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Genome-wide analysis of intracellular pH reveals quantitative control of cell division rate by pH$_c$ in *Saccharomyces cerevisiae*

Rick Orij[1], Malene L Urbanus[2], Franco J Vizeacoumar[2], Guri Giaever[3], Charles Boone[2], Corey Nislow[2], Stanley Brul[1] and Gertien J Smits[1*]

Abstract

Background: Because protonation affects the properties of almost all molecules in cells, cytosolic pH (pH$_c$) is usually assumed to be constant. In the model organism yeast, however, pH$_c$ changes in response to the presence of nutrients and varies during growth. Since small changes in pH$_c$ can lead to major changes in metabolism, signal transduction, and phenotype, we decided to analyze pH$_c$ control.

Results: Introducing a pH-sensitive reporter protein into the yeast deletion collection allowed quantitative genome-wide analysis of pH$_c$ in live, growing yeast cultures. pH$_c$ is robust towards gene deletion; no single gene mutation led to a pH$_c$ of more than 0.3 units lower than that of wild type. Correct pH$_c$ control required not only vacuolar proton pumps, but also strongly relied on mitochondrial function. Additionally, we identified a striking relationship between pH$_c$ and growth rate. Careful dissection of cause and consequence revealed that pH$_c$ quantitatively controls growth rate. Detailed analysis of the genetic basis of this control revealed that the adequate signaling of pH$_c$ depended on inositol polyphosphates, a set of relatively unknown signaling molecules with exquisitely pH sensitive properties.

Conclusions: While pH$_c$ is a very dynamic parameter in the normal life of yeast, genetically it is a tightly controlled cellular parameter. The coupling of pH$_c$ to growth rate is even more robust to genetic alteration. Changes in pH$_c$ control cell division rate in yeast, possibly as a signal. Such a signaling role of pH$_c$ is probable, and may be central in development and tumorigenesis.

Background

Cytosolic pH (pH$_c$) determines the relative protonation state of all weak acid compounds of the cytosol and affects many, if not all, processes in the cell. It is known to affect redox equilibria [1], metabolic rates and energy storing or generating gradients [2,3], protein interactions [4-7], as well as signal transduction [8-10], and it is an important thermodynamic constraint on metabolic reactions [11]. Furthermore, pH$_c$ homeostasis is intricately connected with that of other cations, with membrane potentials, and therefore with cellular energy homeostasis [12,13].

Only relatively recently, with the development of green fluorescent protein (GFP)-based pH sensors, has it become possible to study pH in live, unperturbed cells, in an organelle specific fashion [14-18]. The use of this technology is generating increased insight into intracellular pH (pH$_i$) control, such as the interaction between plasma membrane and vacuolar proton transport [16,19], and nutrient signaling and pH$_i$ control [10]. That pH$_c$ itself directly controls signal transduction and cellular transcriptional responses to environmental conditions was shown recently. A decrease of pH$_c$ from 7 to 6.8, induced by carbon source depletion, abolishes the interaction of the transcription factor Opi1p with phosphatidic acid through direct protonation of the phosphate headgroup of this membrane phospholipid [7]. Considering the known and emerging importance of this parameter, it is remarkable how little is understood of the genetic basis

* Correspondence: G.J.Smits@uva.nl
[1]Molecular Biology and Microbial Food Safety, Swammerdam Institute for Life Sciences, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, the Netherlands
Full list of author information is available at the end of the article

of its control. We decided to carefully study pH_c in growing cultures of the yeast deletion collection [20], to determine the genes that are involved in pH_c control during normal, fermentative growth on glucose. This revealed that pH_c is controlled by the interplay of cation pumps and the mitochondria, even in fermenting cultures. Additionally, we determined that pH_c quantitatively controls yeast cell division rate. Remarkably, deletion of 19 genes could abolish this control, suggesting that pH_c functions as a true signal, transmitting information about external conditions to control cellular decisions.

Results

pH_c is dynamic during growth

Cytosolic pH of yeast cultures is not a static but a highly dynamic parameter. Re-addition of glucose to starved cells leads to a rapid acidification of the cytosol in approximately 30 seconds followed by an alkalinization to neutral pH before growth recommences [18,21,22]. This rapid acidification, which is believed to be the cause of initiation of glycolysis [10,23], is followed by an alkalinization as a result of the activation of the plasma membrane H^+-ATPase Pma1p [24,25].

We assessed pH_c in growing yeast cultures under batch conditions to reveal that pH_c is not constant during growth. pH_c was neutral in the beginning of the exponential growth phase, and then gradually dropped approximately 0.3 pH units in mid- to late exponential phase, before glucose was depleted. Upon glucose depletion pH_c decreased to 5.5 (Figure 1a). We determined that the gradual reduction of pH_c from 7 to 6.7 during growth of the culture was a response to changes in the cellular environment, rather than a property of the cultured cells themselves: we took cell and culture supernatant samples from the beginning of the growth phase (where pH_c was 7.0 and the specific growth rate 0.48 h^{-1}) and at the end of the growth phase, just prior to glucose depletion, when the pH_c and growth rate were decreased. Inoculation of old cells in fresh medium rapidly (within a minute) restored pH_c to 7.0, while the addition of old, depleted culture supernatant to fresh cells set pH_c to 6.85 (Figure 1b). Nutrient depletion at the end of the growth phase was not the cause of this intracellular acidification, as supplementation of the conditioned medium with all fresh nutrients did not restore pH_c. Rather, it appeared that the yeast cells had conditioned the medium such that it now induced a low pH_c. We determined the concentrations of secreted ethanol and weak organic acids such as succinate, acetate, and pyruvate in the conditioned medium. Addition of the same quantity of these compounds to fresh medium did not lead to a decreased pH_c (our unpublished data). In contrast, aeration of the conditioned medium relieved its pH_c lowering effect, strongly suggesting that the main

component of the acidifying activity was dissolved CO_2, acting as a weak acid to acidify the cytoplasm (Figure 1c). Similar acidification occurred even in well shaken Erlenmeyer flask cultures, usually considered properly aerated.

Identification of pH_c mutants

To understand the genetic basis of the control of this central cellular parameter, we performed a genome-wide analysis of pH_c in growing cultures of the deletion mutant array (DMA) [20]. The pH-sensitive GFP ratiometric pHluorin [17,18] was introduced in 4,308 haploid mutants of the DMA using synthetic genetic array (SGA) methodology [26]. All mutants were screened in duplicate during mid-exponential phase in microplates at 30°C in medium buffered at pH 5.0. Candidates were selected based on their deviation from the parent pH_c of 7.08 ± 0.05 (measured in 2,088 biological replicates; Figure 2a). These candidates, along with 432 slow growing mutants that were separately arrayed because they are usually lost during the growth and selection steps of the SGA procedure, were analyzed in six additional biological replicates to obtain statistically valid ($P < 0.01$) hits (Additional File 1, Table S1). Out of a total of 4,740 mutants screened, we identified 177 mutants with significantly high (104) or low (73) pH_c. All significant mutants were microscopically evaluated for aberrant GFP distribution. No indications of aggregation or cell lysis were found. The pH_c of these mutant strains was never more than 0.3 pH units below or 0.5 pH units above parent pH_c. The re-screening of the candidate hits allowed for an accurate false negative estimation (Figure 2b): we applied the criteria for the selection of candidates from the original duplicate screening to the separately arrayed slow grower array, and used this to determine the false negative rate in the initial screening of the 4,308 DMA mutants. This revealed that we successfully identified 86% of the genes with low pH_c and 95% of the genes with high pH_c.

