Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance

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Abstract

Cells balance glycolysis with respiration to support their metabolic needs in different environmental or physiological contexts. With abundant glucose, many cells prefer to grow by aerobic glycolysis or fermentation. Using 161 natural isolates of fission yeast, we investigated the genetic basis and phenotypic effects of the fermentation–respiration balance. The laboratory and a few other strains depended more on respiration. This trait was associated with a single nucleotide polymorphism in a conserved region of Pyk1, the sole pyruvate kinase in fission yeast. This variant reduced Pyk1 activity and glycolytic flux. Replacing the “low-activity” pyk1 allele in the laboratory strain with the “high-activity” allele was sufficient to increase fermentation and decrease respiration. This metabolic rebalancing triggered systems-level adjustments in the transcriptome and proteome and in cellular traits, including increased growth and chronological lifespan but decreased resistance to oxidative stress. Thus, low Pyk1 activity does not lead to a growth advantage but to stress tolerance. The genetic tuning of glycolytic flux may reflect an adaptive trade-off in a species lacking pyruvate kinase isoforms.

Keywords: cellular ageing; fermentation; glycolysis; oxidative stress; respiration

Introduction

Inter-linked pathways for carbon metabolism generate both energy in the form of ATP and fulfil key anabolic roles. Organisms tune their carbon metabolism to environmental conditions, including stress or available nutrients, which affects fundamental biological processes such as cell proliferation, stress resistance and ageing (New et al., 2014; Valvezan & Manning, 2019). Accordingly, aberrant carbon metabolism is the cause of multiple human diseases (Zanella et al., 2005; Wallace & Fan, 2010; Djouadi & Bastin, 2019). Glycolysis converts glucose to pyruvate, which is further processed in alternative pathways; for example, pyruvate can be converted to ethanol (fermentation) or it can be metabolised in mitochondria via the citric acid cycle and oxidative phosphorylation (respiration). Fermentation and respiration are antagonistically regulated in response to glucose or physiological factors (Molenaar et al., 2009; Takeda et al., 2015). In the presence of glucose, many microbes suppress respiration and grow preferentially by glycolysis, even with oxygen being available. This metabolic state, called aerobic glycolysis (Crabtree, 1929), appears paradoxical, because only full glucose oxidation via the citric acid cycle and respiration will maximise the ATP yield generated per glucose. Aerobic glycolysis, found in Crabtree-positive species, may have been selected because it enables higher rates of ATP production (Pfeiffer & Morley, 2014). Analogously, human cancer cells typically grow by aerobic glycolysis, known as the Warburg effect (Warburg, 1927), thought to increase biosynthetic capacity (Diaz-Ruiz et al., 2009; Lunt & Vander Heiden, 2011; Costa & Frezza, 2017). Proposed explanations for how aerobic glycolysis allows faster proliferation involve efficient resource allocation (Basan et al., 2015; Mori et al., 2019), molecular crowding (Andersen & von Meyenburg, 1980; Zhuang et al., 2011; Vazquez & Olvai, 2016; Szenk et al., 2017), an upper limit to the cellular Gibbs energy dissipation rate (Niebel et al., 2019), among others (Dai et al., 2016; de Alteriis et al., 2018; de Groot et al., 2019).
Crabtree-positive organisms, including the model yeasts Saccharomyces cerevisiae and Schizosaccharomyces pombe (Skinner & Lin, 2010), still require some oxygen and basal respiration for optimal cell proliferation (Chan & Roth, 2008). S. cerevisiae cells without mitochondrial genome, and thus without respiratory capacity, feature a slow-growth “petite” phenotype (Ephrussi et al, 1949). S. pombe cannot normally grow without a mitochondrial genome (Haffter & Fox, 1992; Heslot et al, 1970; Chiron et al, 2007), and blocking oxidative phosphorylation with antimycin A leads to moderate or strong growth inhibition, respectively, in rich or minimal glucose media (Malecki et al, 2016). In conditions of low glucose uptake, such as stationary phase, the metabolism of yeast cells is reconfigured towards respiration (DeRisi et al, 1997; Zuin et al, 2010). Thus, cells tune the balance between respiration and fermentation to meet their metabolic needs (Molenar et al, 2009) in a more nuanced way than captured by qualitative descriptions of aerobic glycolysis.

Given its impact on health and disease, it is important to understand the genetic and regulatory factors that affect cellular carbon metabolism. Here, we investigated the genetic basis and physiological implications for the regulatory balance between fermentation and respiration, using our collection of natural S. pombe isolates (Jeffares et al, 2015). A few strains featured a higher reliance on respiration during growth on glucose. This trait was associated with a missense variant in pyruvate kinase (PYK). PYK catalyses the final, ATP yielding step of glycolysis, the conversion of phosphoenolpyruvate to pyruvate. PYK can coordinate the activity of central metabolic pathways (Pearce et al, 2001; Grüning et al, 2011; Yu et al, 2018). Most organisms encode several PYK isoforms that are expressed in specific tissues or developmental stages (Allert et al, 1991; Muñoz & Ponce, 2003; Bleumlein et al, 2011; Israelsen & Vander Heiden, 2015; Bradley et al, 2019). Work in budding yeast has implied that the switch from a high- to low-activity PYK isoform causes increased oxygen uptake, triggering a shift from fermentative to oxidative metabolism (Grüning et al, 2011; Yu et al, 2018). S. pombe possesses only one PYK, Pyk1 (Nairn et al, 1995). Exchanging the Pyk1 variant of the standard laboratory strain triggered increased glycolytic flux, which in turn led to substantial adjustments in the metabolome, transcriptome and proteome. These results show that altered PYK activity is self-sufficient to reprogramme metabolism even in the absence of an evolved regulatory signalling system. These findings define a natural metabolic tuning, consisting of a single amino acid change, possibly reflecting an adaptation in a species lacking multiple PYK isoforms. Notably, the standard laboratory strain is among a minority of natural isolates locked in the low-activity state and is thus metabolically and physiologically unusual. These findings highlight the importance of glycolysis in general, and PYK in particular, as a hub in cross-regulating metabolic pathways and coordinating energy metabolism with cell regulation and physiology, including growth and stress resistance.

Results

Increased respiration dependence is associated with a missense PYK variant

Treating aerobic glycolysis as a complex, quantitative trait, we assessed the amount of residual respiration on glucose-rich media across a set of genotypically and phenotypically diverse wild S. pombe isolates. Resistance to antimycin A, which blocks the respiratory chain by inhibiting ubiquinol-cytochrome c oxidoreductase (Kim et al, 1999), was used as a proxy read-out for cellular dependence on oxidative phosphorylation. The standard laboratory strain 972 h− shows a moderate reduction in maximum growth rate and biomass yield in this condition (Malecki & Bähler, 2016; Malecki et al, 2016). We applied a colony-based assay to determine relative fitness of each strain in rich glucose media with and without antimycin A. The resulting resistance scores, i.e. ratios of growth with vs. without antimycin A, showed a large diversity between strains (Fig 1A, Appendix Fig S1, Dataset EV1). Notably, the laboratory strain was among the most sensitive (score = 1, rank = 10 of 154), with the mean score being 1.25 ± 0.15 for all strains tested.

