**GATA Factor Regulation In Excess Nitrogen Occurs Independently of Gtr-Ego Complex-Dependent TorC1 Activation**

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*Running title: Gtr-Ego Dispensable in Gln3 Response to Excess Nitrogen*

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**ABSTRACT**

The TorC1 protein kinase complex is a central component in a eukaryotic cell’s response to varying nitrogen availability, with kinase activity being stimulated in nitrogen excess by increased intracellular leucine. This leucine-dependent TorC1 activation requires functional Gtr1/2, and Ego1/3 complexes. Rapamycin inhibition of TorC1 elicits nuclear localization of Gln3, a GATA-family transcription activator responsible for the expression of genes encoding proteins required to transport and degrade poor nitrogen sources, e.g., proline. In nitrogen-replete conditions, Gln3 is cytoplasmic and Gln3-mediated transcription minimal, whereas in nitrogen limiting or starvation conditions, or following rapamycin treatment, Gln3 is nuclear and transcription greatly increased. Increasing evidence supports the idea that TorC1 activation may not be as central to nitrogen-responsive intracellular Gln3 localization as previously envisioned. To test this idea directly, we determined whether or not Gtr1/2- and Ego1/3-dependent TorC1 activation was also required for cytoplasmic Gln3 sequestration and repressed GATA factor-mediated transcription by abolishing the Gtr-Ego complex proteins. We show that Gln3 is sequestered in the cytoplasm of gtr1Δ, gtr2Δ, ego1Δ, and ego3Δ strains either long-term in logarithmically glutamine-grown cells or short-term after re-feeding glutamine to nitrogen-limited or -starved cells; GATA factor-dependent transcription was also minimal. However, in all but a gtr1Δ, nuclear Gln3 localization in response to nitrogen limitation or starvation was adversely affected. Our data demonstrate: (i) Gtr-Ego-dependent TorC1 activation is not required for cytoplasmic Gln3 sequestration in nitrogen-rich conditions, (ii) a novel Gtr-Ego-TorC1 activation-independent mechanism sequesters Gln3 in the cytoplasm and (iii) Gtr and Ego complex proteins participate in nuclear Gln3-Myc13 localization, heretofore unrecognized functions for these proteins, (iv) the importance of searching for new mechanisms associated with TorC1 activation and/or the regulation of Gln3 localization/function in response to changes in the cells’ nitrogen environment.

**Keywords:** Gln3 localization, Gtr1/2 complex, Ego1/3 complex, Tor complex one (TORC1), nitrogen catabolite repression (NCR), nitrogen limitation, nitrogen starvation

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**charomyces cerevisiae**, or mTor in animal cells (Broach 2012; Conrad et al. 2014).

Recent advances in our understanding of how TorC1 kinase activity is regulated in yeast derive from studies demonstrating the active participation and requirement of five proteins for TorC1 activation in response to increased concentrations of leucine: Vam6 and two protein complexes consisting of Gtr1-Gtr2 and Ego1-Ego3, respectively (Binda et al. 2009; Bonfils et al. 2012; Zhang et al. 2012; Panchaud et al. 2013). Vam6 is a guanine nucleotide exchange factor or GEF that mediates conversion of the GDP form of Gtr1 to its active GTP form. Gtr1-GTP-Gtr2 associates with the Ego1-Ego3 complex which in as yet to be elucidated manner activates TorC1. In these studies, the reporter of TorC1 kinase activation was the phosphorylation of the Sch9 kinase which is a known regulator of protein synthesis initiation through its phosphorylation of six residues in the C-terminal portion of the protein (Binda et al. 2009; Bonfils et al. 2012; Zhang et al. 2012; Panchaud et al. 2013).

Gln3 and Gat1, the nitrogen-responsive, GATA-family transcription activators, have also been extensively used as reporters of TorC1 activity. In nitrogen-replete conditions, Gln3 is cytoplasmic and transcription of genes encoding the proteins required to transport and catabolize poorly utilized nitrogen sources, e.g., proline, urea or allantoin, is minimal (Cooper 1982, 2004; Hofman-Bang 1999; Magasanik and Kaiser 2002; Broach 2012; Conrad et al. 2014). When the supply of readily utilized nitrogen sources, e.g., YEPD (yeast extract, peptone, dextrose), glutamine, or ammonia, become exhausted or unavailable, Gln3 relocates to the nucleus where Gln3-activated transcription increases dramatically so that cells are able to scavenge a broader range of nitrogenous compounds from their environments. This nitrogen-responsive regulation has long been referred to as nitrogen catabolite repression (NCR).

