



## RESEARCH ARTICLE

# Identification of nuclear genes affecting 2-Deoxyglucose resistance in *Schizosaccharomyces pombe*

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**One sentence summary:** Genes that are required to provide resistance to the anticancer molecule 2-Deoxyglucose when overexpressed or deleted in fission yeast have been identified.

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## ABSTRACT

2-Deoxyglucose (2-DG) is a toxic glucose analog. To identify genes involved in 2-DG toxicity in *Schizosaccharomyces pombe*, we screened a wild-type overexpression library for genes which render cells 2-DG resistant. A gene we termed *odr1*, encoding an uncharacterized hydrolase, led to strong resistance and altered invertase expression when overexpressed. We speculate that *Odr1* neutralizes the toxic form of 2-DG, similar to the *Saccharomyces cerevisiae* *Dog1* and *Dog2* phosphatases which dephosphorylate 2-DG-6-phosphate synthesized by hexokinase. In a complementary approach, we screened a haploid deletion library to identify 2-DG-resistant mutants. This screen identified the genes *snf5*, *ypa1*, *pas1* and *pho7*. In liquid medium, deletions of these genes conferred 2-DG resistance preferentially under glucose-repressed conditions. The deletion mutants expressed invertase activity more constitutively than the control strain, indicating defects in the control of glucose repression. No *S. cerevisiae* orthologs of the *pho7* gene is known, and no 2-DG resistance has been reported for any of the deletion mutants of the other genes identified here. Moreover, 2-DG leads to derepressed invertase activity in *S. pombe*, while in *S. cerevisiae* it becomes repressed. Taken together, these findings suggest that mechanisms involved in 2-DG resistance differ between budding and fission yeasts.

**Keywords:** fission yeast; glucose metabolism; 2-Deoxyglucose resistance; invertase activity; *odr1* overexpression; deletion library

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## INTRODUCTION

There are two main reasons to study the mechanisms of action of the toxic glucose analog 2-Deoxyglucose (2-DG). First, in the budding yeast *Saccharomyces cerevisiae* 2-DG inhibits growth, affects cell wall synthesis, causes abnormal cell morphology and cell lysis, and interferes with glucose metabolism (Biely et al. 1971; Krátký, Biely and Bauer 1975). A series of pioneering papers (Zimmermann and Scheel 1977; Entian and Zimmermann 1980; Neigeborn and Carlson 1987) have identified mutants resistant to 2-DG, and corresponding genes have been characterized leading to insights into the underlying mechanisms (for additional references, see McCartney et al. 2014). Second, 2-DG shows anticancer activity in humans by inhibiting tumor growth with yeast providing a model system to understand its mode of action (Cairns, Harris and Mak 2011; Raez et al. 2013). Aerobic glycolysis is a metabolic pathway that is of particular importance to cancer cells for generating energy, and 2-DG is thought to impede this pathway by inhibiting several of its enzymes (Pelicano et al. 2006). Glycolysis is also the metabolic pathway used by rapidly proliferating yeast cells to ferment glucose to ethanol. After cellular uptake, hexokinase phosphorylates 2-DG to the highly toxic 2-DG-6-phosphate, which in turn cannot be further converted to fructose-6-phosphate (Jaspers and van Steveninck 1975; Lobo and Maitra 1977).

The fission yeast, *Schizosaccharomyces pombe*, is only remotely related to budding yeast and provides a valuable complementary model organism, being in several ways more closely related to humans than to budding yeast (Hoffman, Wood and Fantes 2015). Research by the Hoffman laboratory and others on glucose metabolism has advanced our understanding of glucose signaling in fission yeast. Glucose is sensed by the Git/Protein Kinase A (PKA) pathway (Hoffman 2005) and the glucose repression pathway involving glucose-6-phosphate (Roux et al. 2009). Based on work in *S. cerevisiae*, 2-DG alters glucose sensing and induces a glucose starvation signal (O'Donnell et al. 2015). During glucose starvation, *S. pombe* PKA forms a complex with its regulatory subunit, and it becomes phosphorylated and re-localized to the cytoplasm (Gupta et al. 2011). Glucose starvation triggers the stress-activated protein kinase pathway in *S. pombe* (Madrid et al. 2006, 2013), resulting in a gene expression response (Madrid et al. 2004; Kato, Kira and Kawamukai 2013).

