Research Article

Caenorhabditis elegans F09E10.3 Encodes a Putative 3-Oxoacyl-Thioester Reductase of Mitochondrial Type 2 Fatty Acid Synthase FASII that Is Functional in Yeast

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Caenorhabditis elegans F09E10.3 (dhs-25) was identified as encoding a 3-oxoacyl-thioester reductase, potentially of the mitochondrial type 2 fatty acid synthase (FASII) system. Mitochondrial FASII is a relatively recent discovery in metazoans, and the relevance of this process to animal physiology has not been elucidated. A good animal model to study the role of FASII is the nematode C. elegans. However, the components of nematode mitochondrial FASII have hitherto evaded positive identification. The nematode F09E10.3 protein was ectopically expressed without an additional mitochondrial targeting sequence in Saccharomyces cerevisiae mutant cells lacking the homologous mitochondrial FASII enzyme 3-oxoacyl-ACP reductase Oar1p. These yeast oar1Δ mutants are unable to respire, grow on nonfermentable carbon sources, or synthesize sufficient levels of lipoic acid. Mutant yeast cells producing a full-length mitochondrial F09E10.3 protein contained NAD+-dependent 3-oxoacyl-thioester reductase activity and resembled the corresponding mutant overexpressing native Oar1p for the above-mentioned phenotype characteristics. This is the first identification of a metazoan 3-oxoacyl-thioester reductase (see Note Added in Proof).

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1. Introduction

Eukaryotes have long been thought to undertake de novo fatty acid biosynthesis exclusively in their cytosol. This acyl carrier protein-(ACP-) dependent process relies on a single associative type 1 fatty acid synthase (FASI), which accommodates all the necessary enzyme activities. However, this traditional view has since been updated following the discovery of an additional mitochondrial FASII in yeast and mammals (reviewed in [1, 2]). FASII represents a dissociated system in which each of the enzyme activities occurs within a discrete protein. Although all of the fungal—and most of the mammalian—FASII constituents have been identified, the metazoan 3-oxoacyl-ACP reductase component has hitherto not been reported.

The present work is concerned with identifying the nematode mitochondrial FASII enzyme corresponding to 3-oxoacyl-ACP reductase. The C. elegans genome has been fully sequenced [5], and a cursory glance at the databases (WormBase, http://www.wormbase.org/) reveals that the nematode contains numerous enzymes with amino acid similarities to the mitochondrial 3-oxoacyl-ACP reductase Oar1p of Saccharomyces cerevisiae FASII [6]. In S. cerevisiae, FASII is critical for mitochondrial function and morphology, and a lesion to any one of the genes encoding FASII proteins results in a respiratory growth phenotype, underdeveloped mitochondria lacking cytochromes and, in some cases, loss of mitochondrial DNA [1, 2]. Here, S. cerevisiae was employed as a heterologous system for determining whether any of the candidate nematode proteins might represent a mitochondrial 3-oxoacyl-ACP reductase, by monitoring their ability to replace fungal Oar1p. S. cerevisiae oar1Δ cells heterologously expressing an active nematode 3-oxoacyl-thioester reductase were compared to an otherwise isogenic strain relying on an ectopically expressed native reductase for growth on glycerol, respiration, and lipoic acid production. The results in yeast are discussed with reference to the potential for a dysfunctional FASII in extending nematode lifespan.
The *Escherichia coli* Plasmids and oligonucleotides used are outlined in Table 1.

### Materials and Methods

#### 2.1. *S. cerevisiae* Strain, Plasmids, and Oligonucleotides

Plasmids and oligonucleotides used are outlined in Table 1. The *Escherichia coli* strain TOP10 F<sup>−</sup> was used for all plasmid amplifications and isolations. The mutant yeast BY4741 <del>Δ</del>oar1 <del>Δ</del>CTA1 was derived from BY4741 <del>Δ</del>oar1 <del>Δ</del>CTA1<sup>Δ</sup> MARKED YEp352 plasmid vector [3] and transformants were enriched on solid SD-Uro medium, described below.