The antimycin A resistance trait showed an estimated narrow-sense heritability of 0.54, reflecting the fraction of phenotypic variance explained by additive genetic effects. This heritability was substantially higher than for most of the 223 phenotypes previously reported (Jeffares et al, 2015), which indicates a strong genetic basis...
for the dependence on respiration. We performed a genome-wide association study (GWAS) to identify loci linked to resistance among 118,527 small genetic variants, including single nucleotide polymorphisms (SNPs) and small insertions or deletions (Fig 1B). Compared to a recent GWAS in budding yeast (Peter et al., 2018), our statistical power was lower, partly due to the low number of occurrences.
strains and the strong population substructure (Jeffares et al., 2015). We therefore manually assessed the associated variants, based on P-value, effect size and literature. Among the top-100 associations (by P-value, Dataset EV2), eight were predicted to have moderate or high impact as defined by SnpEff (Cingolani et al., 2012), and six of those were located in genes with functional annotation in PomBase (Wood et al., 2012). Two of these six variants were in S. pombe specific genes: wtf16 and wtf8 (Hu et al., 2017). Other variants were in ubp9, encoding a ubiquitin C-terminal hydrolase, in pfd5, encoding a cell-surface glycoprotein, and in jact, encoding a mitochondrial 2Fe-2S cluster assembly co-chaperone. One missense variant caught our particular attention: this SNP was among the top scoring (Fig 1B) and leads to a T343A amino acid sequence change in Pyk1, encoding the single PYK in S. pombe. Strains with a threonine residue at position 343 (“T-allele”) showed a median resistance score of 1.07, while strains with an alanine (“A-allele”) showed a ~15% higher median resistance of 1.28 (Fig 1C).

An analysis of 26 PYK protein sequences from diverse eukaryotes revealed strong conservation, showing 45–93% agreement with the consensus sequence called from the alignment (Fig 1D). The T343A mutation was in a region of the protein that is annotated as part of the ADP binding pocket in homologous proteins (Schormann et al., 2019). The threonine residue in the reference (laboratory) strain of S. pombe was unique in this highly conserved region of all PYK sequences. All other species featured an alanine residue at this position, including three other Schizosaccharomyces species (Fig 1D). The reference allele (T-allele) in the laboratory strain was the minor allele in our strain collection, found only in 18 of 161 strains (Fig 1E). The rare T-allele occurred in four unique sequences in the phylogenetic tree, split up over two highly divergent lineages (Fig 1E). This result was confirmed by considering a consensus tree based on the entire genome (Jeffares et al., 2015). For 10 of the 18 T-allele strains, the geographical origin is known, with most being isolated in Europe but also one each from Asia and Australia. The substrate is predominantly fermenting grapes (as for most other strains) and one each from lychee and grape syrups, reflecting that most S. pombe strains have been isolated from human-created niches. We conclude that the T-allele at position 343 is a rare, naturally occurring allele which appears to have arisen, and been maintained, independently in two distant lineages.

Replacing pyk1 allele in laboratory strain leads to higher PYK activity and metabolic adjustment

Many species possess two or more PYK isozymes with different activity and/or expression patterns. In S. cerevisiae, the minor isozyme can complement the loss of the major isozyme (Boles et al., 1997). The S. pombe reference genome (Wood et al., 2002), based on the laboratory strain 972, features only one PYK isoform. To test whether this is also the case for the other strains, we searched the de novo assemblies of all wild strain genome (Jeffares et al., 2015) for Pyk1 homologues with tblastn (Camacho et al., 2009). This search consistently produced a single hit only (Pyk1 itself).

We set out to analyse the effect of the pyk1 SNP on cellular metabolism. Using seamless CRISPR/Cas9-based gene editing (Rodríguez-Lópe et al., 2016), we replaced the pyk1 T-allele in the laboratory strain for the more common A-allele. We introduced the A-allele in both a heterothallic h− and a homothallic h0 laboratory strain, without any other genetic perturbations. We then selected three independently edited strains for both h− and h0 backgrounds to use as biological replicates throughout this study. Below, we use the abbreviations “T”-strain for the normal laboratory strains and “A”-strains for the edited pyk1T343A h−/h0 strains. These strains allowed us to study the impact of the pyk1 SNP in a controlled and well-characterised genetic background.

It has been reported that S. pombe features lower PYK activity than S. cerevisiae (Nair et al., 1995, 1998). However, this conclusion has been derived from the laboratory strain, which contains the unusual pyk1 allele. To investigate the impact of the pyk1 SNP on metabolism, we applied a targeted metabolomics workflow based on liquid chromatography–selective reaction monitoring (LC-SRM).

We quantified key metabolites potentially affected by PYK activity (Bluemlein et al., 2012; Gruning et al., 2014), including glycolytic,

**Figure 2. Multi-omic functional investigation of Pyk1 variants.**

A. PCA of metabolite data based on concentrations of 27 central carbon metabolism intermediates. To visualise this high-dimensional data set, we divided the concentration of each metabolite by the median concentration of the T-strain. This normalisation corrects for the large differences in concentrations observed between metabolites but maintains the relative variance within each metabolite. Biological replicates of the T- and A-strains show distinct profiles, largely driven by concentrations of phosphoenolpyruvate, 2-3-phosphoglyceric acid, NADH and NADPH, as indicated by top loading vectors for each principal component. The biological repeats for the three edited A-strains (circles, squares and triangles) behave similarly, with a variance comparable to that of the biological replicates of the single T-strain.

B. Left boxplot: two glycolytic intermediates directly upstream of PYK were strongly depleted in the A-strain (hT-strain = 9, hA-strain = 8). Right barplot: PYK activity was directly measured using a lactate dehydrogenase-coupled colorimetric enzyme activity assay, showing the mean and standard deviation of substrate conversion rate for three biological replicates, each measured in technical duplicates.

C. Concentrations of fructose-1,6-bisphosphate, which correlate with glycolytic flux, are significantly higher in A-strain (ratio = 1.35, hT-strain = 9, hA-strain = 8).

D. Boxplots for selected metabolomics data indicate differences in energy and redox status between T- and A-strains (hT-strain = 9, hA-strain = 8).

E. Heatmap of the 432 genes that are differentially expressed at the RNA level between the T- and A-strains (FDR < 10%) and are measured in all four conditions (columns). First column: genes ordered by increasing fold-changes for RNAs (computed as log2[T]-log2[A]). Second column: fold-changes for proteins (computed as log2[T]-log2[A]). Third column: fold-changes for RNAs in cells treated with rapamycin and caffeine (TORC1 inhibition; computed as log2[treatment]-log2[control]) (data from ref. Rallis et al., 2013). Fourth column: fold-changes for RNAs in cells treated with H2O2 (oxidative stress; computed as log2[treatment]-log2[control]) (data from Chen et al., 2008). Log fold-changes are capped at absolute values of 1 for all columns.

