Down-Regulation of the ALS3 Gene as a Consequent Effect of RNA-Mediated Silencing of the EFG1 Gene in Candida albicans

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ABSTRACT

Background: The most important virulence factor which plays a central role in Candida albicans pathogenesis is the ability of this yeast to alternate between unicellular yeast and filamentous hyphal forms. Efg1 protein is thought to be the main positive regulating transcription factor, which is responsible for regulating hyphal-specific gene expression under most conditions. ALS3 is one of the Efg1-associated genes encoding a multi-functional adhesive polypeptide, which mediates adherence to diverse host substrates. In this study, the EFG1 gene was knocked down by using synthetic siRNA in C. albicans and the regulation in ALS3 as one of the Efg1-dependent genes was investigated.

Method: The 19-nucleotide siRNA was designed based on cDNA sequence of EFG1 gene in C. albicans. Transfection was performed using modified- ployethylene glycol/LiAc method. To quantify the level of EFG1 and the hyphal-specific ALS3 gene expression, the cognate EFG1 and ALS3 mRNA were measured in C. albicans by quantitative real-time RT-PCR.

Results: Fluorescent microscopy pictures indicated that transfection was performed successfully. Also, according to relative expression software tool, expression of EFG1 gene was decreased significantly with 500 nM siRNA as well as 1 µM siRNA ($P<0.05$). However, more significant down-regulations were observed in the expression of ALS3 in both concentrations of 500 nM and 1 µM siRNA ($P<0.05$).

Conclusion: In conclusion, we demonstrated the down-regulation of ALS3 gene as a consequent of applying EFG1-specific siRNA in C. albicans. This may lead us to design anti-fungal-specific agents in order to face with C. albicans-associated infections.

Keywords: Candida albicans, ALS3, RNAi, EFG1

INTRODUCTION

Candida albicans is polymorph diploid yeast, which is widely recognized as the most pathogenic yeast species [1]. While the species is harmless to most individuals, it can opportunistically overgrow and elucidate a variety of infections under certain settings [2]. Identifying the virulence-associated factors in Candida species is rather elaborated due to the fact that they are opportunistic pathogens and are not usually able to cause infections unless the host deficiencies permit [1]. The most important virulence factor which plays a central role in C. albicans pathogenesis is the ability of the yeast to alternate between unicellular yeast and filamentous hyphal forms [3]. Although yeast cells are possibly essential for dissemination and initial colonization, the hyphal cells seems to have a key role in adhesion, invasion and biofilm formation [4]. Moreover, hyphal but not yeast cells are found to involve epithelial cells in infected locations [5]. In general, a combination of the serum and the temperature of 37°C are powerful and robust signals for germ tube formation from yeast cells [6]. However, elevated temperature is essential for hyphae formation, but in embedded matrixes [6]. Efg1 is thought to be the main positive regulating transcription factor, which is responsible for regulation of hyphal-specific gene expression under most conditions, including serum, CO2, neutral pH and GlcNAc in liquid media as well as on solid media [3, 7-9]. The activation region of ALS3 gene is one of the regions where Efg1 binds and as a consequent, this binding leads to ALS3 gene up-regulation [10]. Als3 protein acts as a multi-functional adhesive molecule...
which mediates adherence to diverse host substrates, such as endothelial cells, oral epithelial cells, gelatin, fibrinogen and laminin [11, 12]. The adhesive molecule Als3 is likely to help the yeast to be colonized on solid surfaces. This ability can facilitate biofilm formation, a specialized form of adherence [13]. In addition to adherence, it is well-known that Als3 can mediate C. albicans invasion to oral epithelial and vascular endothelial cells [14]. Therefore, the importance of expression of this hyphal-specific gene is clear in initiating C. albicans-associated infections.