We failed to identify several mutants that we expected to have an altered pHc. We separately tested several of these, among which were *trk1*, *trk2*, *nha1*, *nhx1*. In our analysis, cells growing on defined media with glucose available, these mutants did not have a significantly deviating pH_c. We have shown before [7] that, in such conditions, a *PMA1* hypomorph *ygl007c* and a *trk1* deletion strain do not have a pH_c phenotype, and that such a phenotype only becomes apparent when the cells are challenged with low external pH. At an external pH (pH_{ex}) of 3.0, *trk1*, *trk2*, *nha1* and *nhx1* had pH_c values of 6.93 ± 0.02, 7.02 ± 0.06, 6.99 ± 0.01 and 7.08 ± 0.10, respectively (with average Z-values of -2.77, -0.99, -1.32 and 0.02), which indicates a significant pH_c deviation for *trk1* only. This suggests that, although the gene products
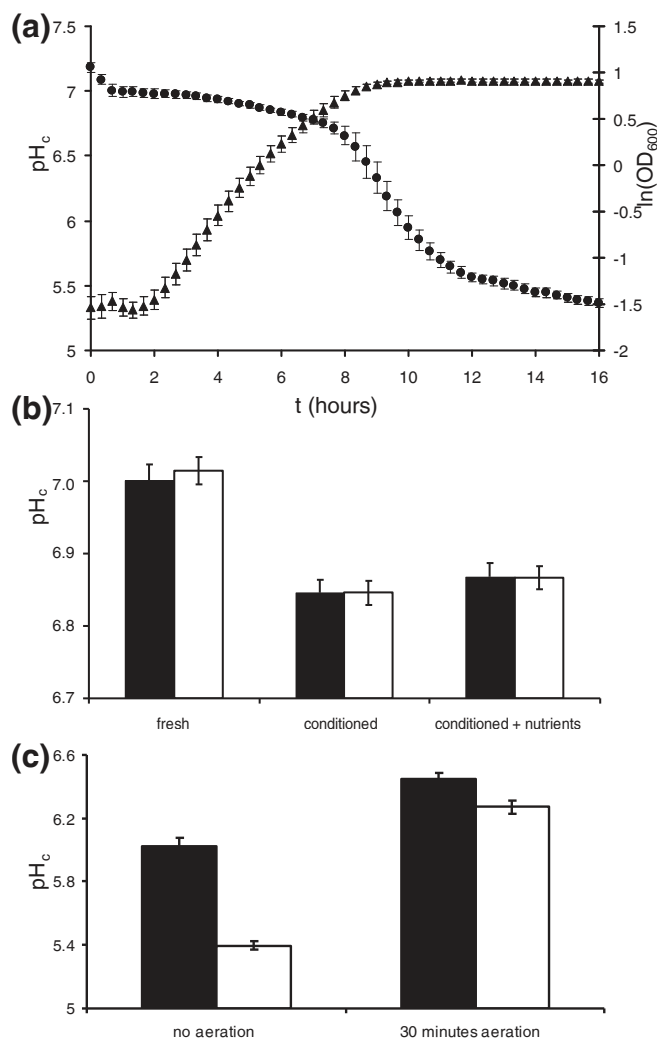
Figure 1 pHc dynamics during growth. **(a)** Growth (filled triangles) and pHc (filled circles) were monitored during growth on glucose in microplates. Data points represent the average of 24 biological replicates, error bars represent standard deviations. **(b)** Medium exchange experiments show that the pHc decrease during the growth phase is determined not by the state of the cell, but the environmental conditions generated in the culture medium. Early and late log phase cells were harvested and resuspended in fresh medium, late log medium, and late log medium supplemented with all nutrients. **(c)** CO_2 causes pHc acidification. Strains were grown for 10 hours in either aerobically (closed bars) or anaerobically (open bars). After 10 hours the pHc of both strains was determined. Cultures were subsequently aerated for 30 minutes by bubbling air through the culture followed by pHc determination.

have well defined functions in cation homeostasis, deletion of these genes when sufficient cellular energy can be generated does not cause a pHc decrease.

Profiling of mutants with aberrant pHc under additional stress conditions reveals involvement of vacuole and mitochondria in pHc control

The pHc mutants were analyzed for functional enrichment based on their gene ontology terms (Figure 2c). As expected, functional groups related to proton and cation homeostasis were strongly enriched, including vacuolar proton pumping [16]. The genes we identified in these functional groups are required to maintain pHc, and we

expected, therefore, that these and our other pHc mutants would have difficulty to control pHc during growth in media conditions that were close to the lower and upper tolerance external pH (pH_{ex}) limits for yeast growth. Most *Saccharomyces* strains will grow at pH_{ex} values of 2.5 to 8.5, and the kinetics of growth and fermentation are not affected between pH 3.5 and 6.0 because of the tight control of intracellular pH [27]. We decided upon media pH values of 3.0 and 7.5, which induce considerable stress, yet allow for significant cell growth and pHluorin expression. Wild-type pHc is unaffected by cultivation at a pH_{ex} of 3.0 compared to a pH_{ex} of 5.0, and slightly increased during cultivation at a pH_{ex}
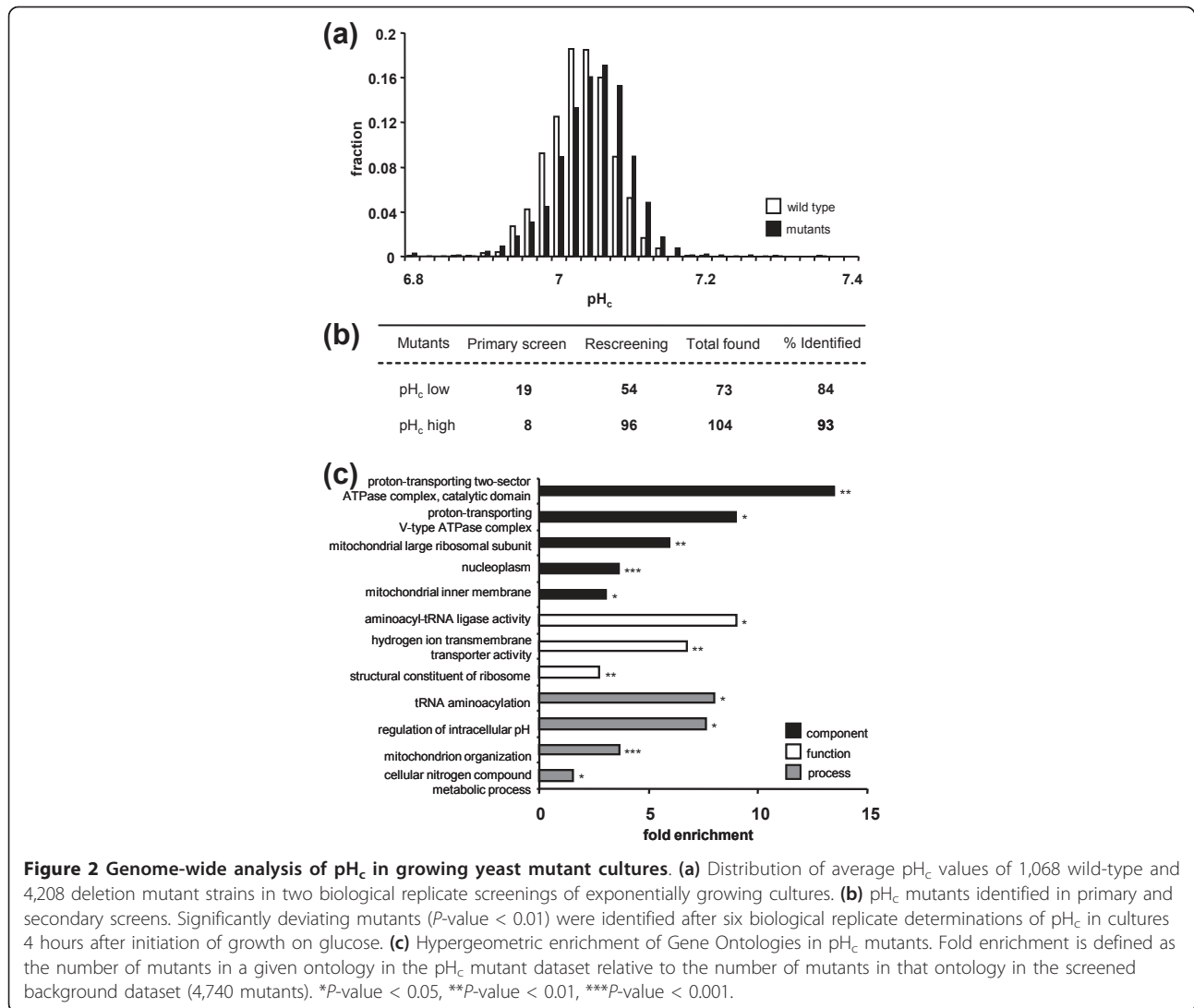
Figure 2 Genome-wide analysis of pH$_c$ in growing yeast mutant cultures. **(a)** Distribution of average pH$_c$ values of 1,068 wild-type and 4,208 deletion mutant strains in two biological replicate screenings of exponentially growing cultures. **(b)** pH$_c$ mutants identified in primary and secondary screens. Significantly deviating mutants (*P*-value < 0.01) were identified after six biological replicate determinations of pH$_c$ in cultures 4 hours after initiation of growth on glucose. **(c)** Hypergeometric enrichment of Gene Ontologies in pH$_c$ mutants. Fold enrichment is defined as the number of mutants in a given ontology in the pH$_c$ mutant dataset relative to the number of mutants in that ontology in the screened background dataset (4,740 mutants). **P*-value < 0.05, **P-value < 0.01, ***P-value < 0.001.