F. Gene Ontology (GO) enrichment analysis of differentially expressed transcripts (using all measured transcripts as background). Shown are Biological Process terms only, with additional plots for Molecular Function and Cellular Component terms in Appendix Fig S5. The length of the bar represents the significance of the enrichment, while its colour indicates the direction and magnitude of differential expression (A- vs. T-strain) of individual genes annotated to this term.

Data information: Significance keys: *P < 0.05, **P < 0.005, ***P < 0.0005 (Welch’s t-test).
pentose-phosphate pathway and citric acid cycle intermediates as well as redox cofactors and adenine nucleotides. Data were obtained for nine replicates of the T-strain and eight replicates of the A-strain (Figs 2A–D and 3, Appendix Figs S2 and S3, Dataset EV3). Technical replicates sampled from the same culture, but prepared and measured separately, were highly correlated (r$_{Pearson} = 0.93$), indicating that our workflow was robust and that most of the observed variation was biological. Over the entire data set, the median coefficient of variation was 17.2%. A principal component analysis (PCA) of metabolite data distinguished all strains based on the SNP in pyk1 (Fig 2A).

We observed a strong depletion of glycolytic intermediates upstream of PYK, with mean levels of phosphoenolpyruvate and 2-/3-phosphoglyceric acid in the A-strains only 25.9% and 12.7% of the AB levels.

Figure 2.
those in the T-strain (Fig 2B, \( P_{\text{adj}} = 8.7 \times 10^{-8} \) and \( 3.7 \times 10^{-6} \), Welch’s \( t \)-test, Benjamini–Hochberg-corrected, \( t \)-tests are unpaired and two-sided throughout). This result suggests that the A343T mutation reduces the activity of the Pyk1 enzyme. We directly tested this hypothesis by determining PYK activity in lysates of 3 biological replicates each of the A- and T-strain grown in rich glucose media, using a lactate dehydrogenase-coupled photometric assay, in technical duplicates. With a buffer composition similar to those previously used (Gehrig et al., 2017), the A-strains showed a 87.3% higher activity compared to the T-strain (\( P = 0.0072 \), Welch’s \( t \)-test) (Fig 2B, Appendix Fig S4).

The metabolomics data allowed us to also estimate several physiological parameters. The A-strains exhibited significantly higher levels of the flux-signalling metabolite fructose 1,6-bisphosphate (ratio 1.35, \( P_{\text{adj}} = 0.015 \); Litisios et al., 2018; Fig 2C). The levels of this metabolite strongly correlate with glycolytic flux in several yeast species (Christen & Sauer, 2011; Huberts et al., 2012), consistent with a higher flux in the A-strain. Furthermore, cellular energy charge was 4.7% higher in the A-strains (Fig 2D; \( P = 0.002 \), Welch’s \( t \)-test; Atkinson & Walton, 1967). These values were within the range reported for other organisms (De la Fuente et al., 2014). We used the ratio of the reduced to oxidised forms of NAD(H), NADP(H) and L-glutathione as read-outs for cellular redox status (Fig 2D). For NAD(H), the A-strains showed an increase from 0.048 to 0.096 (\( P = 0.0001 \), Welch’s \( t \)-test). The same pattern was evident for NADP(H), where the median ratio was 3.24 in the A-strains, but only 2.43 in the T-strain (\( P = 0.024 \)). Data regarding the oxidation state of glutathione were not entirely conclusive: the A-strain showed a significantly higher concentration of the reduced isoform of L-glutathione (ratio 1.30, \( P_{\text{adj}} = 0.015 \), Welch’s \( t \)-test; Appendix Fig S3, Dataset EV3), but no significant difference was apparent in the ratio of the reduced to oxidised isoforms, where the median for the A-strains was 2.01 vs. 1.89 for the T-strain (\( P = 0.289 \), Welch’s \( t \)-test). Overall, these results are in line with the paradigm that NADH/NAD\(^+\) ratios are maintained at low levels to maximise availability of electron acceptors for catabolic processes, while NADPH/NADP\(^+\) ratios are maintained at high levels to provide electrons for anabolic processes and the antioxidant response (Blacker & Duchen, 2016). As part of the antioxidant defence, which includes glutathione-, peroxiredoxin- and thioredoxin-dependent reduction systems, NADPH is limiting when cells are challenged with oxidative stress (Carmel-Harel & Storz, 2000; Drakulic et al., 2005; Vivancos et al., 2006; Veal et al., 2014). While analytical methods cannot distinguish between different compartments or sub-populations of these cofactors (Sun et al., 2012), and our sample extraction method may allow some interconversion between reduced and oxidised isoforms (Lu et al., 2018), these findings are consistent with the hypothesis that the A-strain respires less and thus has a lower oxidative burden.

### Increased PYK activity leads to transcriptome and proteome changes reflecting increased fermentation and decreased respiration

To further analyse the effects of the pyk1 SNP, we characterised the transcriptomes and proteomes of the T- and A-strains using RNAseq and mass spectrometry. We could quantify 7,750 transcripts (including non-coding RNAs) and 3,234 proteins in both strains (Dataset EV4), allowing for a broad analysis of genome regulation. The expression of pyk1 itself was similar in the T- and A-strains at both the transcript (log\(_2\)[fold change] = 0.016, \( P_{\text{adj}} = 0.91 \)) and protein level (log\(_2\)[fold change] = −0.001, \( P_{\text{adj}} = 0.94 \)), indicating that the differences between the two strains were not caused by changes in pyk1 expression. Notably, the pyk1 allele replacement led to substantial changes in both the transcriptome and proteome. Overall, 960 transcripts and 434 proteins were differentially expressed between the T- and A-strains, at a false discovery rate (FDR) of \( \leq 10\% \). While changes at the transcriptome and proteome levels generally correlated well (\( r = 0.65 \) for all genes with differentially expressed transcripts and/or proteins), we also found a large number of genes to be regulated exclusively at the protein level (Appendix Fig S7). These proteins were enriched in functions related to cytoplasmic translation and depleted in functions related to ribosome biogenesis (Appendix Tables S1 and S2). This result raises the possibility that post-transcriptional gene regulation plays an important role in controlling translation in this case.

