

A system to identify inhibitors of mTOR signaling using high-resolution growth analysis in *Saccharomyces cerevisiae*

Mitchell B. Lee · Daniel T. Carr · Michael G. Kifilezghi · Yan Ting Zhao ·
Deborah B. Kim · Socheata Thon · Margarete D. Moore · Mary Ann K. Li ·
Matt Kaeberlein 

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Abstract The mechanistic target of rapamycin (mTOR) is a central regulator of growth and proliferation and mTOR inhibition is a promising therapy for a variety of diseases and disorders. Inhibition of mTOR complex I (mTORC1) with rapamycin delays aging and increases healthy longevity in laboratory animals and is used clinically at high doses to prevent organ transplant rejection and to treat some forms of cancer. Clinical use of rapamycin is associated with several unwanted side effects, however, and several strategies are being taken to identify mTORC1 inhibitors with fewer side effects. We describe here a yeast-based growth assay that can be used to screen for novel inhibitors of mTORC1. By testing compounds using a wild-type strain and isogenic cells lacking either *TOR1* or *FPRI*, we can resolve not only whether a compound is an inhibitor of mTORC1 but also whether the inhibitor acts through a mechanism

similar to rapamycin by binding Fpr1. Using this assay, we show that rapamycin derivatives behave similarly to rapamycin, while caffeine and the ATP competitive inhibitors Torin 1 and GSK2126458 are mTORC1 inhibitors in yeast that act independently of Fpr1. Some mTOR inhibitors in mammalian cells do not inhibit mTORC1 in yeast, and several nutraceutical compounds were not found to specifically inhibit mTOR but resulted in a general inhibition of yeast growth. Our screening method holds promise as a means of effectively assaying drug libraries for mTOR-inhibitory molecules in vivo that may be adapted as novel treatments to fight diseases and extend healthy longevity.

Keywords mTOR · *Saccharomyces cerevisiae* · Yeast

how does it work as immunosuppressive

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M. B. Lee · D. T. Carr · M. G. Kifilezghi · Y. T. Zhao ·
D. B. Kim · S. Thon · M. D. Moore · M. A. K. Li ·
M. Kaeberlein (✉)
Department of Pathology, University of Washington, Seattle, WA,
USA
e-mail: kaeber@uw.edu

M. G. Kifilezghi
Molecular Medicine and Mechanisms of Disease (M3D) Program,
University of Washington, Seattle, WA, USA

Introduction

The budding yeast, *Saccharomyces cerevisiae*, is a premier model system for identifying conserved genetic and pharmacological interventions that extend life span (Longo et al. 2012; Kaeberlein 2010). A particularly good example of this is the mechanistic target of rapamycin (mTOR) pathway that was first genetically implicated in aging in yeast (Fabrizio et al. 2001) and has since emerged as an important target for delaying aging in multicellular invertebrates and mice (Johnson et al. 2013a, 2015). Likewise, the small molecule mTOR inhibitor, rapamycin, was first shown to extend life span in yeast (Powers et al. 2006) and has since been shown

to have similar pro-longevity effects in nematodes (Robida-Stubbs et al. 2012), fruit flies (Bjedov et al. 2010), and mice (Harrison et al. 2009).

In addition to increased life span, rapamycin maintains organismal health during aging in mice, evidenced by decreased occurrence of multiple age-related diseases (Johnson et al. 2013b). Rapamycin treatment in aging mice reduces cancer (Anisimov et al. 2011; Popovich et al. 2014), prevents cognitive dysfunction (Halloran et al. 2012; Majumder et al. 2012), attenuates declining renal and hepatic function (Neff et al. 2013), improves muscle and visual performance (Neff et al. 2013), and reverses cardiac (Flynn et al. 2013; Dai et al. 2014) and immune decline (Chen et al. 2009). Improved cardiac function from rapamycin treatment has recently been similarly observed in middle-aged companion dogs (Urfer et al. 2017a, b), while improved immune function has been observed in healthy elderly people treated with the rapamycin derivative everolimus (RAD001) (Mannick et al. 2014). Transient rapamycin treatment regimens lasting as few as 12 weeks and initiated late in life are also effective at increasing life span and healthspan in mice (Bitto et al. 2016). These findings place rapamycin and other mTOR inhibitors among the leading candidates for translational interventions to promote healthy aging in people and companion animals (Blagosklonny 2010; Kaeberlein et al. 2015, 2016).