RNAi-mediated gene silencing methods have been recently used in several cell systems [15, 16] and ARE NEWLY APPLIED IN fungi [17-20]. The procedure is initiated by the either production or introduction of small RNA (~20-30 nucleotides). These RNA have a sequence complementary to a part of a target mRNA. siRNA generates from dsRNA by involving a member of the ribonuclease Dicer family (RNase H). Afterward, siRNA associates with members of the Argonaute family of proteins to form RNA-induced silencing complexes. These complexes use the siRNA as a guide for the sequence-specific silencing of target messenger RNA through induction of the degradation of the mRNA or repressing their translation [21, 22]. In the present study, the gene EFG1, which encodes a major positive regulator of germ tube production, was knocked down by using synthetic siRNA in C. albicans and the regulation in ALS3 as one of the Efg1-dependent genes was investigated.

MATERIALS AND METHODS

Strains. C. albicans wild-type strain ATCC14053 was used in the present study. The strain was cultured on yeast extract/pepton/dextrose medium plates, incubated at 37°C for 24 h and maintained at 4°C until use.

siRNA. The 19-nucleotide siRNA was designed based on cDNA sequence of EFG1 gene of C. albicans (Accession number: XM_709104.1). The anti-sense and sense sequences are 5’-Fluorescein Amidite-ACAUUGGCGAAUUUUGUUC-3’ and 5’-GAACCGAAUUUGCUCAAGUGU-3’, respectively. Unrelated siRNA, which is a scramble sequence of anti-sense strand, having a sequence 5’-AUAUGCGCAACAUUGUUC-3’ and sense sequences are 5’-Fluorescein Amidite-ACAUGGCAAUUUGGUC-3’. siRNA, which is a scramble sequence of anti-sense strand, having a sequence 5’-AUAUGCGCAACAUUGUUC-3’. Anti-sense strand of siRNA was labeled with a fluorescent dye, Fluorescein Amidite, so as to trace the siRNA localization in yeast cells. Sense anti-sense annealing was performed in an annealing buffer (30 mM HEPES-KOH [pH 7.4], 100 mM KCl, 2 mM MgCl2 and 50 mM NH4Ac) according to the protocol for siRNA annealing (http://www.metabion.com/downloads/siRNA annealing.pdf) to generate siRNA duplex with symmetric 2-nt 3’ overhangs.

C. albicans yeast culture and transfection. Yeast transfection was performed according to the basic protocol previously described for yeast transformation with some modifications [23]. C. albicans strain was grown on yeast nitrogen base medium at an initial absorbance of 0.2 at 623 nm (OD623 ≈ 0.2). The culture was incubated at 37°C with gentle shaking for 18-20 h. Afterward, when most C. albicans cells underwent exponential phase of their lifecycle, a final yeast concentration of 3 × 10^7 cells/ml (OD623 ≈ 0.6) was prepared and used for transfection. The cells were then harvested by centrifugation and washed twice with cold sterile PBS. The final solution was divided into microtubes in such a way that each 1.5 ml microtube contained 1 ml of the final solution (3 × 10^7 cells). Transfection was performed using modified-polyethylene glycol (PEG)/LiAc method. Briefly, to prepare competent yeasts, cells were re-suspended in 500 µl of 100 mM LiCl, mixed gently and centrifuged at 1,500 ×g for 2 min. Then, 240 µl 50% PEG 3350 and 36 µl 1.0 M LiCl were added to the pellet. siRNA was added in such a way that the final concentration of siRNA in each microtube reached to 1,000 nM (1 µM) and 500 nM. Therefore, a volume of 18 and 9 µl of annealed siRNA were added to the solution of each microtube. DEPC-treated water was lastly added to get a final volume of 360 µl. A positive (untransfected yeast cells) and a negative control (yeast cells treated with 1 µM of unrelated siRNA) were also run along with the experiment. Then, the cells suffered a heat shock in a water bath at 42°C for 40 min, followed by centrifugation at 3000 ×g for 30 s and by resuspension in 500 µl of yeast nitrogen base medium so as to allow the transfected cells to be recovered. Finally, the cultures were incubated without shaking at 37°C for 15 h. Transfected yeasts were then subjected to further studies.

siRNA entrance confirmation. To ensure that the entrance of siRNA was successful, samples of exponentially growing siRNA-treated C. albicans cultures were washed twice in sterile PBS. To remove any unused siRNA, samples were treated with RNase (Takara, Japan) and subjected to fluorescent microscopy. Samples of siRNA-treated cells (1 µM) were mounted on slides and examined. Fluorescence images were obtained using 100X objective lens on an Olympus fluorescent microscope (Olympus, UK) with the appropriate fluorescence filters. Photomicroscopy was performed using a Hitachi 12dp camera (Hitachi, USA). The locations of labeled siRNA were then defined.