The differentially expressed genes were enriched in functions related to respiration and energy-demanding processes, like translation and ribosome biogenesis. These enrichments were evident at both the level of the transcriptome (Fig 2F, Appendix Fig S5) and proteome (Appendix Fig S6). Transcripts encoding respiratory chain and oxidative phosphorylation proteins were more highly expressed in the T-strain (Fig 3), while those related to ribosome biogenesis and rRNA processing were more highly expressed in the A-strain. Some functional terms (e.g. NAD-binding) contained genes that were strongly regulated in either direction. Several of the most differentially expressed transcripts and proteins were directly involved in pyruvate metabolism (Fig 3). The mae2 gene was most strongly regulated at both transcript and protein levels, being more highly expressed in the T-strain. Moe2 is an enzyme that catalyses the reaction from malate and oxaloacetate to pyruvate (Viljoen et al., 1994). Thus, the T-strain may up-regulate Moe2 to replenish pyruvate using an alternate way that is largely independent of glycolytic flux; alternatively, Moe2 could function as anaerolic enzyme. The pydc101 and atd1 genes, on the other hand, were expressed more highly in the A-strain. These genes encode pyruvate decarboxylase and aldehyde dehydrogenase, respectively, and their induction is consistent with higher glycolytic flux and increased fermentation (Malecki et al., 2016). These expression changes are consistent with the central role of PYK in glycolysis and the observed metabolic effects mediated by the Pyk1 variants.

The target of rapamycin complex 1 (TORC1) signalling pathway controls carbon metabolism and promotes aerobic glycolysis in response to cellular nutrients (Valvezán & Manning, 2019). Enrichment analysis using AnGeLi (Bitton et al., 2015) revealed substantial overlaps between the differential expression signature of the T- and A-strains and the signature of TORC1 inhibition (Fig 2E; Rallis et al., 2013): 58 transcripts and 33 proteins induced by TORC1 inhibition were more highly expressed in the T-strain (\( P = 6.1 \times 10^{-12} \) and \( 4.1 \times 10^{-7} \), respectively), while 118 transcripts and 72 proteins repressed by TORC1 inhibition were more lowly expressed in the T-strain (\( P = 1.8 \times 10^{-59} \) and \( 2.1 \times 10^{-30} \) respectively). Thus, the expression signature of the T-strain resembles the signature caused by TORC1 inhibition, which leads to reduced glycolysis. Moreover, genes induced in response to oxidative stress were also differentially expressed; examples include gpx1, encoding glutathione peroxidase,
and grx1, encoding glutaredoxin. Accordingly, the differential expression signature between the T- and A-strains also showed substantial overlaps with the core environmental stress response triggered by oxidants and other stresses (Fig 2E; Chen et al, 2003): 63 transcripts induced by oxidative stress were higher expressed in the T-strain ($P = 7.0 \times 10^{-4}$), while 149 transcripts and 94 proteins.

**Gene Expression**
- **green** - higher in A-strain
- **red** - lower in A-strain
- **grey** - not significant or no data

**Metabolomics**
- Transcript
- Protein

**Number** = log2(A/T)

**Figure 3. Metabolic network showing metabolome, transcriptome and proteome changes triggered by pyk1 allele replacement.**

Metabolites, transcripts and proteins are coloured by their abundance ratios in A-strain relative to T-strain (see legend top left for details). For clarity, enzymes without protein or transcript changes are not shown (e.g. most upper glycolysis). Two metabolite pairs are indistinguishable by our LC-MS method (marked as +" and ").
repressed by stress were lower expressed in the T-strain ($P = 2.8 \times 10^{-68}$ and $1.4 \times 10^{-37}$), respectively. Thus, the expression signature of the T-strain also resembles the general signature of cells exposed to different types of stress, likely reflecting the higher load of reactive oxygen species from respiration. Together, the observed gene-expression reprogramming suggests that the T-strain features higher respiration and pentose-phosphate pathway activity (Fig 3). Similarly, budding yeast strains genetically engineered to alter PYK activity reconfigure their metabolism, with a reduced activity leading to higher respiration (to meet energy demands) and pentose-phosphate metabolism (to increase reducing agents required to detoxify reactive oxygen species produced by respiration; Gründing et al, 2011).

**Increased glycolytic flux increases cellular growth and glucose uptake but decreases oxygen consumption and biomass yield**

Given the metabolic and gene-expression changes associated with the pyk1 allele replacement, we expected that the A-strain will feature phenotypic changes at the cellular level, in particular increased growth. We grew the A- and T-strains in biological triplicates in rich media and measured growth by optical density at 600 nm for 6 h of exponential growth. As expected, the A-strain grew more rapidly than the T-strain (Fig 4A). Growth rates were calculated by fitting a line to log-transformed data (Fig 4B). The doubling times were 1.94 and 1.85 h for the T- and A-strains, respectively, a 4.7% decrease. Our metabolomics and gene-expression data suggested that this faster growth rate is due to a shift in the fermentation/respiration balance towards fermentation. Accordingly, we detected less residual glucose in A-strain cultures after 8 h of exponential growth, normalised to the final OD (Fig 4C, $P = 0.04$, Welch’s t-test). Moreover, the A-strain consumed oxygen at a 35% lower rate than the T-strain (Fig 4D). Since energy production from respiration is more efficient than from fermentation, we expected a lower final biomass in the A-strain. Indeed, the final biomass, assessed the ability of the A- and T-strains to endure oxidative stress (Gru¨ning et al., 2011). We therefore assessed the ability of the A- and T-strains to endure oxidative stress triggered by hydrogen peroxide ($H_2O_2$) or diamide. Indeed, the T-strain was substantially more resistant to both oxidants than the A-strain (Fig 5A). Oxidative stress is a by-product of cellular respiration, and the T-strain may feature a higher basal protection from oxidative stress due to higher respiratory activity. This protection is consistent with our observation that core environmental stress response genes were more highly expressed in the T-strain. The environment can also be a source of oxidants, e.g. in microbial communities with H2O2-producing lactic acid bacteria (Ito et al., 2003; Ponomarova et al., 2017). Thus, a natural SNP promoting oxidative stress resistance may be beneficial. Our observation that lower glycolytic flux increases oxidative stress resistance, via higher pentose-phosphate pathway flux, is in line with previous studies in *S. cerevisiae*, where glycolytic flux has been reduced by mutations in triosephosphate isomerase (Ralser et al., 2007; Grüning et al., 2014). We conclude that the slower growth of the T-strain, compared to the A-strain, is offset by an increased resistance to oxidative stress. Both traits may be systemic properties emerging from the up-regulation of respiration at the cost of fermentation, triggered by the T-allele.

We wondered whether the T-strain might feature fitness advantages in stress conditions other than oxidative stress. To this end, we screened for differential growth of the A- and T-strains on 72 different drugs and toxins. The strains appeared to be differentially sensitive to nine compounds (Fig 5D). The A-strain was more resistant to barium chloride, D-L-alanine hydroxamate, caffeine (pleiotropic effects, including TOR inhibition, Rallis et al., 2013), chlorpromazine (causes membrane stress, De Filippi et al., 2007), capreomycin (binds to ribosomes, Lin et al., 2014) and phenylarsine oxide (inhibitor of tyrosine phosphatases, Ous tin et al., 1995). Notably, the A-strain was also more resistant to thallium (I) acetate, which is highly toxic due to its similarity to potassium ions and binds to mammalian PYK with a stronger affinity, but weaker
activating effect, than potassium (Kayne, 1971; Reuben & Kayne, 1971). The T-strain, on the other hand, was more resistant to acriflavine, an antiseptic, and to EGTA, a chelator of bivalent cations (including Mg$^{2+}$ which activates S. cerevisiae PYK, Rhodes et al., 1986). We manually inspected dose–response curves (Appendix Fig S8) to select compounds for validation based on overall difference in maximum growth rate and consistency across concentrations. Using spot assays, we could validate the differential sensitivity to four selected compounds: caffeine, phenylarsine oxide, EGTA and chlorpromazine (Fig 5E). It is striking that the pyk1 SNP differentially affected the resistance to this broad range of stresses, suggesting a general role of glycolysis in stress resistance beyond the known role in oxidative stress.