The mTOR is a nutrient and growth factor responsive kinase that functions in two distinct protein complexes: mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2) (Loewith et al. 2002; Wullschleger et al. 2006). Rapamycin binds to the FK506 binding protein FKBP12 (Fpr1 in yeast), and the FKBP12-rapamycin complex inhibits the activity of mTORC1 by disrupting the physical interaction between the mTOR protein and a second mTORC1 component, raptor (Kog1 in yeast) (Heitman et al. 1991; Lorenz and Heitman 1995). Deletion of *FPR1* confers resistance to rapamycin in yeast (Heitman et al. 1991; Benton et al. 1994). The mTORC1 complex regulates a variety of downstream cellular processes including messenger RNA (mRNA) translation, autophagy, and mitochondrial metabolism, all of which are affected by rapamycin treatment (Saxton and Sabatini 2017). Unlike mTORC1, mTORC2 activity is not directly inhibited by rapamycin (Jacinto et al. 2004). The mTORC2 complex is less well characterized than mTORC1, but is similarly involved in regulating a variety of cellular processes including cytoskeleton

organization and regulation of metabolism. Long-term treatment with rapamycin in mammals is reported to cause indirect inhibition of mTORC2, which is implicated in metabolic defects including insulin resistance and glucose intolerance (Lamming et al. 2012). Both mTOR complexes are essential for viability in yeast and multicellular eukaryotes.

Budding yeast contain two genes that encode the mTOR kinase: *TOR1* and *TOR2*. Tor1 functions exclusively in mTORC1, while Tor2 functions in both complexes (Helliwell et al. 1994). Consistent with this, deletion of *TOR2* leads to inviability due to the complete lack of mTORC2 activity (Kunz et al. 1993), while deletion of *TOR1* results in viable cells that are long lived and sensitive to rapamycin, due to reduced mTORC1 activity (Heitman et al. 1991; Kaeberlein et al. 2005a). Despite their sensitivity to rapamycin, *tor1Δ* yeast cells do not show a substantial reduction in mRNA translation or doubling time (McCormick et al. 2015; Beaupere et al. 2017), indicating that Tor2 provides sufficient mTORC1 activity for relatively normal growth in rich medium.

Multiple pharmaceutical mTORC1 and general mTOR inhibitors are used as chemotherapeutic agents (Folkes et al. 2008; Chresta et al. 2010; Knight et al. 2010; O'Donnell et al. 2017; Liu et al. 2012). Additionally, several natural products and natural product mixtures are reported to inhibit mTOR signaling in cell culture and rodent models, including: curcumin (Beevers et al. 2006, 2009), green tea extract (Zhang et al. 2006), epigallocatechin-3-gallate (Zhang et al. 2006; Van Aller et al. 2011), caffeine (Saiki et al. 2011; Reinke et al. 2006), genistein (Anastasius et al. 2009), lycopene and eicosapentaenoic acid (Liu et al. 2012), sulforaphane (Wiczek et al. 2012), alpha-lipoic acid (Xie et al. 2012; Li et al. 2014), glucosamine (Jiang et al. 2014), quercetin (Meng et al. 2015; Lu et al. 2015), berberine (Fan et al. 2015), and resveratrol (Park et al. 2016). In most cases, the mechanistic basis for inhibition of mTOR via these natural products is unknown, and it remains unclear whether these compounds act via direct inhibition of mTOR, mTORC1, or through indirect effects on components of the mTOR/nutrient response network.

To facilitate identification of new small molecule mTOR inhibitors in vivo, we have developed a simple yeast-based assay that quantifies differential growth inhibition in rapamycin-sensitized and rapamycin-resistant genetic backgrounds using a Bioscreen C

MBR plate reader/shaker/incubator. We have previously optimized the Bioscreen C MBR machine to obtain high-resolution growth curves of budding yeast cells for chronological life span analysis (Murakami et al. 2008; Murakami and Kaerberlein 2009) and assessing differential sensitivities of yeast strains to different chemical and environmental stressors (Delaney et al. 2013). Here, we extend this method by assessing the impact of rapamycin and several other small molecules on doubling time and outgrowth in rich media for wild-type BY4742 cells and isogenic *tor1Δ* and *fpr1Δ* cells. Our method relies on the fact that deletion of *TOR1* confers sensitivity to rapamycin due to diminished mTORC1 activity, while deletion of *FPR1* confers resistance to rapamycin due to the necessary role of Fpr1 in rapamycin-mediated mTORC1 inhibition. Given this, we predict that mTORC1 inhibitors with mechanisms similar to rapamycin will display similar differential growth inhibition across the three genotypes, while compounds that inhibit mTORC1 by a mechanism distinct from rapamycin will have a greater inhibitory effect on growth of *tor1Δ* cells relative to WT or *fpr1Δ* cells, but that WT and *fpr1Δ* cells will show similar inhibition of growth at a given drug concentration. Drugs that do not inhibit mTORC1 will either have no effect on growth in any of the genotypes or will similarly inhibit growth across all three genotypes. We report the validation of this assay using rapamycin, rapamycin derivatives, and mTOR catalytic inhibitors. We also report the effect of several natural product compounds on mTORC1 inhibition and outgrowth, finding that among the natural products tested, only caffeine displays the outgrowth profile expected for an in vivo inhibitor of mTORC1 in yeast.

