

Ospemifene displays broad-spectrum synergistic interactions with itraconazole through potent interference with fungal efflux activities

Hassan E. Eldesouky¹, Ehab A. Salama¹, Tony R. Hazbun^{2,3}, Abdelrahman S. Mayhoub^{4*} and Mohamed N. Seleem^{1,5*}

¹Department of Comparative Pathobiology, College of Veterinary Medicine, Purdue University, West Lafayette, IN 47907, USA

²Department of Medicinal Chemistry and Molecular Pharmacology, College of Pharmacy, Purdue University, West Lafayette, Indiana 47907, USA

³Bindley Bioscience Center, Purdue University, West Lafayette, Indiana 47906, USA

⁴University of Science and Technology, Nanoscience Program, Zewail City of Science and Technology, October Gardens, 6th of October, Giza 12578, Egypt.

⁵Purdue Institute of Inflammation, Immunology, and Infectious Disease, Purdue University, West Lafayette, IN 47907, USA

*Correspondence:

mseleem@purdue.edu

Supplementary Table 1. Source and description of the fungal strains used in this study.

Fungal Strains	Source	Description
<i>C. albicans</i> SC5314	ATCC	Wild-type strain
<i>C. albicans</i> NR-29448	BEI Resources	A fluconazole-resistant bloodstream isolate (Arizona, USA)
<i>C. albicans</i> NR-29437	BEI Resources	Fluconazole-resistant bloodstream isolate (China)
<i>C. albicans</i> ATCC 26790	ATCC	A fluconazole-resistant strain isolated from a patient with pulmonary candidiasis
<i>C. albicans</i> ATCC MYA-573	ATCC	A fluconazole-resistant bloodstream isolate (from an AIDS patient in Germany)
<i>C. albicans</i> TWO7241	Professor Theodore White (University of Missouri-Kansas City)	A fluconazole-resistant clinical isolate that has increased efflux activity (<i>MDR1</i> overexpression) and overexpression of the azole target (<i>ERG11</i>)
<i>C. albicans</i> TWO7243		Fluconazole- and itraconazole-resistant clinical isolate that has increased mRNA levels of <i>CDR1</i> , <i>MDR1</i> , and <i>ERG11</i>
<i>C. albicans</i> SCTAC ^{1R34A}	Professor David Rogers (University of Tennessee)	A mutant strain having a gain-of-function homozygous mutation in <i>TAC1</i>
<i>C. albicans</i> SCMR ^{1R34A}		A mutant strain having a gain-of-function homozygous mutation in <i>MRR1</i>
<i>C. glabrata</i> ATCC 66032	ATCC	Not available
<i>C. glabrata</i> ATCC MYA-2950	ATCC	Not available
<i>C. glabrata</i> ATCC 2001	ATCC	A clinical isolate from human intestinal fluid
<i>C. glabrata</i> HM-1123	BEI-Resources	A clinical isolate from the bronchi of a human patient (Missouri, USA)
<i>C. auris</i> 385	CDC	Resistant to fluconazole, itraconazole, voriconazole, and amphotericin B
<i>C. auris</i> 386	CDC	Resistant to fluconazole, voriconazole, and amphotericin B
<i>C. auris</i> 388	CDC	Resistant to fluconazole, itraconazole, voriconazole, and amphotericin B
<i>C. auris</i> 389	CDC	Resistant to fluconazole, itraconazole, voriconazole, and amphotericin B
<i>C. auris</i> 390	CDC	Resistant to fluconazole, itraconazole, and amphotericin B