The existence of a fundamental link between metabolism and lifespan is well known, e.g. through the observation that dietary restriction extends lifespan from yeast to humans (Al-Regaiey, 2020).

Figure 4. Physiological characterisation of pyk1 variant.
A Growth measured by optical density (OD) at 600 nm for 3 biological replicates each of the T- and A-strains over 6 hrs of exponential growth in YES media. The x-axis refers to the time since inoculation of the culture.
B The same data as in (A) plotted on a log$_2$ scale (solid lines) with lines fitted (dotted lines). The doubling time is the inverse of the slope.
C Media samples were taken from the same cultures ($n$ = 3 for both strains) at the 8 hr timepoint and the remaining glucose was quantified. The consumed glucose was calculated based on the amount of glucose measured in the same, fresh media and normalised to the OD of each culture at the time of sampling.
D Oxygen consumption rates in A- and T-strains (ratio of means = 0.65, $P = 0.0002$, Welch’s t-test, three biological replicates, each measured in technical duplicates).
E Culture dry weight after 24 h was measured reported as a fraction of the weight of glucose put into the media for three biological replicates per strain.

Data information: Vertical bars show the mean of the data. Error bars and shaded areas in all cases denote standard deviation. Significance keys: *$P < 0.05$, ***$P < 0.0005$ (Welch’s t-test).
2016). In various model systems, increased respiration (Bonawitz et al., 2007; Roux et al., 2009; Zuin et al., 2010; Pan et al., 2011) and slower growth (Yang et al., 2011; Rallis et al., 2014; Janssens & Veenhoff, 2016; Smith et al., 2018) correlate with increased lifespan. We therefore expected the T-strain to be longer-lived than the A-strain and measured the chronological lifespan of both strains. Surprisingly, the A-strain was longer-lived, with a mean viability of 25.3% after 3 days, compared to 6.5% for the T-strain (Fig SF). Reduced glycolytic flux has been reported to shorten replicative lifespan in budding yeast (Raiser et al., 2007). We therefore speculate that unrestricted glycolytic flux generally promotes longevity, but mechanistic processes involved will require further investigation.

Our findings show that the pyk1 SNP has substantial effects on growth rate and oxidative stress resistance in the genetic background of the standard laboratory strain. Are such effects generally evident in other strain backgrounds? To address this question, we measured oxidative stress resistance and growth rates for all wild strains. Indeed, the T-allele was significantly associated with higher measured oxidative stress resistance and growth rates for all wild strains and in all other eukaryotes examined, glycolytic flux increased and oxygen consumption decreased. This metabolic adjustment led to changes in gene expression at the transcriptome and proteome levels, resembling the signatures of rapidly proliferating cells with high TORC1 activity and no stress exposure. At the cellular level, the allele replacement led to increased growth and chronological lifespan but decreased resistance to oxidative stress. Cellular growth and stress resistance are linked with gene regulation, although cause-effect relationships are poorly understood (López-Maury et al., 2008; Morano et al., 2012; Pir et al., 2012; Slavov & Botstein, 2013; Tamari et al., 2014; Hesketh et al., 2019).

The extraordinary plasticity in response to altered glycolytic flux, triggered by a single nucleotide change, highlights the fundamental impact of glycolysis on cellular control, physiology and adaptation. Possessing only a single PYK isoform, S. pombe is unlikely to have a pre-existing genetic or signalling programme for the regulation of high- and low-activity PYK states. Yet, a mutation in Pyk1 that changes its activity is sufficient to induce coherent metabolic, regulatory and cellular responses. A PYK-induced change in glycolytic flux is hence the cause, not a consequence, of major changes in cellular metabolism, regulation and physiology. The finding that a new metabolic programme can be triggered by an intracellular event is consistent with a report showing that overexpression of one transcription factor in Komagataella phaffii is sufficient to turn this Crabtree-negative yeast into a Crabtree-positive one (Ata et al., 2018). These findings support the idea that a flux-sensing mechanism could regulate the balance between respiration and fermentation. When we replaced the T-allele of the laboratory strain with the common A-allele, which is broadly conserved in most S. pombe strains and in all other eukaryotes examined, glycolytic flux increased and oxygen consumption decreased. This metabolic adjustment led to changes in gene expression at the transcriptome and proteome levels, resembling the signatures of rapidly proliferating cells with high TORC1 activity and no stress exposure. At the cellular level, the allele replacement led to increased growth and chronological lifespan but decreased resistance to oxidative stress. Cellular growth and stress resistance are linked with gene regulation, although cause-effect relationships are poorly understood (López-Maury et al., 2008; Morano et al., 2012; Pir et al., 2012; Slavov & Botstein, 2013; Tamari et al., 2014; Hesketh et al., 2019).

The extraordinary plasticity in response to altered glycolytic flux, triggered by a single nucleotide change, highlights the fundamental impact of glycolysis on cellular control, physiology and adaptation. Possessing only a single PYK isoform, S. pombe is unlikely to have a pre-existing genetic or signalling programme for the regulation of high- and low-activity PYK states. Yet, a mutation in Pyk1 that changes its activity is sufficient to induce coherent metabolic, regulatory and cellular responses. A PYK-induced change in glycolytic flux is hence the cause, not a consequence, of major changes in cellular metabolism, regulation and physiology. The finding that a new metabolic programme can be triggered by an intracellular event is consistent with a report showing that overexpression of one transcription factor in Komagataella phaffii is sufficient to turn this Crabtree-negative yeast into a Crabtree-positive one (Ata et al., 2018). These findings support the idea that a flux-sensing mechanism could regulate the balance between respiration and fermentation (Huberts et al., 2012).

What might be the evolutionary and ecological role of the pyk1 SNP? We propose that the mutation in the laboratory strain is beneficial given its maintenance at a strongly conserved position, its occurrence in two independent S. pombe lineages, its associated phenotypes and the use of low-activity isoforms in other organisms. The literature suggests that low PYK activity could help cells to retain more carbon intermediates for biosynthesis (Christofk et al., 2008; Lunt et al., 2015; Allen & Locasale, 2018). Our results, and
other recent research (Morita et al., 2018), do not support this hypothesis as cells with low Pyk1 activity grow slower and form less biomass. Our phenotypic assays also do not support the possibility that the pyk1 SNP is adaptive on specific carbon or nitrogen sources. However, we have identified several stress conditions where the laboratory strain exhibits higher fitness than the allele replacement strain, most notably oxidative stress. It is plausible that stress resistance has provided the selection factor for the low-activity Pyk1 allele. Accordingly, we propose that altered stress tolerance provides a biological rationale for the evolution of systems that allow conditional switching between high- and low-activity PYK isozymes.