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RNA extraction and quantitative real-time RT-PCR assay. In order to quantify the level of EFG1 and the hyphal-specific ALS3 gene expression, the cognate EFG1 and ALS3 mRNA were measured in C. albicans by quantitative real-time RT-PCR. Total RNA was extracted from both siRNA-treated (EFG1-specific and unrelated siRNA) as well as untreated cells using FastPure™ RNA kit (Takara, Japan) according to manufacturer’s protocol. RNA concentrations and RNA purity were determined spectrophotometrically using an Eppendorf BioPhotometer (Germany). An equal amount of RNA (1 μg in 20 μl) was subjected to cDNA synthesis by using PrimeScript RT reagent kit (Takara, Japan). EFG1 and ALS3 primers were designed on the bases of published sequences of the EFG1 (NCBI, Accession no.: XM_709104.1), and ALS3 (NCBI, Accession no.: XM_705343.1) genes in C. albicans. The β-actin gene (ACT1) was used as endogenous reference gene. The sequences of forward and reverse primers have been shown in Table 1. Standard curves for each gene were established with four serially diluted cDNA, which was obtained from cells grown to mid-logarithmic phase at 37°C using specific primers under the appropriate PCR conditions.

Real-time RT-PCR was performed with a StepOnePlus™ real-time PCR system (Applied Biosystems, USA) and SYBR® Premix Ex Taq™ II was used as a reagent specifically designed for intercalator-based real-time PCR using SYBR Green I. All PCR reaction mixtures contained: 10 μl SYBR® Premix Ex Taq™ II (2×), 2 μl first strand cDNA, 0.4 μM each primer, 0.4 μl ROX Reference Dye (50×) and dH2O up to the final volume of 20 μl. The program for amplification was 95°C for 30 s as initial denaturation step, followed by 40-cycle PCR consisting of 95°C for 5 s and 60°C for 30 s. Negative control (water as template) was included in each run. Expression of each investigated gene was normalized to the housekeeping ACT1 gene and analyzed by applying REST© (2008 V2.0.7) software, which analyzes data by use of comparative Ct method (ΔΔCt). Expression of EFG1 and ALS3 genes from cells grown under siRNA-treatment condition was indicated as relative expression to that of gene from untreated yeast cells. Each experimental condition was performed in duplicate and each experiment was repeated twice on two different days for reproducibility.

RESULTS

Transfection and siRNA entrance confirmation. To assess the potential of RNAi as a means of gene silencing in C. albicans, we benefited from the modified PEG/LiAc method for double-stranded RNA to be introduced into the cells. Florescent microscopy method was used at the first step of evaluating the efficiency of C. albicans transfection and more important, to trace the siRNA localization in yeasts. Yeast cells were harvested 15 h post transfection, washed, mounted and visualized. Apparently, only yeast cells with labeled-siRNA inside were luminous enough to be traced. Figure 1 indicates that the transfection was performed successfully.

