Tor1/Sch9-Regulated Carbon Source Substitution Is as Effective as Calorie Restriction in Life Span Extension

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Abstract

The effect of calorie restriction (CR) on life span extension, demonstrated in organisms ranging from yeast to mice, may involve the down-regulation of pathways, including Tor, Akt, and Ras. Here, we present data suggesting that yeast Tor1 and Sch9 (a homolog of the mammalian kinases Akt and S6K) is a central component of a network that controls a common set of genes implicated in a metabolic switch from the TCA cycle and respiration to glycolysis and glycerol biosynthesis. During chronological survival, mutants lacking SCH9 depleted extracellular ethanol and reduced stored lipids, but synthesized and released glycerol. Deletion of the glycerol biosynthesis genes GPDL, GPDL2, or RHR2, among the most up-regulated in long-lived sch9Δ, tor1Δ, and ras2Δ mutants, was sufficient to reverse chronological life span extension in sch9Δ mutants, suggesting that glycerol production, in addition to the regulation of stress resistance systems, optimizes life span extension. Glycerol, unlike glucose or ethanol, did not adversely affect the life span extension induced by calorie restriction or starvation, suggesting that carbon source substitution may represent an alternative to calorie restriction as a strategy to delay aging.

Introduction

Mutations that decrease the activities of the Akt/PKB, Tor, and Ras pathways extend the lifespan of several model organisms, suggesting that the underlying mechanisms of longevity regulation are conserved in many eukaryotic organisms [1,2]. Akt/PKB is a highly conserved serine-threonine kinase shown to function in the Daf-2 longevity pathway of Caenorhabditis elegans [3]. Homologous longevity modulating pathways were also identified in Drosophila and mice [2]. In yeast, Sch9, which shares high sequence identity with the mammalian kinases Akt/PKB and S6K, is part of a nutrient-sensing pathway whose downregulation extends the chronological lifespan (CLS, the survival time of a population of non-dividing yeast) by up to 2-fold [4]. The Ras G-proteins are also evolutionary conserved and implicated in cell division in response to glucose/growth factors. The deletion of RAS2 doubles the CLS of yeast [5]. In mammals, a role for Ras in longevity control has not been established conclusively but, together with Akt, Ras is one of the major mediators of IGF-I signaling, which has been shown to promote aging [6,7]. Another conserved nutrient-responsive pathway, regulating cell growth and cell-cycle progression, involves the protein kinase target of rapamycin, TOR, which has been associated with life span regulation in C. elegans and Drosophila. Knockdown of LET-363/CeTOR, starting at the first day of the adult life, more than doubled the life span of worm [8]. Similarly, a reduced activity of Daf-15, the worm ortholog of the mammalian mTOR-interacting protein raptor, promotes life span extension [9]. In flies, overexpression of dominant-negative dTOR or TOR-inhibitory dTsc1/2 proteins also leads to longevity extension [10]. Moreover, knockdown of CeTOR does not further extend the life span of worms subject to dietary restriction (DR) and inhibition of TOR protects flies from the deleterious effects of rich food, suggesting the beneficial effect of DR is, at least in part, mediated by TOR [10,11].

Two TOR orthologs, TOR1 and TOR2, have been identified in yeast. Both Tor1 and Tor2 mediate growth-related signaling in a rapamycin-sensitive manner, whereas Tor2 has an additional rapamycin-insensitive function in controlling the cell-cycle-dependent organization of actin cytoskeleton [12]. Reduction of the TOR complex I (TORC1) activity results in an extension of yeast replicative life span (RLS), the number of daughter cells generated by individual mother cells [13,14], comparable to that obtained when Sch9 is inactivated [15,16]. Furthermore, a high throughput assay to measure the CLS of individual yeast deletion mutants identified several long-lived strains carrying deletions of genes implicated in the Tor pathway [17]. Additional evidence supporting an inverse correlation between Tor1 activity and longevity is provided by individual mother cells [13,14]. Moreover, knockdown of CeTOR does not further extend the life span of worms subject to dietary restriction (DR) and inhibition of TOR protects flies from the deleterious effects of rich food, suggesting the beneficial effect of DR is, at least in part, mediated by TOR [10,11].

The aging-regulatory function of both yeast Tor1 and Sch9 mediates the calorie restriction (CR)-dependent RLS extension. The down-regulation of either pathway mimics the effect of lowering the glucose content of the medium, and no further extension of RLS is observed when the sch9Δ or the tor1Δ mutants...
Author Summary

Studies using model organisms have pointed to the existence of evolutionarily conserved genes and signaling pathways that regulates life span. Changes in the activity of these genes/pathways have also been implicated in mediating the beneficial effect of calorie restriction, a well-recognized intervention that extends the life span from yeast to mammals. We investigated the global gene expression changes and identified genes involved in the metabolism of various kinds of carbon sources that are associated with longevity in the single cell organism, the baker's yeast. Although glucose and ethanol are common carbon sources for growth, they also have detrimental aging effects in yeast. Long-lived yeast mutants actively utilize available glucose and ethanol and produce glycerol, which does not adversely affect the yeast life span extension. Our finding suggest that this "carbon source substitution" observed in long-lived yeast creates an environment mimicking calorie restriction, which together with the direct regulation of stress resistance systems optimizes life span extension. Findings using these simple genetic models will help to elucidate fundamental longevity regulatory mechanisms and identify similar pathways in mammals.

are calorie restricted [19]. Ethanol produced during fermentative growth is used as carbon source during diauxic shift and post-diauxic phase, when the yeast cells switch from rapid growth to slow budding and eventually cease proliferation [20,21]. Switching yeast grown in glucose/ethanol medium to water models an diauxic phase, when the yeast cells switch from rapid growth to growth is used as carbon source during diauxic shift and post-
are calorie restricted [19]. Ethanol produced during fermentative growth is used as carbon source during diauxic shift and post-diauxic phase, when the yeast cells switch from rapid growth to slow budding and eventually cease proliferation [20,21]. Switching yeast grown in glucose/ethanol medium to water models an diauxic phase, when the yeast cells switch from rapid growth to growth is used as carbon source during diauxic shift and post-

Results

Genetic Interactions between SCH9, and RAS2 and TOR1

Using a genetic approach, we examined the relationship between Sch9, Tor1, and Ras2 in regulating cellular protection against stress and life span. The effects on life span and stress resistance caused by deficiency in Tor1 activity are less robust than those observed in the strains lacking Sch9 or Ras2. We did not observe any significant difference in mean lifespan or stress resistance between sch9Δ and the tor1Δ sch9Δ double knockout strains (Figure 1A, G, and Table S1). By contrast, the deletion of TOR1 in a mutant carrying a transposon insertion in the promoter region of SCH9, which only reduces SCH9 expression [4], caused a further increase of resistance to heat and to the superoxide-generating agent menadione, but not to H2O2 (Figure 1B), suggesting that the lack of TOR1 contributes to the further inactivation of the Sch9 pathway. This result is in agreement with the recent study showing that Sch9 is a direct target of rapamycin-sensitive Tor complex 1 (TORC1) [26]. In fact, reducing the TORC1 activity either by deleting TCO89, which encodes a TORC1 component, or by rapamycin treatment increased cellular resistance to heat and H2O2 (Figure S1).