of 7.5 (Additional file 1). We identified 20 mutants that had a low pH$_c$ at all pH$_{ex}$ conditions, and 19 that had a consistently high pH$_c$ (Figure 3a; Additional file 1), and found that these 39 were enriched for global growth-related functions such as RNA polymerase II-mediated transcription and mitochondrial translation. Remarkably, we did not find a clear indication that loss of proton homeostasis mechanisms led to a pH$_c$ phenotype that became much more sensitive to pH$_{ex}$ changes; if we define a pH-fragile mutant as one that has a high pH$_c$ at a pH$_{ex}$ of 7.5, but a low pH$_c$ at a pH$_{ex}$ of 3.0, we could identify only four mutants (*rpl31a∆*, *gpm2∆*, *pet111∆*, and *erg28∆*) that had lost the capacity to maintain pH$_c$ with respect to pH$_{ex}$, which is less than could be expected by coincidence.

Mitochondrial proton pumping functions, as well as functions related to mitochondrial biogenesis and inheritance, were strongly enriched, despite the fact that respiration is not required for energy generation during fermentative growth on glucose. To see if this mitochondrial role in pH$_c$ homeostasis is related to the role of the mitochondria in energy generation, we assessed the pH$_c$ of all pH$_c$ mutants during respiratory growth in glycerol- and ethanol-containing medium (Figure 3b). The average parent pH$_c$ on respiratory medium was reduced by 0.27 pH units, and similarly almost all mutants tested had a lower pH$_c$ on respiratory medium. However, only 13 of the 73 strains with a significantly low pH$_c$ on glucose were also significantly low during respiratory growth, when compared to wild type. Eleven of these (*msf1∆*, *aep3∆*, *pet100∆*, *atp7∆*, *mss116∆*, *mtg2∆*, *mnn9∆*, *plc1∆*, *dep1∆*, *rpl21a∆*, and *snf2∆*) had extremely low growth rates on glycerol/ethanol medium, and were indeed previously shown to have severely reduced growth on respiratory media or to be respiratory growth deficient [28-30]. Only *vps66∆* and *kre28∆* had low pH$_c$ on
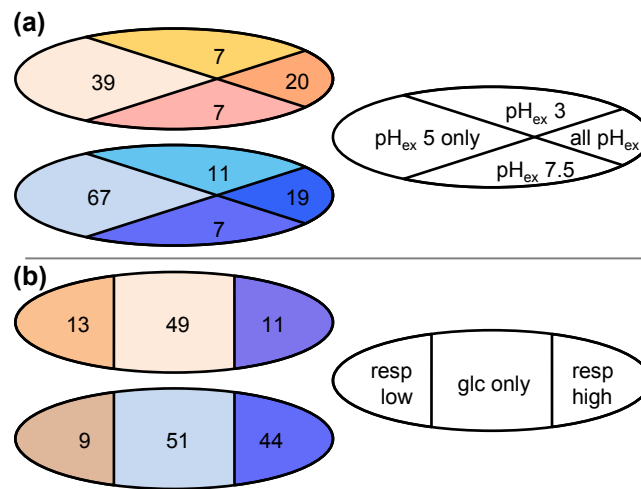
Figure 3 Profiling of mutants with aberrant pH$_c$. (a, b) Venn diagrams of mutants with significantly low pH$_c$ (top) or significantly high pH$_c$ (bottom) during growth at the normal pH$_{ex}$ of 5.0 and during growth at extreme pH$_{ex}$ values of 3.0 and 7.5 (wild-type pH$_c$ of 7.08 ± 0.03 and 7.20 ± 0.15, respectively) (a), or with significantly low pH$_c$ (top) or significantly high pH$_c$ (bottom) during growth in medium with 2% glucose, upon growth on 2% ethanol and 2% glycerol as respiratory carbon source (wild-type pH$_c$ of 6.93 ± 0.06) (b).

respiratory and fermentative carbon sources but were able to grow relatively normally on respiratory media compared to fermentative conditions. The other 60 strains with low pH$_c$ during fermentative growth had normal or even high pH$_c$ during respiratory growth. This apparent rescue of most low pH$_c$ phenotypes shows that pH$_c$ regulation in fermenting cells is very different from that in respiring cells, as suggested before [18]. Together, our data establish the major importance of the vacuole and mitochondria in pH control, and reveal these organelles as central controllers of cytosolic ion concentrations [16,19,31,32].

pH$_c$ controls growth rate

Because many growth-related functions were enriched in the deviant pH$_c$ mutants, we decided to directly analyze the relationship of pH$_c$ and growth rate in detail. We assessed the relation between growth rate and pH$_c$ in the parent strain and found a strong correlation between pH$_c$ and growth rate (μ) over all time points of the experiment after the cells had resumed growth, which could be recapitulated as a linear relation between log(μ) and pH$_c$ (R^2 = 0.99 over all the time points between t = 2 h and t = 16 h from 24 biological replicates) (Figure 4a). Even after glucose depletion (around 8 hours cultivation time in this experiment), when the growth rate is gradually reduced to 0 and the pH is reduced to approximately 5.5, the relationship of pH$_c$ and growth rate is maintained. Only the time points before t = 2 h (grey dots in Figure 4a) do not fit the relationship but cluster around pH 7,0, because pH$_c$ already increased upon re-inoculation in fresh medium before growth was observable. The strong correlation of two such central parameters of cellular functioning

raises the question if pH$_c$ might determine growth rate, growth rate pH$_c$, or whether there is a process that controls both. To establish causality we first note that effects on pH$_c$ are rapid, and precede alterations of growth rate. First, at the beginning of growth, pH$_c$ already increases to 7.0 before growth of the culture starts (Figures 1 and 4a). Second, we established that the gradual reduction of pH$_c$ from 7 to 6.7 during growth of the culture is rapidly induced by the cellular environment at those times, rather than a property of the cells themselves (Figure 1b). The rate at which the pH$_c$ dropped when cells were exposed to this conditioned medium suggests that the pH$_c$ drop precedes the drop in growth rate. The hypothesis that growth rate controls pH$_c$ is also contradicted by the observation that most slow growing mutants (276 out of 432 tested) had a normal pH$_c$ (Additional file 2). Together, these data render it highly unlikely that growth rate controls pH$_c$.

