SYR2, a gene necessary for syringomycin growth inhibition of *Saccharomyces cerevisiae*

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The *Pseudomonas syringae* cyclic lipodepsipeptide syringomycin inhibits the growth of *Saccharomyces cerevisiae*. A novel yeast gene, SYR2, was found to complement two syringomycin-resistant *S. cerevisiae* mutants. SYR2 was cloned, sequenced, and shown to encode a 349 amino acid protein located in the endoplasmic reticulum. SYR2 was identical to SUR2, which is involved in survival during nutritional starvation. Gene disruption or overexpression of SYR2 did not affect cell viability or ergosterol levels, but did influence cellular phospholipid levels. The findings suggest that phospholipids are important for the growth inhibitory action of syringomycin.

Keywords: syringomycin, SYR2, *Saccharomyces cerevisiae*, SUR2, phospholipid biosynthesis

INTRODUCTION

Syringomycin is a small cyclic lipodepsipeptide produced by stone-fruit and grass isolates of *Pseudomonas syringae* pv. *syringae* (Segre et al., 1989; Fukuchi et al., 1990; Takemoto, 1992). Generally considered a nonhost-specific phytotoxin (Gross & Devay, 1977), syringomycin also inhibits the growth of fungi, particularly yeasts such as *Saccharomyces cerevisiae* and *Rhodotorula pilimanae* (Zhang & Takemoto, 1986, 1987). Thus, it may play dual roles as a plant virulence factor and an antifungal agent against fungal competitors on plant surfaces (Takemoto, 1992). Several structurally related cyclic lipodepsipeptides produced by *P. syringae* strains have been identified. These include the syringostatins produced by a lilac isolate (Fukuchi et al., 1992), syringotoxin produced by citrus isolates (Ballio et al., 1990), and the pseudomycins produced from a barley isolate mutated with a transposon (Ballio et al., 1994).

The cellular site of action of syringomycin is the plasma membrane. It alters several membrane functions such as membrane potential, protein phosphorylation, H+-ATPase activity, and cation-transport fluxes (Zhang & Takemoto, 1987, 1989; Bidwai et al., 1987; Bidwai & Takemoto, 1987; Suzuki et al., 1992). The relationships of these activities and their relative importance in the response to syringomycin exposure are not clear. To learn more about the mode of action of syringomycin, recessive syringomycin-resistant strains of *S. cerevisiae* were isolated and characterized (Takemoto et al., 1991, 1993). One class of mutants (yr1) were deficient in membrane ergosterol and sensitive to high external Ca2+ levels. yr1 mutants were complemented by gene *SYR1* (identical to *ERG3*) that encodes the ergosterol biosynthetic enzyme C-5 sterol desaturase (Taguchi et al., 1994). Therefore, ergosterol is necessary for syringomycin action, and the binding of syringomycin to this lipid in the plasma membrane has been proposed (Jumapan et al., 1993). Other classes of syringomycin-resistant mutants with normal ergosterol levels have been identified (Takemoto et al., 1993). Such mutants presumably have defects in other genes whose products are necessary for syringomycin action.

In this paper, we describe the cloning and characterization of yeast gene *SYR2* that complements certain syringomycin-resistant mutants with normal ergosterol levels. *SYR2* is shown to be identical to *SUR2* (Desfarges et al., 1993), which is involved in survival during nutritional starvation. The *SYR2*-encoded protein is shown to associate with the endoplasmic reticulum and to have a role in phospholipid metabolism. The findings suggest that phospholipids are important for syringomycin action.

