Nutrient Control of Yeast Gametogenesis Is Mediated by TORC1, PKA and Energy Availability

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Abstract

Cell fate choices are tightly controlled by the interplay between intrinsic and extrinsic signals, and gene regulatory networks. In Saccharomyces cerevisiae, the decision to enter into gametogenesis or sporulation is dictated by mating type and nutrient availability. These signals regulate the expression of the master regulator of gametogenesis, IME1. Here we describe how nutrients control IME1 expression. We find that protein kinase A (PKA) and target of rapamycin complex I (TORC1) signalling mediate nutrient regulation of IME1 expression. Inhibiting both pathways is sufficient to induce IME1 expression and complete sporulation in nutrient-rich conditions. Our ability to induce sporulation under nutrient rich conditions allowed us to show that respiration and fermentation are interchangeable energy sources for IME1 transcription. Furthermore, we find that TORC1 can both promote and inhibit gametogenesis. Down-regulation of TORC1 is required to activate IME1. However, complete inactivation of TORC1 inhibits IME1 induction, indicating that an intermediate level of TORC1 signalling is required for entry into sporulation. Finally, we show that the transcriptional repressor Tup1 binds and represses the IME1 promoter when nutrients are ample, but is released from the IME1 promoter when both PKA and TORC1 are inhibited. Collectively our data demonstrate that nutrient control of entry into sporulation is mediated by a combination of energy availability, TORC1 and PKA activities that converge on the IME1 promoter.

Author Summary

The cell-fate controlling gametogenesis is essential for all sexual reproducing organisms. In Saccharomyces cerevisiae, entry into gametogenesis or sporulation is dictated by mating type and nutrient availability. These signals regulate the expression of the master regulator of entry into sporulation, IME1. In this manuscript we describe how nutrients control IME1. We show that inhibiting two highly conserved nutrient sensing pathways (PKA and
TORC1) mimics starvation-induced sporulation and drives cells to induce IME1 and complete meiosis in nutrient-rich conditions. In addition, we show that respiration and fermentation are interchangeable energy providers for entry into gametogenesis. Finally, we have uncovered a critical role for TORC1 during entry into gametogenesis. In addition to the known role of TORC1 in repressing IME1, we find that intermediate TORC1 activity is required for entry in gametogenesis. Too much or too little TORC1 activity inhibits gametogenesis. Our data explains how two conserved signalling pathways control a developmental decision essential for sexual reproduction, about which remarkably little is known in all eukaryotes. Thus the activities of two nutrient sensing pathways and energy availability determine whether cells enter gametogenesis or not.

**Introduction**

Cellular differentiation programs are controlled by environmental and cell intrinsic events. How cells integrate multiple stimuli to regulate cell fate choice is poorly understood. The yeast Saccharomyces cerevisiae is an ideal model to study this problem. In response to multiple, well-defined signals, yeast cells induce a differentiation program to form four haploid gametes or spores [1, 2]. Gametogenesis or sporulation is characterized by a specialized cell division called meiosis. During sporulation diploid cells undergo a single round of DNA replication followed by two consecutive nuclear divisions, meiosis, to generate progeny containing half the number of chromosomes of the diploid parent cell.

The initiation of gametogenesis is controlled by cell-intrinsic and cell-extrinsic signals, which together regulate a single master transcription factor called inducer of meiosis I, IME1 [3, 4]. In cells expressing a single mating type, MATa or MATα, IME1 is repressed by transcription coupled repression of the IME1 promoter involving the long noncoding RNA IRT1 [5]. In MATa/α diploid cells Rme1, the transcriptional activator of IRT1, is repressed. As a consequence these cells express IME1 upon nutrient deprivation [6]. For efficient IME1 induction a fermentable carbon source and nitrogen need to be absent from the growth medium. Under these conditions cells produce ATP via oxidative phosphorylation to facilitate IME1 expression [7, 8].

Two conserved signalling pathways have been implicated in nutrient regulation of IME1 expression. First, the presence of glucose in the growth medium activates the Ras/cAMP-dependent Protein Kinase A (PKA) pathway, which in turn inhibits IME1 and entry into sporulation [9, 10]. The second regulator of IME1 is the target of rapamycin complex I (TORC1). TORC1 promotes macromolecule biosynthesis in response to nitrogen and amino acid availability [11]. When nitrogen sources/amino acids are ample, TORC1 is active and inhibits IME1 and sporulation [7, 12]. Whether PKA and TORC1 are the main mediators of nutrient control of IME1, and how the two pathways control entry into sporulation is not well understood.

Here we describe how nutrients control IME1 expression. We find that PKA and TORC1 signalling account for the majority of IME1 regulation by nutrients. Inhibition of PKA and TORC1 activity is sufficient to induce IME1 expression even in the presence of high levels of nutrients. Under these conditions, cells induce IME1, complete meiosis, and generate spores with kinetics that are highly reminiscent of those observed under starvation conditions. The ability to induce sporulation in the presence of ample nutrients further allowed us to investigate the importance of respiration and TORC1 activity for the induction of gametogenesis. We find that respiration and fermentation are interchangeable for IME1 induction. Both metabolic pathways can serve as energy providers during entry into sporulation. Our analysis further
shows that intermediate levels of TORC1 activity are critical for gametogenesis. When TORC1 is fully active or completely inhibited, IME1 is repressed. Finally, we show that the transcriptional repressor Tup1 binds to and represses the IME1 promoter when TORC1 and/or PKA are active, but not when both pathways are inhibited. Importantly, depletion of Tup1 is sufficient to mimic starvation-induced IME1 expression. Our data demonstrate that nutrient control of sporulation is sensed and orchestrated by TORC1 and PKA signalling pathways and by the availability of energy.

**Results**

**Inhibition of PKA and TORC1 in nutrient rich medium mimics starvation induced IME1 expression**

In budding yeast nutrient availability determines whether cells enter sporulation. The PKA and TORC1 pathways as well as respiration have been linked to the regulation of IME1 expression by nutrients and to entry into sporulation (Fig 1A) [1]. To determine whether TORC1 and PKA are the major mediators of nutrient sensing in triggering sporulation, we examined how inactivation of either or both pathways affects IME1 expression. TORC1 can be rapidly and efficiently inhibited using the small molecule rapamycin that reduces cell proliferation rate significantly (S1A Fig). Inhibition of the PKA pathway is more complex because budding yeast encodes three redundant genes encoding the catalytic subunits of PKA, TPK1, TPK2, and TPK3 [13]. To inhibit the PKA pathway, we generated an ATP analogue sensitive strain of PKA that we define as tpk1-as. The strain contains gene deletions in TPK2, TPK3 and a point mutation in TPK1 (tpk1M164G) that transforms this allele into an ATP analog sensitive (as) allele [14]. In the tpk1-as strain, PKA activity can be specifically blocked using the ATP analog 1NM-PP1, which results in a growth arrest (Fig 1B and S1A Fig).