In *S. pombe*, 2-DG leads to deformed cells that lyse at the site of glucan synthesis (Megnet 1965; Johnson 1968). In addition, the 2-DG-resistant *std1* mutant shows defects in glucose transport (Mehta et al. 1998), and other 2-DG-resistant mutants exhibiting derepressed invertase activity and impaired glucose uptake map to four different genetic loci (Kig, Turkel and Temizkan 2005). Some glucose transport-deficient *S. pombe* mutants are also resistant to 2-DG, but 2-DG resistance and glucose transport deficiency have been attributed to different genetic loci (Milbradt and Höfer 1994). Here, we systematically identify genes that cause 2-DG resistance when overexpressed or when deleted to obtain functional information on 2-DG action in fission yeast.

## MATERIALS AND METHODS

### Media, reagents and strains

Standard methods and media were used for growth of *Schizosaccharomyces pombe* strains. The minimal media used were Edinburgh minimal medium 2 (EMM2) (Moreno, Klar and Nurse 1991) and MM as described (Schweingruber and Edenharter 1990), containing either 2% or 0.5% glucose. In contrast to EMM, MM allows to study growth as well as mating and sporulation. It was

**Table 1.** List of strains used in this study.

Strain name	Genotype	Plasmid
wt	972 h <sup>-</sup>	
ura <sup>-</sup>	ura4 D18 h <sup>-</sup>	
pREP4X	ura4D18 h <sup>-</sup>	pREP4X
pODR1	ura4 D18 h <sup>-</sup>	pODR1
pYSP2	ura4D18 h <sup>-</sup>	pYSP2
Parent	ade6 M210 ura4 D18 leu1 h <sup>+</sup>	
odr1Δ	ade6 M210 ura4 D18 leu1 SPBC215.10::KanMX h <sup>+</sup>	
<sup>a</sup> clr5Δ	ade6 M210 ura4 D18 leu1 clr5::KanMX h <sup>+</sup>	
snf5Δ	ade6 M210 ura4 D18 leu1snf5::KanMX h <sup>+</sup>	
fyv7Δ	ade6 M210 ura4 D18 leu1fyv7::KanMX h <sup>+</sup>	
pho7Δ	ade6 M210 ura4 D18 leu1pho7::KanMX h <sup>+</sup>	
ypa1Δ	ade6 M210 ura4 D18 leu1ypa1::KanMX h <sup>+</sup>	

<sup>a</sup>This deletion could not be verified by PCR.

therefore chosen to characterize the 2-DG-resistant strains. The two media differ in their ammonium content. All media contained leucine, adenine and uracil supplements as required by the strains at 50 μg/ml. 2-deoxy D glucose ≥99% pure was purchased from Sigma Aldrich, USA. The GOD-POD assay kit (Autospan liquid gold glucose kit) for measuring invertase activity was obtained from SPAN diagnostics (India). The primers were obtained from Chromous Biotech, Bangalore, India. The *ura4-D18 h<sup>-</sup>* strain and the haploid deletion mutant library, along with the parent control strain *ade6-M210 ura4-D18 leu1-32 h<sup>+</sup>*, were from the collection of the Bähler laboratory. It corresponds to the latest haploid disruption library version from Bioneer (v5.0), covering 98% of all non-essential genes. The generation of this mutant library has been described, and correct genotypes of the deletion mutants have been tested by PCR as described (Kim et al. 2010; Rallis et al. 2014). Table 1 lists the strains used in this study.