The findings that the transcriptome profiles of NCR-sensitive transcription were significantly similar to those observed after treating cells with the specific TorC1 inhibitor, rapamycin, led to the conclusion that nitrogen-responsive regulation of Gln3 and Gat1 was achieved via TorC1 (Beck and Hall 1999; Cardenas et al. 1999; Puria et al., 2008; Hardwick et al. 1999; Bertram et al. 2000; Magasanik and Kaiser 2002; Broach 2012; Conrad et al. 2014). Therefore, one would expect that the proteins required for TorC1 activation would also be required for cytoplasmic Gln3 sequestration and repressed transcription. To address this question, we constructed deletions in the cognate genes for each of the Gtr-Ego complex proteins and then tested Gln3 localization and NCR-sensitive gene expression in these deleted strains. The evidence obtained was remarkable: none of the these proteins were required for the long-term sequestration of Gln3-Myc<sup>13</sup> in the cytoplasm of steady state glutamine-growing cultures or short-term after resupplying excess nitrogen to nitrogen-limited or nitrogen-starved cells. The same results were obtained when NCR-sensitive GDH2 and DAL5 transcription were measured: the expression of these genes was minimal in all of the mutants grown in nitrogen-replete conditions. These data clearly demonstrated that the response of Gln3 to excess nitrogen was mechanistically independent of Gtr1/2-Ego1/3-dependent TorC1 activation thus demonstrating the existence of either (i) another mechanism to achieve cytoplasmic Gln3 sequestration in excess nitrogen or (ii) nitrogen-responsive TorC1 activation that does not require the Gtr-Ego complexes.. On the other hand, nuclear Gln3 localization in response to nitrogen limitation or starvation was adversely affected to varying degrees in all but the gtr1Δ indicating that these proteins play a newly identified role in the regulation of Gln3 localization other than their roles in TorC1 activation. Together the data presented give a more complete and detailed view of the regulatory pathways controlling Gln3 localization and function. In
addition, they provide solid motivation to search for additional mechanisms of activating TorC1 or TorC1-independent mechanisms of regulating Gln3 localization and function in response to changes in the nitrogen environment.

Materials and Methods

Yeast strains and culture conditions

The *S. cerevisiae* strains used in this work appear in Table 1. All deletion mutant strains were derived from TB123. Growth conditions were identical to those described in Tate et al. (2009, 2010). Cultures were grown to mid-log phase (A_{600 nm} = 0.5) in YNB (without amino acids or ammonia) minimal medium containing the indicated nitrogen source (final concentration 0.1%). Appropriate supplements (120 μg/ml leucine, 20 μg/ml histidine, 20 μg/ml tryptophan and 20 μg/ml uracil) were added to cover auxotrophic requirements.

Cells in mid-exponential phase to be transferred from one medium to another were harvested by rapid filtration. The harvested cells were then suspended in fresh, pre-warmed and pre-aerated medium that was the same as the one from which the cells were harvested. When nitrogen (glutamine) was added to a nitrogen-starved culture or a culture that had been previously shifted from glutamine to proline medium, it was added as a solid which quickly dissolved. Between 45 and 60 seconds elapsed between the onset of glutamine addition and sampling of the refed culture.

Strain construction

Deletion strains involving insertion of kanMX or natMX cassettes were constructed using the long flanking homology strategy of Wach (1996) using L1-L4 primers listed in Table 2.

Indirect immunofluorescence microscopy

Cell collection and immunofluorescent staining were performed as previously described (Cox et al. 2004; Tate et al. 2006, 2009; Georis et al. 2008). Stained cells were imaged using a Zeiss Axioplan 2 imaging microscope with a 100x Plan-Apochromat 1.40 oil objective at room temperature. Images were acquired using a Zeiss Axio camera and AxioVision 3.0 and 4.8.1 (Zeiss) software. For presentation, images were processed with Adobe Photoshop and Illustrator programs. Level settings (shadow and highlight only) were altered where necessary to avoid any change or loss in cellular detail relative to what was observed in the microscope; changes were applied uniformly to the image presented and were similar from one image to another.

Determination of intracellular Gln3-Myc\(^{13}\) distribution

We quantitated intracellular Gln3-Myc\(^{13}\) localization by manually scoring its localization in 200 or more cells in multiple, randomly chosen fields from which each image presented was taken. Scoring was performed exclusively using unaltered, primary .zvi image files viewed with Zeiss AxioVision 3.0 and 4.8.1 software.

Cells were classified into one of three categories: cytoplasmic (cytoplasmic Gln3-Myc\(^{13}\) fluorescence only; red bars in the histograms), nuclear-cytoplasmic (Gln3-Myc\(^{13}\) fluorescence appearing in the cytoplasm as well as co-localizing with DAPI-positive material; yellow bars), and nuclear (Gln3-Myc\(^{13}\) fluorescence co-localizing only with DAPI-positive material; green bars). Representative “standard” images demonstrating the differences in these categories is shown in Figure 2 of Tate et al. 2009 along with a description of how the scoring criteria were applied. Time course experiments of the kind presented here do not easily lend themselves to statistical analysis because even small experiment-to-experiment shifts in the overall shape of the response curves destroy the apparent precision of the individual measurements. However, experiments were repeated two or more times with similar results. The reproducibility of our scoring has been repeatedly evaluated (Tate et al. 2006, 2010; Rai et al. 2014). In the latest evaluation, we analyzed the data for three different experimental conditions, each from 10 different experiments performed over a nine month period. The maximum standard deviation observed in our scoring was +/- ~7-8% (Rai et al. 2014). Images accompanying the histograms were selected on the basis that they exhibited intracellular Gln3-Myc\(^{13}\) distributions as close as possible to those observed in the quantitative scoring data.

qRT-PCR analyses

RNA isolation and cDNA synthesis were conducted as described by Georis et al. (2009). Specific DNA targets were quantified by real-time polymerase chain reaction (PCR) performed on a StepOnePlus device (Applied Biosystems, Foster City, CA) using DAL5, GDH2 and TBP1 primers described previously (Georis et al. 2008, 2011). The values reported represent the averages of at least two experiments from independent cultures; error bars indicate standard errors.