To measure IME1 promoter activity in response to modulating PKA activity, we used an IME1-promoter lacZ reporter fusion (pIME1-LacZ) that was integrated at the IME1 locus without disrupting the endogenous IME1. This fusion serves as an accurate readout for IME1 promoter activity [7]. When we shifted control and tpk1-as diploid cells from rich medium containing glucose (YPD) to sporulation medium (SPO), a condition which induces IME1, β-galactosidase activity increased (S1B Fig and Fig 1C). The β-galactosidase levels were comparable between the two strains suggesting that tpk1-as allele does affect IME1 regulation in SPO (S1B Fig). As expected, IME1 promoter activity did not increase when tpk1-as cells were shifted to fresh YPD (Fig 1C).

Using the tpk1-as and pIME1-LacZ system, we first determined whether glucose repression of IME1 is mediated by PKA signalling. Cells were shifted from YPD to SPO, or to SPO medium containing glucose in the presence or absence of the ATP analog 1NM-PP1 (Fig 1D). IME1 promoter activity was strongly reduced in the presence of glucose. In contrast, when PKA was inhibited IME1 promoter activity was comparable with cells grown in the absence of glucose. This result shows that glucose inhibits IME1 expression predominantly via the PKA signalling pathway.

The presence of a nitrogen source also prevents IME1 expression [3]. To test whether TORC1 signalling is responsible for IME1 repression by nitrogen sources and amino acids we examined the effects of rapamycin on IME1 expression. To exclude the effects of glucose repression on IME1, we used a nitrogen and amino acid rich medium containing the non-fermentable carbon source acetate (YPA) but lacking a fermentable carbon source. We found that IME1 promoter activity slightly increased in cells shifted from YPD to YPA, and, inhibition of PKA did not further increase IME1 expression (Fig 1E and S1D Fig). This is expected because it is known that Ras/PKA transmits the glucose signal and thus glucose levels control IME1 via
Fig 1. Inhibition of PKA and TORC1 induces IME1 and meiosis in rich medium. (A) Scheme of the signalling pathways controlling IME1 expression. 1NM-PP1 and rapamycin compounds inhibit tpk1-as and TORC1 respectively. (B) Wild-type (FW1511) cells or cells harbouring the tpk1M164G, tpk2Δ, tpk3Δ alleles (tpk1-as, FW1762) were grown in YPD overnight, diluted to 0.2 (OD600), and subsequently cells were treated with 5μM 1NM-PP1 or untreated. Cell density (OD600) was measured over time at the indicated time points. (C) IME1 promoter activity was measured in a diploid tpk1-as strains and the IME1 promoter fused to LacZ reporter (FW1976). Cells were grown in YPD overnight, diluted into YPD or shifted to sporulation medium (SPO), and samples were taken after 0, 4, 6, 8, 10, and 12 hours. β-galactosidase activity was measured using a quantitative liquid ortho-nitrophenyl-β-galactoside (ONPG) assay (see Materials and Methods for details). The promoter activities are displayed in Miller Units, and the standard error of the mean of at least two biological experiments is shown. (D) Similar to C except that cells were shifted to SPO, SPO plus 2% glucose or SPO with 2% glucose and 5μM 1NM-PP1. Samples were taken at the indicated time points. (E) Similar to C, except that samples shifted to YPD or YP-acetate (YPY), YPA plus rapamycin or YPA plus 1NM-PP1. (F) Similar to C except that cells were shifted to SPO or YPD and treated with rapamycin, 1NM-PP1 or both compounds. (G) IME1 mRNA quantification of cells shifted from YPD to SPO or YPD plus rapamycin, 1NM-PP1, or both compounds. Samples were taken at the indicated time points. Total RNA was isolated, reverse transcribed, and IME1 mRNA levels were measured by quantitative PCR. Signals were normalized to ACT1 levels. The standard error of the mean of at least two biological experiments is shown.

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PKA \([3, 9, 10, 15, 16]\). When we inhibited TORC1, by treating cells grown in YPA medium with rapamycin, \(IME1\) was rapidly induced. The majority of cells (95\%) were also able to form spores within 24 hours (\(S1\) Table). We conclude, as reported previously, that the PKA pathway transmits the glucose signal to the \(IME1\) promoter, and that TORC1 most likely transmits the nitrogen signal \([3, 9]\).

To examine whether PKA and TORC1 are the major mediators of nutrient control of \(IME1\) expression, we inhibited either or both pathways in cells grown in rich medium containing glucose (YPD) (Fig 1F and \(S1\) C Fig). Inhibition of TORC1 had no effect on \(IME1\) expression. In contrast, \(IME1\) promoter activity strongly increased between 8 to 12 hours following treatment with PKA inhibitors. Interestingly, when both PKA and TORC1 were inhibited, \(IME1\) induction was already noticeable at 4 hours, and peaked at 8 hours and was remarkably similar to levels seen in cells incubated in SPO medium (Fig 1F and \(S1\) Fig). Similar results were obtained when \(IME1\) mRNA levels were examined (Fig 1G). These data show that the combined inhibition of PKA and TORC1 activities is sufficient to mimic nutrient control of \(IME1\) expression. We conclude that TORC1 and PKA are two major mediators of nutrient regulation of \(IME1\) expression.

**Inhibition of PKA and TORC1 induces \(IME1\) expression in the majority of cells**

Our results show that inhibition of PKA leads to some degree of \(IME1\) expression in rich medium (YPD) (approximately 50\% of that observed in SPO medium; Fig 1F and 1G). The technique can reliably measure absolute transcript levels in single cells [17]. To ensure that the signals were specific and probes entered the cells, we first measured \(IME1\) and \(ACT1\) transcript levels in wild-type and \(ime1\)Δ diploid cells that were induced in SPO medium (\(S2\) Fig). While \(IME1\) was expressed in the wild type, no transcripts were detected in \(ime1\)Δ cells. As expected, \(ACT1\) levels were comparable between the two strains (\(S2B\) Fig). Next, we counted the mean number of \(IME1\) transcripts in cells grown in rich medium shifted to SPO medium, or treated with PKA or PKA/TORC1 inhibitors (Figs 2A and 1B). The \(IME1\) expression pattern matched the RT-PCR experiment (compare Figs 1G and 2B). In cells treated with the PKA inhibitor \(IME1\) levels increased after 8 hours to about 10 copies per cell on average. When both TORC1 and PKA were inhibited, \(IME1\) was transcribed efficiently and cells contained on average 30 copies per cell at 8 hours after treatment, which was comparable to \(IME1\) levels in SPO medium (Fig 2B).