To positively demonstrate that pH$_c$ dictates growth rate, we postulated that it should then be possible to titrate pH$_c$, which should allow us to set the growth rate to the values predicted by the quantitative relationship previously determined (Figure 4a). In wild-type strains, the plasma membrane ATPase ensures pH$_c$ control in different pH$_{ex}$ conditions [18,33], and titration of pH$_{ex}$ leads to only minute changes in pH$_c$ (Figure S1 in Additional file 3). However, in a mutant with a hypomorphic allele of *PMA1* (*pma1-007*), with approximately 50% reduced plasma membrane ATPase levels and activity [7,34], acidification of the culture medium with HCl from pH 5.0 to pH 2.0 resulted in a pH$_c$ decrease from 7.0 to 6.2 (Figure 4b), while nutrient abundance is not affected. Cultivation in these conditions revealed that growth was also progressively decreased (Figure 4c). Direct comparison of growth
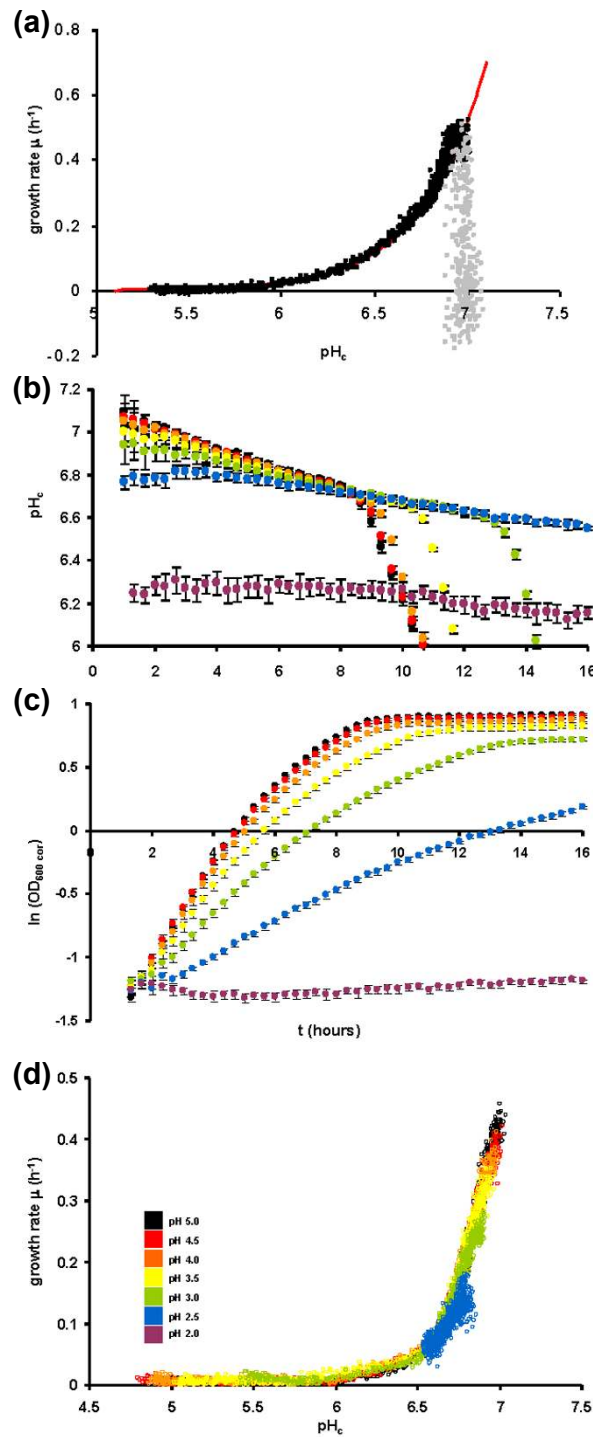
Figure 4 Cause and effect in the relationship between pH$_c$ and growth rate. **(a)** Wild-type pH$_c$ plotted against growth rate μ. Dots represent the time course data of 24 independent biological replicates of full 16 hour growth curves. The data were fit to an exponential dependence of μ on pH$_c$ (Additional file 1). Grey dots represent points from the first 1.5 hours after inoculation into fresh medium.
(b-d) Titration of pH$_c$ sets growth rate. Strain *pma1-007* was cultivated in unbuffered, pH$_{ex}$ controlled batch fermentors, and titrated to pH$_{ex}$ values indicated using strong acid (HCl). Figures represent pH$_c$ (b), growth (c), and pH$_c$ plotted against growth rate μ (d). Data points represent the average of 12 technical replicates, error bars represent standard deviations.

rate and pH_c revealed that the growth rate was decreased exactly to the extent expected from the lowering of pH_c (Figure 4d), thus showing that pH_c determines the growth rate.

pH_c appears to have a signaling role

Now that we have determined that pH_c controls growth rate, we could analyze the genes that are required for maintaining this relationship. Analysis of all pH_c mutants with respect to this same pH_c-growth rate relationship revealed three distinct classes of mutants (Figure 5a; Figure S2 in Additional file 3; Additional file 4). Category I had a pH_c that significantly deviated from wild type pH_c during exponential growth, but the normal relationship between pH_c and growth rate was maintained. Wild-type strains analyzed of course cluster with this category. The genes mutated in this case can be considered upstream of pH_c, and thus control pH_c. The effect they have on growth rate is through their effect on pH_c only. This category contained the majority of the mutants identified in our screen (92 out of 173 mutant strains). Most of the cation and pH homeostasis-related genes identified in the screen fell into this category, as well as many involved in mitochondrial translation and oxidative phosphorylation (Figure 5b). Category II (62 out of 173 mutant strains) had a significantly low growth rate compared to the pH_c, which suggests that these mutations limit growth rate though mechanisms other than pH_c. Indeed, many of these mutants had a high pH_c in our screen (45 out of 62), even while growth rate was reduced compared to wild-type. We selected a set of slow growing mutants with deletions in genes involved in ribosome biogenesis and central carbon metabolism that do not exhibit aberrant pH_c, and used the same analysis of growth rate/pH_c relationship, to show that these would fall into the same category (Figure S3 in Additional file 3). Indeed, very general functions are enriched in this cluster, such as polymerase II-mediated transcription, and ATP generating processes (Figure 5c). Any effect of such functions on pH_c is likely indirect - for instance, because expression of pH regulatory genes is RNA polymerase II mediated [35,36], or proton homeostatic processes depend on ATP [2,3]. Finally, mutants in category III had a low pH_c and regularly also a low growth rate, but, more importantly, their growth rate was no longer as constricted by this low pH_c as in the wild type. Only 19 of 173 mutants fall into this category (Table 1), suggesting a coupling that is robust to mutations in single genes. The fact that the deletion of single genes can lead to (partial or full) evasion of the control of pH_c over growth rate shows that pH_c is not somehow rate limiting for growth because of the complex integrated effect of protonation of many cellular components. This strongly suggests that pH_c