RESULTS
Our previous work demonstrating that the model describing nitrogen-responsive regulation of TorC1 activity was insufficient to account for control of the GATA factors Gln3 and Gat1 prompted an important question that directly tests whether or not nitrogen-dependent TorC1 activation, as we currently understand it, regulates GATA factor localization and function. Do the Gtr1/Gtr2 and Ego1/Ego3 complexes, required for TorC1 activation and downstream Sch9 phosphorylation in nitrogen-replete medium, also participate in cytoplasmic Gln3 sequestration during nitrogen excess and/or nuclear Gln3 localization and subsequently Gln3-dependent gene expression during nitrogen limitation/starvation? To frame these questions in a context that permitted overall comparisons of present Gln3 localization data with that reported for growth recovery and Sch9 phosphorylation (Binda et al. 2009), we used an experimental format similar to the one originally employed to establish that Gtr1, Gtr2, Ego1, and Ego3 were required for recovery from rapamycin-induced growth arrest and TorC1 activation. In those investigations, wild type and mutant cells, growing in complex nitrogen rich medium, were treated with rapamycin for 6 hrs to mimic nutrient starvation. The cells were then transferred to nitrogen-free rich (YPD) medium where growth arrest and TorC1 activation. In those investigations, wild type (Figure 2A and B, left side). When these cells were resupplied with excess nitrogen, by adding glutamine to the nitrogen-free medium, Gln3-Myc13 immediately relocated from the nucleus to the cytoplasm. In fact, Gln3-Myc13 relocation to the cytoplasm was so rapid that it was already half complete before we could collect our first sample (~1 min). It totally relocated within 10 mins (Figure 2A and B, right side), and then remained completely cytoplasmic over the next hr.

Transferring cells from nitrogen-replete to nitrogen-limiting conditions, i.e., from glutamine to proline medium, generated a less strong response. Gln3-Myc13’s initial entry into the nucleus occurred more quickly than with nitrogen starvation in that maximum relocation was largely achieved within 30 mins (Figure 2C and D, left side). The degree of nuclear localization was similar to that observed in short-term nitrogen starvation (1-2 hrs). However, the overall extent of Gln3-Myc13 relocation was less than seen with nitrogen starvation. In contrast, the response to re-feeding glutamine to cells growing in proline medium was exactly the same as occurred when re-feeding nitrogen starved cells. Gln3-Myc13 began relocating to the cytoplasm immediately and was completely cytoplasmic within 10 mins (Figure 2C and D, right side).

Effects of deleting GTR1 and GTR2 on Gln3-Myc13 movement in and out of the nucleus

The first mutant analyzed was a gtr1Δ (FV406). Consistent with the growth data (Figure 1), there was no demonstrable effect of deleting GTR1 other than a small shift in the kinetics of Gln3-Myc13 movement from the cytoplasm to the nucleus during short-term nitrogen limitation or long-term nitrogen starvation (Figure 3A and B). Otherwise, the gtr1Δ exhibited a wild type phenotype (Figure 2 vs. Figure 3A and B). We were also unable to demonstrate a significant change in the behavior of Gln3-Myc13 localization for up to 5 hrs after transferring gtr1Δ cells from a rich to a poor nitrogen source (Figure 3C and D). Some Gln3-Myc13 movement out of the nucleus did occur, however, between the 5th and 6th hrs following the transfer to proline medium; the significance of this observation is unclear.
On the other hand, addition of glutamine to nitrogen-starved or nitrogen-limited \( \text{gtr1} \Delta \) cells elicited rapid and dramatic exit of Gln3-Myc\(^{13}\) from the nucleus. Gln3-Myc\(^{13}\) was cytoplasmic or nuclear-cytoplasmic in over half of the cells before the first sample could be collected irrespective of whether glutamine was added to nitrogen starved \( \text{gtr1} \Delta \) cells or in those provided with a derepressive nitrogen source (Figure 3, right side). Thus, Gtr1 was not required for cytoplasmic Gln3-Myc\(^{13}\) sequestration in glutamine re-fed cells. Similarly, Gtr1 was not required for cytoplasmic Gln3 sequestration when the cells were growing logarithmically in nitrogen-rich, glutamine medium, a growth condition where TorC1 is activated (zero time points in Figure 3).

Gtr1 and Gtr2 are members of a heterodimeric complex that associates with the Ego1/Ego3 complex also reported to be required for TorC1 activation (Binda \textit{et al.} 2009; Bonfils \textit{et al.} 2012; Zhang \textit{et al.} 2012; Panchaud \textit{et al.} 2013). As such, we expected \( \text{gtr1} \) and \( \text{gtr2} \) deletions to exhibit similar phenotypes. Therefore, we were somewhat surprised to find that their phenotypes were different. Short- and long-term nitrogen-starved and nitrogen-limited, (transferred to proline for 6 hrs) \( \text{gtr2} \Delta \) (FV359) cells behaved similarly (Figure 4A-D). In all three cases, alteration of the cells’ nitrogen supplies elicited rapid initial Gln3-Myc\(^{13}\) movement into the nucleus; the effects were clearly evident within 30 mins of altering the medium (Figure 4). However, further Gln3-Myc\(^{13}\) relocation then abruptly ceased and remained at this intracellular distribution for the duration of the experiment again with Gln3-Myc\(^{13}\) situated equally in the nuclear, nuclear-cytoplasmic and cytoplasmic scoring categories (Figure 4).

There were two conditions where the phenotypes of the \( \text{gtr1} \Delta \) and \( \text{gtr2} \Delta \) mutants exhibited striking and identical phenotypes. Cytoplasmic Gln3-Myc\(^{13}\) sequestration following addition of glutamine to nitrogen-limited and starved cultures did not require functional Gtr1 and Gtr2 (Figure 3 and 4, right side). The same absence of a Gtr2 requirement was also observed in logarithmically, glutamine-growing cells (Figure 4, left side, zero time points).