Results

TOR1 mutants are hypersensitive, and FPR1 mutants are resistant to rapamycin and rapalogs

We tested the effect of known mTORC1 inhibitors on growth kinetics in three haploid yeast strains: wild-type (WT) BY4742 and isogenic *tor1Δ*, and *fpr1Δ* single-gene deletion mutants. We began by analyzing dose responses for rapamycin and two rapalogs, everolimus and temsirolimus. As expected, all concentrations of rapamycin tested reduced *tor1Δ* outgrowth to a greater extent than WT cells, while *fpr1Δ* cells were resistant to

growth inhibition (Figs. 1 and 2). Everolimus and rapamycin produced remarkably similar growth inhibitory responses, while higher concentrations of temsirolimus were necessary to achieve growth inhibition comparable to the other two drugs.

Sensitivity of the *tor1Δ* strain to mTORC1 inhibitors can be seen at 2.5 ng/mL rapamycin or everolimus and at 20 ng/mL temsirolimus, where deletion of *TOR1* results in a significantly greater increase in doubling time relative to WT (Fig. 2 and Supplemental Table 1). Resistance of the *fpr1Δ* strain is most evident at the highest concentration of each drug tested, where both WT and *tor1Δ* strains have doubling times exceeding 200 min, while the *fpr1Δ* cells are still growing as rapidly as in the vehicle control (doubling time 80–90 min).

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One consequence of diminished mTORC1 signaling is diminished protein translation (Steffen et al. 2008; Beretta et al. 1996). To determine if diminished protein translation is sufficient to recapitulate rapamycin-like patterns of growth inhibition, we tested concentrations of the general protein translation inhibitor cycloheximide (CHX) ranging from 1 to 500 ng/mL. Cycloheximide treatment potently and similarly inhibits growth of all three strains at concentrations of 50 ng/mL and greater (Supplemental Fig. 1), demonstrating that general translation inhibition does not recapitulate the differential effects of rapamycin on growth of these three yeast strains.

ATP competitive inhibitors of mTORC1 produce a distinct growth inhibitory profile compared to rapamycin treatment

In addition to rapamycin-like compounds that inhibit mTORC1 signaling via interaction with Fpr1, several drugs have been developed that act as ATP-competitive inhibitors of mTOR in mammalian cells. To understand how these compounds differentially impact growth in our yeast strains, we tested dose responses for Torin 1, GSK2126458, GDC-0941, and AZD8055 (Fig. 3, Supplemental Fig. 2, and Supplemental Table 2). All of the ATP-competitive inhibitors required micromolar concentrations to inhibit growth, compared to nanomolar concentrations when using rapamycin and rapalogs. At 10 μM Torin 1, *tor1Δ* cells were strongly growth inhibited, while WT cells or *fpr1Δ* cells were less strongly affected (Fig. 3 and Supplemental Table 2). At 25 μM Torin 1, growth of all three strains was