#### 2.2. Plasmid Constructions

DNA work and plasmid assembly were undertaken according to standard methods [8]. The F09E10.3 and D1054.8 genes were isolated from cDNA by polymerase chain reaction using Phusion high fidelity DNA polymerase (Finnzymes Oy, Espoo, Finland) and the appropriate oligonucleotide pairs (Table 1). Subsequent processing of the resultant amplicons, including their electrophoresis, purification, and insertion into an *EcoRV*-digested *pBluescript* plasmid vector (Stratagene, La Jolla, CA) was performed as described [9]. The *pBluescript* inserts were isolated following digestion with *XbaI* and *Xhol* restriction enzymes, and ligated behind the *CTA1* promoter to *pYE352*:<del>CTA1</del> [4] from which the *CTA1* open reading frame encoding yeast peroxisomal catalase A was removed using the appropriate oligonucleotides Ce OAR1-1 refer to F09E10.3 and Ce OAR1-2 to D1054.8. The *CTA1* gene was then introduced into BY4741 <del>Δ</del>oar1 <del>Δ</del>CTA1<sup>Δ</sup> from which the *CTA1* open reading frame encoding yeast peroxisomal catalase A was removed using the appropriate oligonucleotides Ce OAR1-1 refer to F09E10.3 and Ce OAR1-2 to D1054.8.

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#### 2.3. Media, Growth, Enzyme Assays, Respiration Competence and Lipoic Acid Measurements

Standard media were prepared for yeast [10] and *E. coli* [11]. Episomal plasmids based on the *URA3*-marked *YEp352* plasmid vector [3] were retained in transformed *S. cerevisiae* strains by applying selective pressure using solid SD-Ura medium consisting of 0.67% (wt/vol) yeast nitrogen base without amino acids, 2% (wt/vol) D-glucose, 3% (wt/vol) agar, and with all necessary supplements added except for uracil (Sigma-Aldrich Inc, St. Louis, MO USA). Solid synthetic complete glycerol medium (SCglycerol) was prepared essentially as the aforementioned SD-Ura medium, with the exceptions that uracil was added and glucose was replaced with 3% (wt/vol) glycerol as the sole carbon source.

For high levels of protein expression prior to enzyme assays, yeast cells were grown on oleic acid medium as described [12]. Cells were broken with glass beads in a buffer consisting of 50 mM KP<sub>p</sub> (pH 7.0), 200 mM KCl, and 0.1% (wt/vol) Triton X-100. Protein concentrations [13] and reductase activities [14] were determined as described. The reductase activity assay mixture consisted of 50 mM KP<sub>p</sub> (pH 8.0) and 50 μM bovine serum albumin, 2 μM purified protein representing the hydratase 2 domain from human MFE2 (1/10 dilution of a 3 mg/ml stock), 125 μM NAD<sup>+</sup> or NADP<sup>+</sup>, and 60 μM 2-trans-hexenoyl-CoA [15]. In this assay, the reverse reaction was monitored, whereby the 2-trans-hexenoyl-CoA substrate was first hydrated by the aforementioned hydratase 2 domain of human MFE2 into the 3-hydroxyacyl-CoA, followed by the removal of two electrons from C3 by 3-oxoacyl-thioester reductase leaving behind a carbonyl group within the 3-oxoacyl-CoA product. To improve the sensitivity of the reductase assay, which was designed to be performed on crude extracts, the coincidental reduction of NAD<sup>+</sup> or NADP<sup>+</sup> into the corresponding NAD(H) and NADP(H) species was monitored spectrophotometrically at 340–385 nm, instead of just 340 nm, using a dual wavelength spectrophotometer (Shimadzu Corp., Kyoto, Japan) [16]. Respiration competence was monitored using an overlay consisting of 0.1% (wt/vol) 2,3,5-triphenyltetrazolium chloride (TTC) in phosphate-buffered saline and 1.5% (wt/vol) low-melting temperature agarose [17].