**Effects of deleting EGO1 and EGO3 on Gln3-Myc\(^{13}\) localization**

The next complex in the cascade required for TorC1 activation, consists of Ego1 and Ego3 (Binda \textit{et al.} 2009; Bonfils \textit{et al.} 2012; Zhang \textit{et al.} 2012; Panchaud \textit{et al.} 2013). There were several measurable effects of losing Ego1 on cells starved for nitrogen or transferred from excess to growth limiting proline medium. First, nuclear Gln3-Myc\(^{13}\) localization in response to short-term nitrogen starvation was lower than in wild type (compare Figures 2A and B with Figure 5A and B, 0 to 1 hr). Although the Gln3-Myc\(^{13}\) response to long-term nitrogen starvation was initially the same as in wild type cells, nuclear Gln3-Myc\(^{13}\) localization was not sustained as nitrogen starvation extended beyond 4 hrs (Figure 5A and B). Gln3-Myc\(^{13}\) began exiting the nucleus between the fifth and sixth hours. However, the significance of this observation is uncertain.

The initial response of shifting ego1\( \Delta \) cells from glutamine to proline medium was much the same as occurred with short-term nitrogen starvation, again a smaller response than observed in wild type during the first hr. Thereafter, up to 5 hrs, Gln3-Myc\(^{13}\) became more nuclear than occurred in wild type as though the cells were becoming increasingly starved even though they were being cultured in a stable condition with proline as sole nitrogen source. Then, as with long-term starvation, Gln3-Myc\(^{13}\) began exiting from the nucleus between hrs five and six (Figure 5C and D).

As occurred with the previous two deletion mutants, we could demonstrate no Ego1 requirement for relocating Gln3-Myc\(^{13}\) from the nucleus to the cytoplasm when glutamine was added to re-feed the nitrogen-starved and nitrogen-limited cultures (Figure 5A-D, right side). Supporting this result we observed no requirement of Ego1 to sequester Gln3 in the cytoplasm of cells growing logarithmically in YNB-glutamine medium (Figure 5A-D, left side, zero time point).

The final TorC1 activation pathway component we investigated was Ego3. For the first 1/2 hr of nitrogen starvation, the response of Gln3-Myc\(^{13}\) in an Ego3\( \Delta \) was largely wild type, Gln3-Myc\(^{13}\) began relocating from the cytoplasm to the nucleus (Figure 6A and B, left side). At that point, however, Gln3-Myc\(^{13}\) movement ceased with it remaining more or less equally distributed in the three localization scoring categories just as occurred when the \( \text{gtr2} \Delta \) was nitrogen starved (compare Figure 6A and B with Figure 4A and B). Long-term nitrogen starvation-elicited nuclear Gln3-Myc\(^{13}\) localization did not occur. Again Gln3-Myc\(^{13}\) was distributed equally in the three scoring categories. When the ego3\( \Delta \) was transferred from glutamine to proline medium, the phenotype was the same as with nitrogen starvation and as previously observed with the \( \text{gtr2} \Delta \).

At this point we were no longer surprised by our inability to demonstrate a requirement of Ego3 for Gln3-Myc\(^{13}\) to be relocated from the nucleus to the cytoplasm following re-feeding of glutamine to nitrogen-starved cultures or a culture growing in proline medium. And as before, Ego3 was not required to sequester Gln3-Myc\(^{13}\) in the cytoplasm of steady state glutamine-grown cells (Figure 6, zero time points). In sum, none of the TorC1 activation pathway components previously shown to be required for TorC1-dependent Sch9 phosphorylation...
were required for cytoplasmic Gln3 sequestration in steady state glutamine-grown cultures, or when glutamine was added to nitrogen-starved cultures or those provided with a poor nitrogen source.

Effects of deleting Gtr-Ego complex components on Gln3-Myc\textsuperscript{13} localization in steady state cultures provided with proline as sole nitrogen source

Above experiments demonstrated Gtr2, Ego1 and Ego3 were required to varying degrees for nuclear Gln3-Myc\textsuperscript{13} localization when cells were shifted from glutamine to proline medium. It was conceivable, however, these requirements resulted from insufficient time being allowed for the transition from nitrogen-replete to nitrogen-poor medium and would disappear over time. To assess this possibility, wild type and mutant cultures were grown in proline medium (Figure 7). Both Gtr2 and Ego3 were required for high level nuclear Gln3-Myc\textsuperscript{13} localization supporting conclusions reached during the time course studies. When the steady state Gln3 localization profiles were compared with the values observed at 4-6 hours, data for ego1\textsuperscript{Δ} correlated relatively well, but there was an even greater Ego3 requirement in proline-grown cells than at 4-6 hours after they were transferred from glutamine to proline medium (compare Figures 5-7). As observed in cells transferred to proline, GTR1 was not required for Gln3 localization in proline-grown cells.

The Gln3-Myc\textsuperscript{13} localization profiles in wild type, gtr1\textsuperscript{Δ} and gtr2\textsuperscript{Δ} strains paralleled the growth of these strains in proline medium (compare Figures 1 and 7). There was, however, less positive correlation when ego1\textsuperscript{Δ} and ego3\textsuperscript{Δ} mutants were analyzed. Gln3-Myc\textsuperscript{13} localization in steady state proline-grown cells would lead to the prediction that the ego1\textsuperscript{Δ} would grow well, whereas the ego3\textsuperscript{Δ} would not (compare Figure 7 with Figure 1). In fact, both ego1\textsuperscript{Δ} and ego3\textsuperscript{Δ} mutants grew poorly in proline (Figure 1). Importantly, both mutants also grew poorly in glutamine medium where Gln3-Myc\textsuperscript{13} is cytoplasmic and NCR-sensitive transcription is minimal. This strongly suggests that the growth of these mutants was dependent on more than Gln3-Myc\textsuperscript{13} localization, which likely accounts for the poorer correlation between Gln3-Myc\textsuperscript{13} localization and growth of the ego1\textsuperscript{Δ} and ego3\textsuperscript{Δ} mutants.