<i>C. neoformans</i> NR-41291	BEI Resources	A clinical isolate of human cerebrospinal fluid was identified in July 2011 (China)
<i>C. neoformans</i> NR-41295	BEI Resources	A Fluconazole-resistant human cerebrospinal fluid clinical isolate was identified in February 2012 (China)
<i>C. neoformans</i> NR-41298	BEI Resources	A clinical isolate obtained in February 2012 from human cerebrospinal fluid (China)
<i>A. fumigatus</i> NR-35304	BEI-Resources	A clinical isolate identified in 1998 from human sputum tracheal suction in California, USA
<i>A. fumigatus</i> NR-35312	BEI Resources	An environmental isolate was identified in 2002 (Montréal, Québec, Canada)
<i>A. fumigatus</i> NR-35302	BEI Resources	Clinical isolate obtained in 1998 from peritoneal fluid of a human patient in California, USA
<i>S. cerevisiae</i> AD/CaCDR1	Professor Richard D. Cannon (University of Otago, New Zealand)	Recombinant <i>S. cerevisiae</i> strain overexpressing <i>CDR1</i> from <i>C. albicans</i>
<i>S. cerevisiae</i> AD/CaCDR2		Recombinant <i>S. cerevisiae</i> strain overexpressing <i>CDR2</i> from <i>C. albicans</i>
<i>S. cerevisiae</i> AD/CaMDR1		Recombinant <i>S. cerevisiae</i> strain overexpressing <i>MDR1</i> from <i>C. albicans</i>

Supplementary Table 2. Effect of ospemifene-fluconazole (FLC) combination against different fungal strains.

Fungal Strains	MIC ($\mu\text{g/ml}$)				ΣFICI^1	Interaction
	FLC		Ospemifene			
	Alone	Combined	Alone	Combined		
<i>C. albicans</i> SC5314	0.125	0.125	> 256	4	1.02	IND
<i>C. albicans</i> NR-29448	256	4		2	0.02	SYN
<i>C. albicans</i> NR-29437	128	4		4	0.05	SYN
<i>C. albicans</i> ATCC MYA 573	128	128		4	1.02	IND
<i>C. albicans</i> TWO7241	32	32		4	1.02	IND
<i>C. albicans</i> TWO7243	64	64		4	1.02	IND
<i>C. albicans</i> SC-TAC1 ^{G980E}	2	2		4	1.02	IND
<i>C. albicans</i> SC-MRR1 ^{P683S}	2	2		4	1.02	IND
<i>C. glabrata</i> ATCC 66032	4	4		4	1.02	IND
<i>C. glabrata</i> ATCC MYA-2950	8	8		4	1.02	IND
<i>C. glabrata</i> ATCC 2001	4	4		4	1.02	IND
<i>C. glabrata</i> HM-1123	4	4		4	1.02	IND
<i>C. auris</i> 385	256	256		4	1.02	IND
<i>C. auris</i> 386	256	256		4	1.02	IND
<i>C. auris</i> 388	256	256		4	1.02	IND
<i>C. auris</i> 389	256	256		4	1.02	IND
<i>C. auris</i> 390	256	256		4	1.02	IND
<i>C. neoformans</i> NR-41291	8	1		0.5	0.13	SYN
<i>C. neoformans</i> NR-41295	8	4		1	0.50	SYN
<i>C. neoformans</i> NR-41298	2	0.5		0.5	0.25	SYN
<i>A. fumigatus</i> NR-35304	> 256	> 256	4	1.02	IND	
<i>A. fumigatus</i> NR-35312	> 256	> 256	4	1.02	IND	
<i>A. fumigatus</i> NR-35302	> 256	> 256	4	1.02	IND	

¹ ΣFICI (fractional inhibitory concentration index) values, rounded to the nearest two decimal places, were used to measure the interaction between the tested combinations. ΣFICI interpretation corresponded to the following definitions: synergism (SYN), $\Sigma\text{FICI} \leq 0.50$; additivity (ADD), $\Sigma\text{FICI} > 0.50$ and ≤ 1 ; and indifference (IND), $\Sigma\text{FICI} > 1$ and ≤ 4 .