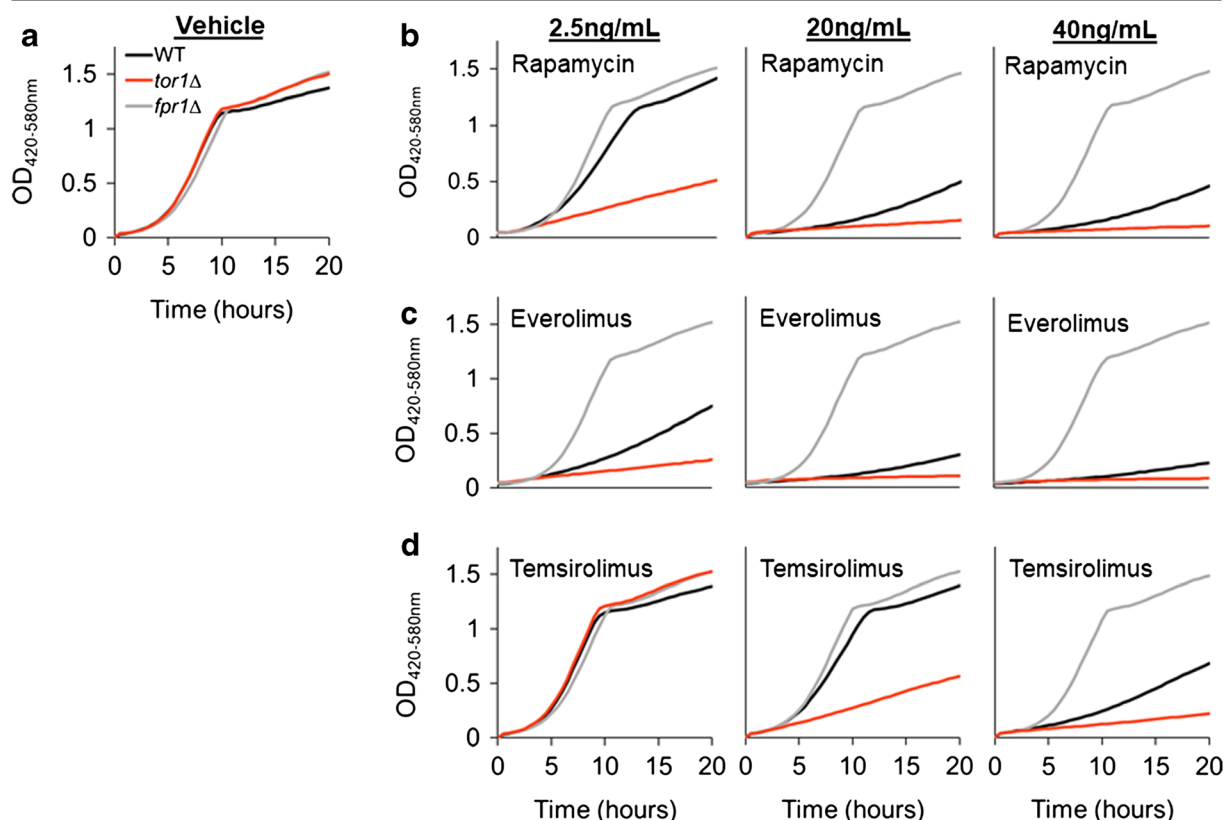


Fig. 1 Differential growth of wild-type (WT), *tor1Δ*, and *fpr1Δ* strains in the presence of rapamycin and rapalogs. *tor1Δ* mutants are hypersensitive, and *fpr1Δ* mutants are resistant to rapamycin and rapalogs. Representative growth curves of WT (black), *tor1Δ*

(red), and *fpr1Δ* (gray) yeast grown in YPD with (a) 1.5% DMSO (vehicle) or 2.5–40 ng/mL (left to right) (b) rapamycin, (c) everolimus, or (d) temsirolimus (color figure online)

severely impacted, with WT and *fpr1Δ* cells showing similar reductions in growth rate, as expected for a catalytic inhibitor of mTOR that does not act through Fpr1.

GSK2126458, another catalytic inhibitor of mTOR, only weakly impacted yeast growth (Supplemental Fig. 2 and Supplemental Table 2). Doubling time was modestly increased by 100 μ M GSK2126458 in all three strains, while growth of only the *tor1Δ* cells was impacted by lower concentrations. Interestingly, neither GDC-0941 nor AZD8055 produced a measurable change in growth in any yeast strains (Supplemental Fig. 2 and Supplemental Table 2).

Among several putative mTORC1 inhibitory nutraceuticals, **caffeine shows specificity for mTORC1 in yeast**

Many nutraceutical compounds are described as having an mTORC1 inhibitory effect, particularly in the context

of human cancer cell culture models. To identify and validate mTORC1-modulating nutraceuticals in yeast, we tested a subset of these compounds in our Bioscreen C MBR assay (Table 1). Most of the tested nutraceuticals produced no effect on growth at concentrations up to 100 μ g/mL (Table 1). Quercetin significantly inhibited WT and *tor1Δ* doubling time by 23 and 25%, respectively, at the highest concentration tested ($p < 0.01$, Welch's t test), but did not produce a significant difference in *fpr1Δ* doubling time ($p = 0.24$, Welch's t test) even though a trend toward increased doubling time is seen in the strain. Two compounds tested, berberine and lycopene, inhibited growth in a genotype-independent manner. Lycopene only modestly impacted growth, while berberine strongly inhibited growth at 100 μ g/mL.