Repressed reporter gene expression is unaffected in Gtr-Ego complex mutants

We and others often use reporter gene transcription to evaluate nitrogen-responsive regulation in yeast and other organisms. Therefore, we extended the above studies by determining the extent to which DAL5 and GDH2 transcription correlated with the Gln3-Myc\textsuperscript{13} localization responses in the various mutants. After two hours of nitrogen starvation, DAL5 and GDH2 expression markedly increased relative to that in glutamine-grown cells, positively correlating with increased Gln3-Myc\textsuperscript{13} localization (Figure 8A and B), irrespective of whether the assays were performed in wild type, gtr1\textsuperscript{Δ}, gtr2\textsuperscript{Δ}, ego1\textsuperscript{Δ} or ego3\textsuperscript{Δ} mutant strains. A similarly positive correlation was observed when wild type or mutant cells were transferred from glutamine to proline medium (Figure 8, Gln>Pro 1 hr). Thus, deleting components of the Gtr-Ego complex did not demonstrably affect overall NCR-sensitive gene expression. There was, however, one striking lack of correlation between Gln3-Myc\textsuperscript{13} localization and NCR-sensitive gene expression. It was the low GDH2 level after shifting ego1\textsuperscript{Δ} cells from glutamine to proline medium. The reason for this discrepancy isn’t known. We also observed a minor lack of correlation between Gln3-Myc\textsuperscript{13} localization and NCR-sensitive gene expression. It occurred with DAL5 expression in the gtr1\textsuperscript{Δ} and ego1\textsuperscript{Δ} mutants during steady state growth in glutamine medium. Transcription was modestly higher in the mutants than wild type yet Gln3-Myc\textsuperscript{13} localization was similarly sequestered to the cytoplasm in all three cases. It is difficult to know whether this difference in transcription is meaningful given how close it was to basal levels, but in any case the reason for the difference is unknown.

There was an important correlation between Gln3-Myc\textsuperscript{13} localization and DAL5 and GDH2 transcription. The two processes responded in absolute lock-step when wild type and mutant cells were growing in steady state with nitrogen-rich glutamine as the nitrogen source. Gln3-Myc\textsuperscript{13} was totally excluded from the nucleus under these conditions and DAL5 and GDH2 transcription was just barely detectable. The same outcome occurred when glutamine was re-fed to nitrogen-starved cells or those growing in a derepressive nitrogen source (Figure 8). Together, these data indicated little if any required participation of Gtr1, Gtr2, Ego1 or Ego3 in the responses of overall DAL5 and GDH2 gene expression to nitrogen limitation or starvation. More importantly, they unequivocally demonstrated that these proteins were completely dispensable when it came to short- or long-term control of Gln3-Myc\textsuperscript{13} localization and function in cells provided with excess nitrogen either in steady state or transition.

DISCUSSION
Multiple mechanisms participate in the Gln3 response to nitrogen excess

The data presented clearly demonstrate cytoplasmic Gln3-Myc\textsuperscript{13} sequestration in logarithmically growing cells provided with excess nitrogen or upon re-feeding
excess nitrogen to nitrogen-starved cells or those growing with a poor nitrogen source does not require Gtr1/2-Ego1/3-dependent TorC1 activation. GATA factor-mediated, NCR-sensitive DAL5 and GDH2 transcription closely correlate with Gln3 localization, further supporting the conclusion. These striking observations raise two pivotal questions about TorC1 activation/inactivation and its role in the regulation of Gln3 localization and function. (i) Is there more than one way that TorC1 can be activated, both short and long term, by the cell’s nitrogen supply? (ii) Is Gln3-Myc\textsuperscript{13} localization and function determined by mechanisms beyond nitrogen-responsive TorC1 activation/deactivation, a previously suggested possibility (Cox et al. 2004; Tate et al. 2005, 2006, 2009, 2013; Georis et al. 2011; Feller et al. 2013; Rai et al. 2013, 2014)?

Considering the first question, two possibilities are pertinent. Binda et al. observed a very small amount of residual Sch9 phosphorylation (TorC1 activation) when gtr1\textsuperscript{Δ}, gtr2\textsuperscript{Δ}, ego1\textsuperscript{Δ}, ego3\textsuperscript{Δ} and tco89\textsuperscript{Δ} mutants were growing in nitrogen rich medium (2009). Therefore, one could conceivably argue this residual activity was sufficient to trigger cytoplasmic Gln3 sequestration. However, this interpretation depends on two premises: (i) that the observed Sch9 phosphorylation was in fact catalyzed exclusively by TorC1 kinase in the absence of rapamycin and (ii) cytoplasmic Gln3 sequestration is exquisitely sensitive to TorC1 kinase activity. Without a double mutant (Gtr-Ego complex component and unknown component responsible for residual TorC1 activation) abolishing detectable Sch9 phosphorylation, this possibility cannot be rigorously evaluated. We do not particularly favor the second premise because three hours were required after increasing the intracellular pools of amino acids with 200 µg/ml cycloheximide, conditions that abolish protein synthesis elongation and strongly activate TorC1 kinase, for ~85% of Gln3 to become cytoplasmic (Tate and Cooper 2013). In contrast Sch9 phosphorylation increased dramatically under similar conditions after a 30 min. 25 µg/ml of cycloheximide treatment (Binda et al. 2009).