### Growth experiments

Resistance to 2-DG of strains on solid MM media was tested by growing cells in liquid MM to mid-log phase at 30°C, the cell density was normalized, and in a volume of 5 μl ~1.6 × 10<sup>4</sup> and 0.4 × 10<sup>4</sup> cells were applied on the plates shown in Figs 1 and 3.

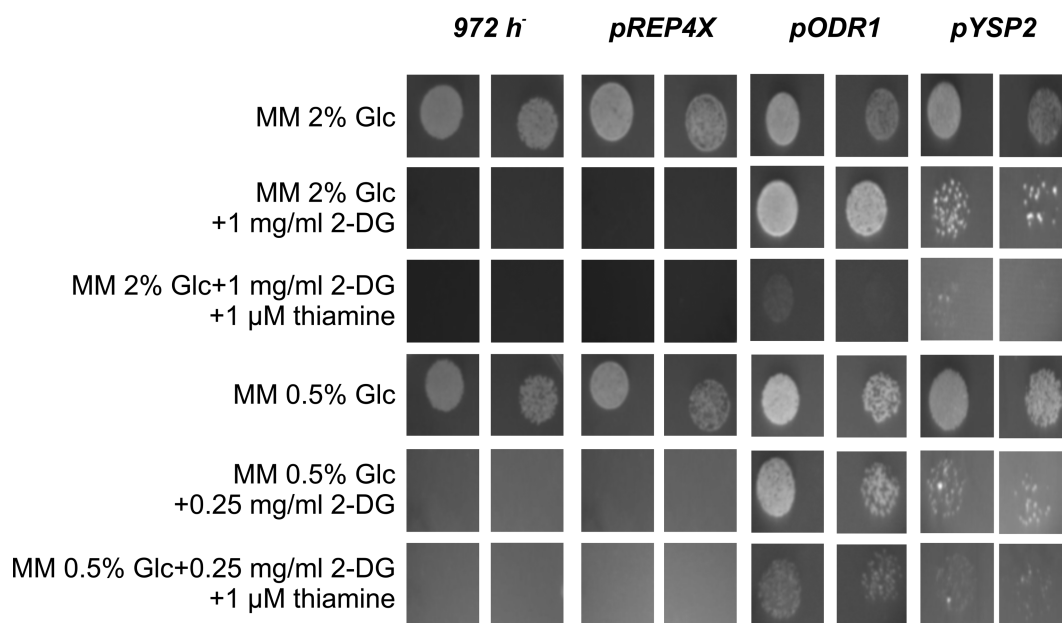
Growth in liquid media was tested by inoculating cells pre-cultured to early mid-log phase in the liquid media given in Figs 2 and 4, and growing cells at 30°C in a rotary shaker at 180–200 rpm. To estimate growth, the optical density was measured at 600 nm and percentage growth inhibition was determined by calculating the percentage decrease between growth in the absence and presence of 2-DG.

### Plasmids

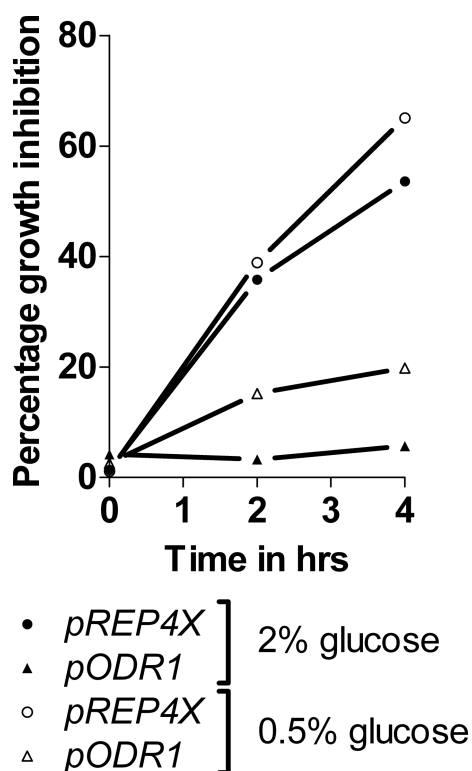
To overexpress wild-type genes, we used a partial *Sau3A* genomic library ligated into the shuttle vector pURL18 as described previously (Barbet, Muriel and Carr 1992) (a gift from Viesturs Simanis). To check for accurate structure of the plasmid, we sequenced it (Chromous Biotech, India) (data not shown). Plasmid pREP4X, containing the thiamine repressible *nmt1* promoter, was obtained from Susan Forsburg (Forsburg 1993).