functions as a true signal that must be transduced. Although again the genes in this category were enriched for basic mitochondrial functions, we also found enrichment for genes involved in signal transduction and inositol pyrophosphate metabolism (Figure 5d). These high-energy metabolites are proposed to be involved in the sensing of a cell's energy status [37]. Interestingly, $kcs1\Delta$ and $plc1\Delta$, involved in inositol pyrophosphate metabolism, both show growth that is no longer limited by pH_c as it is in the wild type (Figure 5e). For $kcs1\Delta$, this entails a growth rate of 0.30 h^{-1} instead of the expected 0.18 h^{-1} at a pH_c of 6.7, and the difference is most apparent at relatively normal pH_c values. For $plc1\Delta$ the phenotype is even more striking, with growth rate being more or less constant (although never very high) until pH_c values of 5, below which growth suddenly collapses. These two mutants are both among the mutants with the lowest pH_c in the screen (Additional file 1). The pH dependence of the charge of the many phosphates on inositol poly- or pyrophosphates renders these metabolites exquisitely suitable for pH_c sensing. Three other mutants in the inositol pyrophosphate synthesis pathway, $vip1\Delta$ and $ipk1\Delta$ (deletion of genes encoding enzymes responsible for pyrophosphorylation of inositol hexakisphosphate (InsP6) at the 1-P or 3-P position) and $ddp1\Delta$ (deletion of the gene encoding the phosphatase that removes the pyrophosphates) [38,39], did not affect pH_c or pH_c signaling to growth rate (Figure S4 in Additional file 3).

Discussion
Complex control of a simple parameter

It is becoming apparent that pH_c is controlled not just by simply pumping protons out of the cytosol into the vacuole or across the plasma membrane. The pH of the various compartments is heavily influenced by that of others [16]. Vacuolar ATPases are not only important for maintenance of the low pH in the secretory pathway, but also for control of cytosolic pH. This could be a buffering activity, a transient and rapid mode of removing protons from the cytosol, to be made permanent by true proton efflux. It should be noted, however, that a transient storage of protons in the secretory pathway or the vacuole conserves the energy in the cell as a membrane potential. Most of the components of the vacuolar ATPases have been identified based on the *vma* phenotype, which comprises the inability to grow at high extracellular pH and at high Ca^{2+} concentrations [40,41]. It is remarkable, therefore, that not all *vma* mutants have a pH_c phenotype at a pH_{ex} of 5.0, and of the ones that do, not all have a pH_c phenotype at a pH_{ex} of 7.5 (2 out of 7). Similarly, we found very little correlation between our screen for pH_c and a recent screen for mutations leading to deviating vacuolar pH, although conditions were different [42].
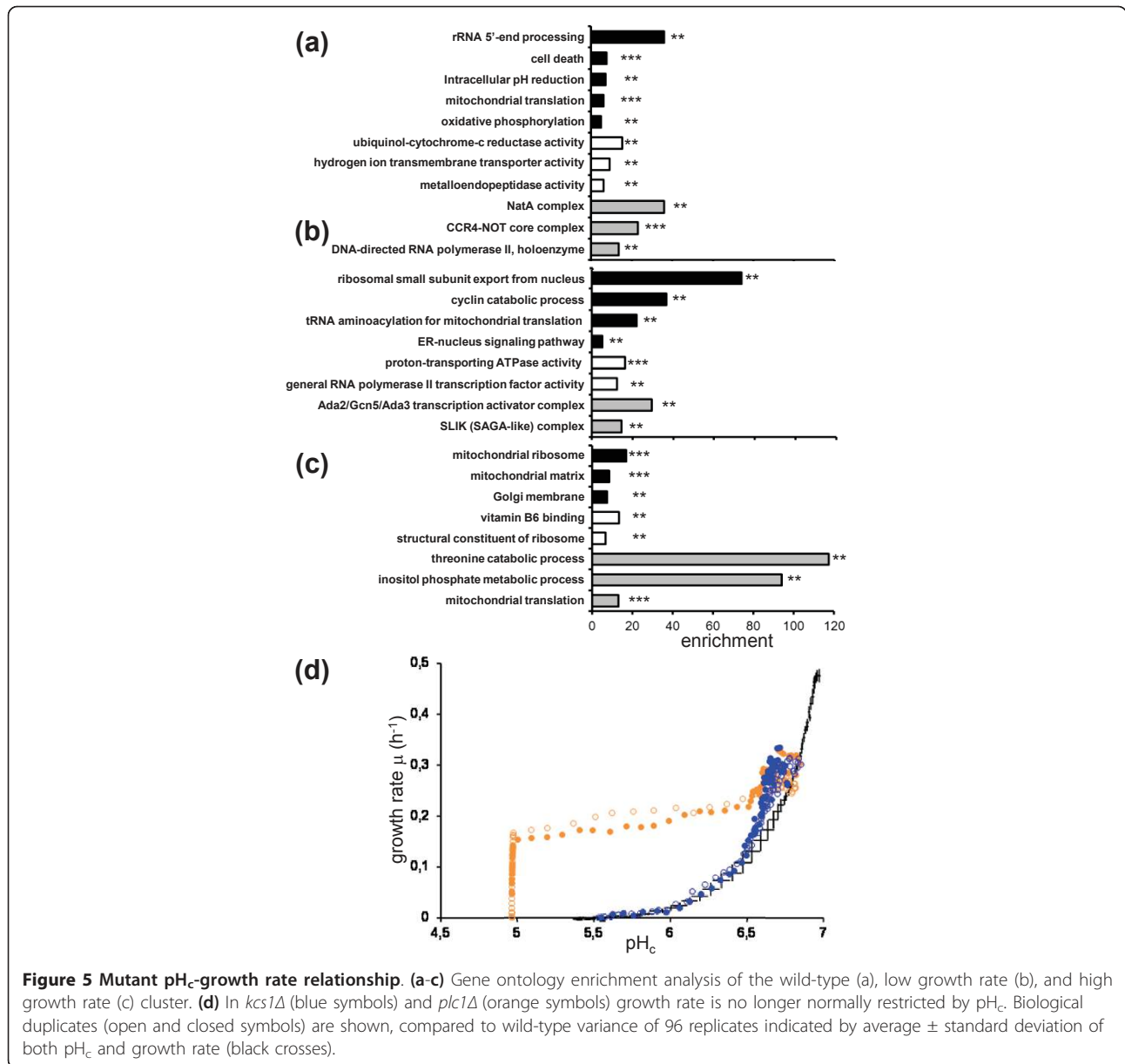
Figure 5 Mutant pH$_c$-growth rate relationship. **(a-c)** Gene ontology enrichment analysis of the wild-type (a), low growth rate (b), and high growth rate (c) cluster. **(d)** In *kcs1Δ* (blue symbols) and *plc1Δ* (orange symbols) growth rate is no longer normally restricted by pH$_c$. Biological duplicates (open and closed symbols) are shown, compared to wild-type variance of 96 replicates indicated by average ± standard deviation of both pH$_c$ and growth rate (black crosses).

This suggests that even if the mechanisms for pH$_c$ control share components with those for vacuolar pH control, the organelles control their pH independently.