Alternatively and more likely there exists a means of activating TorC1 in response to nitrogen availability that does not involve the Gtr-Ego complexes. Although this possibility might explain some of our observations, it would not explain a significant number of others. For example, if there is a Gtr-Ego complex-independent TorC1 activation pathway regulating Gln3-Myc\textsuperscript{13} localization, it would have to support both short-term TorC1 activation in response to re-feeding excess nitrogen to nitrogen-limited or -starved cells as well as long-term activation in response to steady state growth in nitrogen-replete environments. Further, if there is a Gtr1/2-Ego1/3 complex-independent way of activating TorC1, we would have to conclude that the outcomes of the two routes of TorC1 activation, i.e., phosphorylation of Sch9 and cytoplasmic sequestration of Gln3-Myc\textsuperscript{13} and down regulation of GATA factor-mediated transcription also follow separable routes of implementation because Sch9 phosphorylation requires all of the proteins studied in this work, whereas cytoplasmic Gln3-Myc\textsuperscript{13} sequestration on re-feeding glutamine or in steady state growth in glutamine medium required none of them.

Alternatively, we prefer to suggest that our data likely indicate the existence of a separate means of implementing cytoplasmic sequestration of Gln3 in the presence of excess nitrogen that does not involve TorC1. Several observations support this idea. We have previously shown that mutations in URE2 and GLN3 themselves are able to abrogate a response to rapamycin treatment without adversely affecting NCR-sensitive Gln3 regulation (Feller et al. 2013; Rai et al. 2013). Further, amino acid substitutions that abolish the Gln3-Tor1 interaction do not result in constitutively nuclear Gln3 localization as expected in nitrogen-rich medium where TorC1 is active (Rai et al. 2013). Rather, Gln3 becomes only partially nuclear exhibiting a distinct intracellular distribution in which Gln3 is about equally distributed in the three scoring categories used to assess its localization. This is precisely the behavior that would be expected if one of two mechanisms participating in cytoplasmic Gln3 sequestration were inactivated.

**Gtr2 and Ego3 participation in nuclear Gln3 localization in response to nitrogen limitation or starvation**

Our results also demonstrate that loss of Gtr2 and Ego3 diminished the responses of Gln3-Myc\textsuperscript{13} localization to nitrogen availability in a way very similar to that observed in gln3 amino acid substitution mutants in which the Gln3-Tor1 interaction was abolished (Rai et al. 2013). This would again be expected if Gtr2 and Ego3 were participating in only one of two or more Gln3 regulatory mechanisms. There is an unexplained issue, however, in these data. Gtr2 and Ego3 are both members of complexes, Gtr1/2 and Ego1/3. Normally one would expect that abolishing one member of a two-member complex would generate a functional phenotype similar to abolishing the other member. This, of course, did not occur with Gln3-Myc\textsuperscript{13} localization. Deleting GTR1 had no demonstrable effect on Gln3-Myc\textsuperscript{13} localization and although deleting EGO1 did affect nuclear Gln3-Myc\textsuperscript{13} localization, the response profile was not the same as in the gtr2\textsuperscript{Δ} and ego3\textsuperscript{Δ}. The above expectation, however, derives from the assumption that the Gtr and Ego proteins can function only as members of their respective complexes. The Gln3-Myc\textsuperscript{13} data raise the possibility...
that Gtr and Ego proteins may be able to function both in complexes and as individual molecules or members of yet to be discovered additional complexes. From this perspective, it is interesting that deletion of either GTR2 or EGO3 yielded similar phenotypes raising the possibility that they are participating in the same overall process leading to nuclear Gln3 localization.

**Gln3-Myc<sup>13</sup> localization and Gln3 supported transcription in gtr1Δ, gtr2Δ, ego1Δ and ego3Δ mutants**

Where it counted most, Gln3-Myc<sup>13</sup> localization and nitrogen-responsive DAL5 and GDH2 reporter gene transcription closely correlated. Indeed, irrespective of the deletion mutant assayed, Gln3-Myc<sup>13</sup> was sequestered in the cytoplasm of steady state glutamine-grown cells or when glutamine was added to nitrogen limited/starved cultures, and DAL5 and GDH2 transcription was minimal.

There is a final important point that should not be overlooked. The landmark investigation of the Gtr1/2-Ego1/3 complexes employed Sch9 phosphorylation as the proxy of TorC1 activity (Binda et al. 2009; Bonfils et al. 2012; Zhang et al. 2012; Panchaud et al. 2013). Sch9 being a central regulator of protein synthesis (Powers 2007; Urban et al. 2007). We, on the other hand, used intracellular Gln3-Myc<sup>13</sup> localization to measure responses to various nitrogen environments. Gln3 is a central activator of all nitrogen catabolism which generates rather than utilizes nitrogenous precursors. Therefore, it is not too surprising that control of pathways generating and utilizing nitrogenous precursors might share similarities on the one hand and exhibit distinct differences on the other. An analogous situation occurs with general amino acid control by the GCN proteins (Riego et al. 2002; Sosa et al. 2003; Hernandez et al. 2011). It is well known that the regulation of protein synthesis by the GCN proteins is mechanistically distinct from the NCR-sensitive regulation of Gln3 and its control of nitrogen catabolism even though Gln3 provides the nitrogen for that protein biosynthesis. Additionally, the two regulatory systems often collaborate to fine tune expression of some, but not all, nitrogen catabolic genes.