It is worth noting that \(IME1\) mRNA levels decline sharply 12 hours after inhibition of the PKA and TORC1 pathways but remained elevated in cells incubated in SPO medium for the same amount of time (Fig 2B). Given that expression of \(IME1\) is known to decline when cells undergo meiotic divisions, a plausible explanation is that progression into meiosis differs between the two conditions [18]. Indeed, when PKA and TORC1 were inhibited the majority of cells underwent meiotic divisions within 12 hours (see next section for details). In contrast, when cells were directly transferred from YPD medium into SPO medium sporulation did not occur efficiently, and it is likely that many (more than 50\%) of the cells were arrested in intermediate stages of meiosis (\(S1\) Table). Therefore a decline in \(IME1\) was not observed at 12 hours (Fig 2B). Finally, we would like to point out that we did not see a decline in \(pIME1\)-\(LacZ\)
Fig 2. Single cell quantification of IME1. (A) Representative images used for the analyses of IME1 and ACT1 transcript levels in single cells. Cells harbouring tpk1-as (FW1762) were grown in YPD overnight and were either shifted to SPO, or diluted into fresh YPD plus rapamycin, 1NM-PP1 or 1NM-PP1/rapamycin. Cells were fixed, hybridized with probes directed against IME1 (AF594) and ACT1 (Cy5), and were imaged (see Materials and Methods for details). ACT1 was used as an internal control and only ACT1 positive cells were selected for the analysis. (B) Mean of IME1 and ACT1 transcripts’ number among single cells as described in A.
Cells harbouring tpk1-as (FW1762) were grown in YPD overnight, diluted into fresh YPD plus 1NM-PP1 or 1NM-PP1/rapamycin and samples were taken at the indicated time points. Cells were imaged and quantified (see Materials and Methods for details). At least, 60 cells (n = 60) were quantified per time point. The standard error of the mean of at least two biological experiments is shown. (C) Distribution of IME1 and ACT1 transcripts among single cells grown in YPD as described in A and B. Cells were binned in five classes of transcript levels (0 to 5; 6 to 10; 11 to 15; 16 to 20 and 21 or more transcripts per cell) and the percentages of each class contributing to the total population are indicated. At least, 60 cells (n = 60) were quantified per time point. The standard error of the mean of at least two biological experiments is shown. (D-G) Similar to C except that cells were grown in YPD overnight and transferred to YPD plus rapamycin (D), YPD plus 1NM-PP1 (E), YPD plus 1NMPP and rapamycin (F), or SPO (G). Samples were taken at the indicated time points. Cells were binned in five classes of transcript levels (0 to 5; 6 to 10; 11 to 15; 16 to 20 and 21 or more transcripts per cell) and the percentages of each class contributing to the total population are indicated. doi:10.1371/journal.pgen.1006075.g002

Fermentation and respiration are interchangeable energy providers for IME1 transcription

Respiration is needed for IME1 transcription and for entry into sporulation [7, 8]. However, it is not clear whether IME1 expression is dependent on the energy produced by respiration or...
whether it requires a signal from active mitochondria. The system we developed to induce sporulation in the presence of ample nutrients allowed us to investigate this question. First, we analysed how IME1 expression is affected in respiratory deficient cells. Pet100 is required for the assembly of cytochrome c oxidase. Yeast cells lacking the PET100 gene cannot respire. In line with previous observations, pet100Δ cells did not induce IME1 in SPO medium (Fig 4A, compare lanes 1–5 to 6–8) [7]. Likewise, cells treated with the drugs antimycin A (antimycin), which inhibits cytochrome c reductase, or oligomycin, which inhibits the Fo subunit of the mitochondrial ATP synthase, did not induce IME1 (Fig 4B, compare lanes 1–5 to 8–9 and 10–12). Uncoupling of respiration from energy production by treating cells with CCCP which disrupts the proton gradient and thus reduces the ability of the ATP synthase to function...
Fig 4. Respiration is not essential to IME1 induction. (A) Northern blot analysis of IME1 expression in control (FW1762, lanes 1–4) and pet100Δ mutant (FW1770, lanes 5–8). Cells were grown overnight in YPD medium and shifted to sporulation medium (SPO), and samples were taken at the indicated time points. (B) Similar to A except that cells (FW1762) were grown in pre-sporulation medium before shifted to SPO. Subsequently, cells were either not treated (lanes 1–4), treated with antimycin A (50 μM, lanes 5–8), oligomycin (10 μM, lanes 9–12), or with CCCP (20 μM, lanes 13–16). (C) Similar to A, except that cells were diluted into 1NM-PP1 and rapamycin containing YPD (lanes 1–16), and treated with antimycin A (lanes 5–8) or oligomycin (lanes 9–12). The pet100Δ mutant (lanes 13–16) was also included in the analyses. (D) IME1 promoter activity was measured using a diploid strain harbouring tpk1-as and the IME1 promoter fused to LacZ reporter (FW1976). Cells were grown in YPD overnight, diluted into YPD plus 1NM-PP1/rapamycin or shifted to sporulation medium (SPO) in the absence or presence of oligomycin (10 μM). Samples were taken after 0, 4, 6, 8, and 12 hours. β-galactosidase activity was measured using a quantitative liquid ortho-Nitrophenyl-β-galactoside (ONPG) assay (see Materials and Methods for details). The promoter activities are displayed in Miller Units, and the standard error of the mean of at least two biological experiments is shown. (E) Quantification of IME1 mRNA levels in a strain harbouring the GAL1 promoter fused to IME1 and GAL4-ER (FW3243). Cells were grown in YPD, shifted to pre-sporulation medium, and transferred to SPO in the absence or presence of antimycin A. The GAL1 promoter was activated using estradiol. Total RNA was isolated, reverse transcribed, and IME1 mRNA levels were measured by quantitative PCR. Signals were normalized to ACT1 levels. The standard error of the mean of at least two biological experiments is shown. (F) Quantification of sporulation efficiency of strains and treatments described in C. At least n = 200 cells were counted at 48 hours after treatment. Untreated diploid cells were included as a negative control.

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led to similar results (Fig 4B, compare lanes 1–4 and 13–16). Thus, respiration is required for induction of IME1 expression in sporulation medium.

Next, we induced sporulation by inhibiting PKA and TORC1 in cells grown in glucose-rich medium, and tested whether respiration is required for IME1 expression. To our surprise, IME1 expression levels were comparable between control cells, and antimycin or oligomycin treated cells (Fig 4C, compare lanes 1–4 to 5–8 or 9–12). pet100Δ cells grown in YPD strongly induced IME1 when the PKA and TORC1 pathways were inhibited (Fig 4C, compare lanes 1–4 to 13–16). To further quantify IME1 promoter activity in respiratory deficient cells, we measured pIME1-LacZ reporter expression in oligomycin treated cells. As expected, in SPO medium the IME1 promoter stayed repressed when cells were treated with oligomycin. In YPD plus TORC1 and PKA inhibitors, IME1 expression accumulated with slightly slower kinetics in the presence of oligomycin but peaked to similar levels as control cells (Fig 4D). Finally we examined whether IME1 can be induced from a heterologous promoter in SPO medium when respiration is inhibited (Fig 4E). When we induced IME1 from the GAL1 promoter using a Gal4-estrogen receptor fusion (GAL4-ER) that can be activated by the addition of estradiol, IME1 was strongly induced. However, in cells treated with antimycin IME1 stayed repressed. Previous work showed that expression of mRNAs from different genes is also affected under this condition [7]. We propose that the effects are not specific for IME1, but either transcription or mRNA stability or both are generally affected when cells are starved and cannot respire. Notably, even though cells were able to express IME1 when respiration was inhibited in YPD medium with TORC1 and PKA inhibitors the vast majority of these cells did not complete gametogenesis (Fig 4F) indicating that other stages of sporulation require respiration. In conclusion, when sporulation is induced in the presence of ample nutrients, respiration is not required for IME1 expression. This result suggests that either respiration or fermentation can serve as energy providers for induction of IME1 transcription.