Materials and Methods

Wild strain phenotyping and GWAS

We constructed two arrays of 384 strains, each containing a reference grid of 96 JB22 colonies (standard laboratory strain 972), around which 159 wild isolates from our collection (Jeffares et al., 2015) were randomly arranged in triplicates, with additional internal, interspersed JB22 controls. A RoToR HDA pinning robot (Singer Instruments) was used to copy the arrayed strains onto various growth media. Plates were grown for 2 days at 32°C, and images were acquired by transmission scanning (Epson V800 Photo). Colony sizes were determined with jitter (Wagih & Parés, 2014) and corrected for spatial biases using reference-grid normalisation (Zackrisson et al., 2014) and thinning predictors, then calculating their weights and finally using the direct method for obtaining the kinship matrix. All steps used default options. Heritability estimates were obtained by REML as implemented in LDAK5. Linear mixed-model association was performed in LDAK5, using the previously generated kinship matrix to correct for population structure.

Phylogenetics

The phylogenetic tree in Fig 1 was constructed by filtering biallelic SNPs in the region ± 500 bp around the pyk1 gene ([1:3,844,243–3,847,145] using bcftools. This vcf was converted to a pseudo alignment in fasta format with VCF-kit (Cook & Andersen, 2017). The tree was constructed by the neighbour-joining method, implemented in ClustalW2 (Larkin et al., 2007), accessed through the EBI web interface (Goujon et al., 2010) and drawn in seaview (Gouyon et al., 2010).

Construction of allele replacement strains

The allele replacement strains were generated using the CRISPR-Cas9 system. The plasmid containing the gRNA targeting the pyk1 SNP in 968 h\(^{–}\) (homothallic) and 972 h\(^{–}\) (heterothallic) was generated as described (Rodríguez-López et al., 2016) using the following primers: gRNA.JB50-F: GCTTTCCGGTGAGACTACCAgttttagagctagaa atagc and gRNA.JB50-R: TGGTAGTCTCACCGGAAAGCttcttcggtaggtta.

Proper gRNA cloning was assessed by Sanger sequencing. The template for homologous recombination was generated using the following primers (underlined is the point mutation introduced in t-strain to convert it to the A-strain):

```
HR_JB50-R: GTAAGGGATGGAAGCCTCAGCAACACGGGCAGTCT
CAGCATTAGTGGTAACCGGCTTCAACCGGTAGAAGACTG
ACTCCAAAGGGTTCTTA
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HR_JB50-R: GTAAGGGATGGAAGCCTCAGCAACACGGGCAGTCT
CAGCATTAGTGGTAACCGGCTTCAACCGGTAGAAGACTG
ACTCCAAAGGGTTCTTA
```