By this reasoning, results obtained using Sch9 phosphorylation and Gln3-Myc<sup>13</sup> localization as reporters may, as we saw throughout this work, reveal both distinct and overlapping functions of TorC1- and NCR-dependent regulation in the control of nitrogenous compound degradation and reuse of the products it generates in biosynthetic reactions.

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FIGURE LEGENDS

Figure 1. Requirements of Gtr1, Gtr2, Ego1 and Ego3 for growth with repressive (glutamine) and derepressive (proline and allantoin) nitrogen sources. Wild type and mutant cells were streaked on the same plates containing YNB-glutamine, -proline or –allantoin medium. Cultures were incubated at 30°C for 72 hrs and photographed. Strain numbers and pertinent genotypes are indicated to the left of the images.

Figure 2. Time course of Gln3-Myc13 localization in wild type cells (TB123) following nitrogen starvation (panels A and B), or transfer from nitrogen-replete to nitrogen-limiting medium (panels C and D), and resupplying excess nitrogen to all of the cultures (panels A-D). Cultures were originally grown to mid-log phase (A600nm = 0.5) in YNB-glutamine medium. At zero time the first culture was sampled and the remainder transferred to nitrogen-free-YNB medium (panels A and B) and the second culture was sampled at zero time and the remainder transferred to YNB-proline medium (panels C and D). Samples of each culture were taken as indicated. After 6 hrs of incubation, glutamine was added to each culture (final concentration of 0.1%) and sampling continued for an additional hr. Samples were then processed for indirect fluorescence microscopy as described in Materials and Methods. Time course experiments as presented here do not easily lend themselves to statistical analysis because even small experiment to experiment shifts in the overall shape of the response curves destroy the precision of the individual measurements. However, we have repeatedly assessed the precision of our scoring; see Methods and Materials and Tate et al. 2006, 2010; Rai et al. 2014.

Figure 3. Time course of Gln3-Myc13 localization in gtr1Δ (FV406) cells following nitrogen starvation (panels A and B), transfer from nitrogen-replete to nitrogen-limiting medium (panels C and D), and resupplying excess nitrogen to all of the cultures (panels A-D). The experimental format and treatment of the samples were identical to those in Figure 2.

Figure 4. Time course of Gln3-Myc13 localization in gtr2Δ (FV359) cells following nitrogen starvation (panels A and B), or transfer from nitrogen-replete to nitrogen-limiting medium (panels C and D), and resupplying excess nitrogen to all of the cultures (panels A-D).

Figure 5. Time course of Gln3-Myc13 localization in ego1Δ (FV515) cells following nitrogen starvation (panels A and B), or transfer from nitrogen-replete to nitrogen-limiting medium (panels C and D), and resupplying excess nitrogen to all of the cultures (panels A-D).

Figure 6. Time course of Gln3-Myc13 localization in ego3Δ (RR216) cells following nitrogen starvation (panels A and B), or transfer from nitrogen-replete to nitrogen-limiting medium (panels C and D), and resupplying excess nitrogen to all of the cultures (panels A-D).

Figure 7. Gtr2 and Ego3 are required for nuclear Gln3-Myc13 localization for steady state growth in minimal-proline medium. Wild type (TB123), gtr1Δ (FV406), gtr2Δ (FV359), ego1Δ (FV515) and ego3Δ (RR216) were grown of a density of A600nm = 0.5-0.55 in YNB-proline medium. Intracellular distribution of Gln3-Myc13 was then determined in each of the cultures as described in “Materials and Methods”.

Figure 8. Transcriptional responses to nitrogen excess, limitation and starvation are unaffected in the Gtr/Ego complex mutants. Total RNA was isolated from GLN3-MYC13 wild type (TB123), gtr1Δ (FV406), gtr2Δ (FV359), ego1Δ (FV515) and ego3Δ (RR216) cells grown in YNB-glutamine medium to mid-exponential phase, transferred to nitrogen-free medium or to proline-containing medium, with or without glutamine re-feeding. Incubation times are indicated on the figure. DAL5 (panel A) and GDH2 (panel B) mRNA levels were quantified as described in “Materials and Methods”.
### Table 1
Saccharomyces cerevisiae strains used in this work.

| Strain  | Pertinent genotype     | Complete genotype                                                                 |
|---------|------------------------|-----------------------------------------------------------------------------------|
| TB123   | Wild type Gln3-Myc\(^{13}\) | MATa, leu2-3, 112, ura3-52, trp1, his4, rme1, HMLa, GLN3-MYC\(^{13}\)[KanMX]     |
| FV359   | gtr2\(\Delta\)-Gln3-Myc\(^{13}\) | MATa, leu2-3, 112, ura3-52, trp1, his4, rme1, HMLa, GLN3-MYC\(^{13}\)[KanMX]\(\text{gtr2}\Delta::\text{natMX}\) |
| FV406   | gtr1\(\Delta\)-Gln3-Myc\(^{13}\) | MATa, leu2-3, 112, ura3-52, trp1, his4, rme1, HMLa, GLN3-MYC\(^{13}\)[KanMX]\(\text{gtr1}\Delta::\text{natMX}\) |
| FV515   | ego1\(\Delta\)-Gln3-Myc\(^{13}\) | MATa, leu2-3, 112, ura3-52, trp1, his4, rme1, HMLa, GLN3-MYC\(^{13}\)[HIS3]ego1\(\Delta::\text{natMX}\) |
| RR216   | ego3\(\Delta\)-Gln3-Myc\(^{13}\) | MATa, leu2-3, 112, ura3-52, trp1, his4, rme1, HMLa, GLN3-MYC\(^{13}\)[KanMX]ego3\(\Delta::\text{natMX}\) |