TORC1 activity enables efficient IME1 induction and meiosis

Our results show that inhibition of PKA and TORC1 activity is sufficient to initiate entry into sporulation. Although it is well established that PKA signalling inhibits sporulation, inhibition of TORC1 by rapamycin treatment has been reported to affect sporulation with different outcomes. We and others have shown that rapamycin can stimulate sporulation by inducing IME1 expression [7]. Moreover, inactivation of TORC1 was shown to stabilize Ime1 and promotes its nuclear localization [20]. However, others have found that rapamycin can also inhibit spore formation in budding and fission yeast when added to the SPO medium [21, 22]. These seemingly conflicting results prompted us to further examine how rapamycin and TORC1 control sporulation.

First, we tested whether there is a concentration dependent effect of rapamycin on cell growth and sporulation. Rapamycin treatment at the concentration which ensures efficient sporulation (1000 ng/ml) diminished, but did not stop cell proliferation (190 min versus 90 min in control cells; Fig 5A). This observation suggests that TORC1 is still active. When we used 50 fold less rapamycin (20 ng/ml), cell proliferation was somewhat affected (145 min versus 90 min in control cells), and cells sporulated efficiently when combined with inhibition of PKA (Fig 5A, right panel). Lower concentrations of rapamycin had no observable effect on growth and sporulation. These results indicate that the TORC1 pathway is not completely blocked upon entry into sporulation and meiosis.

In line with our observation that rapamycin does not abolish growth completely, a recent study showed that rapamycin, irrespective of the concentration used, does not fully inhibit TORC1 activity [23]. Depletion or inactivation of the Kog1 subunit of the TORC1 complex,
Fig 5. TORC1 activity is required for sporulation. (A) Cells (FW1762) were treated with different concentrations of rapamycin, and doubling times (left panel) as well as the fraction of cells that underwent meiosis (right panel) were quantified. Left panel, cells were grown in YPD, shifted to YPD plus 0, 5, 20, or 1000 ng/ml rapamycin and doubling times were measured during exponential growth. Right panel, cells were diluted into YPD plus PKA inhibitors and treated with different concentrations of rapamycin as indicated. DAPI masses were counted after 48 hours of treatment. (B) Control (FW1762) and KOG-AID/pTEF1-osTIR1 (FW1904)
cells harbouring tpk1Δ were grown in YPD overnight, diluted into fresh YPD and treated with 1NM-PP1, rapamycin or IAA. The nuclei number in cells was counted after 48 hours of treatment by DAPI staining, and percentage of cells that underwent meiosis (MI+MII) was quantified. (C) Quantification of IME1 mRNA levels in control (FW1762) and KOG1-AID/pTEF1-osTIR1 (FW1904) cells harbouring tpk1Δ and treated with 1NM-PP1. KOG1-AID/pTEF1-osTIR1 cells were also treated with IAA. Samples were taken at the indicated time points. Total RNA was isolated, reverse transcribed, and IME1 mRNA levels were measured by quantitative PCR. Signals were normalized to ACT1 levels. The standard error of the mean of at least two biological experiments is shown. (D) Percentage of cells that underwent meiotic divisions (MI+MII) was determined in gene deletion strains, all harbouring tpk1Δ and plME1-LacZ (FW1976, control). The following gene deletion mutants were used for the analyses: control (FW1976), tco89Δ (FW2154), gtr1Δ (FW2164) or tor1Δ (FW2162). Samples were grown in YPD medium, fixed, and DAPI masses were counted at 48 hours after treatment with 1NM-PP1 or with 1NM-PP1 and rapamycin. (E) IME1 promoter activity was measured in strains described in D. Cells were grown in YPD overnight, diluted into YPD plus 1NM-PP1 and/or rapamycin, and samples were taken after 0, 4, 8, and 12 hours. β-galactosidase activity was measured using a quantitative liquid ortho-Nitrophenyl-β-galactoside (ONPG) assay (see Materials and Methods for details). The promoter activities are displayed in Miller Units, and the standard error of the mean of at least two biological experiments is shown. (F) IME1 promoter activity was measured as described in E for control (FW1976) and tco89Δ (FW2154) strains. Cells were grown in YPD overnight, diluted into YPD plus 1NM-PP1 and/or rapamycin, and samples were taken after 0, 2, 4, 6, 8, 10, 12 and 24 hours. (G) Kinetics of meiotic division (MI+MII) of strains and treatments described in F. Samples were taken at the indicated time points, fixed, and DAPI masses were counted.

However, causes a complete growth arrest and a starvation response [24, 25]. We therefore depleted Kog1 using an auxin induced degradation system (AID) system [26] and examined the effects on IME1 expression and sporulation. The system relies on *Oryza sativa* TIR1 (pTEF1-osTIR1), which interacts with the SCF ubiquitin ligase, and the chemical indole-3-acetic acid (IAA), which allows for the SCF-TIR1 and E2 ubiquitin ligases to come together to polyubiquitinate and subsequently degrade AID by the proteasome [26]. Tagging Kog1 with the AID-tag decreased Kog1 activity as judged by reduced proliferation of cells carrying the KOG1-AID allele (S3A Fig). However, when KOG1-AID cells expressing pTEF1-osTIR1 were treated with IAA to deplete Kog1, growth and proliferation were completely abolished (S3A and S3B Fig). The AID tag also partially interfered with sporulation as Kog1-AID cells exhibited reduced meiosis efficiency following treatment with PKA inhibitors and rapamycin (Fig 5B). Nonetheless, it was evident that depletion of Kog1 strongly affected IME1 expression and as a result meiosis did not occur (Fig 5B and 5C). In conclusion, when we induce sporulation by inhibiting PKA in nutrient rich conditions, Kog1 is required for entry into sporulation.

Given that inactivation of TOR1 by depleting Kog1 abolished the cell’s ability to sporulate, we hypothesized that some TORC1 activity is needed for entry into sporulation. To test this hypothesis we modulated TORC1 activity. A number of TORC1 pathway mutants have been isolated previously and have been shown to reduce basal TORC1 activity [27–29]. Typically, these mutants are hypersensitive to rapamycin and some mutants cannot recover growth after rapamycin treatment. If reduced TORC1 activity is necessary for entry into sporulation, such mutants should sporulate in the presence of a nitrogen source and/or amino acids. To test this, we generated gene deletion mutants in two nonessential subunits of TORC1, TCO89 and the kinase TOR1. In addition, we mutated the GTPase GTR1, an upstream activator of TORC1 and a component of EGO complex. As reported previously, vegetative growth was strongly reduced in gtr1Δ and tor1Δ mutants when treated with rapamycin, and was abolished completely in tco89Δ cells [S3C Fig] [27, 30]. Upon inhibition of PKA more than 80 percent of mutant cells (tco89Δ, tor1Δ, and gtr1Δ) completed meiosis compared to approximately 20 percent of control cells (Fig 5D). The ability to undergo meiosis was abolished in tco89Δ and gtr1Δ cells when treated with PKA inhibitor and rapamycin (Fig 5D). Meiosis was not affected in tor1Δ cells treated with rapamycin. This can be explained by the presence of the functionally similar Tor2 kinase in TORC1, which can compensate for the tor1Δ [27, 29].