### Table 1: Plasmids and oligonucleotides used.

<table>
<thead>
<tr>
<th>Plasmid&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Description</th>
<th>Source/reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1) pBluescript KS II (+)</td>
<td>pKS cloning vector</td>
<td>Stratagene</td>
</tr>
<tr>
<td>pkS:F09E10.3&lt;sup&gt;1&lt;/sup&gt;</td>
<td>F09E10.3 in pBluescript</td>
<td>This study</td>
</tr>
<tr>
<td>pkS:D1054.8&lt;sup&gt;1&lt;/sup&gt;</td>
<td>D1054.8 in pBluescript</td>
<td>This study</td>
</tr>
<tr>
<td>(2) YEp352</td>
<td>URA3-marked multicopy plasmid</td>
<td>[3]</td>
</tr>
<tr>
<td>(3) YEp:CTA1&lt;sup&gt;2&lt;/sup&gt;</td>
<td>CTA1 behind its own promoter</td>
<td>[4]</td>
</tr>
<tr>
<td>YEp:F09E10.3&lt;sup&gt;3&lt;/sup&gt;</td>
<td>F09E10.3 behind the CTA1 promoter</td>
<td>This study</td>
</tr>
<tr>
<td>YEp:D1054.8&lt;sup&gt;5&lt;/sup&gt;</td>
<td>D1054.8 behind the CTA1 promoter</td>
<td>This study</td>
</tr>
<tr>
<td>YEp:OAR1&lt;sup&gt;3&lt;/sup&gt;</td>
<td>OAR1 behind the CTA1 promoter</td>
<td>Z.-J. Chen</td>
</tr>
</tbody>
</table>

<sup>a</sup>The superscripts following the plasmid designations refer to their parental vectors, for example, pKS:F09E10.3 was derived from (1) pBluescript KS II (+).

<sup>b</sup>Oligonucleotides Ce OAR1-1 refer to F09E10.3 and Ce OAR1-2 to D1054.8.
The content of lipico acid in yeast strains was estimated using a biological assay relying on lipico acid-deficient bacterial cells described previously [18, 19]. The assay determined the growth of these defective bacterial cells in liquid medium to which extracts were added that were generated from control and test yeast strains, and the growth values were converted to the amount of lipico acid present in the yeast cells based on a standard curve. Each yeast strain was grown in triplicates for 48 h in liquid SD-Ura medium selecting for plasmid presence. Acid hydrolysis was carried out in 0.5 ml 9 N H₂SO₄, and the assay products of both D1054.8 and F09E10.3 contained amino acid residues that appeared to correspond to the catalytic residues of 3-oxoacyl-ACP reductase gene whose RNAi inactivation might code for 3-oxoacyl-ACP reductases, the genes were oar1 like 3-oxoacyl-ACP reductase gene whose RNAi inactivation it was previously chronicled as the sole potential FASII-arrangement of the sequences for best fit. Black shadings refer to strictly conserved amino acid residues among all four sequences whereas the darker and lighter grey shadings denote regions with more relaxed residue similarities not necessarily shared by the full set of sequences. MitoProt (MP), PSORT II (PS), and TargetP (TP) algorithms were used to analyze the deduced amino acid sequences of the candidate genes, resulting in a prediction that the sequence relating to F09E10.3 (MP, 0.9232, 0.439, 0.505) had a probability of representing a mitochondrial protein that was equivalent to or higher than that calculated for the known yeast mitochondrial protein Oar1p (0.9166, 0.1, 0.244). In addition to F09E10.3, D1054.8 that calculated for the known yeast mitochondrial protein Oar1p (0.9119; PS, 0.1; TP, 0.540) had a probability of representing a mitochondrial protein that was equivalent to or higher than that calculated for the known yeast mitochondrial protein Oar1p (0.9166, 0.1, 0.244). In addition to F09E10.3, D1054.8 (0.9232, 0.439, 0.505) was also selected for investigation as it was previously chronicled as the sole potential FASII-like 3-oxoacyl-ACP reductase gene whose RNAi inactivation affected worm longevity [23]. The conceptual translation products of both D1054.8 and F09E10.3 contained amino acid residues that appeared to correspond to the catalytic triad previously characterized in bacterial FabG [24], albeit only within the amino acid sequence encoded by the latter nematode gene was the distance across the triad region fully conserved (Figure 1).