Quality control and effect of siRNA on EFG1 gene expression. EFG1, ALS3 and ACT1 mRNA levels were monitored over a 15-h period of yeast incubation with both unrelated and EFG1-specific siRNA. Positive control (untreated C. albicans cells) was also included in each run of experiment. EFG1, ALS3 and ACT1 primers demonstrated similar efficiency in titration experiment using C. albicans cDNA in serial dilutions (data not shown). Expression of each gene was indicated as expression ratio relative to that of untreated logarithmic-phase grown yeasts. REST© (2008 V2.0.7) software was applied to analyze the obtained data of quantitative real-time RT-PCR. On the basis of REST© output, expression of EFG1 gene was decreased about 2 folds using 500 nM siRNA. Meaningfully, a 5.5-fold decrease in EFG1 gene expression was observed when applying 1 μM of siRNA (P<0.05). The level of EFG1 mRNA in cells affected with unrelated siRNA was the same as positive control and unchanged (P>0.05). Figure 2 shows the relative expression ratio of EFG1 and ALS3 genes under different conditions. Furthermore, the expression of ALS3, the hyphal-specific genes regulated by EFG1, was considerably down-regulated and there were significant differences between ALS3

**Table 1. PCR primers for real-time RT-PCR analysis.**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer name</th>
<th>Sequence (5'-3')</th>
<th>PCR product size (bp)</th>
<th>GenBank</th>
</tr>
</thead>
<tbody>
<tr>
<td>EFG1</td>
<td>Fefg140</td>
<td>TgCCAATAATgTgTCggTtg</td>
<td>140</td>
<td>XM_709104.1</td>
</tr>
<tr>
<td></td>
<td>Refg140</td>
<td>CCCATCTCTCTCACACACgTgTC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ACT1</td>
<td>Fact110</td>
<td>ACggTATTgtTTCCAATgAAgCg</td>
<td>110</td>
<td>XM_717232.1</td>
</tr>
<tr>
<td></td>
<td>Ract110</td>
<td>TggAgCTTCgTgTCAACAAAACgTgg</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ALS3</td>
<td>Fals141</td>
<td>gCTggTggTTATTgCAAGCgTgC</td>
<td>141</td>
<td>XM_705343.1</td>
</tr>
<tr>
<td></td>
<td>Rals141</td>
<td>TggTAAGgTggTCACgCgg</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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gene expression in positive control (untreated cells) and test sample yeasts ($P < 0.05$). An 8-fold reduction in the expression $ALS3$ gene was observed when $500$ nM siRNA was added to $EFG1$ mRNA (Table 2).

**DISCUSSION**

During $C. albicans$ infection, epithelial cells are invaded by two distinct routes: in the first route, hyphal cells induce endocytosis by the host cells in which the adhesive molecule $ALS3$ is necessary [24]. In the second route, hyphal cells penetrate actively in the plasma membrane [8]. Invasion of oral epithelial cells occurs through both routes, while active penetration is the only route by which $C. albicans$ invades intestinal epithelial cells [8]. Despite the roles of hyphae during infections due to $C. albicans$, the issue that the hyphae are required for virulence is still difficult to prove [6]. One of the crucial functions of Efg1 is up-regulation of $ALS3$ gene expression [10]. $ALS3$ is one of the members of agglutinin-like sequence gene family in $C. albicans$ [25, 26]. The family of this gene comprises eight members ($ALS1-7$ and $ALS9$), which encode cell surface proteins with the same overall structure [27]. $ALS3$ gene encodes a protein called Als3, which is now considered as a multi-functional adhesion and invasion. This adhesive molecule mediates adherence to various kinds of substrates, such as laminin, gelatin, salivary pellicles etc. This function can be led to produce biofilm, which is a kind of specialized form of adherence [11, 12]. Moreover, endocytosis is one of the strategies by which $C. albicans$ can invade to both epithelial and endothelial cells. However, hyphae of $C. albicans$ are more likely to be endocytosed rather than yeast-phase organisms. This suggests that hyphae express specific molecule such as Als3, which can bind to one or more receptors in host cells and induce endocytosis [24]. This adhesive molecule is able to form a mixed-species biofilm with *Streptococcus*.
gene silencing is likely to be considered as a promising approach to discover new gene targets. This may lead
generation of new gene targets. This may lead
generate silencing protein among fungal species, RNA previously applied before.
for yeast transfection described here had not been
generated spores from media. However, the method
transfection, except for Khatri as a model system. In all mentioned studies, vector-
transduction of gene expression in the fungus. In 2007, Khatri
expression of genes, have been investigated and significant reductions in both gene
regulations were indicated. Outputs for real-time RT-
expression in the yeast of control and sample groups are significant as well as the expression of
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silencing pathway appears to have been diversified in
this kingdom [30]. In the case of C. albicans, it was reported that the RNA silencing machinery is probably
absent because the Dicer involved in the silencing pathway lacks both a helicase and PAZ (Piwi Argonaute
and Zwille) domain [33]. According to Candida Genome Database, the genome of C. albicans holds a
typical Argonaute homologue (orf19.2903; www.
candidagenome.org), and a non-canonical Dicer (orf19.3796; www.candidagenome.org). Interestingly, the
nucleotide sequence of the Dicer (orf19.3796) is only conserved among Candida species. However, the
deduced amino acid sequence has quite high homology with ribonuclease of other fungal species. Moreover,
the yeast C. albicans harbors a probable ribonuclease III protein. Remarkably, the homology of the amino
cid acid sequences of ribonuclease III protein and the so-called Dicer protein (orf19.3796) is 100% after
contains DSRM (double-stranded RNA binding motif) and ribonuclease III C terminal domain. Despite that
Candida Dicer lacks a PAZ and helicase domain, it contains a DSRM and ribonuclease III C terminal
domain. DSRM domain binding is not sequence specific, but is highly specific for double stranded
RNA. Therefore, based on the above mentioned arguments and the results obtained in this study, it
supposed that the Dicer of C. albicans is functional and effectively participate in RNAi silencing pathway. The
Argonaute protein of the pathogenic yeast C. albicans holds both PiWi and PAZ domains, which are essential
motifs for Argonaute function and dsRNA binding. Therefore, it can be suggested that the RNAi gene
silencing pathway is functional in this microorganism.