While the role of vacuolar proton pumping in pH$_c$ homeostasis has been relatively well studied, the important role of the mitochondria is novel. In an analysis of mutations affecting the 'ionome' of yeast, a similar enrichment of both vacuolar and mitochondrial genes was observed [31], suggesting that the homeostasis of cations in general requires the proper function of both organelles. However, this analysis does not distinguish the organelle-specific ion concentrations. A role for mitochondria in pH$_c$ homeostasis is less surprising if one considers the fact that proton translocation over the mitochondrial inner membrane is the driving force for energy generation in mitochondria. However, in the glucose-rich conditions of our screen the mitochondrial respiratory chain is not required for energy generation in yeast. Still, we identified a large number of mutants in mitochondrial genes in which pH$_c$ was affected. The genes were classified as part of the proton translocating machinery and the mitochondrial respiratory chain, but also as involved in mitochondrial translation and biogenesis. The same mutations did not necessarily affect pH$_c$ in respiratory conditions, which suggests that the role of these genes in pH$_c$ homeostasis is indeed not linked to energy generation.

Clearly, the control of pH$_c$ in yeast, and in other eukaryotes [32,43] is distributed over various organelles, as is

Table 1 Mutations that reduce growth control by pH$_c$

Category	Gene	ORF	Absolute pH$_c$[a]	GO process
Inositol polyphosphates	PLC1	YPL268W	6.92 (0.035)	Inositol phosphate biosynthetic process
	KCS1	YDR017C	6.76 (0.047)	Inositol phosphate biosynthetic process
Signal transduction	LCB5	YLR260W	6.99 (0.034)	Calcium-mediated signaling
	RHO5	YNL180C	7.02 (0.025)	Rho protein signal transduction
Lipid synthesis	CAX4	YGR036C	6.93 (0.057)	Lipid biosynthetic process
	PDX3	YBR035C	6.99 (0.025)	Fatty acid metabolic process
Vesicular transport	RGP1	YDR137W	6.92 (0.031)	Retrograde transport, endosome to Golgi
	CLC1	YGR167W	7.01 (0.049)	Endocytosis
Mitochondria	RSM24	YDR175C	7.01 (0.024)	Mitochondrial translation
	MRPL27	YBR282W	7.00 (0.019)	Mitochondrial translation
	MRPL16	YBL038W	6.97 (0.028)	Mitochondrial translation
	MRPL37	YBR268W	6.98 (0.032)	Mitochondrial translation
	MRPS5	YBR251W	7.00 (0.027)	Mitochondrial translation
Various	MSS2	YDL107W	7.00 (0.035)	Protein insertion
	ILV1	YER086W	6.98 (0.035)	Isoleucine biosynthetic process
	REF2	YDR195W	6.97 (0.072)	mRNA processing
	CYC8	YBR112C	7.00 (0.032)	Chromatin remodeling
Unknown	AIM44	YPL158C	6.97 (0.024)	Biological process unknown

[a]Wild-type pH average is 7.08 ± 0.05. Mutants were clustered according to pH$_c$ with respect to growth rate (Materials and methods) and grouped according to functionally related gene ontology (GO) processes.

control of organellar pH. Also, the same functions are not responsible for pH$_c$ control in different conditions. This shows that pH$_c$ is a seemingly simple outcome of diverse and intricate regulation. This renders pH$_c$ an excellent signal of cellular status.

pH$_c$ as a signal integrating multiple environmental cues to control growth

In yeast it has long been known that pH$_c$ transiently responds to the addition of nutrients [18,23]. The transient pH$_c$ reduction upon glucose addition plays a role in the activation of the nutrient signaling, growth-promoting activation of protein kinase A [44]. How exactly pH$_c$ functions in the activation of protein kinase A is not yet fully understood, but it is clear that a lowered pH$_c$ promotes the activity of the adenylate cyclase Cyr1p through the activity of Ira2p and Ras2p [45], and possibly also the increase in the affinity of Cyr1p for ATP upon a decrease in pH$_c$ [46]. Additionally, the gradual decrease of pH$_c$ upon glucose depletion was shown to lead to inactivation of protein kinase A, through the disassembly of the vacuolar proton ATPases [10,19]. Decrease of pH$_c$ upon glucose depletion also affects other signal transduction pathways. The activation of inositol biosynthetic gene transcription upon inositol depletion is inhibited in the absence of a proper energy source, through direct control of the activity of the transcriptional inhibitor Opi1p. This inhibitor is recruited to phosphatidic acid in membranes upon inositol depletion, directly binding to the negatively charged phospholipid. Upon pH$_c$ decrease the phosphate headgroup of

the phospholipid is protonated, and Opi1p is released [7,47]. Therefore, as phosphates can be protonated at physiological pH$_c$ values, and this can affect interactions with proteins, it is very likely that other phosphate groups, such as those on proteins or those on small metabolites, may be protonated and this protonation could then affect recognition by enzymes or effector proteins.

We identified three different classes of pH$_c$ mutants with respect to their cell division rate. The three classes are suggestive of different modes of functional interference with the pH$_c$-growth rate interdependence (Figure 6). We reasoned that any integrated effect of increased protonation of many cellular compounds that would lead to reduced growth by reduced pH$_c$ could not possibly be relieved by deletions of single ORFs. The fact, therefore,
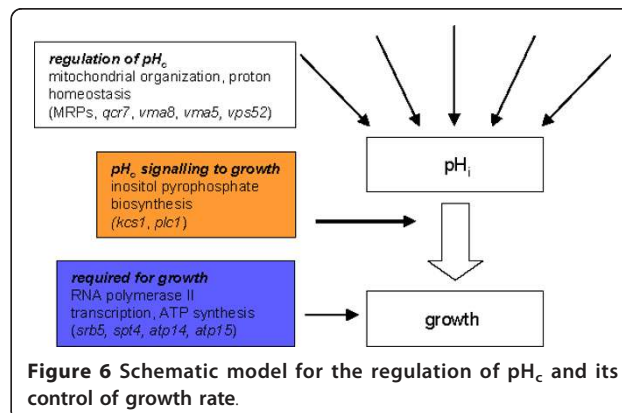

Figure 6 Schematic model for the regulation of pH$_c$ and its control of growth rate.

that strains mutated for a single gene have a higher than expected growth rate at a given pH_c based on the wild-type pH_c-growth rate relationship suggests that pH_c would function as a true second messenger [7,10], providing a signal that is improperly transduced in only a very small number of deletion strains. This last observation reveals that the tight control of growth rate by pH_c has evolved to become robust towards mutation, suggesting a high importance for cell or population fitness.

There is some evidence that pH_c varies during the cell cycle [48,49], but others have not been able to confirm this [50]. We show that pH_c quantitatively controls cell division rate. This may or may not be through cell cycle phase-dependent fluctuations. However, the fact that the changes in pH_c that we observed are in the range at which phosphate groups can be protonated, and the observation that such protonation can interfere with protein interactions [7], would allow many opportunities for pH_c interference with cell cycle signaling.

Previously, is has been shown that the Vip1p pyrophosphorylation of InsP6 is important for phosphate regulation of growth [51,52]. Interestingly, they reveal an inhibitory interaction of inositol pyrophosphate with the alternative CDK Pho85p, suggesting that such interactions could control kinase function [39,52]. We now show that Kcs1p-mediated pyrophosphorylation of InsP6 is important for pH_c signaling to set growth rate. It is tempting to speculate that these inositol pyrophosphate species appear to integrate signals from two major regulatory metabolites to determine growth rate. Indeed, a recent publication shows that inositol pyrophosphates contribute to cellular energy control [53], which is completely in line with the potential role of pH_c in nutrient status sensing. The authors find that inositol pyrophosphates affect mitochondrial function and fermentation rates to control cellular ATP content. This suggests that pH_c, inositol pyrophosphates and mitochondria function in an interdependent network to control cell division, resource distribution, and therefore potentially the balance between growth and cellular robustness [53-57].