METHODS

Organisms and general genetic methods. *S. cerevisiae* syringomycin-resistant mutants 13N-F2 and 3N-H1 were isolated from haploid strain KZ1–1C (*MATa his3 leu2 trp1 ura3*), and were previously described by Takemoto et al. (1993). Syringomycin-
resistant mutant 28N-D6 was also derived from KZ1-1C and was shown by diploid analysis to be in the same genetic complementation group as 13N-F2. Resistant mutant 3N-H1 was defective in SYR1 (also designated ERG3), which encodes the sterol biosynthetic enzyme C-5 sterol desaturase (Taguchi et al., 1994). For gene cloning, *Escherichia coli* strains DH5 and HB101 were used (Sambrook et al., 1989). Yeast plasmid shuttle vectors YCPN1 (Liu et al., 1991), YCP50 (Rose et al., 1987), YEp24 (Rose & Broach, 1991) and pYES2 (Invitrogen) were used. Genomic libraries of KZ1-1C were prepared in YCp50 and YCPN1 as described by Rose & Broach (1991). Yeast extract-peptone-dextrose (YPD), minimal salts-dextrose minus uracil (SD-URA) and minimal salts-galactose minus uracil (SG-URA) growth media were prepared as described by Rose et al. (1990). Syringomycin was added to growth media at concentrations ranging from 0.5 to 2.0 μg ml⁻¹. Yeast transformations were done using the lithium acetate method (Ito et al., 1983) or by electroporation (Becker & Guarente, 1991). After transformation, yeast cells from single colonies growing on selective agar media were suspended in 100 μl water in microtitre plate wells. Cells were replica-plated onto YPD agar medium and YPD agar medium containing syringomycin. After 48 h the plates were visually inspected for clones showing little or no growth on syringomycin-containing plates but normal growth on plates without syringomycin. Genetic complementation tests of syringomycin-resistant strains were performed as previously described by Takemoto et al. (1993).

**SYRINGOMYCIN PURIFICATION.** Syringomycin (E form) was purified as described previously by Bidwai & Takemoto (1987).

**NESTED DELETION SUBCLONING OF SYR2.** Nested deletions were performed using the Erase-a-Base system (Promega). A 4.8 kb SYR2 clone (Spdl—Spbl) contained in pBluescript II (Stratagene) was used. The plasmid was linearized at KpnI and SalI restriction sites, and then subjected to exonuclease III digestion for varying lengths of time to unidirectionally excise portions of insert DNA. After exonuclease III excision, the DNA was treated in succession with S1 nuclease, Klenow DNA polymerase and T4 DNA ligase according to the manufacturer's protocol. The resulting SYR2 subclones were transferred to pBluescript I1 (Stratagene) and used for hybridization to the RNA fragments. A HindIII site was borrowed from the fragment Scll—Spbl was ligated with blunt ends to the SmaI site of the pGEX-KG vector. A HindIII site was inserted in-frame with the GST end of SYR2 into pGEX-KG at the corresponding site. HpaI—Spbl product was produced. The fusion protein was purified and the GST—Syr2 fusion protein was cleaved with thrombin as described by Smith & Johnson (1988). Peptide Syr2 was purified by SDS-PAGE using a 8–15% (w/v) gradient polyacrylamide gel. After staining with Coomassie Blue, the Syr2 fragment was excised, and the N-terminus (31 amino acids) was sequenced at the lower and upper interfaces, respectively. Vanadate-sensitive H⁺-ATPase and NADPH-cytochrome-c oxidoreductase activities were used to verify the identification of the plasma and endoplasmic reticulum membrane fractions, respectively (Marriott & Tanner, 1979). Samples (30–50 μg protein per lane) were analysed by SDS-PAGE. After electrophoresis, the proteins were transferred to nitrocellulose membranes and Western-blotted as described by Harlow & Lane (1988).

**PROTEIN DETERMINATION.** Protein concentrations were determined using Coomassie Protein Assay Reagent (Pierce) and BSA as standard.

**ALKALINE PHOSPHATASE TREATMENT OF CRUDE MEMBRANES.** Crude membranes (50 μg protein) in 200 μl phosphate buffer (10 mM Tris/HCl, pH 9, 1 mM ZnCl₂, 1 mM MgCl₂) were treated with 17 U alkaline phosphatase (Boehringer Mannheim) at 37°C for 30 min.