### Transformations

Strains were transformed by the alkali cation method as described (Moreno, Klar and Nurse 1991) or by the more rapid transformation method (Kanter-Smolter, Dahlkvist and Sunnerhagen 1994).



**Figure 1.** Growth of *odr1* and *ysp2* overexpressor strains on solid media in presence and absence of thiamine. Cells containing the plasmids *pODR1* and *pYSP2* under the control of the *nmt1* promoter, along with the control cells containing the plasmids *pREP4X* and wild-type cells 972, were spotted at two different cell densities on solid MM containing 2% and 0.5% glucose (Glc). Plates contain thiamine and 2-DG as indicated (Materials and Methods). Growth resulting after plating  $\sim 1.6 \times 10^4$  and  $0.4 \times 10^4$  cells as  $5 \mu\text{l}$  drops was assayed. When cells were diluted more, they were not growing at all or only very poorly on 2-DG plates, indicating that 2-DG resistance is highly dependent on initial cell density.



**Figure 2.** Growth inhibition by 2-DG of the *odr1* overexpressor strain in liquid medium. Cells containing the plasmids *pODR1* and control cells containing the plasmid *pREP4X* were grown at  $30^\circ\text{C}$  in MM containing 2% or 0.5% glucose as indicated, the presence and absence of 2-DG (0.25 mg/ml). Growth was tested at 2 and 4 h, and percentages of growth inhibition by 2-DG were plotted. The given values represent the mean of two independent experiments.

### Screening of the disruption strain library

Screening was performed as described (Rallis et al. 2014), but with each mutant represented in quadruplicate. The initial screening was performed on EMM containing 1 mg 2-DG/ml. We re-tested the 2-DG-resistant strains on solid MM containing 1 mg 2-DG/ml. The strains examined in more detail have been tested for co-segregation of the 2-DG and kanamycin resistance marker. In addition, the deletions were validated by colony PCR as previously described (Rallis et al. 2014) (Supplementary Table 2, Supporting Information; Supplementary Fig. 2, Supporting Information)

### Construction of plasmids containing *odr1* and *ysp2* under control of *nmt1* promoter

Using standard PCR-based methods (Moreno, Klar and Nurse 1991), the genes starting with the translation start codon were fused to the *nmt1* promoter. The primers used were for *odr1* TAAGCACTCGAGATGCCGTCTAAAGAA (forward primer) and TAAGCAGGATCCTTATTATTAATTAATAATCAGGAGGGATATTAT (reverse primer) and for *ysp1* TAAGCACTCGAGATGAAGGGT-TTAGGTCT and TAAGCAGGATCCTTATTACTAATACTTGCGAGCG. The REP4X plasmid was cut using a Xho1 and BamH1 double digest. The correct sequences of the constructs were verified by sequencing. We call the plasmids containing the *odr1* and *ysp2* genes under the control of the *nmt1* promoter *pODR1* and *pYSP2*, respectively.

### Invertase assay

Cells were harvested and washed twice with ice-cold 10 mM sodium azide. Cells were pelleted and resuspended in sterile water to an optical density of 1 at 600 nm, corresponding to  $\sim 10^7$  cells/ml. A total of  $100 \mu\text{l}$  cell suspensions were aliquoted into fresh tubes, centrifuged, cell pellets were resuspended in  $50 \mu\text{l}$

of 50 mM sodium acetate pH 5.1 and invertase activity was determined as described (Harkness and Arnason 2014), using the GOD-POD assay kit. Activities are given as units (micromolar glucose produced per minute) per  $10^6$  cells. Statistical analysis was performed using GraphPad Prism 5<sup>®</sup> (GraphPad Software Inc., La Jolla, CA, USA). Results are expressed as mean  $\pm$  SEM ( $n = 3$ ).