2.4. Mitochondrial Localisation Predictions and Sequence Comparisons. MitoProt (http://www.mips.biochem.mpg.de/cgi-bin/proj/medgen/mitofilter), PSORT II (http://psort.ims.u-tokyo.ac.jp/form2.html), and TargetP (http://www.cbs.dtu.dk/services/TargetP/) were used to calculate the N-terminal region of proteins that could support a mitochondrial targeting sequence [21, 22] and Multalin (http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_multalin.html) and Genedoc (http://www.nrbsc.org/gfx/genedoc/index.html) to generate the sequence comparison in Figure 1.

3. Results

3.1. Selection of Nematode F09E10.3 and D1054.8 for Analysis. The WormBase homology group identifier KOG1200, which refers to “mitochondrial/plastidial beta-ketoacyl-ACP reductases” (3-oxoacyl-ACP reductases), lists Y39A1A.11/dhs-11 and F09E10.3/dhs-25 as potentially encoding this activity in the nematode. However, there are approximately 28 additional genes annotated with the dhs designation (alcohol dehydrogenase/short chain). Moreover, the C. elegans genome contains a multitude of genes whose products are homologous to yeast mitochondrial Oar1p. To determine which of these genes might encode proteins residing in mitochondria, the MitoProt (MP), PSORT II (PS), and TargetP (TP) algorithms were used to analyze the deduced amino acid sequences of the candidate genes, resulting in a prediction that the sequence relating to F09E10.3 (MP, 0.9119; PS, 0.1; TP, 0.540) had a probability of representing a mitochondrial protein that was equivalent to or higher than that calculated for the known yeast mitochondrial protein Oar1p (0.9166, 0.1, 0.244). In addition to F09E10.3, D1054.8 (0.9232, 0.439, 0.505) was also selected for investigation as it was previously chronicled as the sole potential FASII-like 3-oxoacyl-ACP reductase gene whose RNAi inactivation affected worm longevity [23]. The conceptual translation products of both D1054.8 and F09E10.3 contained amino acid residues that appeared to correspond to the catalytic triad previously characterized in bacterial FabG [24], albeit only within the amino acid sequence encoded by the latter nematode gene was the distance across the triad region fully conserved (Figure 1).

3.2. Nematode F09E10.3 Restores Respiratory Growth to Yeast oar1Δ Cells. To determine whether F09E10.3 or D1054.8 might code for 3-oxoacyl-ACP reductases, the genes were expressed behind the promoter of yeast CTA1 encoding peroxisomal catalase A (Cta1p), which is only moderately derepressed on nonfermentable carbon sources such as glycerol, used here for complementation assays. On glycerol medium, yeast cells shift their metabolism to respiration, which requires an operational FASII within functional mitochondria [1, 2]. An extra fungal mitochondrial leader sequence was not fused to the nematode proteins. Yeast
strain, mutant cells expressing F09E10.3 could thrive on glycerol, whereas those mutant cells expressing CTA1 were not able to proliferate on this medium type. Hence, the respiratory-deficient phenotype of mutant oar1Δ cells was rescued following the expression of F09E10.3, indicating functional complementation.

Yeast cells lacking the native OAR1 gene have been shown before to lack assembled cytochrome complexes [6], and so their rehabilitation to normal respiratory growth was expected to occur contemporaneously with the assembly of cytochrome complexes and the regeneration of the electron transport chain. To examine whether mutant cells expressing Oar1p or the F09E10.3 protein contained a regenerated electron transfer chain, respiration competence was assayed by applying to the cells spotted onto solid SD-Ura medium an overlay consisting of 2,3,5-triphenyltetrazolium chloride (TTC). The results revealed that only mutant oar1Δ cells expressing Oar1p or the F09E10.3 protein could rapidly metabolize TTC to generate the red chromophore, whereas those expressing Cta1p were essentially white (lower panel; Figure 2).