**PREPARATION OF SYR2 FUSION PROTEIN AND ANTISERUM.** The bacterial vector pGEX-KG (Guan & Dixon, 1991) was used to prepare a Syr2–glutathione-S-transferase (GST) fusion protein. Initially, an EcoRI—SalI fragment containing intact SYR2 was cloned into the vector. Expression of this GST–Syr2 fusion protein severely restricted the growth of E. coli and the fusion protein was not isolated in sufficient quantities. Subsequently, the HpaI—Spbl fragment from SYR2 (encoding the C-terminal 124 amino acids) (Fig. 2b) was inserted in-frame with the GST sequences to produce a GST–Syr2 fusion protein. The 5' end of the fragment (HpaI) was ligated with blunt ends to the SalI site of the pGEX-KG vector. A HindIII site was borrowed from pBluescript II phagemid (Stratagene) and used to clone the 3' end of SYR2 into pGEX-KG at the corresponding site. E. coli HB101 was transformed with the construct. Upon IPTG induction, a 40 kDa polypeptide presumed to be the fusion product was produced. The fusion protein was purified and the Syr2 peptide was cleaved with thrombin as described by Smith & Johnson (1988). Peptide Syr2 was purified by SDS-PAGE using a 8–15% (w/v) gradient polyacrylamide gel. After staining with Coomassie Blue, the Syr2 band was cut from the gel. The gel slice was fragmented and prepared for injection as described by Harlow & Lane (1988). Rabbit antisera was prepared by immunizing rabbits with 75 μg protein in Freund's complete adjuvant. Booster injections of 40 μg protein in Freund's incomplete adjuvant were given 10–14 d before collection of sera. The sera were used directly for Western blot analysis.

To confirm the Syr2 peptide sequence, the peptide was transferred to Immobilon-P membrane (Millipore) using the method of LeGendre & Matsuda (1989). The membrane was stained with Coomassie Brilliant Blue, the Syr2 fragment was excised, and the N-terminus (31 amino acids) was sequenced at the Utah State University Biotechnology Center (Logan, UT, USA). The sequence included two residues (Gly—Ser) encoded by vector sequences remaining after thrombin cleavage.
**SYR2 disruption.** A 2.3 kb pBluescript clone of SYR2 created by nested deletion was used to construct the SYR2-disruptant strain. Plasmid C1 was constructed by replacing the HpaI–EcoRV segment of SYR2 with a 1.2 kb HindIII fragment containing URA3 from plasmid YEp24. The C1 plasmid was digested with SalI and SphI, and the resulting 3.14 kb linear fragment was purified and used to transform diploid strain W303–1A (MATa/MATr bis3 leu2 trpl1 ura3). The one-step gene disruption method was used (Rothstein, 1983). Transforms were induced to sporulate, and the spores were dissected for tetrad analysis (Rose et al., 1990). A typical SYR2-disrupted segregant was selected and designated strain W303ΔSYR2 and a corresponding non-disrupted strain was selected and designated W303C.

**SYR2 overexpression.** The PstI–SphI fragment of SYR2 was cloned into the GAL1 promoter-containing vector pYES2 to yield pY3SYR2. pYSYR2 allowed overexpression of SYR2 in SG-URA growth medium. The PstI–SphI fragment was missing the first ATG start codon and the following 24 codons, yielding an expressed protein that was shorter than intact Syr2.

**Chromosomal localization.** Yeast chromosomes were separated by PFGE using a Bio-Rad CHEF DR-II system. Chromosomal DNA was electrophoresed in 1% (w/v) agarose at 200 V. Pulse time was 60 s for 15 h followed by 90 s for 9 h. DNA for Southern blotting was digested with appropriate restriction enzymes and separated on 0.7% (w/v) agarose gels. DNA was transferred to nylon membranes as described by Sambrook et al. (1989). The SYR2 probe was the same as described above for Northern blot analysis. A Dictyostelium actin-8 probe was also used, prepared by digesting an actin-8 clone contained in pMB9 with HindIII and labeling by PFGE using a Bio-Rad CHEF DR-I1 system. Chromosomal localization. Yeast chromosomes were separated by PFGE using a Bio-Rad CHEF DR-II system. Chromosomal DNA was electrophoresed in 1% (w/v) agarose at 200 V. Pulse time was 60 s for 15 h followed by 90 s for 9 h. DNA for Southern blotting was digested with appropriate restriction enzymes and separated on 0.7% (w/v) agarose gels. DNA was transferred to nylon membranes as described by Sambrook et al. (1989). The SYR2 probe was the same as described above for Northern blot analysis. A Dictyostelium actin-8 probe was also used, prepared by digesting an actin-8 clone contained in pMB9 (Romans & Firtel, 1985) (supplied by Dr Dennis L. Welker, Utah State University, UT, USA) with HindIII and labeling with the ECL system as described above.