Since Sch9 activity is associated with an age-dependent increase of mutation frequency [23], we examined the interaction between Sch9 and Tor1 in the regulation of genomic instability during chronological aging. Whereas the tor1Δ mutant was slightly less susceptible than wild type cells to genomic instability (measured as age-dependent frequency of mutations of the CAN1 gene) between day 1 and 7, there was no additive effect of TOR1 and SCH9 double deletion in the mutation frequency compared to that of the sch9Δ mutant (Figure 1E). Overexpression of TOR1 only slightly reduced the stress resistance phenotype of sch9Δ (data not shown). However, resistance to stress and life span extension of tor1Δ was abolished by overexpressing SCH9 (Figure 1F and data not shown). Taken together, these data are in agreement with a shared signaling pathway between Tor and Sch9 in life span regulation and suggest an upstream role of Tor1 in Sch9 signaling (Figure 1H).

Both Tor and Ras/cAMP-PKA pathways are known to regulate stress-responsive (STRE) genes [27]. Elevating Ras activity by ectopically expressing constitutively active Ras2 (ras2Val19) reversed the life span extension and the stress resistance of tor1Δ mutants (Figure 1F and data not shown). Conversely, deletion of RAS2 had an additive effect to tor1Δ with respect to stress resistance but not life span (Figure 1C, G, and Table S1), suggesting an overlap in longevity modulation by Tor1 and Ras2.

We have previously shown that longevity regulation controlled by Tor1, Sch9 and Ras2 converges on the protein kinase Rim15 [24]. Rim15 positively regulates stress response transcription factors (TFs) Msn2/4 and Gis1, which activate genes involved in cellular protection. Interestingly, enhancement of stress resistance and life span extension associated with Ras2 deficiency requires both the STRE-binding TFs Msn2/4 and PDS-binding Gis1, whereas the sch9Δ-mediated longevity regulation mainly depends on the latter [4,24]. These results indicate that the common downstream effectors are differentially modulated by the Sch9 and Ras2. In fact, the ras2Δ sch9Δ double knockout cells exhibited higher stress resistance than either of the single deletion mutants (Figure 1D). It also showed a 5-fold increase in mean life span compared to wild type cells (Figure 1G and Table S1). The triple sch9Δ ras2Δ tor1Δ deletion mutant, however, did not show any further increase of life span or stress resistance (Figure 1D, G, and Table S1). These results depict a life-span regulatory network composed of parallel but partially connected signaling pathways controlled by Tor1/Sch9 and Ras2 (Figure 1H).

Gene Expression Profiles of Long-Lived Mutants

To identify the mediators of life span extension downstream of the Tor/Sch9 and Ras pathways, we carried out DNA microarray
Figure 1. Genetic interactions between Sch9, Tor1, and Ras2 in regulating stress resistance and life span. (A–D) Day 3 wild type (DBY746) and cells lacking Tor1, Sch9, or Ras2 were challenged with heat shock (55°C; A, 105 min; B, 75 min; C, 150 min; and D, 120 min) or oxidative stresses (H$_2$O$_2$, 100 mM for 60 min; or menadione, 250 μM for 30 min). (E) Mutation frequency over time measured as Can$^r$ mutants per million cells. The average of four experiments is shown. Error bars represent SEM. (F) Chronological survival in minimal complete medium (SDC) of wild type, tor1Δ, and mutants overexpressing either SCH9 or constitutively active Ras2 (ras2Val19). (G) Chronological survival of wild type and mutants lacking Tor1, Sch9, Ras2 or combinations. The data represent average of at least 4 experiments. Error bars show SEM. For mean life span calculated from non-linear curve fitting see Table S1. (H) Longevity regulatory pathways in yeast. The nutrient sensing pathways controlled by Sch9, Tor, and Ras converge on the protein kinase Rim15. In turn, the stress response transcription factors Msn2, Msn4, and Gis1 transactivate stress response genes and enhance cellular protection, which lead to life span extension. Pro-longevity effects of CR are partially mediated by Sch9, Tor, and Ras, and may also require additional yet-to-be indentified mechanism(s).

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analyses for all three long-lived mutants: sch9Δ, tor1Δ and ras2Δ. Total RNA was extracted from 2.5 day-old cultures of long-lived mutants and wild type cells. This age was selected to avoid both the noise that may arise from a small fraction of cells that are still dividing at younger ages (day~2) and the general decrease in metabolism and consequently in gene expression that normally occurs at older ages (day 4–5) [22]. The cRNA obtained from total RNA was hybridized to gene chips that allow the detection of 5841 genes present in S. cerevisiae. Three independent populations of each genotype were analyzed. A total of 900 genes showed a greater than 2-fold change in expression relative to those in wild type cells. Among these, 63 genes were consistently up-regulated more than 2-fold in all three mutants, and 25 genes were consistently down-regulated (Figure 2A, for complete microarray data, see Table S2). The mRNA levels of seven of the most up-regulated and one most down-regulated genes in both the tor1Δ and sch9Δ mutants were confirmed by quantitative RT-PCR and/or Northern blot (Figure S2). Based on the pair-wise comparison of the long-lived mutants, the up- and down-regulation of genes in these long-lived mutants are significantly overlapping, suggesting that the Ras, Tor, and Sch9-centered longevity regulatory network controls a common set of downstream genes (Table 1 and Table S3). To identify features common to the three long-lived mutants, we performed a gene ontology (GO) analysis of the microarray data by Wilcoxon rank test. Although the data point to common changes in all 3 long-lived mutants, the GO category analysis indicated a divergence in expression pattern between ras2Δ and the other two mutants (Table S4), which is in agreement with our genetic analysis of two parallel signaling pathways controlled by Sch9 and Tor1 in combination with that of one of the most up-regulated genes, the expression of glycolytic/fermentative genes, but not of gluconeogenic genes, was instead up-regulated (Table S5C). Interestingly, several genes coding for high-affinity glucose transporters or putative glucose transporters, known to be inhibited by high glucose concentrations [28], were up-regulated indicating that the long-lived mutants may have entered a starvation-like mode in which glucose uptake is maximized (Table S5D). Considering that the extracellular glucose was exhausted in mutants as well as wild type cells by day 1–2 (data not shown), the major substrate available for fermentation by day 2.5 is probably glycerol, which is normally accumulated by yeast in the late phases of exponential growth [29].