3.3. Yeast oar1Δ Cells Expressing F09E10.3 Contain 3-Oxoacyl-Thioester Reductase Activity. FASII enzyme activities can often be measured in soluble protein extracts made from mutant yeast cells ectopically expressing heterologous proteins. For example, enzyme activities for 2-trans-enoyl-thioester reductase can be detected in protein extracts made from yeast etr1Δ mutant cells producing S. cerevisiae Etr1p [25], Candida tropicalis Etr1p or Etr2p [25, 26], and Mycobacterium tuberculosis InhA [9]. However, other FASII enzyme activities are less amenable to detection using this procedure. Although discernible levels of 3-hydroxyacyl-thioester dehydratase activity can be measured in extracts made from yeast htd2Δ mutants producing mycobacterial HadAB, HadBC, HtdX, HtdY, and HtdZ [27, 28], the sole documented measurement of dehydratase activity in mutant cells enriched for native Htd2p could only be undertaken following the laborious preparation of pure mitochondria [29].

To examine whether the F09E10.3 protein contained reductase activity, yeast cells were grown in triplicate cultures on oleic acid medium [12] under which conditions the CTA1 promoter is highly induced [30]. Oleic acid has not been shown previously to interfere with yeast FASII [9, 25, 27, 28]. The cells were broken with glass beads, and the ensuing soluble protein extracts were subjected to spectrophotometric analysis for reductase activity (in the reverse orientation), which ostensibly could depend on either NAD+ or NADP+ as co-factor. Enzyme assays performed on extracts from oar1Δ cells over-expressing native Oar1p, a presumed NADP+-dependent enzyme, did not yield appreciable levels of activity using the present assay. Likewise, mutant cells over-expressing Cta1p also failed to produce extracts with a specific reductase activity. On the other hand, soluble protein extracts obtained from mutant cells over-expressing the F09E10.3 protein gave rise to an NAD+-dependent oxidation of the 2-trans-hexenoyl-CoA substrate at the rate of 0.97 ± 0.18 (S.D., n = 3)
µmol/mg protein x min⁻¹. NADP⁺ did not act as co-factor when examining the nematode protein for reductase activity. Hence, ectopic expression of C. elegans F09E10.3 in yeast oar1Δ mutant cells resulted in clearly discernible levels of catalytic activity in an assay designed to expose 3-oxoacyl-thioester reductases.

3.4. Expression of F09E10.3 Restores Lipoic Acid Production in the oar1Δ Mutant. Lastly, to couple the expression of the F09E10.3 protein with fatty acid biosynthesis in yeast mitochondria, lipoic acid synthesis was measured in these strains. The results showed that the negative control strain (oar1Δ cells expressing peroxisomal catalase A) yielded extracts supporting only a minimal growth level of the mutant bacterial cells that was equivalent to 25 ± 3 ng lipoic acid per gram wet weight yeast cells, whereas levels of lipoic acid in mutant cells expressing fungal Oar1p or the nematode F09E10.3 protein gave rise to a bacterial growth that corresponded to 138 ± 22 or 80 ± 4 ng lipoic acid per or gram wet weight, respectively. Hence, the combined results demonstrated that mutant oar1Δ cells could grow on glycerol since their formerly defective mitochondrial functions were restored due to the expression of the full-length F09E10.3 protein, indicating that it represented a putative mitochondrial 3-oxoacyl-thioester reductase.

4. Discussion

The present study demonstrated a physiological function for the gene product of C. elegans F09E10.3/dhs-25 as a possible 3-oxoacyl-thioester reductase of mitochondrial FASII. The F09E10.3 protein could reach its designated subcellular compartment in fungi without resorting to a dedicated yeast mitochondrial targeting sequence, so as to replace the mitochondrial 3-oxoacyl-thioester reductase of mitochondrial FASII. The gene product of the oar1Δ mutation in C. elegans has hitherto not been identified in nematodes, its involvement in C. elegans lifespan extension could not be specifically addressed. If the lifespan extension observed with the RNAi intervention of C. elegans W09H1.5 [23], which encodes a potential homologue of the aforementioned yeast Etr1p, is in any way indicative, then a dysfunctional mitochondrial FASII might be conducive to longer nematode life. Worm longevity notwithstanding, the issue is that yeast FASII mutants will likely continue to play an important role in exposing FASII enzymes in metazoan mitochondria.

Note Added in Proof: Identification of human NAD(H)-dependent 3-oxoacyl-ACP reductase, HSKAR, of mitochondrial FASII, and the description of pYE352:OAR1 have been published online [35].

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References