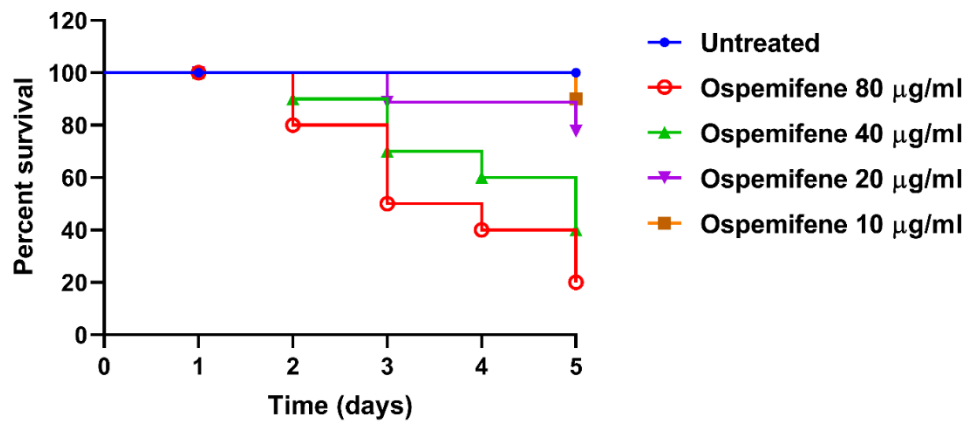
Supplementary Table 3. Effect of ospemifene-voriconazole (VRC) combination against different fungal strains.

Fungal Strains	MIC ($\mu\text{g/ml}$)				ΣFICI^*	Interaction
	VRC		Ospemifene			
	Alone	Combined	Alone	Combined		
<i>C. albicans</i> SC5314	0.031	0.031	> 256	4	1.02	IND
<i>C. albicans</i> NR-29448	4	0.125		8	0.06	SYN
<i>C. albicans</i> NR-29437	0.125	0.015		4	0.14	SYN
<i>C. albicans</i> ATCC MYA 573	0.25	0.25		4	1.02	IND
<i>C. albicans</i> TWO7241	0.125	0.062		1	0.50	SYN
<i>C. albicans</i> TWO7243	0.50	0.50		4	1.02	IND
<i>C. albicans</i> SCTAC1R34A	0.062	0.062		4	1.02	IND
<i>C. albicans</i> SCMRR1R34A	0.015	0.015		2	1.01	IND
<i>C. glabrata</i> ATCC 66032	0.125	0.125		2	1.02	IND
<i>C. glabrata</i> ATCC MYA-2950	0.125	0.125		2	1.01	IND
<i>C. glabrata</i> ATCC 2001	0.062	0.062		2	1.01	IND
<i>C. glabrata</i> HM-1123	0.062	0.062		2	1.01	IND
<i>C. auris</i> 385	2	2		4	1.02	IND
<i>C. auris</i> 386	1	1		4	1.02	IND
<i>C. auris</i> 388	1	1		4	1.02	IND
<i>C. auris</i> 389	2	2		4	1.02	IND
<i>C. auris</i> 390	0.50	0.50		4	1.02	IND
<i>C. neoformans</i> NR-41291	0.125	0.062		0.5	0.50	SYN
<i>C. neoformans</i> NR-41295	0.25	0.062		0.5	0.25	SYN
<i>C. neoformans</i> NR-41298	0.031	0.015		0.5	0.50	SYN
<i>A. fumigatus</i> NR-35304	0.125	0.125		4	1.02	IND
<i>A. fumigatus</i> NR-35312	0.125	0.125		4	1.02	IND
<i>A. fumigatus</i> NR-35302	0.125	0.125		4	1.02	IND