## RESULTS

### *odr1* and *ysp2* cause increased 2-DG resistance when overexpressed

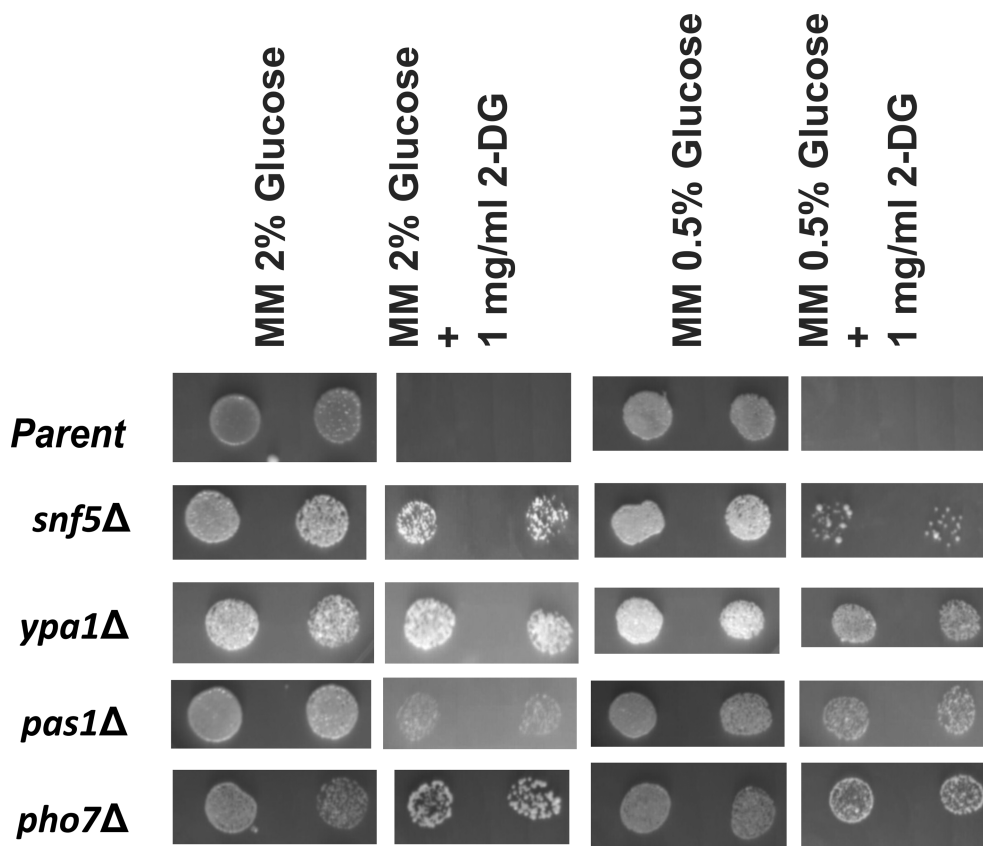
To identify genes involved in 2-DG toxicity, we first screened for strains that are resistant to 2-DG when transformed with the wild-type gene library pURL18. Out of 77 resistant transformants, we could only isolate two intact nuclear genes. The remaining cells either contained plasmids that harbored truncated nuclear or mitochondrial genes, or the plasmids could not be recovered.