Genes involved in stationary phase survival, sporulation, meiosis, and stress response (EMP45, GRE1, IME1, RPI1, SPS100, and TAI1) were among the most up-regulated genes in all three long-lived mutants (Table S2). To test their contribution to life span extension and stress resistance in long-lived mutants, we originated a set of double mutants carrying the deletion of SCH9, RAS2 or TOR1 in combination with that of one of the most up-regulated genes. Whereas the deletion of either EMP45 or YDR126W slightly reduced the mean life span of the sch9Δ mutants (Figure 2B), they have no effect on ras2Δ mutants (Figure S3B). The deletion of IME1 or RPI1 did not affect either the stress resistance or the life span extension caused by the lack of Sch9 (Figure 2B and data not shown). Deletion of YLR012C, the most down-regulated gene, did not affect significantly the life span or the stress resistance of the cell (Figure S3A).

Several genes coding for proteins that function in the ergosterol biosynthesis were up-regulated in the long-lived mutants (Table S7). Ergosterol is the predominant sterol in yeast and is structurally closely related to cholesterol. Besides being a structural component of the cellular membrane, ergosterol affects phospholipid synthesis, lipid rafts formation, signal transduction as well as aerobic energy metabolism [30]. The deletion of either ERG4 or ERG20 caused a small decrease in both heat and oxidative stress resistance in the sch9Δ mutants (Figure S3D). However, the deletion of ERG3, the most up-regulated ergosterol biosynthesis gene in our microarray analysis, did not reverse longevity extension or reduce stress resistance associated with the sch9Δ mutants (data not shown). Notably, the ergosterol biosynthetic genes that were upregulated in all three long-lived mutants are those involved in converting squalene to ergosterol, which require molecular oxygen and often

**Figure 2. Gene-expression profiles of long-lived mutants.** (A) Venn diagram of genes up- or down-regulated more than 2-fold in the tor1Δ, sch9Δ, and ras2Δ mutants, at day 2.5, compared to wild type cells (DBY746). Microarray analyses were carried out in triplicates. The number of up- or down-regulated genes was shown in red or green, respectively. For the significance of overlapping in up- and down-regulated genes see Table S3. (B) Life span of mutants with deletions of genes most upregulated in long-lived mutants in the sch9Δ background. Data represent mean and SEM of pair matched, pooled experiments. For mean life span calculated from non-linear curve fitting see Table S1.

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Whereas the genes encoding the lipases responsible for the acetone-phosphate (DHAP), a glycolysis intermediate (Figure 3A). Glycerol is produced from either triacylglycerol or dihydroxyacetone phosphate (DHAP), a glycolysis intermediate (Figure 3A). 

glycerol is produced from either triacylglycerol or dihydroxyacetone phosphate (DHAP), a glycolysis intermediate (Figure 3A). In yeast, biosynthesis. A search in the 800 bp upstream promoter region of glucose utilized by these mutants is redirected towards glycerol from DHAP, showed higher levels of expression in all the long-lived mutants has little effect on life span. The most up-regulated in long-lived mutants was DAK1, indicating that regulation of glycerol biosynthesis is part of the regulatory repertoire of Sch9 signaling.

Increased Expression of Glycerol Biosynthetic Genes in Long-Lived Mutants

In addition to the lower expression of TCA cycle and respiratory genes and higher expression of glycolytic/fermentative genes, we also observed an up-regulation of the genes implicated in the metabolism of glycerol, a byproduct of the overflow metabolism when there is enhanced glycolytic flux and limited respiration capacity (Figure 3A and B). Significant up-regulation of genes involved in glycerol metabolism (21 genes, Table S6) was observed in sch9Δ and ras2Δ mutants (p-value of 0.0058 and 0.0142, Wilcoxon rank test, one-sided, respectively). In yeast, glycerol is produced from either triacylglycerol or dihydroxyacetone-phosphate (DHAP), a glycolysis intermediate (Figure 3A). Whereas the genes encoding the enzymes responsible for the hydrolysis of triacylglycerol were slightly up-regulated, GPD1 and GPD2, encoding the key enzymes required for glycerol production from DHAP, showed higher levels of expression in all the long-lived mutants (Figure 3B and C), suggesting that part of the glucose utilized by these mutants is redirected towards glycerol biosynthesis. A search in the 800 bp upstream promoter region of the glycerol biosynthesis genes revealed that GPD1, GPD2, HOR2, DAK1, and DAK2 contain the DNA binding elements of Gis1- and Msn2/4 (Figure 3B), stress resistance transcription factors downstream of Tor1, Sch9, and Ras2 [24]. Furthermore, the up-regulation of glycerol biosynthesis genes was partially reversed in sch9Δ gis1Δ double mutants (Figure 3C; Figure S2J and K), indicating that regulation of glycerol biosynthesis is part of the regulatory repertoire of Sch9 signaling.

In fact, higher level of intracellular glycerol was observed in the sch9Δ mutants compared to that in wild type cells at day 3 (Figure 4A). In wild type cells the level of extracellular glycerol peaked at day 2 but was mostly depleted by day 3. In the sch9Δ culture, however, a much elevated level of glycerol was measured in the medium up to day 9 (Figure 4B). By contrast, ethanol produced during the exponential growth, and most likely in the post-diauxic phase as well, was depleted early in sch9Δ mutants but not in wild type cells (Figure 4C and D) [23], suggesting a metabolic switch from biosynthesis and release of ethanol in wild type cells to that of glycerol in sch9Δ mutants. Glycerol accumulation could be accompanied by the depletion of other carbon sources as well. Nile red staining of the lipid body indicated that the levels of triacylglycerol and other neutral lipids in sch9Δ mutants were consistently lower compared to that in wild type cells across all ages (Figure 4E and data not shown), which is in agreement with a modest but consistent increase of lipolytic enzyme mRNA levels (Table S6). Accumulation of extracellular glycerol also occurred in tor1Δ and ras2Δ mutants, but was lower than that observed in sch9Δ mutants (Figure S4).