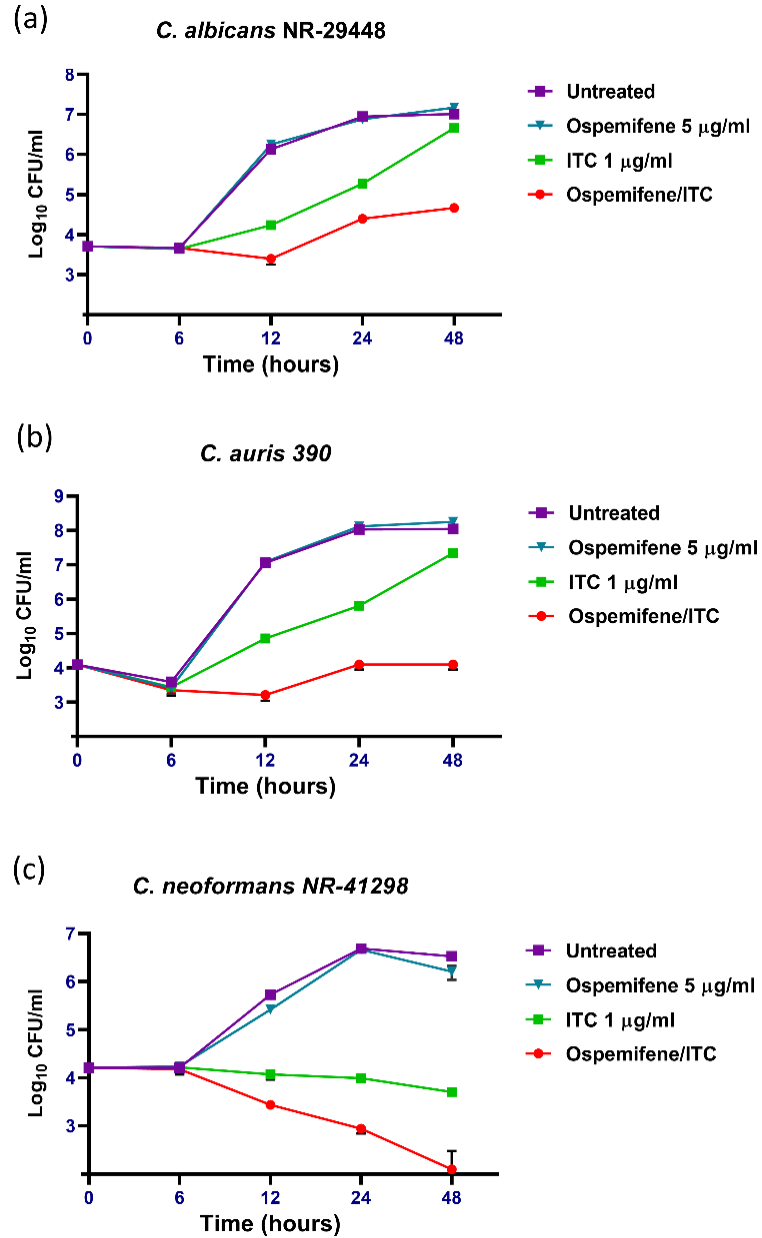
¹ ΣFICI (fractional inhibitory concentration index) values, rounded to the nearest two decimal places, were used to measure the interaction between the tested combinations. ΣFICI interpretation corresponded to the following definitions: synergism (SYN), $\Sigma\text{FICI} \leq 0.50$; additivity (ADD), $\Sigma\text{FICI} > 0.50$ and ≤ 1 ; and indifference (IND), $\Sigma\text{FICI} > 1$ and ≤ 4 .

Supplementary Table 4. Primers used in this study.