Next, we examined how IME1 promoter activity was affected by tco89Δ, gtr1Δ, or tor1Δ mutations. In cells treated with PKA inhibitor, LacZ activity was significantly higher in all three mutants compared to the control (6h after treatment) (Fig 5E). Moreover, the kinetics
and levels of IME1 induction in the mutant cells treated with PKA inhibitor alone closely resembled that of control cells treated with both PKA inhibitor and rapamycin. The tco89Δ and gtr1Δ cells treated with rapamycin and PKA inhibitors did not express IME1, which is consistent with the observation that these mutants did not induce meiosis under this condition. As expected, in tor1Δ mutant cells, rapamycin only had a minor effect on IME1 promoter activity.

In order to compare the tco89Δ mutant to control cells more closely, we monitored IME1 induction and meiosis in a detailed time-course. When PKA was inhibited in tco89Δ cells, IME1 promoter activity increased significantly faster than in control cells (Fig 5F). In contrast, the IME1 promoter was not induced even at later time points (12h or 24h) in tco89Δ cells treated with rapamycin and PKA inhibitors. Moreover, the kinetics of meiosis in tco89Δ cells treated with PKA inhibitor alone closely resembled that of control cells treated with PKA and TORC1 inhibitors and both underwent meiosis efficiently (Fig 5G). These data show that a certain level TORC1 activity is required for IME1 transcription and entry into sporulation. When TORC1 activity is high or completely blocked, IME1 expression and sporulation are repressed.

Inactive TORC1 represses IME1 mRNA expression

Several mechanisms could be responsible for the observation that complete inactivation of TORC1 prevents plME1-LacZ activity. Given that TORC1 regulates translation and ribosome biogenesis, one plausible explanation is that the β-galactosidase protein is not produced [11]. Another possibility is that mRNA production or stability is affected by inactive TORC1. To distinguish between these two possibilities, we measured IME1 mRNA and protein levels in tco89Δ cells, rather than IME1 promoter activity. We found that both IME1 mRNA and protein levels were strongly reduced, but not completely abolished, in tco89Δ cells treated with rapamycin (Fig 6A and 6B, compare lanes 6–9 to 10–13). Furthermore, we observed a small increase in Ime1 protein that correlated with IME1 mRNA levels following 4 hours of treatment. We conclude IME1 mRNA accumulation is predominantly affected when TORC1 is completely inhibited.

TORC1 regulation of IME1 is mediated by Sch9 kinase

The TORC1 complex has multiple effectors that regulate cellular processes such as autophagy, nitrogen and amino acid sensing, as well as ribosome biogenesis [11]. We investigated whether the Sch9 branch of TORC1 is important for IME1 regulation.

Sch9 is a serine/threonine kinase that controls ribosome biogenesis, autophagy, and entry into stationary phase [31–33]. It is also directly phosphorylated by Tor1 [34]. First, we quantified IME1 promoter activity in sch9Δ mutant cells shifted from YPD to SPO medium. We found that IME1 promoter activity was only slightly higher in sch9Δ cells compared to control cells (Fig 7A). We next measured IME1 promoter activity in cells grown in rich medium using the tpk1-as allele. Upon inhibition of PKA, IME1 promoter activity was overall higher and accumulated with faster kinetics in sch9Δ cells compared to control cells (Fig 7B). These data indicate that Sch9 is a repressor of IME1. If Sch9 is the only downstream target of TORC1 that represses IME1 than lowering TORC1 activity in sch9Δ cells should not further affect IME1 expression. Indeed, rapamycin treatment did not further increase IME1 promoter activity in sch9Δ cells (Fig 7B, compare pink bars with light green bars). These results indicate that Sch9 mediates repression of IME1 by TORC1.

To further analyse how Sch9 controls sporulation we measured IME1 levels in single cells by smFISH. We observed that in sch9Δ cells treated with PKA inhibitors the majority (more than 60%) of cells expressed more than 21 copies per cell (Fig 7C). Only a small fraction of cells did not induce IME1. Furthermore, the IME1 mRNA distribution pattern in sch9Δ cells
closely resembled that of tco89Δ cells, which supports our finding that TORC1 repression of IME1 is mediated by Sch9. Finally, we measured how meiosis is affected in sch9Δ cells. In line with the IME1 expression data, the percentage of cells that completed meiosis was significantly higher (60% versus less than 20% in the control) in sch9Δ cells treated with PKA inhibitor (Fig 7D). In addition, in sch9Δ cells shifted from YPD to SPO the percentage of cells that underwent meiosis was substantially higher than in wild-type cells induced to sporulate under these conditions (90% versus 20%). Given that we only observed a small increase in IME1 under this conditions (Fig 7A), the result suggests that Sch9 may also inhibit meiotic progression downstream of IME1 induction and regulate events such as IME2 and NTD80 induction. In conclusion, TORC1-Sch9 signalling contributes to repressing IME1 expression and entry in sporulation in nutrients-rich conditions.

Tup1 mediates TORC1 and PKA control of IME1 expression

Having established that PKA and TORC1 control IME1 expression, we next determined how both signalling pathways control the association of transcription factors with the IME1 promoter. Several regulators of IME1 have been identified that regulate IME1 including the Tup1--Cyc8 complex [5, 35]. This transcriptional repressor is recruited to promoters by sequence specific transcription factors and represses transcription by masking and inhibiting the transcriptional activation domains of transcription factors at gene promoters [36–38]. Several lines of evidence indicate that Tup1 contributes to IME1 repression. TUP1 and CYC8 mutants have been identified in a screen for genes that repress IME1 expression [35]. In addition, when we plotted the nucleosome occupancy at the IME1 locus using data from a published genomewide study, we found that in tup1Δ mutant cells the IME1 promoter is almost completely depleted for nucleosomes suggesting that the promoter is de-repressed (Fig 8A) [39]. Finally,
ChIP sequencing data indicated that depletion of Tup1 leads to increased binding of RNA polymerase II to the IME1 ORF and up-regulation of IME1 transcription [38].