### Table 2
Primers used in strain constructions.

| Primer   | Sequence                                          |
|----------|---------------------------------------------------|
| EGO1-L1  | 5’-GTGTTCGACGGAACTGTGAA-3’                        |
| EGO1-L2  | 5’-GGGGATCCGACCCATTGCAGCAGCTTCAAGTCTGCG-3’        |
| EGO1-L3  | 5’-AACGAGCTCAATTCATCGATGAACCTTGTATAAATTGATG-3’   |
| EGO1-L4  | 5’-AGGATGTTTTCCCGGCAAATG-3’                      |
| EGO3-L1  | 5’-GCGAGTTATACGCAGCAAAACGGTATCCAAAAATATTGAAGCAATTGCTGTGACGT-3’ |
| EGO3-L2  | 5’-AGAAGCGCATGAAAAGGTGGCTCAGATAAAATTGTTATCCACATCGACTTAAACTTGACGT-3’ |
| GTR1-L1  | 5’-TCTCCCCTCCTCGGGTTGTG-3’                        |
| GTR1-L2  | 5’-GGGGATCCGACCCATTACTACAAATTGCTGAGTAAACGGTATTTGTTCT-3’ |
| GTR1-L3  | 5’-CGAGCTCGATATTACGCATGAGTGAGGTGAGTACGAGAACATTTCCGCGCATTG-3’ |
| GTR1-L4  | 5’-CCCGTTGGTGGCTTAATGACC-3’                       |
| GTR2-L1  | 5’-TCTACCATTGTTTATTTTACTTG-3’                    |
| GTR2-L2  | 5’-GGGGATCCGACCCATTGAGTGATGTTGAGTGATATTACCGTAGTCC-3’ |
| GTR2-L3  | 5’-CGAGCTCGATATTACGCATGAGTGAGGTGAGTACGAGAACATTTCCGCGCATTG-3’ |
| GTR2-L4  | 5’-GCTGTTGTAACCGTCCGTACG-3’                       |
|                      | Glutamine | Proline | Allantoin |
|----------------------|-----------|---------|-----------|
| **W.T. (TB123)**     | ![Image](A) | ![Image](B) | ![Image](C) |
| **gtr1Δ (FV406)**    | ![Image](A) | ![Image](B) | ![Image](C) |
| **gtr2Δ (FV359)**    | ![Image](A) | ![Image](B) | ![Image](C) |
| **ego1Δ (FV515)**    | ![Image](A) | ![Image](B) | ![Image](C) |
| **ego3Δ (RR216)**    | ![Image](A) | ![Image](B) | ![Image](C) |
Figure 2
Wild Type (TB123)

(A) Hrs After Onset of Nitrogen Starvation | Mins After Gln Addition

Gln3-Myc

DAPI

(B) Hrs After Onset of Nitrogen Starvation | Mins After Gln Addition

Percentage of Cells

Cytoplasmic | Nucl.-Cyto. | Nuclear

(C) Hrs After Transfer from Gln to Pro | Mins After Gln Addition

Gln3-Myc

DAPI

(D) Hrs After Transfer from Gln to Pro | Mins After Gln Addition

Percentage of Cells

Cytoplasmic | Nucl.-Cyto. | Nuclear
Figure 3

\(gtr1\Delta\) (FV406)

(A) Hrs After Onset of Nitrogen Starvation | Mins After Gln Addition
---|---
0 | 1
0.25 | 10
0.5 | 30
1 | 60
3 | 6
6 | 6

(B) Stem plots showing the percentage of cells at various time points. The x-axis represents hours after the onset of nitrogen starvation and minutes after Gln addition. The y-axis represents the percentage of cells.

(C) Hrs After Transfer from Gln to Pro | Mins After Gln Addition
---|---
0 | 1
0.25 | 10
0.5 | 30
1 | 60
3 | 6
6 | 6

(D) Stem plots showing the percentage of cells at various time points. The x-axis represents hours after transfer from Gln to Pro and minutes after Gln addition. The y-axis represents the percentage of cells.
Figure 4
gtr2Δ (FV359)

(A) Hrs After Onset of Nitrogen Starvation          Mins After Gln Addition

Gln3-Myc13

DAPI

(B) Percentage of Cells

Hrs After Onset of Nitrogen Starvation          Mins After Gln Addition

Cytoplasmic  Nucl.-Cyto.  Nuclear

(C) Hrs After Transfer from Gln to Pro          Mins After Gln Addition

Gln3-Myc13

DAPI

(D) Percentage of Cells

Hrs After Transfer from Gln to Pro          Mins After Gln Addition

Cytoplasmic  Nucl.-Cyto.  Nuclear
Figure 6

ego3Δ (RR216)

(A) Hrs After Onset of Nitrogen Starvation

(B) Hrs After Transfer from Gln to Pro

(C) Mins After Gln Addition

(D) Mins After Gln Addition

Gln3-Myc

DAPI

Percentage of Cells

Cytoplasmic  Nucl.-Cyto.  Nuclear

0  0.25  0.5  1  2  3  4  5  6  1  10  30  60

0  0.5  2  4  5  6  1  10  30  60

0  0.25  0.5  1  2  3  4  5  6  1  10  30  60

0  0.25  0.5  1  2  3  4  5  6  1  10  30  60

0  20  40  60  80  100

0  20  40  60  80  100

0  20  40  60  80  100

0  20  40  60  80  100