Table 1. Gene ontology (GO) analysis of expression profiles of long-lived mutants.

| Positively affected GO categories | sch9Δ | tor1Δ | ras2Δ |
|----------------------------------|-------|-------|-------|
| GO* GO ID Genes # Annotation     | p     | q     | p     | q     | p     |
| C G00005842 93 cytosolic large ribosomal subunit | 0.00E+00 | 0.00E+00 | 0.00E+00 | 0.00E+00 | 1.64E-12 | 2.37E-10 |
| C G00005843 63 mitochondrial large ribosomal subunit | 0.00E+00 | 0.00E+00 | 0.00E+00 | 0.00E+00 | 7.49E-09 | 6.49E-07 |
| P G00016125 37 sterol metabolism | 5.65E-03 | 6.20E-02 | 7.50E-03 | 7.56E-02 | 7.51E-05 | 2.32E-03 |
| P G00046365 33 monosaccharide catabolism | 1.32E-03 | 2.01E-02 | 2.94E-05 | 1.02E-03 | 8.81E-06 | 3.81E-04 |

Significantly up-or down-regulated categories were shown in bold (p<0.01). q-value was also calculated to correct the multi-testing error.

GO categories: C, Cellular component; F, molecular function; and P, biological process.

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involve oxidation of NADPH to NADP⁺ (Table S7). The upregulation may reflect a hypoxic environment during the post-diauxic phase survival of these long-lived mutants and suggests a link between redox state of the cell and survival. Taken together, these results indicate that the single deletion of many genes among the most up-regulated in long-lived mutants has little effect on life span.
Glycerol Biosynthesis Genes Are Required for Life Span Extension in *sch9Δ*

To further examine the role of glycerol biosynthesis in life span regulation, we generated strains lacking Rhr2, the yeast DL-glycerol-3-phosphatase, in the *sch9Δ* background. The *rhr2Δ* *sch9Δ* double mutant failed to accumulate glycerol extracellularly (Figure 5A). Deletion of *RHR2* abolished the life span extension as well as the resistance to heat and oxidative stresses associated with the *sch9Δ* mutants in the DBY746 genetic background (Figure 5B and C). Interestingly, ethanol was still present in the medium of *rhr2Δ* *sch9Δ* mutants at day 5 (Figure 5D), when ethanol is mostly depleted in the *sch9Δ* culture (Figure 4D), although in 3 independent cultures (3 independent isolates) assayed, we observed high variation in ethanol concentration. Utilizing the yeast KO collection (BY4741 genetic background), we deleted *SCH9* in strains lacking key glycerol biosynthetic genes. Deficiency in either of the NAD-dependent glycerol 3-phosphate dehydrogenase genes, *GPD1* or *GPD2*, did not cause a significant life span change in wild type BY4741 cells (Figure S5A). However, the deletion of either *GPD1* or *GPD2*, led to the reversion of the longevity extension associated with *Sch9* deficiency (Figure 5E). Similarly, the deletion of *RHR2* abolished the life span extension in the *sch9Δ* mutant (Figure 5E).

In contrast, lack of Hor2, a redundant isoenzyme of DL-glycerol-3-phosphatase, did not affect the life span of the *sch9Δ* mutant (data not shown). The difference between these two isoenzymes may be explained by the fact that Rhr2 is the predominant isoenzyme in the cell [31]. In agreement with the major role of Rhr2, the mRNA level of *HGI1*, coding for an inhibitor of Rhr2 [32], was down-regulated in all long-lived mutants (Figure 3B). Notably, the life span of *rhr2Δ* mutants in the BY4741 genetic background was similar to that of wild type cells, although some *rhr2Δ* cultures showed regrowth/gasping (data not shown) [33].

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**Figure 3. Expression of the glycerol biosynthesis genes.** (A) Schematic representation of glycerol metabolism. For illustration purpose, genes up- or down-regulated more than 20%, compared to wild type (DBY746) in all three long-lived mutants, are labeled in red or green, respectively. (B) Fold change in expression levels of glycerol biosynthetic genes in *sch9Δ*, tor1Δ, and ras2Δ mutants compared to wild type at day 2.5 (for complete microarray data, see Table S2 and Table S6). Data were expressed in fold change, WT = 1. Gene expression levels that are 20% higher or lower than wild type cells are marked in red or green. 1 Predicted PDS motif: AWAGGGAT; 2 predicted STRE motif: ARGGGG; 3 predicted STRE motif: AGGGG. (C) Real time quantitative PCR analysis of *GPD1* mRNA level *sch9Δ* and *sch9Δ gis1Δ* cells at day 2.5. Data represent mean and SEM, n = 4. *p*< 0.05, t-test, two-tailed, *sch9Δ* vs. WT. doi:10.1371/journal.pgen.1000467.g003

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Figure 4. Sch9 deficient mutants metabolize ethanol and accumulate glycerol. (A) Intracellular glycerol contents of wild type (DBY746) and cells lacking Sch9 were measured on day 1 and day 3. Data represent mean and SEM of 8 cultures analyzed. (B) Glycerol concentration in the medium of wild type and sch9Δ cultures. Data represent mean and SEM of 5–7 cultures analyzed. ** p<0.01, unpaired t-test, two-tailed, sch9Δ vs. WT. (C–D) Glycerol and ethanol concentrations in the medium of wild type (C) and sch9Δ (D) cultures. Data represent mean and SEM of 3–5 cultures analyzed. (E) Nile red staining of neutral lipids of day 1 wild type and sch9Δ mutants. Nile red staining is shown on the right, and phase contrast left. Bar, 10 µm. doi:10.1371/journal.pgen.1000467.g004
Cells lacking both Rhr2 and Hor2 have been shown to be hypersensitive to the superoxide anion generator, paraquat, suggesting a role for glycerol biosynthesis in cellular protection beyond osmotic stress [34]. We also tested the role of glycerol biosynthetic genes in the stress resistance of sch9Δ mutants in the BY4741 background. Hypersensitivity to heat and hydrogen peroxide-induced oxidative stress was observed in the RHR2-null strain, but not in gpd1Δ, gpd2Δ, or hor2Δ mutants in the BY4741 background (Figure 5F). Furthermore, cells lacking Yig1, the Rhr2 inhibitor, were slightly more resistant to stress compared to wild type cells (Figure 5F). The stress resistance phenotype of sch9Δ mutants was reversed by the deletion of GPD1 or GPD2, but not of RHR2 or HOR2 (Figure 5F). There appears to be redundancy in glycerol-mediated response to stress such that deficiency of one enzyme can be compensated by activation of others in the glycerol biosynthesis pathway. Deletion of SCH9 greatly enhanced stress resistance to heat and H2O2 of rhr2Δ mutants (Figure 5F), possibly due to the upregulation of the Hor2 level. Since glycerol phosphatases (Rhr2 and Hor2) are not the rate-limiting enzymes for glycerol production [34], the upregulation of Gpd1 and Gpd2 may also contribute to the rescue of the rhr2Δ stress sensitive phenotype in cells lacking SCH9. A similar redundancy exists between Gpd1 and Gpd2. Although little or no effect was seen in either of the single deletion mutants, gpd1Δ/2 Δ double knockout strain is hypersensitive to heat and hydrogen peroxide treatment (data not shown). The triple sch9Δ gpd1Δ gpd2Δ mutant showed severe growth defects and low saturation density in the liquid culture, which