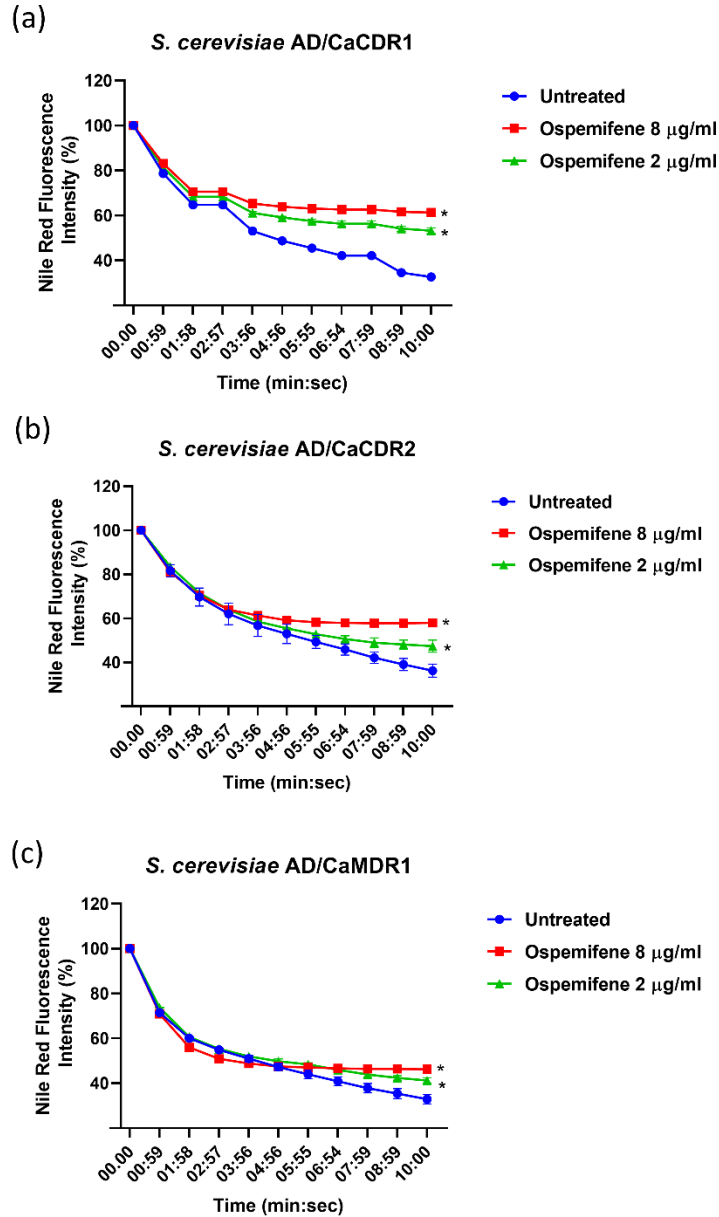
Gene	Protein	GeneBank accession no.	Primer	Sequence
<i>ACT1</i>	Actin	XM_019475182	Forward Reverse	TTGGTGATGAAGCCCAATCC CATATCGTCCCAGTTGGAAACA
<i>MDR1</i>	Major facilitator superfamily transporter	XM_714072	Forward Reverse	TTACCTGAAACTTTTGGCAAACA ACTTGTGATTCTGTCGTTACCG
<i>CDR1</i>	ABC transporters CDR1	XM_718116	Forward Reverse	TTTAGCCAGAACTTTCATCATGAT T TATTTATTTCTTCATGTTTCATATGG ATTGA
<i>CDR2</i>	ABC transporters CDR2	XM_718076	Forward Reverse	GGTATTGGCTGGTCCTAATGTGA GCTTGAATCAAATAAGTGAATGGA TTAC