Among the nutraceuticals tested, caffeine was the only compound that showed growth inhibition consistent with an mTOR inhibitory effect, increasing doubling time specifically in the *tor1Δ* mutant cells at

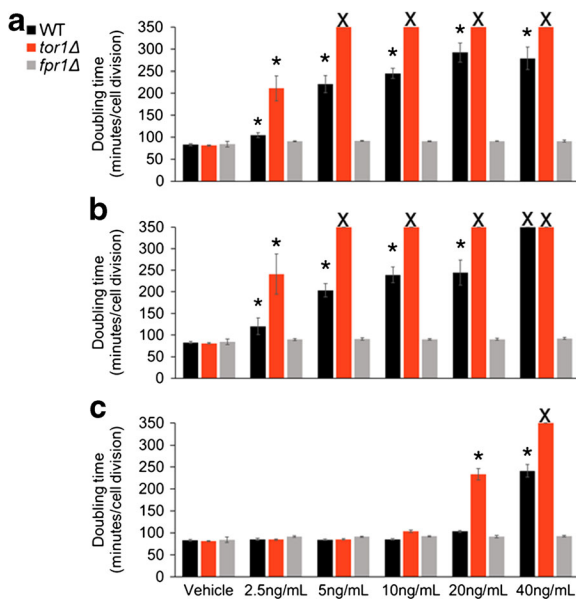


Fig. 2 Effect of rapamycin and rapalogs on maximal doubling time of wild-type (WT), *tor1Δ*, and *fpr1Δ* yeast cells. Maximal doubling times of wild-type (black), *tor1Δ* (red), and *fpr1Δ* (gray) in vehicle or 2.5–40 ng/mL (a) rapamycin, (b) everolimus, or (c) temsirolimus ($n = 3$ –5 biological replicates for each treatment). Error bars = SEM. Asterisk means significantly different from 1.5% DMSO control (vehicle) ($p < 0.05$, Welch's t test). X = doubling time could not be calculated due to no growth, indicated by $OD \leq 0.3$ after 20 h (color figure online)

100 μ g/mL (Fig. 4). Caffeine also increased WT and *fpr1Δ* doubling times at concentrations greater than 750 μ g/mL. To assess epistatic relationships between Fpr1 and mTORC1, we constructed a *tor1Δ fpr1Δ* double mutant. Growth inhibitory profiles in *tor1Δ fpr1Δ* were identical to those of *tor1Δ* in our caffeine dose response (Fig. 3c), confirming that Fpr1 is not required for caffeine-mediated growth inhibition in yeast.

Discussion

Rapamycin and other mTOR inhibitors have emerged as one of the most promising classes of molecules for treating a variety of diseases and promoting healthy longevity (Kaeberlein 2013). The largest barrier to clinical utilization of these compounds for such purposes is the perceived risk of adverse side effects. While it remains unclear how significant an issue this is in relatively healthy people at lower doses, the perception that mTOR inhibitors are risky drugs remains a significant

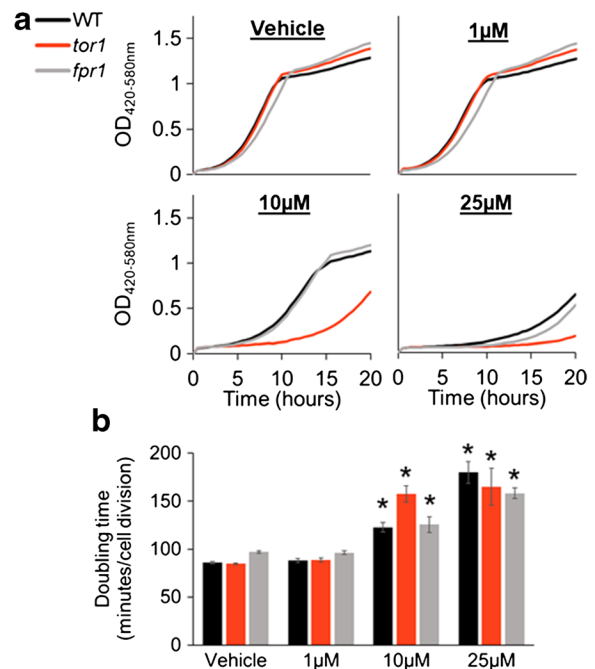


Fig. 3 The catalytic mTOR inhibitor Torin 1 produces a distinct growth inhibitory profile relative to rapamycin. *tor1Δ* mutants are hypersensitive to Torin 1, and *fpr1Δ* mutants are not resistant. a Representative growth curves of WT, *tor1Δ*, and *fpr1Δ* outgrown in the presence of 2.5% DMSO (vehicle) (top left), 1 μ M Torin 1 (top right), 10 μ M Torin 1 (bottom left), or 25 μ M Torin 1 (bottom right). b Maximal doubling time (minutes/cell division) for WT, *tor1Δ*, and *fpr1Δ* strains grown in either 2.5% DMSO (vehicle) ($n = 9$ biological replicates for WT and *fpr1Δ*, and biological replicates $n = 10$ for *tor1Δ*) or 1–25 μ M Torin 1 ($n = 4$ biological replicates for each strain in 1 μ M Torin 1 and $n = 5$ biological replicates for each strain in 10 and 25 μ M Torin 1). Asterisk means significantly different from vehicle ($p < 0.05$, Welch's t test). Error bars = SEM

challenge. Thus, there is utility in developing or identifying novel mTOR inhibitors that are effective in vivo and which may have fewer side effects. Of particular interest are natural product “nutraceutical” mTOR inhibitors.