Figure 5. Deletion of glycerol biosynthesis genes reverses life span extension and stress resistance associated with Sch9 deficiency. (A) Glycerol concentration in the medium. Data represent mean and SEM of 4 cultures analyzed. * p<0.05, ** p<0.01, unpaired t-test, two tailed, sch9Δ vs. rhr2Δ sch9Δ. (B) Life span of wild type (DBY746), sch9Δ, rhr2Δ, and Sch9-deficient mutants lacking Rhr2. Glycerol (1%, final concentration) was added to the one day-old rhr2Δ sch9Δ culture. Data represent mean and SEM of 4–5 cultures analyzed. (C) Day3 cells were exposed to heat shock (55°C for 105 min) or H2O2 (150 mM for 60 min). Strains shown are wild type (DBY746), rhr2Δ, sch9Δ, and rhr2Δ sch9Δ. (D) Ethanol concentration in the medium. Data represent mean and SEM, n = 3. Ethanol in sch9Δ culture at day 5 was at the lower detection limit of the assay. (E) Life span of wild type (BY4741), sch9Δ, and Sch9-deficient mutants lacking Gpd1, Gpd2, or Rhr2. Data represent mean and SEM of 3 experiments. (F) Heat shock (55°C) and oxidative stress (H2O2, 500 mM, 60 min) resistance of day 3 mutants lacking glycerol biosynthesis genes (in the BY4741 genetic background). doi:10.1371/journal.pgen.1000467.g005
Glycerol can protect against stress in part because of its function as a chemical chaperone [33-37]. To test the role of glycerol in protecting against heat-induced protein misfolding, we examined the activity loss and recovery of a heat-sensitive bacterial luciferase [38] in wild type and sch9Δ cells. Whereas exposing wild type cells to heat stress (42°C for 1 hour) led to a ~80% reduction of luciferase activity, only a 20-40% loss of activity was observed in sch9Δ mutants (Figure 6A), which is consistent with the enhanced stress resistance phenotype of sch9Δ (Figure 1). However, pre-treatment of wild type cells with low concentration of glycerol had no protective effect on the heat-induced loss and the recovery of luciferase activity (Figure 6B), indicating the heat resistance phenotype of sch9Δ does not depend on the short-term exposure to extracellular glycerol. Similar results were obtained in the BY4741 genetic background (Figure S5B and C).

Intracellular accumulation of glycerol also contributes to protection against osmotic stress [37,39]. Addition of 0.1% of glycerol to the medium slightly enhanced the resistance to osmotic stress of wild type yeast (Figure 6C). When exposed to high concentration of NaCl, the sch9Δ and rasΔ mutants exhibited enhanced resistance to hyperosmolarity compared to the tor1Δ mutant, which in turn was better protected than wild type yeast cells (Figure 6C and Figure S4B), suggesting that increased resistance against hyperosmolarity may be part of the general stress response shared by all long-lived mutants. These data are also consistent with the reports that high osmolarity growth conditions extend both RLS and CLS in yeast [40,41]. With regard to life span, however, extracellular supplementation of glycerol (0.1% and 1%) to the wild type yeast culture at day 3, when the glycerol level is high in the long-lived sch9Δ mutants (Figure 4B), did not show any beneficial effect (Figure 6D).

Glycerol Provides a Carbon Source without Blocking the Anti-Aging Effect of Calorie Restriction

Ethanol, as a carbon source, elicits pro-aging signaling and promotes cell death. Removing ethanol either by evaporation or by switching yeast cells from expired medium to water, which represents a condition of extreme calorie restriction/starvation, extends yeast chronological life span [23]. The metabolic switch to ethanol utilization and glycerol biosynthesis removes the detrimental effect of pro-aging carbon sources (glucose and ethanol) and creates an environment that mimics calorie restriction in the sch9Δ mutant culture (Figure 4D). To elucidate the role of different carbon sources on life span, we used an in situ assay to monitor chronological survival of yeast on plate [42], which allowed us to: a) study the effect of different carbon sources in the presence of all the other nutrients, b) control the exact amount of carbon source to which the cells are exposed over the whole experiment, similarly to the experimental conditions used for the RLS studies of caloric restriction.

The survival curve of approximately 200 wild type DBY746 cells plated onto SC-Trp plates supplemented with 2% glucose is reminiscent of that in the standard liquid medium paradigm (Figure 6E). Extreme CR/starvation (agar plate) or removal of carbon source from the SC-Trp plates leads to life span extension, which was partially reversed by the presence of low concentration of ethanol (Figure 6E) in agreement of our earlier findings [23]. The adverse effect of glucose on life span was also observed on the long-lived sch9Δ and ras2Δ cells (Figure S6C and D). Substitution of glucose with high level of glycerol (3%), however, did not trigger the pro-aging signaling as seen with glucose or ethanol (Figure 6E). Thus, the metabolic switch to glycerol biosynthesis in the long-lived sch9Δ mutants may represent a genetically induced “carbon source substitution” that can be as effective as calorie restriction in the regulation of protection.