In conclusion, we established that RNAi is an applicable tool for functional silencing of EFG1 gene
expression in C. albicans in a dose-dependent manner. We have also demonstrated the consequence effect of
this gene silencing on the down-regulation of ALS3 gene expression in C. albicans. Post transcriptional
gene silencing is likely to be considered as a promising approach to discover new gene targets. This may lead

Table 2. Output for relative expression of EFG1 and ALS3 genes by use of ΔΔCt method (REST®, 2008 V2.0.7). Results indicate
the differences between EFG1 expression in the yeast of control and sample groups are significant as well as the expression of
ALS3 gene.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Type</th>
<th>Reaction Efficiency</th>
<th>Expression</th>
<th>Standard Error</th>
<th>95% C.I.</th>
<th>P(H1)*</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACT1</td>
<td>REF</td>
<td>1.0</td>
<td>1.000</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EFG1</td>
<td>TRG</td>
<td>1.2</td>
<td>1.046</td>
<td>0.636 - 1.820</td>
<td>0.482 - 2.277</td>
<td>0.638</td>
<td></td>
</tr>
<tr>
<td>EFG1</td>
<td>TRG</td>
<td>1.2</td>
<td>0.357</td>
<td>0.209 - 0.674</td>
<td>0.153 - 0.858</td>
<td>0.000</td>
<td>DOWN*</td>
</tr>
<tr>
<td>ALS3</td>
<td>TRG</td>
<td>0.8</td>
<td>0.122</td>
<td>0.066 - 0.288</td>
<td>0.049 - 0.347</td>
<td>0.000</td>
<td>DOWN</td>
</tr>
<tr>
<td>ALS3</td>
<td>TRG</td>
<td>1.0</td>
<td>0.179</td>
<td>0.101 - 0.394</td>
<td>0.080 - 0.487</td>
<td>0.000</td>
<td>DOWN</td>
</tr>
</tbody>
</table>

*P(H1), probability of alternate hypothesis that difference between sample and control groups is due only to chance. *TRG, target; *REF, reference; *down-regulation of ALS3 and EFG1 genes after using siRNA; C.I., confidence interval.

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us to design anti-fungal-specific agents in order to face with C. albicans-associated infections via inhibiting the production of true hyphae and subsequently hyphal-wall specific proteins of the yeast C. albicans.

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