By utilizing yeast strains with differential sensitivity to mTORC1 inhibition, we developed an in vivo screening platform that allows us to preliminarily categorize compounds as growth inhibitory, mTOR inhibitory, and/or rapamycin mimetics. Compounds that inhibit WT, *tor1Δ*, and *fpr1Δ* cells similarly are general growth inhibitors, but are unlikely to be either direct or indirect mTOR inhibitors, at least in yeast. Compounds that induce growth inhibition preferentially or specifically in *tor1Δ* cells are candidate mTOR inhibitors, and if *fpr1Δ* cells are resistant to these compounds, then they

Table 1 Maximum doubling time of wild-type (WT), *tor1Δ*, and *fpr1Δ* cells grown in rich YPD medium supplemented with the indicated nutraceuticals. Doubling time (DT) (minutes/celldivision), standard error of the mean (SEM), percent change, and number of biological replicate cultures tested (*n*) for putative mTOR-inhibitory nutraceutical compounds

Treatment	WT			<i>tor1Δ</i>			<i>fpr1Δ</i>		
	DT (SEM)	% change	<i>n</i>	DT (SEM)	% change	<i>n</i>	DT (SEM)	% change	<i>n</i>
1% DMSO	83.3 (0.9)	—	13	82.8 (0.9)	—	13	90.8 (1.0)	—	13
100 μg/mL Alpha-lipoic acid	85.4 (2.3)	2.6	3	85.2 (1.2)	2.9	3	91.7 (2.1)	−6.2	3
100 μg/mL Broccoli concentrate	83.3 (1.1)	0.0	3	82.7 (2.8)	−0.2	3	89.2 (1.9)	−1.8	3
100 μg/mL Glucosamine	81.0 (2.5)	−2.8	4	81.2 (2.1)	−2.0	4	87.5 (2.6)	−3.6	4
100 μg/mL Lycopene	95.8 (0.3)	15.0*	3	101.1 (2.8)	22.2*	3	107.7 (0.7)	18.6*	3
100 μg/mL Quercetin	104.1 (3.1)	25.0*	4	102.0 (6.0)	23.2*	4	105.4 (10.2)	16.1	4
100 μg/mL Resveratrol	82.7 (0.8)	−0.7	3	82.4 (0.5)	−0.5	3	87.0 (1.5)	−4.2	3
1 μg/mL Berberine	80.2 (2.4)	−3.7	3	79.7 (2.6)	−3.7	3	87.0 (4.2)	−4.2	3
10 μg/mL Berberine	102.2 (1.9)	22.7*	3	95.2 (1.8)	14.9*	3	101.8 (2.3)	12.1*	3
100 μg/mL Berberine	227.1 (6.7)	172.6*	3	228.6 (2.9)	176.1*	3	238.1 (2.5)	162.3*	3

**p* < 0.05, compared to 1% DMSO, Welch's (unequal variance) *t* test

are likely inhibiting mTOR by a mechanism similar to rapamycin. The assay system performed as expected here for rapamycin, the rapalogs everolimus and

temsirolimus, the catalytic mTOR inhibitors Torin 1 and GSK2126458, and the natural product mTOR inhibitor caffeine. Therefore, we conclude that this assay