Calorie restriction-induced cellular protection and life span extension in yeast depends on the protein kinase Rim15 and the activation of its downstream stress response transcription factors, which are negatively regulated by Sch9, Tor, and Ras [24]. Extreme CR/starvation, achieved by switching yeast to water, activates Msn2/4 and Gis1 transactivation, via the STRE and PDS elements, respectively [24]. Addition of glucose and, to a lesser extent, ethanol significantly represses CR-induced STRE- and PDS-driven LacZ reporter gene expression (Figure 6F and G). However, no reduction in STRE and PDS transactivation were observed when CR yeast were exposed to glycerol (Figure 6F and G). Similar to extreme CR/starvation, reduction concentration of glucose in the culture medium also extends yeast life span [43-47] and requires the Msn2/4 and Gis1 [24]. When yeast were grown in medium containing either low glucose (1%) or glucose/glycerol (1% each), a 1.5-fold increase in mean life span was observed compared to that in the standard medium (Figure 6H). This pro-longevity effect of the low glucose/glycerol diet was mostly dependent, as is that of calorie restriction, on the stress response transcription factors (Figure 6H). Notably, the beneficial effect of calorie restriction on longevity does not require glycerol biosynthesis. Cells deficient of RHR2 still lived long when cultured in reduced glucose or incubated in water (Figure S6A and B).

The metabolic switch in the sch9Δ mutants may not only remove the pro-aging/death signaling from glucose/ethanol or other carbon sources but also produce a carbon source, glycerol, for long-term survival. We switched wild type cells from the ethanol-containing medium to water containing 0.1% glycerol. A small extension of life span was observed in addition to that of extreme calorie restriction (Figure 6I), suggesting that glycerol may provide nutritional support or additional protection under the starvation condition. In fact, we show that yeast cells actively uptake the exogenous [1,2,3-3H] glycerol during the post-diauxic phase, entered by S. cerevisiae after most of the extracellular glucose is depleted (Figure 6J and Figure S4C). The utilization of glycerol is also supported by our microarray analysis, which showed that the genes involved in the catabolic metabolism of glycerol are up-regulated under the extreme CR/starvation (water) condition in wild type cells (Table S6).

Discussion

Model organisms such as yeast, worms, and flies have been instrumental in the discovery of life span regulatory pathways that have a common evolutionary origin. Among these, the insulin/IGF-1-like pathways control longevity in organisms as phylogenetically distant as yeast and mice. Akt, Tor, and Ras function in the mammalian IGF-1 signaling pathway and have been implicated in life span regulation in different model organisms [1,48]. In this study, we show that longevity regulatory pathways control the shift from respiration to glycolysis and glycerol biosynthesis. This metabolic switch, which leads to the removal of pro-aging carbon sources and glycerol accumulation, creates an environment in the sch9Δ culture that mimics calorie restriction (Figure 7).

The genetic and genomic data revealed two parallel longevity signaling pathways controlled by Tor1/Sch9 and Ras, in agreement with our previous work [4]. The beneficial effects of reduced activities of both pathways is additive (Figure 1D and G),
and the \( sch9\Delta ras2\Delta \) double mutant is one of the longest lived genetic mutants [49]. In agreement with the genetic data, the gene expression profile of the day 2.5-old \( ras2\Delta \) mutant shows that approximately 67% of the genes differentially expressed are not significantly changed in the other two mutants (Figure 2A). Our genetic analysis of the interactions between the Tor, Sch9 and Ras2 indicates a stronger overlap between the Tor1 and Sch9 pathways in the regulation of stress resistance, longevity, and age-dependent genomic instability. It also suggests that TORC1 functions upstream of Sch9 in the regulation of these readouts in agreement with what has been proposed by others [50] and with the demonstration of the direct phosphorylation of Sch9 by TORC1 [26]. Our microarray analysis indicates similarities but also differences between the set of genes controlled by Tor and Ras. On the one hand, \( TOR1 \) deletion further increased the heat-shock resistance of \( ras2\Delta \) mutants, and on the other hand no additional life span extension was observed. Furthermore, the overexpression of constitutively active Ras2 abolished CLS extension associated with deficiency of \( TOR1 \), suggesting an overlapping of the two pathways and possibly an upstream role of TORC1.

Despite the higher degree of differential expression profile observed in \( ras2\Delta \) mutants, there are remarkable similarities in the expression pattern of genes involved in key metabolic pathways in
The metabolic changes in long lived mutants generate a calorie restriction-like environment, which contributes to enhanced stress resistance and longevity modulation in both long-lived mutants and cells under calorie restriction (Figure 6) [24]. Since glycerol was taken up by the cells and caused a minor enhancement of survival under starvation conditions, it is likely that its uptake provides nutritional support for long term survival (Figure 6F). Second, production and accumulation of glycerol may contribute to cellular protection since glycerol enhances resistance to osmotic stress and functions as molecular chaperone stabilizing/renaturing the newly synthesized or heat-inactivated proteins. However, our present and past results indicate that Sch9 also down-regulates stress resistance systems independently of the generation of glycerol. For example, in the BY4741 background Sch9 deficiency increased the resistance to multiple stresses in mutants with defects in glycerol biosynthesis (Fig. 5F). Third, glycerol production may affect aging through the modulation of the redox balance of the cell, since its production contributes to enhanced stress resistance and longevity modulation in both long-lived mutants and cells under calorie restriction (Figure 6) [24]. Once glycerol was taken up by the cells and caused a minor enhancement of survival under starvation conditions, it is likely that its uptake provides nutritional support for long term survival (Figure 6F). Additionally, we overexpressed in wild type cells the malate-aspartate NADH shuttle components to enhance replicative life span [57]. The latter two mechanisms, however, are less likely to contribute significantly to chronological life span extension, as addition of exogenous glycerol to the culture had little or no effect on heat-induced protein inactivation (Figure 6B) or chronological survival in wild type cells (Figure 6D). Additionally, we overexpressed in wild type cells the bacterial NADH oxidase (NOX) or alternative oxidase (AOX), both of which increase NADH oxidation in yeast [58], did not significantly alter the life span of the wild type cells (unpublished data).

In summary, we presented data showing enhanced expression of glycerol biosynthetic genes in three long-lived yeast mutants lacking SCH9, TOR1, or RAS2, whose homologs also play important roles in life span modulation in organisms ranging

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**Figure 7. Inhibition of the Tor1/Sch9 and Ras pathways activates stress response transcription factors and glycerol biosynthesis.** The metabolic changes in long lived mutants generate a calorie restriction-like environment, which contributes to enhanced stress resistance and extended life span. doi:10.1371/journal.pgen.1000467.g007
from worms, flies, to mammals. Our data also suggest that the switch to glycerol biosynthesis is required for life span extension in the *sch9*Δ mutants. We argue that the genetically induced carbon source substitution in the long-lived *tor1*Δ and *sch9*Δ cells creates a beneficial environment that mimics calorie restriction which, together with the intracellular regulation of stress resistance via transcription factors Gis1 and Msn2/4, results in life span extension and stress resistance (Figure 7). In light of the conservation of the longevity regulatory pathways and the role of calorie restriction in extending life span of a wide range of species, it will be important to investigate further the possibility of an anti-aging role for glycerol in higher eukaryotes.