**Phospholipid and ergosterol analyses.** Cells were extracted with chloroform/methanol (3:1, v/v) and the phospholipids were purified as described by Radin (1969). Total lipid masses were determined after drying the chloroform/methanol lipid extracts. Total phospholipid phosphate amounts were determined using a modified Fiske & Subbarow method described by Cooper (1977). Individual phospholipids were resolved by one-dimensional TLC (silica gel G-60, Merck; 20 × 20 cm) using chloroform/methanol/acetic acid/water (25:15:4:2, by vol.) as the developing solvent. For phospholipid detection, plates were sprayed with molybdenum blue reagent (Dittmer & Lester, 1964). Authentic samples of phosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, phosphatidylserine and cardiolipin (Sigma) were used as standards. For ergosterol analysis, nonsaponifiable lipid extracts (Radin, 1969) were chromatographed on silica gel G-60 (Merck; 20 × 20 cm) thin-layer plates using n-hexane/diethyl ether/acidic acid (70:30:1, by vol). After chromatography, the plates were sprayed with phosphomolybdic acid spray reagent (Sigma) for visualization of ergosterol.

**RESULTS**

**SYR2 cloning.** Genetic complementation analyses showed that syringomycin-resistant strains 13N-F2 (Takekoto et al., 1993) and 28N-D6 had closely linked mutant alleles designated syr2. In contrast to other mutations that conferred syringomycin resistance, syr2 mutations did not affect ergosterol biosynthesis (Takekoto et al., 1993; Taguchi et al., 1994). Strains 13N-F2 and 28N-D6 were transformed with genomic libraries prepared in yeast centromeric vectors YCP11 and YCP50. Inserts for the two libraries averaged 12 kb. Approximately 5000 transformants of each strain were screened for phenotypic complementation of syr2. Transformants were replicated onto YPD medium containing 1–2 μg syringomycin ml⁻¹ and inspected for growth after 48 h. Plasmids were isolated from transformants that showed little or no growth with syringomycin. Five clones were isolated with inserts ranging from 10.5 to 14 kb. Restriction fragment analysis revealed that the clones were allelic, containing large overlap regions (data not shown). The smallest clone, 246-D6 (derived from a YCpN1 library), was selected for isolation of the SYR2 gene (Fig. 1). The gene was subcloned on a 2.5 kb BstBI fragment with restriction endonucleases and then on a 1.68 kb fragment by nested deletion. Smaller subclones generated by S1 nuclease treatment were not expressed in yeast, suggesting that coding or upstream regulatory sequences had been excised.

A portion of the 1.68 kb fragment was used as a probe for chromosomal mapping of SYR2. Yeast chromosomes of strain KZ1–1C were separated by CHEF gel electrophoresis and blotted onto nylon membranes. Hybridization of the SYR2 probe to chromosomal blots revealed that SYR2 is located on chromosome IV (Fig. 2). To look for genes having similar or overlapping function with SYR2, the strain KZ1–1C genome was hybridized to the SYR2 probe using low stringency conditions. No similar genes were found under hybridization conditions that allowed Dictyostelium actin-8 (Romans & Firtel, 1985) to bind yeast actin genes (approximately 78% identity) (data not shown).

**Sequence analyses**

A 2 kb fragment that included the 1.68 kb fragment was sequenced. An ORF sequence was located, beginning at ATG position 270, containing 1047 nucleotides and...
Fig. 2. Mapping of SYR2 to chromosome IV by hybridization to a CHEF gel blot. An ethidium-bromide-stained CHEF gel is shown in lane 1. Hybridization of the SYR2 probe to a blot of the CHEF gel is shown in lane 2.

predicted to encode a protein of 349 amino acids (Fig. 3). The ORF was preceded by regulatory sequences (CAAT) and (TATAA) beginning at positions -259 and -128, respectively. Northern blot analysis showed a transcript of approximately 1-4 kb (data not shown), consistent in size with a polyA-modified transcript encoded by the ORF. The predicted amino acid sequence was confirmed by sequencing the N-terminal 31 amino acids of a thrombin-cleaved GST-Syr2 (derived from a HpaI-SphI fusion protein. The determined sequence (Thr227–Ala253) corresponded to the predicted sequence.