The implications of pH_c as a signal for growth and more
In humans, pH_c changes have been implicated in tumorigenic transformation and tumor growth and metastasis [58-60]. The reduction of oxygen availability in solid tumors causes a fermentative metabolism, described already in 1927 by Otto Warburg. This change leads to the production of lactate, which causes the acidification of the tumor exterior space and the surrounding tissue. Tumor cells themselves almost invariably overexpress pH homeostatic pumps [61,62], leading to a selective advantage of transformed over non-transformed cells. Interestingly, our data suggest that the acidification of the non-transformed cells might result in a growth

suppression, but also that the slightly alkaline tumor cell cytosol might have growth promoting activity. Indeed, it has been suggested that tumor alkalinization might already be a very early event in tumorigenic transformation [60], and an even slightly increased replication rate of the alkalinized cells could benefit the accumulation of mutations promoting the transformation to malignancy.

Conclusions
Intracellular pH is a determinant of the properties of the molecules that make up living cells, and changes in pH_c rapidly and reversibly alter these properties. In yeast, pH_c is highly dynamic. Although intracellular pH is hardly affected by changes in extracellular pH, it is affected by the changes occurring during normal growth on glucose (Figure 1), and decreases as a consequence of CO_2 produced by cellular metabolism. In respiratory conditions, either after glucose depletion or during growth on glycerol- and ethanol-containing media, pH is much lower than during fermentation.

To understand the genetic basis of pH_c control during growth on glucose, we expressed the pH-sensitive GFP pHluorin in all strains of the yeast haploid deletion collection. We analyzed pH_c in liquid cultures of these strains during the exponential growth phase, and identified 177 mutants in which pH_c deviated significantly from wild type. The genes affecting pH_c control were strongly enriched for functions in the vacuole, including vacuolar proton pumping, but also for many mitochondrial functions, both in proton pumping and energy generation as well as in mitochondrial translation, biogenesis and inheritance. The fact that the same mutations did not lead to pH_c alterations in respiratory conditions indicates that pH_c control is condition dependent.

The most striking functional enrichment of the mutants was in very general growth-related functions. This could imply that pH_c is reduced as a consequence of reduction in growth rate or as a consequence of the metabolic conditions that lead to a reduced growth rate, but it also opens up the possibility that growth rate is reduced as a consequence of the reduction in pH_c. We note that while conditions that decrease growth rate also generally reduce pH_c, mutations that reduce growth rate do not necessarily reduce pH_c. Also, pH_c responds much more rapidly to external conditions than growth rate does. This suggests that either environmental conditions affect pH_c and metabolism that sets growth rate in parallel, or that pH_c in fact controls growth rate. To distinguish between these two options, we titrated pH_{ex} with strong acid in cultures of the plasma membrane ATPase hypomorph *pma1-007* that were otherwise unaffected in nutrient availability, and thereby reduced pH_c. This indeed led to a reduction of growth rate, quantitatively matching the relationship between pH_c and growth rate observed in wild type. This

proves that pH_c directly controls growth rate. A further analysis of the genetic basis of this control shows that it was relaxed in only 19 out of 177 mutants. The fact that pH_c control can be relaxed demonstrates that pH_c must function as a signal, whereas the fact that this signal is not properly sensed in only 19 mutants suggests that it has evolved to be robust to mutation, and therefore that it is central and important.

Indeed, there is evidence that similar control takes place in mammalian cells. Although a link between pH control and tumorigenesis has been established, most research in this field focuses on the acidified cell exterior, which appears to affect metastatic propensity [59]. Very little is known about the role of the alkalinization of the cell interior. However, recent literature also suggests that, in mammalian cells too, pH_c affects signal transduction [8,9] and cell division rate [63-65]. The fact that we now show that cytosolic pH controls growth rate, and functions as a signal to do so, suggests that the relevance of pH_c for growth control is conserved. How exactly this quantitative signal is controlled, and how it is transmitted to control the cell cycle, remains to be elucidated, but the involvement of the inositol pyrophosphate kinase Kcs1p, and of Plc1p gives promising targets for investigation.

Materials and methods
Growth conditions
In all experiments strains were pre-cultured by transfer from solid medium to liquid and incubated overnight (o/n) in round-bottom 96-well microplates (Greiner Bio-One, Kremsmünster, Austria)) stacked in microplate holders (New Brunswick, Enfield, CT, USA) under constant shaking at 30°C in 200 μl low fluorescence synthetic defined monosodium glutamate medium buffered at pH 5.0 with 25 mM sodium citrate. This medium contained 1.7 g yeast nitrogen base without (w/o) ammonium sulfate, w/o folic acid, w/o riboflavin (MP Biochemicals, Santa Ana, CA, USA), 1 g L-glutamic acid sodium salt hydrate (Sigma-Aldrich, St. Louis, MO, USA), 2 g drop-out amino acids supplement powder mixture without uracil (Sigma-Aldrich; Acros Organics, Geel, Belgium; Thermo Fisher Scientific, Waltham, MA, USA), 20 g glucose (Thermo Fisher Scientific) and 7.35 g sodium citrate (Sigma-Aldrich) per liter. For pH titration experiments, strains were cultivated in 500 ml batch fermenters with a steady airflow (500 ml minute^{-1}) and stirring rate (600 r.p.m.). The pH of batch fermenter cultures was controlled by titration with 0.2 M KOH using an Applikon ADI 1030 controller (Applikon Biotechnology, Foster City, CA, USA).

Strain construction
The plasmid pYES-P_{ACT1}-pHluorin [18] was introduced into the *MATα* query strain Y7092 and crossed with the *MAT*a DMA using SGA technology [26], yielding a complete set of mutants expressing pHluorin in the cytosol. Mutants that displayed a slow growing phenotype were set up in a separate array, allowing for longer incubation times on the different SGA media.

Metabolite analysis
Ethanol, acetate, succinate and pyruvate concentrations in the medium were determined by high pressure liquid chromatography. To this extent, 1.0 ml of sample was quenched with 100 μl of 35% perchloric acid followed by a neutralization with 55 μl of 7 M KOH. Samples were analyzed on a Phenomenex Rezex ROA-Organic Acid H^+ column (Phenomenex, Utrecht, The Netherlands) using 7.2 mM H_2SO_4 as mobile phase.

Screening for mutants with deviating pH_c
Unless stated otherwise, strains were pre-cultured o/n in microplates, diluted 10-fold into fresh medium in CELL-STAR black polystyrene clear-bottom 96-well microplates (Greiner Bio-One) and grown for 4 hours to ensure exponential growth. Plates were transferred to the Automated Cell, Compound and Environment Screening System (ACCESS) [66] and incubated at 30°C under constant shaking until automatically transferred to a Safire^2 microplate reader (Tecan, Männedorf, Switzerland). Optical density at 600 nm (OD_{600}) was measured followed by two fluorescence measurements at 390 nm and 470 nm excitation, both with 512 nm emission. After background subtraction the ratio of the two fluorescence measurements was compared to a calibration curve to determine pH_c as described in [18]. The array was screened twice and the 2,136 wild-type measurements were used to determine an average wild-type pH_c with according standard deviation. For every mutant in the array the average pH was converted to a Z-value defined as the number of standard deviations their measured pH was removed from the average wild-type pH_c in that replicate. Mutants with a Z-value at least higher than 2 or lower than -2 once and higher than 1 or lower than -1 in the other screening were selected as 'candidate hits' and combined with the slow grower array for additional confirmatory screening. Candidate hits and slow grower arrays were precultured as described and subjected to six rescreening runs where OD_{600} was measured with a SpectraMax Plus384 microplate spectrophotometer (Molecular Devices, Sunnyvale, CA, USA) followed by pHluorin fluorescence measurements using a SpectraMax Gemini XS microtitre plate spectrofluorometer (Molecular Devices). In each of these replicates, mutant pH_c values were converted to Z-values with respect to average and standard deviation of the wild-type population in that replicate. Significant scores were determined based on a two-tailed *t*-test of