**Materials and Methods**

*S. cerevisiae* Strains and Growth Conditions

Mutant strains used were originated in DBY746 (*MATa*, *leu2-3,112, his3Δ, trp1-289, ura3-52, GAL*) or *BY4741* (*MATa*, *his3Δ1*, *leu2Δ0*, *met15Δ0*, *ura3Δ0*) by one-step gene replacement as described previously [59]. Strains overexpressing SCH9 or ras2Δco319 were generated by transforming DBY746 with plasmids pHA-SCH9 (a gift from Dr. Morano University of Texas Medical School) or pMW101 (plasmid RS416 carrying *CIA I-ras2Δco319-Hind III* fragment of pMF100, a gift from Dr. Broach, Princeton University), respectively. Strains expressing a heat sensitive bacterial luciferase (Parsell, 1994) were generated by transforming yeast with plasmid pGPD-luxAB (Addgene.com). Yeast chronological life span was measured as described previously [22]. For *in situ* viability assay [42], day 1 SDC cultures of tryptophan auxotrophic strains were diluted and plated on to SC-Trp plates without glucose, 1 ml of 5% glucose was added to the plates every 2–3 days, 0.5 ml of 2 mg/ml tryptophan was added to the plates. For oxidative stress resistance assays, cells were treated with 250 μM of menadione for 30 min in K-phosphate buffer (pH7.4). Silico dilutions of control or treated cells were spotted onto YPD plates and incubated at 30°C for 2–3 days. For osmotic stress resistance assay, cells were washed twice with water and resuspended in salt buffer (2 or 4 M NaCl). After incubating at 30°C for 24 h with shaking, cells were washed with water to eliminate salt, serially diluted, and then plated on to YPD plates. Plates were incubated 2–3 days at 30°C.

Nile Red Staining

Cells (1 ml SDC culture) were washed once with PBS and resuspended in 1 ml PBS. 10 μl of Nile Red (0.1 mg/ml in acetone) was added to the cell suspension and incubated at room temperature, in the dark, for 5 min. Cells were washed once with PBS and imaged with a Leica fluorescence microscope.

Glycerol and Ethanol Measurements

For intracellular glycerol content, cells were washed three times with water. Cell pellets from 1 ml culture were resuspended in 0.5 ml of Tris buffer (0.1 M, pH7.4) and, then, boiled for 5 min followed by a 30 sec spin to remove cell debris. The supernatant from the cell extract or the medium cleared of cells was used to determine intracellular or extracellular glycerol level, respectively. Glycerol concentration was measured using an UV-based glycerol assay kit (Boehringer Mannheim/R-Biopharm). The manufacturer recommended protocol was modified to adapt the assay to a 96-well plate format. Each sample was assayed in duplicates and data were fitted to standard curve generated by serial dilutions of stock glycerol. For intracellular glycerol measurement, glycerol concentrations were normalized to cell number based on viability assay. Ethanol concentration in medium was measured using the UV-based ethanol assay kit (Boehringer Mannheim/R-Biopharm) according to the manufacturer recommended protocol.

Luciferase Assay

Heat inactivation of luciferase was measured as previously described [Parsell, 1994]. Briefly, cells expressing heat-sensitive bacterial luciferase were subject to heat shock (42°C for 60 min). Ten minutes before the end of heat shock, cycloheximide (20 μM, final) was added to the culture. The culture was sampled and mixed with the luciferase substrate decanol (Sigma) and the signal was immediately measured in a luminometer (Luminoskan Ascent, Thermo Scientific).

LacZ Reporter Gene Assay

DBY746 strains with either 4xSTRE- or 1xPDS-LacZ integrated in the *URA3* locus have been described previously [24]. One-day old cells grown in SDC were washed 3 times with water and resuspended in water (extreme CR/starvation). Four hours after the initiation of CR, glucose, glycerol, or ethanol (0.8%, final) were added to the cultures. Samples were collected after 2 and 4 hours of further incubation at 30°C with shaking. LacZ activity was measured as described previously [24].

DNA Microarray Analysis and Real Time PCR

Total RNA were extracted from 2.5-day old wild type and mutants cultures (in SDC, n = 3) by the acid phenol method. The cRNA was hybridized to Affymetrix GeneChip Yeast 2.0 array to obtain the measurement of gene expression. Procedures for microarray data analysis have been described previously [51,60]. The Gene Ontology (GO, ftp://genome-ftp.stanford.edu/pub/go/ontology/) data were organized as a directed acyclic graph, in which each node corresponded to a set of genes with specific annotations. Only the GO categories that were well annotated and contain ≥30 genes were included, which were defined as terminal informative GO (TIGO) categories: 44 cellular components, 53 molecular functions, and 109 biological processes. Wilcoxon rank test was performed to examine whether a TIGO category was significantly up- or down-regulated. Finally, q-values for each test were calculated to correct the multiple testing errors using the “qvalue” package [61]. For quantitative RT-PCR analysis, total mRNA was extracted from cells harvested from 2.5-day-old cultures. RNA was reverse-transcribed using RetroScript III (Invitrogen). Quantitative real time PCR was performed using the DNA Engine Opticon 2 (BioRad). Primers used are listed in Figure S2 legend. Gene expression levels were normalized to actin (*ACT1*) and expressed as the percentage of wild type.
Supporting Information

Figure S1 Reduced Tor complex I (TORC1) activity enhances stress resistance. (A) Heat shock and oxidative stress resistance of wild type (DBY746) and cells deficient of either TOR1 or TORC1 subunit TCO89. Day 3 cells were subject to heat stress (55°C for 10 min) or oxidative stress (H2O2, 100 mM for 60 min). (B) Overnight culture of wild type cells were diluted into fresh SDC medium (initial OD600 0.3) and allowed to grow. Rapamycin was added to the culture after 5.5 hours (OD600 ~1) and 9.5 hours (OD600 ~6). Heat shock assay (55°C for 75 min) was performed at day 3. (C) Rapamycin was added to the SDC medium at the start of the culture with the concentrations indicated. Heat resistance assay (55°C for 75 min) was performed at day 3. Found at: doi:10.1371/journal.pgen.1000467.s002 (0.06 MB PDF)