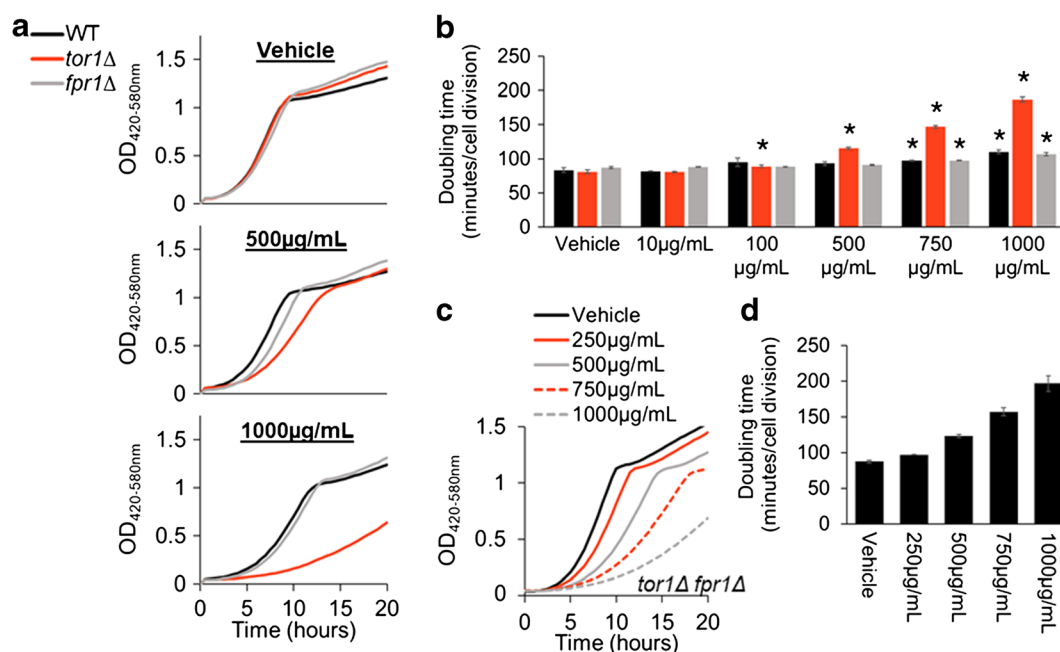


Fig. 4 Caffeine inhibits yeast growth in *tor1Δ* cells independent of Fpr1. **a** Representative growth curves of 6.67% H₂O (vehicle) (top left), 500 μg/mL (middle), and 1000 μg/mL (bottom). **b** Maximal doubling time (minutes/cell division) for WT, *tor1Δ*, and *fpr1Δ* yeast grown in vehicle or 10–1000 μg/mL caffeine (*n* = 3–5 independent cultures for each strain-treatment tested). Asterisk means significantly different from vehicle control

(*p* < 0.05, Welch's *t* test). Error bars = SEM. **c** *tor1Δ fpr1Δ* are sensitive to caffeine, indicating that caffeine-mediated growth inhibition in *tor1Δ* cells is independent of Fpr1. **d** Peak doubling times for *tor1Δ fpr1Δ* grown in vehicle or 250–1000 μg/mL caffeine (*n* = 6 biological replicate cultures for each strain-treatment tested). Error bars = SEM

system is likely to be suitable for identification of novel, unknown pharmaceutical and natural product mTOR inhibitors.

Our analyses also confirmed previously observed cases of differential sensitivity between yeast and mammals with regard to the catalytic mTOR inhibitors AZD8055 and GDC-0941, which may be due to sequence differences between the mammalian and yeast proteins (Wu et al. 2015). It is also likely that equivalent doses of some compounds will yield different intracellular concentrations in yeast cells relative to mammalian cells, and that yeast may be able to clear or otherwise detoxify certain compounds more or less effectively. Thus, it is important to recognize that any hits identified in the yeast-based screening system described here will need to be validated in mammalian cells to confirm similar mTOR-inhibitory effects, and that **failure to detect mTOR inhibition in this system for a given compound does not rule out the possibility that the compound could inhibit mTOR in mammalian cells.** Nonetheless, given the biochemical and mechanistic similarities between yeast and mammalian mTORC1 and mTORC2, we anticipate that many compounds will behave similarly in both systems, as is the case for several examples reported here.

It is of particular interest that, among the nutraceutical compounds tested, only **caffeine demonstrated growth kinetics consistent with mTORC1 inhibition in our yeast assay.** This supports prior studies of caffeine on mTOR activity in budding yeast (Reinke et al. 2006; Wanke et al. 2008) and fission yeast (Rallis et al. 2013), and is of interest in light of numerous reports that caffeine can extend life span in invertebrate models (Sutphin et al. 2012; Bridi et al. 2015) and that coffee consumption is associated with reduced mortality in people (Loftfield et al. 2015; Je and Giovannucci 2014). It is intriguing to speculate that these effects could be related to the caffeine's mTOR inhibitory activities.

The absence of effects from the other nutraceutical compounds tested suggests that they may not be true mTOR inhibitors. One potential explanation is that some of these compounds, which were generally reported to inhibit mTOR in cancer cell culture models, act via indirect mechanisms through targets that are not present or not similarly affected in yeast. Another possibility is that some of these compounds inhibit mammalian cell growth or nutrient uptake, perhaps specifically in the context of cancer cell culture models, which could have

indirect effects on mTOR signaling in response. One interesting example is resveratrol, which is reported to have numerous targets in mammalian cells and to inhibit mTOR through both direct and indirect mechanisms. In one study, resveratrol was found to enhance the physical interaction between mTOR and its inhibitor DEPTOR (Liu et al. 2010), which has no obvious yeast ortholog. Resveratrol has also been suggested to inhibit mTOR by indirect mechanisms including regulation of phosphoinositide 3-kinase (PI3K), Akt (Brito et al. 2009), and AMP-activated protein kinase (AMPK) (Tillu et al. 2012). We found no evidence here to support an mTOR-inhibitory role for resveratrol in yeast, nor any effect on growth at all, consistent with prior work showing that resveratrol does not impact yeast growth or replicative life span (Kaeberlein et al. 2005b).