To examine whether Tup1 directly regulates IME1, we measured Tup1 binding across the IME1 promoter by ChIP in nutrient rich conditions (Fig 8B). We found that Tup1 binds strongly (more than 30 fold over background) to the IME1 promoter in a region around 800 to 1000 base pairs upstream of the translation start side. To determine whether Tup1 binding to the IME1 promoter is regulated by nutrients, we treated tpk1-as diploid cells with 1NM-PP1 or rapamycin for 4 hours. Tup1 binding to the IME1 promoter was not affected. However, when we inhibited PKA and TORC1, Tup1 binding to the IME1 promoter was lost (Fig 8C). Finally, we tested whether the degree of TORC1 activity affected Tup1 binding to the IME1 promoter. In tco89Δ mutant cells Tup1 was bound to the IME1 promoter in rich medium. Inhibition of

**Fig 7. Sch9 controls IME1 and entry into sporulation.** (A) IME1 promoter activity was measured in strains harbouring tpk1-as and pIME1-LacZ (control, FW1976) and sch9Δ (FW2498). Cells were grown in YPD overnight shifted to SPO and samples were taken at the indicated time points. β-galactosidase activity was measured using a quantitative liquid ortho-Nitrophenyl-β-galactoside (ONPG) assay (see Materials and Methods for details). The promoter activities are displayed in Miller Units, and the standard error of the mean of at least two biological experiments is shown. (B) Similar to A except that cells were diluted into YPD with 1NM-PP1 or 1NM-PP1 plus rapamycin. (C) IME1 transcript distribution among single cells in control (FW1762), tco89Δ (FW1966) and sch9Δ (FW2437) strains (all in tpk1-as background). After 8 hours treatment with 1NM-PP1, cells were fixed, hybridized with probes directed against IME1 (AF594) and ACT1 (Cy5). Finally, cells were imaged and transcript levels were quantified (see Materials and Methods for details). ACT1 was used as an internal control and only cells positive for ACT1 were selected for the analysis. At least 120 cells (n = 120) were quantified. The error bars represent the standard error of the mean of two biological experiments. (D) Same treatments and strains as A and B, but here the percentage of cells that underwent meiotic divisions (MI+MII) was determined after 48 hours of treatment.

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Fig 8. Tup1 binds, represses, and mediates nutrient control of the IME1 promoter. (A) Data taken from Rizzo et al. [39] showing the nucleosome distribution at the IME1 locus in control (closed circles) and tup1Δ mutant (open squares) cells. The x-axis shows the coordinates of the IME1 locus at chromosome X in kilobases (kb), and y-axis shows the nucleosome occupancy score as described in [39]. The position of each dot or point on the graph represents the coordinate of the nucleosome dyad center at the IME1 locus. Regions lacking dots are depleted for nucleosomes. (B) Binding of Tup1 to the IME1 promoter measured by chromatin immunoprecipitation. Diploid cells harbouring tpk1-as (control, FW1762) and tpk1-as plus Tup1 tagged

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PKA in this mutant background was sufficient to disassociate Tup1 from the IME1 promoter (Fig 8C). Interestingly, when we treated tco89Δ cells with rapamycin to inactivate TORC1, Tup1 binding to the IME1 promoter was also not detectable. We conclude that Tup1 binding to the IME1 promoter is controlled by PKA and TORC1 activity.

Depletion of Tup1 leads to rapid activation of IME1 transcription

We next tested whether Tup1-Cyc8 association with the IME1 promoter is important for IME1 repression. We found that Tup1 depletion was sufficient for the activation of the IME1 promoter (Fig 8D). In diploids cells harbouring a TUP1-AID fusion and expressing pTEF1-osTIR1, IME1 promoter activity (pIME1-LacZ) increased after treatment with IAA. In contrast, β-galactosidase expression was not induced in untreated cells or cells that only expressed Tup1-AID. Finally, we compared the level of IME1 induction between Tup1 depleted cells, wild type starved cells (SPO medium), and cells treated with PKA and TORC1 inhibitors grown in rich medium (Fig 8E). Overall IME1 promoter activity was similar under the different conditions, but increased more rapidly in Tup1 depleted cells compared to cells starved in SPO medium or treated with PKA and TORC1 inhibitors. We conclude that Tup1-Cyc8 is a key repressor of the IME1 promoter, and that PKA and TORC1 control Tup1 association with the IME1 promoter.

Discussion

In yeast, the decision to stop vegetative growth and enter gametogenesis is dictated by nutrient availability regulating the expression of the master regulator IME1. Here, we describe how nutrient sensing and signalling regulate IME1 expression.

Entry into sporulation requires cooperation between PKA and TORC1 signalling

Previous work implicated both the PKA and TORC1 signalling pathways in regulating IME1. Constitutively active PKA, as observed in hyperactivated RAS2 and in BCY1 loss of function mutants, inhibits sporulation [9, 10]. Conversely, when PKA signalling is inhibited or reduced, sporulation occurs in a subpopulation of cells even in nutrient-rich conditions. Furthermore, inhibition of TORC1 with rapamycin leads to IME1 induction and sporulation in saturated

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YPD cultures [7, 21]. Our work shows that entry into sporulation can be achieved in nutrient-rich conditions by inhibiting PKA and lowering TORC1 signalling. Inhibition of these pathways leads to sporulation with similar kinetics and efficiency as starvation induced sporulation. It has been shown that multiple other signalling pathways can also contribute to IME1 regulation including G1 cyclins, several MAPK pathways and the Snf1 pathway [40–45]. Given that PKA and TORC1 signalling control the phosphorylation status of a large number of proteins [46, 47], we propose that some of the previously described regulators of IME1 act downstream of PKA and TORC1 signalling. Further work is needed to decipher how the different signalling networks are connected to each other and how they control entry into sporulation.

Our data suggests that TORC1 and PKA do not only control IME1, but also downstream events such as meiotic divisions and packaging into spores. For example, in cells with low PKA, inhibition of TORC1 with rapamycin further stimulates IME1 induction but also has a profound effect on progression into meiotic divisions and spore formation (Fig 3A). How PKA and TORC1 control other stages of sporulation is not well understood. Our observation that triad formation is significantly enhanced and spore viability is reduced when PKA and TORC1 are inhibited implicates that the two pathways must be tightly regulated during gametogenesis. Further analyses is needed to dissect how PKA and TORC1 themselves are controlled throughout sporulation.

How is repression of IME1 by TORC1 and PKA mediated?

In our efforts to understand how TORC1 and PKA repress IME1, we identified two factors: Sch9 and Tup1. We find that Sch9, a major mediator of TORC1 signalling, negatively regulates IME1. Interestingly, Sch9 and PKA are genetically redundant and functionally overlap [48]. Global gene expression analyses indicate that Sch9 and PKA regulate a common set of genes [49]. These observations suggest that PKA and Sch9 may share one or multiple downstream effectors to control IME1 and entry into sporulation. Indeed, it is known that Sch9 and PKA phosphorylation inhibits the protein kinase Rim15, which is required for quiescence, IME1 expression and sporulation [32, 50]. However, a constitutive active allele of RIM15 cannot derepress IME1 in the presence of ample nutrients suggesting that Rim15 is not the only target of Sch9 and PKA [51]. PKA and TORC1 could also repress IME1 expression by controlling G1 cyclins. It was previously shown that the G1 cyclins CLN1, 2 and 3 repress IME1 [40]. Given that TORC1 and PKA control CLN1-3 expression, it is possible that CLN1-3 partially mediate PKA and TORC1 repression of IME1 [52–54]. PKA is also known to phosphorylate the transcription factors Sok2, Msn2/4, Sko1 and Com2, which directly bind and control the IME1 promoter [15, 42, 55]. Further efforts are needed to identify downstream effectors of PKA and TORC1 that mediate the regulation of IME1.