The following primers were used to identify and confirm successful mutants, of which three were kept (referred to as A,B,C in this manuscript) and used for experiments in order to reduce the risk of observing the effects of off-target mutations:

```
Pyk1ck-F: GATGTTGTAACCGGCGTTCT
Pyk1ck-R: GGACCGGTTACGAGGCAG
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Cell culture for multi-omics experiments

Transcriptomes and proteomes were measured from the same cell culture, in five biological repeats per strain. Strains were woken up on yeast extract with supplement (YES) agar and incubated for 2 days at 32°C. Then, 50 ml pre-cultures (YES medium, 32°C, 170 rpm) were grown overnight and used to inoculate 200 ml cultures (YES medium) at an OD\(_{600}\) of 0.1. These cells were then grown until OD\(_{600}\) of 0.8 and harvested as described below.
Transcriptomics experiments

When cells reached OD 0.8, 25 ml was collected by centrifugation and snap-frozen in liquid nitrogen. RNA was extracted with a hot phenol method as described in Ref. Lyne et al. (2003). RNA was further purified with Qiagen RNAeasy columns, and DNase treatment was performed in the columns (as suggested by manufacturer) prior to library preparation. RNA quality was assessed with a Bioanalyzer instrument (Agilent), and all samples presented a RIN (RNA Integrity Number) > 9. cDNA libraries were prepared with the Illumina TruSeq stranded mRNA kit, according to the manufacturer’s specifications, by the Cologne Center for Genomics (CCG) facility. The samples were sequenced on a single lane of an Illumina HiSeq4000 to produce 2 × 75 nt reads.

Reads were trimmed with Trimmomatic (Bolger et al., 2014) v0.36, with the following parameters differing from default settings: LEADING:0 TRAILING:0 SLIDINGWINDOW:4:15 MINLEN:25. The reference genome was indexed with bowtie2 with default settings (v2.3.4.1) (Langmead & Salzberg, 2012). In the case of the A-strain, the reference genome was edited to reflect the base substitution within the genome. Bowtie2 was aligned to the reference genome using bowtie2 with default settings (v2.3.4.1) (Langmead & Salzberg, 2012). The annotations were downloaded from PomBase (uploaded on 1st Sept 2015; Wood et al., 2012). The transcriptome and proteome were tested separately. All genes with an FDR ≤ 10% were included in the test set, while all other genes formed the background. Importantly, only those genes with available measurements were included in the background to avoid false-positive enrichments. The nodeSize was set to 10. We performed Fisher’s exact tests with the elim-algorithm. All terms with $P \leq 0.01$ were included in the plots. We used AngELi (Bitton et al., 2015) for functional enrichment analysis to confirm the GO enrichments and to reveal overlap with core environmental stress and TORC1 response genes.

Proteomics experiments

For sample preparation, cells were washed with PBS and centrifuged (3 min, 600 g, RT). Subsequently, cells were washed with 1 ml RT lysis buffer (LB: 100 mM HEPES, 1 mM MgCl₂, 150 mM KCl, pH 7.5) and transferred to 1.5-ml tubes and centrifuged (5 min, 600 g, RT). Cell pellets were flash-frozen and stored at -80°C. Cell pellets were resuspended in 400 µl cold LB, mixed with the same volume of acid-washed glass beads (Sigma-Aldrich), transferred to a FastPrep-24TM 5G Instrument (MP Biomedicals), and disrupted at 4°C by 8 rounds of bead-beating at 30 s with 200 s pauses between the runs. Samples were centrifuged (2 min, 1,000 g, 4°C), supernatants collected, and protein concentrations determined with the bicinchoninic acid assay (Thermo Fisher Scientific). Then, 100 µg of proteome samples was subjected to the sample preparation workflow for MS analysis as reported (Piazza et al., 2018). Peptide samples were analysed on a Q Exactive HF Orbitrap mass spectrometer (Thermo Fisher Scientific), equipped with a nano-electrospray ion source and a nano-flow LC system (Waters-M-class). For shotgun LC-MS/MS data acquisition (DDA), 1 µl peptide digests from each sample were injected independently at a concentration of 1 µg/µl. MS1 spectra were acquired as described (Piazza et al., 2018). One µl peptide digest from the same samples was also measured in data-independent acquisition (DIA) mode on using the DIA settings reported (Piazza et al., 2018). The collected DDA spectra were searched against the S. pombe fasta database (Clément-Ziza et al., 2014), using the Sorcerer+SEQUEST database search engine (Thermo Electron) as reported (Piazza et al., 2018). For generation of spectral libraries, the DDA spectra were analysed with Proteome Discoverer 2.2 as described above and imported in the Spectronaut software (version 8, Biognosys AG). DIA-MS targeted data extraction was performed with Spectronaut version 8 (Biognosys AG) with default settings.

Analyses of protein abundance were performed with the MSStat package (Choi et al., 2014) using default parameters, unless stated otherwise. Spectronaut output was converted to the input format of MSstats with the SpectronauttoMSstatsFormat function. The normalised peak areas were further processed with the function dataProcess and intensity = “NormalizedPeakArea”. This included log₂ transformation, median normalisation, the summary of fragments to peptides, and the summary of peptides to proteins. The parameter featureSubset was set to “all”. We used the groupComparison function with linear mixed models to compare protein abundances between the replicates for the two strains. The FDRs and log2 fold-changes between strains returned by groupComparison were used for further analyses.

Functional enrichment analyses

Gene ontology (GO) enrichment analysis was performed with the topGO package (v2.30.1) (Alexa et al., 2006). The annotations were downloaded from PomBase (uploaded on 1st Sept 2015; Wood et al., 2012). The transcriptome and proteome were tested separately. All genes with an FDR ≤ 10% were included in the test set, while all other genes formed the background. Importantly, only those genes with available measurements were included in the background to avoid false-positive enrichments. The nodeSize was set to 10. We performed Fisher’s exact tests with the elim-algorithm. All terms with $P \leq 0.01$ were included in the plots. We used AngELi (Bitton et al., 2015) for functional enrichment analysis to confirm the GO enrichments and to reveal overlap with core environmental stress and TORC1 response genes.

Metabolomics experiments

Overnight, cell pre-cultures were diluted to OD₆₀₀ of 0.1, and 5 ml was quenched in 20 ml dry-ice-cold methanol when an OD₆₀₀ of 0.8 was reached. This suspension was spun down (600 g, 3 min, 4°C), and the supernatant was discarded by inversion. The pellet was resuspended in the remaining liquid and transferred to a small tube and spun down again with the same parameters. The supernatant was removed completely, and the pellet was frozen in liquid nitrogen and stored at -80°C until further processing.

The samples were extracted as described (Bligh & Dyer, 1959). Acid-washed Zirkonia beads were added to the pellet, together with 140 µl of 10:4 MeOH/water, and cells were lysed mechanically (FastPrep Instrument, 40 s, 6.5 m/s). Then, 50 µl chloroform was added and mixed thoroughly, followed by 50 µl water and 50 µl chloroform. Insoluble components were removed by centrifugation at 5,000 g for 10 min. The aqueous phase was recovered and used without further conditioning. One microtitre was injected for LC-MS/MS analysis. The sample was diluted 1:20 for the analysis of free amino acids, except for glutamine which was quantified without dilution.

The compounds were resolved on an Agilent 1290 liquid chromatography system, using a HILIC amide column (Waters BEH Amide, 2.1 × 100 mm, 1.7 µm particle size) with acetonitrile (solvent A) and 100 mM aqueous ammonium carbonate (solvent B) for
gradient elution at a constant flow rate of 0.3 ml/min and column temperature of 35°C. The gradient programme started at 30% B and was kept constant for 3 min before a steady increase to 60% B over 4 min. Solvent B was maintained at 60% for 1 min before returning to initial conditions. The column was washed and equilibrated for 2 min resulting in a total analysis time of 10 min. Compounds were identified by comparing retention time and fragmentation patterns with analytical standards. The samples were analysed by tandem mass spectrometry coupled to an Agilent 6470 triple quadrupole. The sample was acquired using the Agilent dynamic MRM (dMRM) approach with polarity switching. Peak areas were converted to concentrations using external calibration by standard curves and corrected for the optical density of the culture at the time of harvesting.

