were transformed into *E. coli* cells to express the *pfa* genes. The *E. coli* cells were transformed by electroporation according to the method of Miller and Nickoloff [19]. The coding region of each gene was placed downstream of the *E. coli lac* promoter for inducible expression. The procedure to construct these expression vectors is described in the Supplemental Materials and methods.

2.4. Culture conditions

A. marina was cultivated at 25 °C on Sap2 medium [0.5 × artificial seawater (1.5% NaCl, 0.035% KCl, 0.54% $MgCl_2$, 0.27% $MgSO_4$, and 0.05% $CaCl_2$), 0.1% tryptone, 0.1% yeast extract, and 1.5% agar] [13]. Transformants of *E. coli* cells were cultivated by shaking in Luria–Bertani (LB) medium supplemented with 50 mg/L ampicillin, 10 mg/L kanamycin, and 20 mg/L chloramphenicol. A portion of the *E. coli* cells precultured at 30 °C was inoculated into fresh LB medium supplemented with antibiotics and 1 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) and then cultivated at 20 °C for 40 h. After the incubation, the *E. coli* cells were collected and used for lipid analysis.

2.5. Lipid analysis

Total lipids were extracted from *E. coli* by the method of Bligh and Dyer [20]. The extracted lipids were separated on thin-layer chromatography plates with a solvent system (chloroform/methanol:acetic acid, 65:25:5, by volume). The isolated lipids were subjected to methanolysis with 5% HCl in methanol at 85 °C for 2.5 h. The resulting fatty acid methyl esters (FAMEs) were analyzed by gas chromatography (GC; GC-2010; Shimadzu, Tokyo, Japan) with a flame-ionization detector and a capillary column (ULBON HR-SS-10, 0.25 mm in diameter and 25 m in length; Shinwa Kako, Bangkok, Thailand). Column temperature was maintained at 190 °C for 30 min. The flow rate of the carrier gas (nitrogen) was 1.35 ml min^{-1}. FAMEs were identified by comparing the retention time of each FAME with those of authentic standards and by analyzing each FAME by gas chromatography–mass spectrometry (GC–MS; GCMS-2010; Shimadzu). The positions of the double bonds in the FAMEs were determined by analyzing the pyrrolidide derivatives of FAMEs by GC–MS as described by Andersson and Holman [21]. A ULBON HR-52 capillary column (0.25 mm in diameter and 25 m in length; Shinwa Kako) was used for the GC–MS analysis. Column temperature was kept at 220 °C for 30 min. The flow rate of the carrier gas (helium) was 1.03 ml min^{-1}. Mass spectra were scanned every 0.3 s.

3. Results and discussion

3.1. Identification of a candidate PUFA synthase gene cluster involved in ARA biosynthesis

To identify a PUFA synthase gene cluster involved in ARA biosynthesis, we searched a gene cluster that shows similarities to a *S. oneidensis* MR-1 gene cluster for EPA biosynthesis [22] in the draft genome sequence of *A. marina*. We found a gene cluster containing five open reading frames (Fig. 1), which were homologous to the *pfaE*, *pfaA*, *pfaB*, *pfaC*, and *pfaD* genes of *S. oneidensis* MR-1. As described below, these genes encode components of the PUFA synthase responsible for ARA biosynthesis. Thus, we named these genes *pfaE*, *A*, *B*, *C*, and *D* (GenBank, accession number AB980240).

Domain analyses of the proteins encoded in the isolated *pfa* gene clusters revealed many enzyme and acyl-carrier protein (ACP) domains similar to PUFA synthases, which are responsible for EPA and DHA biosynthesis. As described by Lee et al. [22], the PUFA synthase of *S. oneidensis* MR-1 for EPA production is encoded in a gene cluster consisting of five genes (Fig. 1). The encoded proteins contained 10 enzyme domains and six repeated ACP domains: a 3-ketoacyl-ACP synthase (KS), a malonyl-CoA:ACP transacylase (MAT), six repeat ACP and a 3-ketoacyl-ACP reductase (KR) domains in PfaA; an acyltransferase (AT) domain in PfaB, a KS, a chain length factor (CLF), and two repeat 3-hydroxyacyl-ACP dehydratase (DH) domains in PfaC; an enoyl-ACP reductase (ER) domain in PfaD, and a phosphopantetheinyl transferase (ppTase) domain in PfaE. Although the structure of the gene cluster and domain organization of the *S. oneidensis* MR-1 encoded proteins for EPA production were similar to those of *M. marina* MP-1 for DHA production, there were some differences between the two