SYR2 (GenBank accession no. SCU10427) was identical to SUR2 (GenBank accession no. SCU07171), identified in S. cerevisiae and related to survival during nutrient starvation (Desfarges et al., 1993). No other homologues of the encoded Syr2/Sur2 protein were found in the standard protein computer databases.

Syr2 possessed the C-terminal dilysyl motif for retrieval to the endoplasmic reticulum (Letourneur et al., 1994). Syr2 hydropathy profiles suggested six potential membrane-spanning regions with hydrophobicity exceeding 1.25 using the parameters of Kyte & Doolittle (1982) (Fig. 4). The C-terminus contained 26% lysine residues within a stretch of 50 residues, giving Syr2 an overall basic character. A pI of 9.32 was calculated. Potential protein phosphorylation and N-glycosylation sites were revealed using computer programs PROFILES and MOTIF (GCG Corporation, Madison, WI, USA) (Altschul et al., 1990).

SYR2 disruption

All four meiotic segregants recovered after SYR2 disruption in diploid strain W303-1A were viable in YPD growth medium. A 2:2 cosegregation of syringomycin...
resistance and \( \text{ura}^+ \) phenotypes occurred, indicating \( URA3 \) replacement in the wild-type \( SYR2 \) allele (Fig. 5). Disruption was confirmed by Southern blot hybridization (Fig. 5c). No \( SYR2 \) transcripts were detected by Northern blot analyses in the disruptant strains. The \( \Delta SYR2 \) segregants were viable in SD media and insensitive to ethanol, heat shock and high concentrations of sorbitol (1.25 M) and \( \text{Na}^+ \) (1 M). They grew with maltose, galactose, glycerol and acetate as carbon sources.

**Syr2 detection and cell localization**

Western blot analysis using antisera directed against Syr2 identified an approximately 43 kDa immunoreactive protein, which was slightly larger than the predicted mass of Syr2. The protein was detected in whole-cell extracts, microsomal fractions and endoplasmic reticulum membranes, but not the plasma membrane (Fig. 6). The strongest immunoreaction occurred with the cellular fractions enriched for endoplasmic reticulum markers. Syr2 was not detected in extracts of the \( \Delta SYR2 \) disruptants nor in extracts of strain 28N-D6. It was, however, detected in strain 13N-F2 membrane fractions.

In extracts from \( SYR2 \)-overexpression strains, two equally intense immunoreactive bands on Western blots were often observed. This observation raised the possibility that Syr2 exists in two forms. To test the possibility that one form may be phosphorylated, crude membrane preparations were treated with alkaline phosphatase before SDS-PAGE and Western blotting. Both forms were still detected in the phosphatase-treated samples (data not shown). Likewise, no glycosylated form of Syr2 was evident after staining equivalent gels and blots with periodic acid/Schiff base reagent (data not shown).
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**Ergosterol**

KZ1-1C(pYSYR2) SG-URA
KZ1-1C(pYSYR2) SD-URA
W303C
WASYR2

![Fig. 7. Ergosterol levels in SYRZ-overexpressing and disruption strains. Equal amounts (1 mg) of total cell nonsaponifiable lipid extracts were chromatographed on thin-layer silica gel plates and stained with phosphomolybdic acid reagent. Authentic ergosterol (1 mg) was applied for comparison. The chromatographic origin (o) is indicated.](image)

**Table 1. Total cell phospholipid levels of SYR2-overexpression and disruption strains**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Growth medium</th>
<th>Lipid phosphate [μg (mg dry wt cells)-1]*</th>
</tr>
</thead>
<tbody>
<tr>
<td>KZ1-1C(pYSYR2)</td>
<td>SD-URA</td>
<td>1.35 (0.31)</td>
</tr>
<tr>
<td>KZ1-1C(pYSYR2)</td>
<td>SG-URA</td>
<td>2.47 (1.19)</td>
</tr>
<tr>
<td>WASYR2</td>
<td>YPD</td>
<td>1.71 (0.73)</td>
</tr>
<tr>
<td>W303C</td>
<td>YPD</td>
<td>3.88 (1.03)</td>
</tr>
</tbody>
</table>

*Values are means from three separate experiments. Standard deviations (n-weighted) are indicated in parentheses.