**Enzyme assays**

Pyruvate kinase activity was assayed as described (Gehrig et al., 2017). The homothallic A- and T-strains were grown overnight in 3 ml of YES pre-cultures, diluted to OD 0.15, and grown for a further 5 h. The OD600 of cultures at the time of sampling was approximately 3 ml of lysis buffer (10 mM Tris at pH 7, 100 mM KCl, 5 mM MgCl2, 1 mM DTT), breaking the cells with a FastPrep instrument (MP Biomedicals), operated at 4°C, three times for 40 s with 1-min breaks in between, spinning at 8,000 g (3 min, 4°C), and transferring the supernatant to a fresh tube kept on ice and used fresh. Reactions with a total volume of 200 μl in a 96-well plate contained 10 mM Tris at pH 7, 100 mM KCl, 5 mM MgCl2, 20 μg L-lactate dehydrogenase from rabbit muscle, 5 mM ADP (all by Sigma-Aldrich), 10 mM PEP (Molekula) and 200 μM NADH (Bioworld). The reaction mix was warmed to 32°C for 1 min and the reaction was started by adding 4 μl of lysisate. The absorbance at 340 nm was measured every ~15 s in a Tecan Infinite M200 Pro plate reader set to 32°C. Absorbance values below 0.2 were set to NA. Absorbance values were converted to concentration using the extinction coefficient 6220 M⁻¹ cm⁻¹ and a path length of 0.5411 cm (calculated from reaction volume and well diameter). The slope of the concentration trace was determined using the linregress function from the scipy python package, background subtracted (reaction mix without lysisate), and divided by the OD of the culture at the time of sampling.

**Measurement of growth rates**

For each biological replicate, a colony was picked and grown overnight in a 5 ml YES pre-culture. The pre-culture was diluted to OD600 0.2 and grown for 6 h, centrifuged (400 g, 4 min, RT), discarding the supernatant, adding a small amount of glass beads and 200 μl of lysis buffer (10 mM Tris at pH 7, 100 mM KCl, 5 mM MgCl2, 1 mM DTT), breaking the cells with a FastPrep instrument (MP Biomedicals), operated at 4°C, three times for 40 s with 1-min breaks in between, spinning at 8,000 g (3 min, 4°C), and transferring the supernatant to a fresh tube kept on ice and used fresh. Reactions with a total volume of 200 μl in a 96-well plate contained 10 mM Tris at pH 7, 100 mM KCl, 5 mM MgCl2, 20 μg L-lactate dehydrogenase from rabbit muscle, 5 mM ADP (all by Sigma-Aldrich), 10 mM PEP (Molekula) and 200 μM NADH (Bioworld). The reaction mix was warmed to 32°C for 1 min and the reaction was started by adding 4 μl of lysisate. The absorbance at 340 nm was measured every ~15 s in a Tecan Infinite M200 Pro plate reader set to 32°C. Absorbance values below 0.2 were set to NA. Absorbance values were converted to concentration using the extinction coefficient 6220 M⁻¹ cm⁻¹ and a path length of 0.5411 cm (calculated from reaction volume and well diameter). The slope of the concentration trace was determined using the linregress function from the scipy python package, background subtracted (reaction mix without lysisate), and divided by the OD of the culture at the time of sampling.

**Glucose uptake measurements**

After 8 h of growth, media samples were taken, cleared of cells by centrifugation and stored at ~80°C until further processing. Glucose concentrations were determined using a commercial, colorimetric kit (Glucose (HK) Assay Kit, Sigma-Aldrich, catalogue number GAHK20), following the instructions of the manufacturer with the following modifications. A standard curve was prepared from a twofold dilution series of the supplied standard. Samples were diluted 1:20 in water. Then, 10 μl of diluted sample was added to 190 μl of assay buffer in a 96-well plate and incubated for 15 min. The absorbance at 340 nm was measured with a plate reader (Tecan Infinite M200 Pro). Values were subtracted by the water blank and converted to concentrations using the standard curve and dilution factor. For each sample, the measured concentration was subtracted from the amount of glucose in fresh media (determined by the same method) and divided by the OD of the culture at the time of sampling.

**Dry weight measurements**

We inoculated 100 ml YES cultures from overnight 5 ml YES precultures at an initial OD600 of 0.2 and grew them for 24 h. Cultures were centrifuged, washed once in dH2O, dried at 70°C for 48 hrs and weighed on a high-resolution balance.

**Oxygen consumption rate measurements**

YES cell cultures (100 ml) were grown overnight to an OD600 between 1 and 3. A ~25 ml sample was put into a 25-ml Erlenmeyer flask and stirred at 900 rpm using a magnetic stirrer bar. An oxygen probe (Hanna HI 98193), held with a clamp, was inserted into the flask, resulting in it being completely filled with no remaining air inside it, and the flask was sealed with multiple layers of parafilm. The oxygen saturation of the culture was followed over 7 min and recorded every ~1 min. The slope of the concentration trace was determined using the linregress function from the scipy python package and divided by the OD of the culture.

**Carbon source screen**

We used Edinburgh minimal medium (EMM) or YES, depending on the nitrogen source in the final assay medium (Moreno et al., 1991). Cells were pre-cultured overnight (5 ml), diluted to approximately OD600 0.2 in the morning, grown for 6 h, centrifuged (400 g, 4 min, RT), washed once in EMM without glucose or YES, resuspended and diluted to OD600 0.2 in EMM without glucose or YES. Carbon sources were used at the same molarity as glucose in standard EMM (2% w/w, 111 mM), except for sucrose, maltose and raffinose (where amount was corrected for number of monosaccharides they contain), pectin (where a saturated solution was used), and glutamine (16% w/w due to low solubility). The OD600 was recorded in 384-well plates, every 15 min, with short shaking (15 s) before each measurement in a plate reader (Tecan Infinite M200 Pro). Growth curves were smoothed by first applying a median filter of size 5 and a Gaussian filter with sigma = 3. We obtained maximum slopes for each well by fitting all linear regression models for 12 timepoints over the course of the growth curve and retaining the best one.

**Biolog phenotyping screen**

The resistance to various chemical compounds was assessed using Biolog Phenotype MicroArray plates PM22, PM23 and PM25. JB50 and pyk1-A-allele h80 were grown overnight in EMM, diluted to OD600
0.15 in fresh EMM and grown for 6 h at 25°C. Cultures were then diluted to OD_{600} 0.05, and 100 µl was added to each well. For each plate type, two individual plates were used (one per strain). Growth curves were recorded by measuring the absorbance at 610 nm every 30 min in an EnVision 2104 plate reader (PerkinElmer) with stacker module. The room was not strictly temperature controlled but was stable at 23.5 ± 1°C over the course of the experiment. Growth curves exhibited considerable noise levels and were smoothed by first applying a median filter of size 5 and a Gaussian filter with sigma = 3. We obtained maximum slopes for each well by fitting all linear regression models for 12 timepoints over the course of the growth curve and retaining the best one. Each plate contained multiple concentrations of the same compound, and dose–response curves were plotted for all, with hits identified by manual inspection.

To assess the ability of both strains for using different nitrogen sources (Biolog Phenotype MicroArray plate PM3), we applied the same strategy with the following modifications. We used strains with the heterothallic h+ mating type to prevent mating and sporulation in poor nutrient conditions. Pre-cultures were diluted to OD_{600} 0.2 and grown for 6 h at 25°C. Cultures were then centrifuged (300 g, 3 min, RT), washed in EMM without nitrogen or carbon (EMM-N-C), resuspended in EMM-N at an OD_{600} of 0.2 and 100 µl of cells was added to each well of the assay plates. OD_{610} was recorded in 15-min intervals, and the fit range for maximum slope extraction was accordingly doubled to 24 timepoints. Growth curves were otherwise acquired and analysed similarly. Nitrogen sources in which both strains had a maximum growth rate < 0.015 were excluded from further analysis.

Spot assays

Three independent pre-cultures were used for the T-strain and one pre-culture per independent CRISPR-engineered mutant. Pre-cultures were grown in either YES or EMM media depending on the plate used for the actual assay. Overnight cultures were diluted to an OD_{600} of 0.15 and grown for an additional ~6 h. Cultures were then diluted to a OD_{600} of 0.4, with a threefold dilution series prepared in a 96-well plate (one culture per column). The “1 to 16 array single source” program of the RoToR HDA (Singer Instruments) was used to create the read-out plates. For each batch, a control plate without toxin was prepared to check for any accidental bias in strain dilutions.

Chronological lifespan assays

Chronological lifespan assays were performed as previously described (Rallis et al, 2013). Single colonies were picked and inoculated in YES. Cells were grown for 48 h, which was treated as the beginning of stationary phase (Day 0). For the A-strain, three independent CRISPR-engineered mutants were used as biological repeats.

Data availability

The datasets produced in this study have been made available as described below:

- Mass spectrometry proteomics data: PRIDE (Perez-Riverol et al, 2019) PXD017833 (http://www.ebi.ac.uk/pride/archive/projects/PXD017833)
- GWAS top hits: Dataset EV2
- Metabolomics data: Dataset EV3
- Gene-expression data: Dataset EV4
- Carbon source screen: Dataset EV5
- Nitrogen source screen: Dataset EV6

**Expanded View** for this article is available online.

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**Author contributions**

SK, AB, MR and JB conceived the study. SK, JG, MR-L, SJT, MM, VC, GS and CC-M performed the experiments. SK and JG analysed the data. PP, AB, MR and JB supervised the work and acquired funding. SK and JB drafted the manuscript. All authors read and approved the final submission.

**Conflict of interest**

The authors declare that they have no conflict of interest.

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