Figure S2 qRT-PCR validation of DNA microarray results. (A) Northern blot analysis of YDL218W and SPS100 mRNA levels in wild type (DBY746), tor1Δ and sch9Δ at day 2.5 (equal amounts of total RNA were loaded). The PCR products of YDL218W (93 bp, see primer list below) and SPS100 (99 bp) labeled with random-priming (Promega) were used as probes. (B-K) Quantitative RT-PCR analysis of mRNA levels in wild type (DBY746), tor1Δ, sch9Δ, gis1Δ, and sch9Δ gis1Δ mutants at day 2.5. Gene expression levels were normalized to actin (ACT1) and expressed as the percentage of wild type. 2–3 independent cultures were analyzed. * p<0.01, ** p<0.001, ANOVA, Tukey’s multiple comparison test, compared to wild type. Primers used for qRT-PCR: ACT1, F, 5′-AGCTCTCAAT- GAACCTTTAAXTCA-3′; R, 5′-ACGAGCTGATAGAAAC- ATCACG-3′; ERG5, F, 5′-TATCTTGCTAAGCCCTTGGG- 3′; R, 5′-AACACAAACTCTTTACACCC-3′; FMP45, F, 5′- TCAATTTTACCATCGTTC-3′; SPS100, F, 5′-AATGAGGAAATCCAAAGTCG-3′; GPD1, F, 5′-GTTGTTAACATGT- GGCTCT-3′; GD1, F, 5′-GCCATAGCATACAAACGATCAA-3′; R, 5′-ACGACGTGAGTAACACC-3′; FMP45, F, 5′- TCAATTTTACCATCGTTC-3′; SPS100, F, 5′-AATGAGGAAATCCAAAGTCG-3′; GPD1, F, 5′-TCTTCCAGAATCCTAAGGTG- TCCTGT-3′; R, 5′-GGGACCTTTCTCATTGGTA-3′; GAP2, F, 5′-TTTTCCTAAGTTCAAAAGTGTC-3′; R, 5′-GGGACCTTTCTCATTGGTA-3′; RHR2, F, 5′-GAATACCTGCCACCA- GAACCA-3′; R, 5′-CAAGCAATTTCACGACCA-3′; GRE1, F, 5′-CCCAACACTCCGGAACAAATC-3′; R, 5′-ATGACGG- GTTACTTTGAGCAGT-3′; RHR2, F, 5′-GAATACCTGCCACCA- GAACCA-3′; R, 5′-CAAGCAATTTCACGACCA-3′; GRE1, F, 5′-CCCAACACTCCGGAACAAATC-3′; R, 5′-ATGACGG- GTTACTTTGAGCAGT-3′; RHR2, F, 5′-GAATACCTGCCACCA- GAACCA-3′; R, 5′-CAAGCAATTTCACGACCA-3′; GRE1, F, 5′-CCCAACACTCCGGAACAAATC-3′; R, 5′-ATGACGG- GTTACTTTGAGCAGT-3′; RHR2, F, 5′-GAATACCTGCCACCA- GAACCA-3′; R, 5′-CAAGCAATTTCACGACCA-3′; GRE1, F, 5′-CCCAACACTCCGGAACAAATC-3′; R, 5′-ATGACGG- GTTACTTTGAGCAGT-3′.

Table S1 Chronological life span. Mean and maximum life span (10% survival) was calculated from cube fitting of the survival data (from pair matched, pooled experiments) with the statistical software Prism (GraphPad Software). * n, the number of cultures analyzed. ** p-value for mean CLS of mutants compared to that of wild type, ANOVA, Tukey’s Multiple Comparison Test, except for tor1Δ ss, wild type, unpaired t-test, two-tailed.

Table S2 Microarray analysis of gene expression profiles at day 2.5. Data represent the log ratio of sch9Δ, tor1Δ, and ras2Δ cells to wild type (DBY746), n = 3. Found at: doi:10.1371/journal.pgen.1000467.s007 (0.05 MB PDF)

Table S3 The significance of overlapping in up- and down-regulated genes between long-lived mutants based on hypergeometric distribution and Fisher’s exact test. Found at: doi:10.1371/journal.pgen.1000467.s009 (0.01 MB PDF)

Table S4 Gene ontology (GO) analysis of expression profiles of long-lived mutants. Significantly up- or down-regulated categories were shown (p<0.05), q-value was also calculated to correct the multi-testing error. *GO categories: C, Cellular component; F, molecular function; and P, biological process.

Table S5 Expression levels of genes involved in ribosomal structure (a and b), glycolysis-glucogenesis (c), glucose transport (d), TCA cycle (e), and oxidative phosphorylation (f) in long-lived mutants compared to wild type cells at day 2.5. Data were expressed in fold change, WT = 1. For illustration purpose, gene expression levels that are 20% higher or lower than wild type cells are marked in red or green, respectively.
Table S6 Expression levels of genes involved in glycerol metabolism in long-lived \( sch9^{Δ}, tor1^{Δ}, \) and \( ras2^{Δ} \) mutants at day 2.5. The glycerol biosynthesis gene subset contains 21 genes. Denote the gene subset by \( S \) and the entire gene as a whole by \( G \). We compared expressions of \( S \) against those in the complement of \( S \) in \( G \) denoted by \( G-S \). The Wilcoxon rank test (one-sided) was performed. We found that glycerol biosynthesis gene set is upregulated with \( p \)-value 0.0058 in \( sch9^{Δ} \), 0.0614 in \( tor1^{Δ} \), and 0.0142 in \( ras2^{Δ} \). For illustration purpose, gene expression levels that are 20% higher or lower than wild type cells are marked in red or green, respectively. 

1 Data were expressed in fold change, \( WT = 1 \). Array probe specificity.

2 Day 1.5-old SDC wild type cells in SDC.

3 Water for 24 or 48 hours. Data represent fold change compared to (DBY746) cells were washed 3 times with water and incubated in water for 24 or 48 hours. Data represent fold change compared to wild type cells in SDC.

Table S7 Schematic representation of ergosterol biosynthesis and expression levels of genes involved in the process. Data were expressed in fold change, \( WT = 1 \). For illustration purpose, gene expression levels that are 20% higher or lower than wild type cells are marked in red or green, respectively.

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Author Contributions

Conceived and designed the experiments: MW PF VDL. Performed the experiments: MW PF. Analyzed the data: MW PF FM JH. Conceived and designed the experiments: MW PF VDL. Performed the experiments: MW PF FM JH. Analyzed the data: MW PF HG LML VDL. We are grateful to Changhan Lee, Fernando M. Safdie, and Chao Cheng for their assistance on DNA microarray methodology.

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