**SYR2 overexpression**

To further analyse SYR2 function, overexpression vector pYSYR2, containing the PstI-SphI portion of SYR2 under the regulation of the GAL7 promoter, was constructed. When syr2 mutant strains 13N-F2 and 28N-D6 were transformed with pYSYR2 and grown in SG-URA medium, sensitivity to syringomycin was restored. Transformants W303C(pYSYR2) and KZ1-1C(pYSYR2) displayed syringomycin sensitivities comparable to the corresponding nontransformed strains, W303C and KZ1-1C, when grown in galactose-containing media. Also, pYSYR2 transformants of syr1 mutant 3N-H1 maintained levels of resistance to syringomycin in SG-URA medium similar to those of non-transformants. SYR2 overexpression was confirmed by Northern blot and Western blot analyses.

**Sterol and phospholipid compositions**

The cellular ergosterol levels of disruptant strain WASYR2 and strain W303C were similar (Fig. 7). Also, the ergosterol levels of KZ1-1C(pYSYR2) cells grown in minimal medium with either galactose or glucose were similar (Fig. 7). In contrast, WASYR2 had lower levels of total cellular phospholipid (Table 1) and of phosphatidylethanolamine, phosphatidylserine and phosphatidylinositol (Fig. 8) than W303C. On the other hand, KZ1-1C(pYSYR2) cells grown with galactose had higher total cellular levels of phospholipids (Table 1) and of phosphatidylethanolamine, phosphatidylserine and phosphatidylinositol when compared to cells grown with glucose (Fig. 8).

**DISCUSSION**

It was determined in the present study that a novel gene, SYR2, is required for yeast growth inhibition by syringomycin. SYR2 differs from other identified syringomycin response genes since it does not involve ergosterol biosynthesis (Takemoto et al., 1993). Although its precise biochemical function is not known, SYR2 appears to have a role in cellular phospholipid biosynthesis. SYR2 is not essential for viability and, therefore, it is unlikely that it catalyses a critical step in the phospholipid biosynthetic pathways. Mutant syr2 alleles, however, lead to syringomycin resistance, indicating that normal phospholipid
levels are required for syringomycin action. Previous work showed that the plasma membrane is the site of action of this lipodepsipeptide (Takemoto, 1992), and we suggest that the two major lipid classes of the yeast plasma membrane, ergosterol and phospholipids, are important for its action.

SYR2 is identical to the yeast gene SUR2. Mutant sur2/sur2 alleles, as well as sur1, sur3 and sur4 mutations, are suppressors of rvl61 (Desfarges et al., 1993), which impairs survival of yeast during nutrient starvation. Like sur2/sur2, sur1 and sur4 lead to alterations in the relative levels of various phospholipids. Desfarges et al. (1993) have hypothesized that all four identified SUR genes function in the same biochemical pathway.

Sequence analysis of Syr2 revealed several potential sites for phosphorylation and N-glycosylation. However, evidence for covalent modification of Syr2 was not observed. Syr2 was often seen as a doublet on Western blots of crude extracts obtained from SYR2-overexpression strains. The doublet may reflect a modified or degraded form of Syr2. The overexpressed Syr2 did not possess an N-terminal signal sequence, eliminating the possibility that one form resulted from cleavage of a signal peptide.

Hydropathy profiles suggested that Syr2 is a membrane protein. As expected for an enzyme involved in phospholipid biosynthesis, an association with the endoplasmic reticulum was demonstrated. This location is consistent with the dilytsyl motif at the C-terminus, which is an endoplasmic reticulum retrieval and coatamer interacting signal (Letourneur et al., 1994). Yeast proteins Wbp1p and C-5 sterol desaturase (encoded by ERG3/SYR1) also contain this signal (Taguchi et al., 1994; Arthington et al., 1991; Te Heesen et al., 1992; Letourneur et al., 1994), and in the former, the dilsyl motif occurs in the cytoplasmic domain (Townsley & Pelham, 1994; Gaynor et al., 1994). By analogy, we suggest that the Syr2 hydrophilic C-terminus is exposed on the cytoplasmic side of the endoplasmic reticulum.

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