Our data show that the Tup1-Cyc8 complex is a direct repressor of IME1 that mediates the signals coming from PKA and TORC1. Tup1 binds to the IME1 promoter in nutrient rich conditions, but dissociates from the promoter when both PKA and TORC1 are inhibited. The Tup1-Cyc8 complex functions as a global repressor of transcription and is recruited to promoters by sequence specific DNA binding proteins [36–38]. Identifying transcription factors that recruit Tup1 to the IME1 promoter will give important insights into how IME1 is regulated by TORC1 and PKA signalling. Interestingly, Tup1 depleted cells do not enter sporulation, even though these cells strongly induce IME1. It is possible that other downstream factors, which control entry into sporulation, are not activated under these conditions. For example it has been known that Ime1 translation, phosphorylation, and localization are also affected by nutrients [20, 56–58]. In addition, Tup1 is also required for sporulation. Starving Tup1 depleted
cells to induce sporulation, did not result in spore formation. We hypothesize that Tup1 also regulates the transcription of genes that are important for preventing sporulation.

Intermediate levels of TORC1 activity are required for entry into sporulation

Our analyses revealed a positive role for TORC1 in inducing sporulation. When TORC1 is completely inactive, IME1 is not induced and entry into sporulation does not occur (Figs 5 and 9). We propose that downstream effectors of TORC1 must have opposite effects on IME1 expression and entry into sporulation. Reduced levels of TORC1 activity are required to inactivate Sch9 (discussed in previous section). Some TORC1 signalling however is needed to induce IME1 expression via as yet unidentified downstream mediators. Our findings also reconcile two previous contradictory observations regarding the effect of rapamycin on sporulation. Rapamycin treatment was shown to induce IME1 and sporulation [7, 12, 21] but when rapamycin was combined with nutrient starvation, sporulation was reduced [21]. The observation that intermediate levels of TORC1 are needed for IME1 induction also implies that there is a defined window of activity to induce sporulation. Given that sporulation is energy consuming, perhaps TORC1 senses whether there are sufficient nutrients available for cells to induce IME1 and undergo sporulation.

The effect of ATP/energy production on IME1

To facilitate the energy and metabolic needs throughout sporulation, metabolism is finely and dynamically controlled [59, 60]. Mitochondrial respiration activity is essential for both IME1 expression and sporulation in starvation medium [7, 8]. Previous work showed that inhibition of TORC1 in rich medium induces IME1 in respiration competent, but not in respiration deficient cells [7]. However, in this study TORC1 activity was inhibited in cells grown to a relatively high density (OD600 = 5.5). It is likely that glucose was already consumed from the medium for some extent and not abundant enough to support IME1 expression when respiration is blocked. Our system enabled us to challenge the role of respiration during IME1 induction in rich medium plus glucose. By inhibiting both PKA and TORC1 pathways, we demonstrate that IME1 can be expressed in respiration deficient cells when a fermentable carbon source such as glucose is available. Thus ATP/energy production via either respiration or fermentation is required for IME1 activation. It is interesting to speculate that IME1 functions as an energy sensor that ensures that sporulation is induced by the lack of nutrients and only occurs when the energy source is sufficient for cells to complete sporulation. We further note that the kinetics of IME1 induction in respiration deficient cells is somewhat slower than in wild-type cells (Fig 4C). Even though we cannot exclude the possibility that other functions of mitochondria are contributing to IME1 expression, we favour the idea that in wild-type cells glycolysis is simply not sufficient to produce the energy needed for rapid activation of IME1 expression due to a reduced glucose uptake from the medium. Taken together, we propose that respiration is an essential provider of ATP during starvation induced sporulation.

Concluding remarks

Signal sensing and signal integration are key determinants of cell fate specification and development. In mammalian cells multiple signals often integrate at master regulatory genes to control cell specialization. The IME1 promoter serves as a model for signal integration at complex promoters because it can sense multiple nutrient signals and is regulated by transcription of long noncoding RNAs. Understanding the regulation of yeast entry into gametogenesis may shed light on how complex cell fate choices are made in mammalian cells during development.
Materials and Methods

Strains and plasmids

SK1 strain background was used for the experiments throughout this manuscript and the genotypes are listed in S2 Table. Gene deletions were generated using one-step deletion protocol as described in [61]. The tpk1-as allele was realized by deleting tpk2, tpk3, and by making a point mutation in tpk1M164G as described in [14, 33]. The C-terminal auxin induced degron (AID) tag (used for the KOG1-AID and TUP1-AID alleles), which also includes three copies of the V5 epitope, was generated using one step PCR integration (the plasmid was a gift from Leon Chan, UC Berkeley). A plasmid expressing Oryza sativa TIR1 (osTIR1) ubiquitin E3 ligase from the TEF1 promoter was integrated at the HIS3 locus by digestion with Pme1 (the pTE-F1-osTIR1 plasmid was a gift from Leon Chan, UC Berkeley). Indole-3-acetic acid (IAA) was used to induce depletion of Kog1-AID and Tup1-AID [26].

Growth conditions

In general, cells were grown overnight in YPD to saturation (1% yeast extract, 2% peptone, 2% glucose) at 30°C, then diluted to fresh YPD (OD600 = 1) and treated with different drugs or shifted to sporulation medium (SPO, 0.3% potassium acetate, 0.002% raffinose, pH 7.0). In some experiments cells were grown overnight in YPD, diluted to pre-sporulation medium (BYTA, 1% yeast extract, 2% tryptone, 1% potassium acetate, 50 mM potassium phthalate) for 16 hours, and subsequently shifted to YPD or SPO [62]. Rapamycin was added to cells in a final concentration of 1000 ng/μl unless written otherwise. INM-PP1 was added to cells in a final concentration of 3 μM.

Northern blot analysis

The northern blot protocol for IME1 was described previously [5].

RT-PCR

The RT-PCR protocol was described previously [5]. In short, total RNA was treated with DNase and purified. 750 ng of total RNA was used for the reverse transcription reaction, and single stranded cDNA were quantified by real-time PCR using a SYBR green mix (Life Technologies) on a 7500 Fast Real-Time PCR system (Life Technologies). Signals were normalized to ACT1 transcripts levels. The primer sequences used are included in S3 Table.
Western blot analysis and antibodies

A tricarboxylic acid (TCA) extraction protocol was used to make total protein extracts. Samples were separated by SDS page, blotted onto PVDF blotting membrane, and subsequently incubated with anti V5/1:2000 dilution (Life Technologies) and anti-hexokinase/1:8000 dilution (Stratech Scientific) antibodies. As secondary antibodies IRDye800CV/1:15000 dilution (anti-mouse, LI-COR Biosciences) and IRDye680RD/1:15000 dilution (anti-rabbit, LI-COR Biosciences) were used. Western blot images generated using the Odyssey system (LI-COR Biosciences).