Overall, the system described here represents a sensitive, high-throughput, and inexpensive approach to identify growth inhibitory molecules with specificity for mTOR in vivo. It may be possible to further optimize this system, for example, by screening compounds in a drug sensitized background or by **humanizing the system through expression of human proteins in the mTOR signaling pathway in yeast.** Additionally, this method is easily adapted for testing drug interactions by adding a mixture of two or more compounds, as well as for investigating the impact of genetic diversity on mTORC1 inhibition through use of large-scale genetic libraries or wild isolate yeast strains (Fay and Benavides 2005; Liti et al. 2009). The identification of new mTOR inhibitors and genetic variants that impact sensitivity to mTOR inhibition will facilitate the development of new therapies and personalized approaches for a breadth of conditions where mTOR signaling is perturbed.

Methods

Yeast strains and culture conditions

All yeast strains used were in the BY4742 genetic background (*MAT α his3 Δ 1 leu2 Δ 0 lys2 Δ 0 ura3 Δ 0*). BW1121 (BY4742) was purchased from Thermo Fisher Scientific (Waltham, MA). GS668 (*fpr1 Δ ::kanMX4*) and GS983 (*tor1 Δ ::kanMX4*) were obtained from the haploid *MAT α* yeast deletion collection (Winzeler et al. 1999). PCR was used to confirm knockout identity. For GS983, 5'-TTGAATCCTAATTCTTGCTCAATC-3' and 5'-AAGGCATATATTGATGCTCAAAAAG-3'

primers were used to confirm knockout. For GS668, 5'-GTTACTTGATGATATTAAGCACGGG-3' and 5'-ACAAAAATGAACCATTAGCAAAGAG-3' primers were used to confirm knockout. The *tor1Δfpr1Δ* double deletion strain was constructed by mating *tor1Δ::URA3* (Kaeberlein et al. 2005a) and *fpr1Δ::kanMX4* and selecting for Ura⁺ G418^r haploid spores after sporulation and tetrad dissection. PCR was used to verify presence of gene deletions. For overnight culture and growth analysis, yeast extract peptone dextrose (YPD) (1% w/v Bacto™ yeast extract (BD), 2% w/v Bacto™ peptone (BD), 2% w/v dextrose) media were used. Yeast were cultured at 30 °C for all experiments. All experiments were repeated at least three times with biological replicates. The number of biological replicates is indicated in each figure legend. Error bars in each figure represent standard error of the mean (SEM).

Growth analysis using Bioscreen C MBR

Growth analysis of maximal growth rate in yeast strains was performed using a Bioscreen C CMB (Growth Curves USA, Piscataway, NJ, USA) as previously described (Murakami et al. 2008, 2011; Burtner et al. 2009). Briefly, colonies outgrown from frozen stocks were inoculated into 5 mL YPD and incubated at 30 °C in a roller drum for 12–16 h. Two microliters of outgrown culture was used to inoculate 148 µL YPD into 100-well honeycomb plates for growth analysis. At least three colonies per strain were analyzed in triplicate for each drug treatment. Doubling times were calculated identifying the slope of the inflection point along growth curves using the online web tool Yeast Outgrowth Data Analyzer (YODA) (Olsen et al. 2010). Welch's (unequal variance) *t* test was used to assess statistical significance.

Drug preparation and suppliers

All drugs except caffeine and cycloheximide were suspended in DMSO (these drugs were suspended in H₂O). Rapamycin, everolimus, and temsirolimus were purchased from LC Laboratories (Woburn, MA, USA). Cycloheximide and berberine were purchased from Sigma-Aldrich (St. Louis, MO, USA). Torin 1 was purchased from Cayman Chemical (Ann Arbor, MI, USA). AZD8055, GDC-0941, and GSK2126458 were kind gifts from Jason Pitt. Caffeine was purchased from MP Biomedicals (Santa Ana, CA, USA). Resveratrol was purchased from AstaTech Inc. (Bristol, PA, USA).

Alpha-lipoic acid, broccoli concentrate, glucosamine, lycopene, and quercetin were provided by USANA Health Sciences, Inc. (Salt Lake City, UT, USA).

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