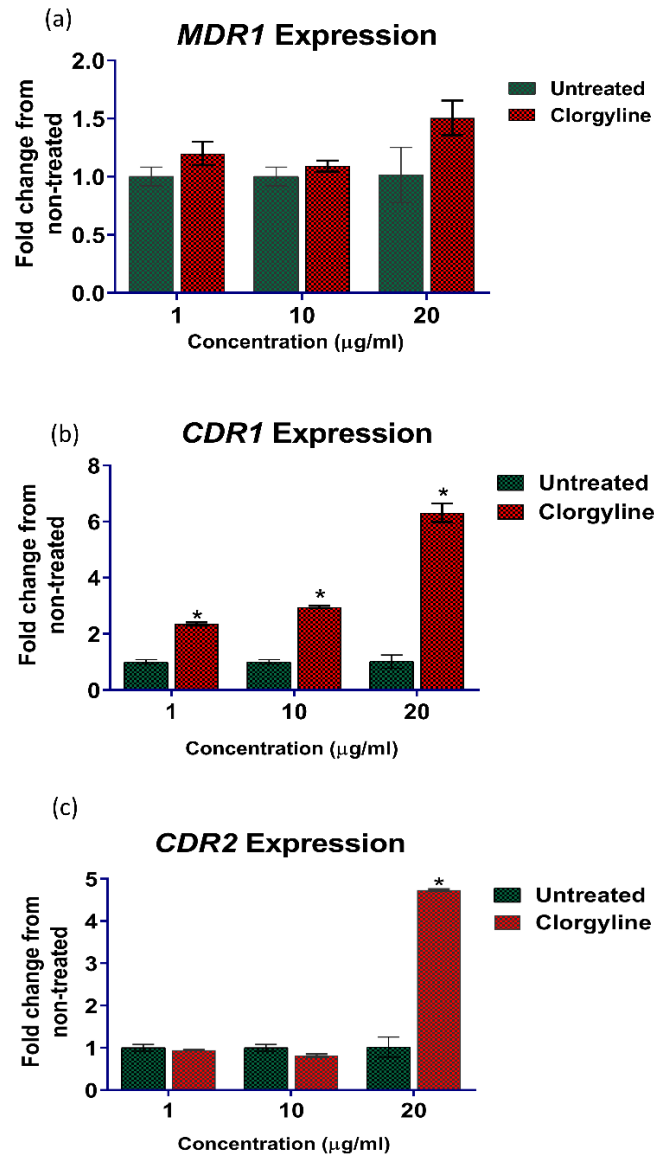
Supplementary Figure 1. Toxicity assessment of ospemifene in *C. elegans*. Adult (L4-stage) nematodes were exposed to ospemifene at four different concentrations (80, 40, 20, and 10 μg/ml) and viability was recorded for five consecutive days.



Supplementary Figure 2. Time-kill analysis of ospemifene (5 µg/ml), itraconazole (1 µg/ml), or a combination of both. Test agents were evaluated against (a) *C. albicans* NR-29448, (b) *Candida auris* 390, and (c) *C. neoformans* NR-41298 over a 48-hour incubation period at 35 °C. DMSO served as a negative untreated control. Error bars represent standard deviation values.



Supplementary Figure 3. Effect of ospemifene on Nile red efflux by recombinant *Saccharomyces cerevisiae* strains. Effect of ospemifene on Nile red efflux was evaluated against recombinant *S. cerevisiae* strains (a) Recombinant *S. cerevisiae* AD/CaCDR1 overexpressing *C. albicans* CDR1 (b) Recombinant *S. cerevisiae* AD/CaCDR2 overexpressing *C. albicans* CDR2, and (c) Recombinant *S. cerevisiae* AD/CaMDR1 overexpressing *C. albicans* MDR1. Energy-depleted cells were loaded with Nile red (7.5 µM) and were treated with ospemifene (2, and 8 µg/ml). Efflux was initiated by adding glucose (40 mM) to all treatment groups. The Nile red fluorescence intensity was then monitored over 10 minutes and is expressed as the percentage of change in the fluorescence intensity. (*) indicates a significant statistical difference in the fluorescence intensity of the treated cells relative to the untreated control ($P < 0.05$), as determined by multiple t-tests using the Holm-Sidak statistical method for multiple comparisons.



Supplementary Figure 4. Effect of clorgyline on the expression of azole resistance-related efflux genes a) *MDR1*, b) *CDR1*, and c) *CDR2*. *C. albicans* SC5314 was treated with either DMSO or ospemifene (1, 10, 20 µg/ml) for 3 h in RPMI 1640 and harvested. The expression of *CDR1*, *CDR2*, and *MDR1* was determined by quantitative RT-PCR. Bars show the mean fold change for ospemifene-treated cells relative to untreated cells, and error bars indicate standard deviations of three biological replicates. * indicates a significant difference between clorgyline treatments relative to the untreated control ($P < 0.05$), as determined by multiple t-tests using the Holm-Sidak statistical method for multiple comparisons.