Nuclei/DAPI counting

Cells were fixed overnight in 80% ethanol, and stained with 0.05 μg/ml 4’,6-diamidino-2-phenylindole (DAPI) solution in 100 mM phosphate buffer (pH 7). The number of DAPI masses in at least one hundred cells (n = 100) was counted.

β-galactosidase liquid assay

Liquid ortho-Nitrophenyl-β-galactoside (ONPG) assay was performed as described previously [5]. In short, 2 ml of OD600 = 1 cell pellets were washed with buffer Z (Phosphate buffer pH 7, KCl 10 mM, MgCl 1mM) and were snap frozen in liquid nitrogen. Samples for each biological replicate were collected on different days, but ONPG assays were performed together at the same time. Cells were chemically disrupted using Y-PER buffer (Thermo Scientific). Subsequently cells were incubated with ONPG (Sigma) (1 mg/ml in Z buffer plus 50 mM β-mercaptoethanol) till yellow colouring occurred. The reaction was quenches using sodium carbonate (1 mM) and cell debris was cleared by centrifugation. Absorption of each sample was measured at OD420 using a 96 well plate reader. Miller Units were calculated according to a standard formula [63]: Miller Unit = (signal from plate reader (OD420) x 1000) / (cell density (OD600) x time of incubation with ONPG (min)). The data from the experiments represents the standard error of the mean of at least two biological experiments.

Chromatin immunoprecipitation

Chromatin immunoprecipitation (ChIP) experiments were performed as described previously [5]. Cells were fixed with 1% formaldehyde for 20 min, the reaction was quenched with 125 mM glycine. Cells were disrupted using mini beadbeater (BioSpec), and crosslinked chromatin was sheered by sonication using Bioruptor (Diagenode, 6 cycles of 30 sec on/off). Chromatin extracts were then incubated with anti V5 agarose beads (Sigma) for 2 hours at room temperature, and beads were washed accordingly. To measure Tup1 binding, input and ChIP samples were quantified by real-time PCR using SYBR green mix (Life Technologies) and primers corresponding to the IME1 promoter on a 7500 Fast Real-Time PCR system (Life Technologies). The mating type locus (HMR) was used as a non-binding negative control. The primer sequences used are included in S3 Table.

Single molecule RNA FISH

The single molecule RNA fish was performed as described previously [5]. In short, cells were fixed with formaldehyde overnight, treated with zymolyase and further fixed in 80% ethanol. Subsequently cells were hybridized with fluorophore labelled probes directed to IME1 (AF594) and the internal control ACT1 (Cy5). Cells were imaged using a 100x oil objective, NA 1.4, on a Nikon Ti-E imaging system (Nikon). DIC, DAPI, AF594 (IME1), Cy5 (ACT1) images were collected every 0.3 micron (20 stacks) using an ORCA-FLASH 4.0 camera (Hamamatsu) and
NIK-element software (Nikon). ImageJ software was used to make maximum intensity Z projections of the images [64]. Subsequently, StarSearch software (http://rajlab.seas.upenn.edu/StarSearch/launch.html, Raj laboratory, University of Pennsylvania) was used to determine number transcripts in single cells. Comparable thresholds were used to count the RNA foci in single cells. Only cells positive for the internal control ACT1 were used for the analysis. At least a total n = 60 cells were counted for each experiment.

Supporting Information

S1 Fig. (A) Cells harbouring the tpk1M164G, tpk2Δ, tpk3Δ alleles (tpk1-as, FW1762) were grown in YPD overnight, diluted to 0.2 (OD600), and subsequently were treated with 1NM-PP1, rapamycin, both or untreated. Cell density (OD600) was measured over time at the indicated time points. (B) IME1 promoter activity was measured in a diploid control strain harbouring the IME1 promoter fused to LacZ reporter (pIME1-LacZ) (FW612), and a strain harbouring tpk1-as and pIME1-LacZ (FW1976). Cells were grown in YPD overnight, shifted to sporulation medium (SPO), and samples were taken at the indicated time point. β-galactosidase activity was measured using a quantitative liquid ortho-nitrophenyl-β-galactoside (ONPG) assay (see Materials and Methods for details). The promoter activities are displayed in Miller Units, and the standard error of the mean of at least two biological experiments is shown. (C) Similar as B except that IME1 tpk1-as (FW1976) cells were diluted into YPD and treated with rapamycin (1000 ng/ml), 1NM-PP1, or both compounds, or shifted to SPO. Samples were taken after 0, 1, 2, and 4 hours. (D) Similar to C, except that samples shifted to YPA, YPA plus rapamycin or YPA plus 1NM-PP1. (PDF)

S2 Fig. Single molecule RNA FISH of IME1 in control and ime1Δ cells. (A) Representative images used for the analyses of IME1 and ACT1 transcript levels in diploid control (FW1511) and ime1Δ (FW81) cells. Cells were grown overnight in YPD and shifted to sporulation medium for 3 hours. Cells were fixed, hybridized with probes directed against IME1 (AF594) and ACT1 (Cy5), and imaged (see Materials and Methods for details). ACT1 was used as an internal control and only ACT1 positive cells were selected for the analysis. (B) Mean of IME1 and ACT1 transcripts’ number among single cells as described A. At least, 60 cells (n = 60) were quantified per time point. The standard error of the mean of at least two biological experiments is shown. (PDF)

S3 Fig. Inactive TORC1 represses IME1. (A) Spot assay of strains harbouring KOG1-AID (FW1894), Oryza sativa TIR1 (pTEF1-osTIR1) (FW1818), and the combined KOG1-AID/pTEF1-osTIR1 in haploid (FW1887) and diploid (FW1905) cells. Cells were grown in YPD overnight and spotted in five-fold serial dilutions on YPD agar plates in the absence or presence of indole-3-acetic acid (IAA) (500 μM). (B) Western blot analysis of Kog1-AID in the absence or presence of IAA. KOG1-AID/pTEF1-osTIR1 expressing cells (FW1887) were grown in YPD overnight, diluted into fresh YPD, and treated with IAA. Samples were taken at the indicated time points. Kog1-AID protein levels were quantified by western blot with antibodies directed against V5 and Hxk1 (control). (C) Doubling times of control (FW1976), tco89Δ (FW2154), gtr1Δ (FW2164) and tor1Δ (FW2162) strains. Cells were grown overnight, diluted into fresh YPD in the absence of presence of rapamycin and a growth curve was determined by OD600 readings. Doubling times were calculated from the exponential part of the growth curve. (PDF)
S1 Table. Sporulation efficiencies. Sporulation efficiencies during different conditions as described in Fig 1. (DOCX)

S2 Table. Table of yeast strains. (DOCX)

S3 Table. Oligonucleotide sequence information. (DOCX)

S1 Data. Supporting data. (XLSX)

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Author Contributions
Conceived and designed the experiments: HW AA FJvW. Performed the experiments: HW FJvW FM GS. Analyzed the data: HW FJvW. Contributed reagents/materials/analysis tools: HW FJvW. Wrote the paper: HW FJvW AA.

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