these rescreening Z-values compared to the wild-type data ($P < 0.01$). For the analysis of the candidate hits based on the initial two genome-wide screens, for rigidity we did not include the pH_c values used for identification in the determination of significance. Doing so would have improved *P*-values for all pH_c mutants identified. For the slow growing mutants, to avoid bias originating from outliers, we performed a second analysis discarding the lowest and highest replicate value for each mutant (Jackknife), and retesting significance. Mutants with *P*-values > 0.1 in this analysis were discarded as significant. Both average Z-values and average pH_c values are presented. All mutants identified as significant were subjected to microscopical analysis: strains were grown in microplates for at least 2 hours as described above. After washing with phosphate-buffered saline, cells were transferred to agarose-coated glass slides. Images were obtained using a Canon A620 camera (Canon, Tokyo, Japan) on an Axiovert 40 CFL microscope with a Plan Neofluar 100 X/NA 1.3 oil objective (Carl Zeiss, Oberkochen, Germany), using Endow GFP narrow-band excitation filter sets (Chroma Technology, Bellows Falls, VT, USA) for fluorescent images.

Profiling of mutants with aberrant pH_c under additional stress conditions

After o/n inoculation in described conditions, cells were transferred to fresh medium buffered at pH 3.0 with 25 mM potassium citrate (Sigma-Aldrich), pH 7.5 with 25 mM MOPS (Sigma-Aldrich) or 2% ethanol and 2% glycerol as the carbon source. These experiments were conducted at least three times. Deviation was determined using *t*-tests comparing to the parent strain.

Hypergeometric distribution analysis

Enrichment of data sets for gene ontology terms was performed using the Yeast GO-term finder [67].

Growth curve analysis

After o/n inoculation hits identified in the initial screen were re-inoculated and subsequently monitored for 16 hours by OD_{600} and pH_c measurements every 10 minutes in a FLUOstar OPTIMA microplate reader (BMG labtech, Ortenberg, Germany). Growth data were corrected for the non-linearity of optical recording at higher cell densities similar to the method in [68], correcting OD_{600} values recorded in the microplate reader (OD_{obs}) to reflect linear OD_{600} determinations of the same cultures in a Novaspec II spectrophotometer (Pharmacia LKB Biochrom, Cambridge, UK) (always diluting the cultures to yield measured values between 0.05 and 0.3 OD units) using the formula $OD_{cor} = 1.1252(OD_{obs})^2 + 0.6808(OD_{obs}) - 0.0002$. Growth rates

of cultures in time were determined by calculating the slope of six consecutive data points (1 hour) of the entire $\ln(OD_{cor})$ curve.

Cluster analysis

For cluster analysis 190 independent 12-hour pH_c-growth curves of the wild-type strain were used to fit the variables in:

$$\mu = 10^{\dfrac{pH_c + a}{b}} \tag{1}$$

where *a* was determined be to -7.24 ± 0.06, and *b* to 0.73 ± 0.08. We used this fit to predict the growth rate at each time point based on the pH_c measured at that time, for all wild-type and mutant strain time courses. We next determined the biological variance at each time point of the measured μ values around the predicted μ values of the 190 individual wild-type replicates, resulting in a mean and standard deviation of the wild-type divergence from the prediction at each time point. Using this mean and standard deviation, we transformed individual wild-type and mutant curves to Z-values at all time points. *t*-Test analyses of the average mutant Z-values compared to all wild-type replicates for all time points between t = 4 h to t = 9 h was multiplied by a correction factor to eliminate false positives based on *P*-values of wild-type time courses in a same *t*-test. Z-values of mutant and wild-type μ/pH_c curves, from t = 4 h to t = 9 h, were hierarchically clustered using Euclidean distances with full linkage.

Additional material

Additional file 1: All mutants with deviating pH_c at various pH_{ex}, and during respiratory growth. Mutants with aberrant pH_c under the standard condition (glucose, pH 5.0) were subjected to growth in pH 3.0, 7.5, as well as 2% ethanol/2% glycerol pH 5.0. Mutants were pre-grown overnight under standard conditions except for the 2% ethanol/2% glycerol experiment, in which case mutants were pre-grown in 2% ethanol/2% glycerol because of the long adaptation time to non-fermentable carbon source conditions. Cells were re-inoculated in described conditions and grown for 4 hours prior to measurements. Mutants were measured at least six times at pH 5.0 and at least three times at all other conditions. Mutants with significantly low pH_c in any condition are indicated in orange, while mutants with significantly high pH_c are indicated in blue.

Additional file 2: pH_c analysis of 432 slow growing mutants. All strains were grown in standard conditions (2% glucose, pH_{ex} of 5.0) and fluorescence was registered in three to six biological replicates, and are presented as average and 95% confidence interval. pH_c was compared to wild-type (WT) controls in the same replicate, to determine a Z-value. Significance of the pH_c difference with WT was determined using a two-tailed *t*-test assuming equal variance with a *P*-value < 0.05. ND refers to mutants for which fewer than three replicates were successfully measured. Significantly low pH_c values are shown in orange, significantly high pH_c values in blue.

Additional file 3: Classification of mutants. Mutants are classified as having a growth rate-pH_c relationship similar to wild type (WT; no significant deviation from the predicted growth rate based on pH_c-

growth rate relationship of the parent strain, low growth rate/pH_c (significant positive deviation from the parent fit), or high growth rate/pH_c (significant negative deviation from the parent fit), and are categorized according to functional classification.

Additional file 4: Figures S1 to S4. See Additional file 5 for further data pertaining to Figure S3.

Additional file 5: Data belonging to the hierarchical cluster plot in Figure S3 in Additional file 4. Mutants are listed in the order in which they appear in the cluster plot, for all three clusters. Mutant growth profiles were fitted to the parent strain pH_c-growth rate relationship, and at each time point the Z-value of the digression from the fit was determined compared to the average and variance of 96 parent strain growth curves at the same time point. Time courses during the growth phase (t = 4 h to t = 9 h) of these Z-values were used to statistically categorize the mutants as wild type (WT; 92/173 mutants; 96 parent strain profiles also fall in this category), significantly (corrected P-value < 0.01) slow growing (62/173 mutants), or significantly fast growing (19/173 mutants) with respect to pH_c.

Abbreviations

DMA: deletion mutant array; GFP: green fluorescent protein; InsP6: inositol hexakisphosphate; OD: optical density; ORF: open reading frame; pH_c: cytosolic pH; pH_{ex}: external pH; SGA: synthetic genetic array.

Author details

[1]Molecular Biology and Microbial Food Safety, Swammerdam Institute for Life Sciences, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, the Netherlands. [2]Banting and Best Department of Medical Research, Terrence Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario M5S 3E1, Canada. [3]Department of Molecular Genetics, Terrence Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Ontario M5S 3E1, Canada.

Authors' contributions

RO designed and performed most of the experiments and their analysis, and participated in drafting the manuscript. MLU set up the genome-wide screening. FJV performed the SGA recombination experiments. GG, CB, CN and SB assisted in experimental design, analysis, and drafting of the article. GJS conceived of the study, participated in its design and coordination, performed most data analysis and drafted the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

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