The identified genes were put under the control of the expression vector pREP4X containing the thiamine-repressible promoter *nm1*; 2-DG resistance was then examined by growing strains in the presence and absence of thiamine. Knowing from work in *Saccharomyces cerevisiae*, growth conditions such as carbon sources can drastically alter 2-DG resistance (McCartney et al. 2014). We therefore tested the strains both under glucose repressing (2%) and derepressing (0.5%) conditions, and identified two genes leading to 2-DG resistance when

overexpressed. For gene SPBC215.10, called here *odr1* (for overexpression causing deoxyglucose resistance), the effect of thiamine was strong under glucose-repressing conditions, while under glucose-derepressing conditions, the overexpressing strain still weakly grew in the presence of thiamine (Fig. 1). This effect is not surprising given that full repression of the *nm1* promoter occurs only at 15  $\mu$ M thiamine (Forsburg 1993), a concentration that causes weak 2-DG resistance for unknown reasons (unpublished results). The other gene, *ysp2*, showed only weak 2-DG resistance when overexpressed (Fig. 1). The few resistant colonies growing on 2-DG-containing plates probably represent cells containing high plasmid copy numbers. The resistant colonies were unlikely to reflect spontaneous 2-DG-resistant mutants, given that no resistant cells were observed for the wild-type cells, parent control cells and the deletion cells (Fig. 3). Given its weak resistance, we did not further study *ysp2*.

To quantify 2-DG resistance of the *odr1* overexpressor strain, we tested its growth in liquid medium. Neither the wild-type nor parent strain did grow with 1 mg/ml 2-DG, so growth was examined at 0.25 mg/ml 2-DG. Cells were inoculated in the presence and absence of 2-DG and growth was measured after 2 and 4 h incubation. Figure 2 shows the growth inhibition by 2-DG. The data confirm that *odr1* overexpression leads to 2-DG resistance, although the effect was weaker in liquid low-glucose medium than in high-glucose medium.

Knowing that overexpression of *odr1* causes resistance to 2-DG, we tested whether the corresponding deletion mutant (*odr1::kanMX ade6-M210 ura4-D18 leu1-32*) was more sensitive than its parent strain. However, quantitative measurements in



**Figure 3.** Growth of deletion mutants in absence and presence of 2-DG on solid media. The mutants as indicated, along with the parent strain (*ade6-M210 ura4-D18 leu1-32 h<sup>+</sup>*), were spotted at two different cell densities on MM and MM containing 2-DG plates, both under glucose-repressing and derepressing conditions as given for Fig. 1.



liquid medium showed no increased sensitivity to 2-DG for the *odr1* mutant (data not shown).

### Identification of four genes causing 2-DG resistance when deleted

In a complementary approach to identify genes involved in 2-DG toxicity, we pre-screened a haploid deletion library for mutants resistant to 2-DG on EMM plates containing 1.0 mg/ml 2-DG. This first screen identified 14 mutants exhibiting 2-DG resistance phenotypes in both of the two independent repeats carried out (Supplementary Fig. 1, Supporting Information; Supplementary Table 1, Supporting Information). We also performed a second screen for mutants resistant to 2-DG on EMM plates containing the lower dose of 0.5 mg/ml 2-DG. This screen identified 59 mutants exhibiting 2-DG resistance phenotypes in both of the two independent repeats carried out. The hits of the second screen included all 14 mutants of the first screen (Supplementary Table 1, Supporting Information).

To characterize growth of the 14 resistant mutants from the first screen, we tested them under the same physiological conditions as the *odr1* overexpressor strain in MM containing 2-DG (1.0 mg/ml). For seven mutant strains, deleted for the genes *plc1*, *iec1*, *adn3*, *vps38*, *rx13*, *trk2* and *moe1*, resistance to 2-DG was weak (data not shown), while one mutant, deleted for the gene *snz1*, did not grow after re-streaking on either MM or EMM for unknown reasons (data not shown). These differences in resistance and growth under the two conditions tested highlight the effect that physiological conditions can have for experiments involving glucose metabolism. For one mutant, deleted for the gene *fyv7*, the kanamycin resistance did not co-segregate with 2-DG resistance, revealing that the resistance was not caused by the deletion.

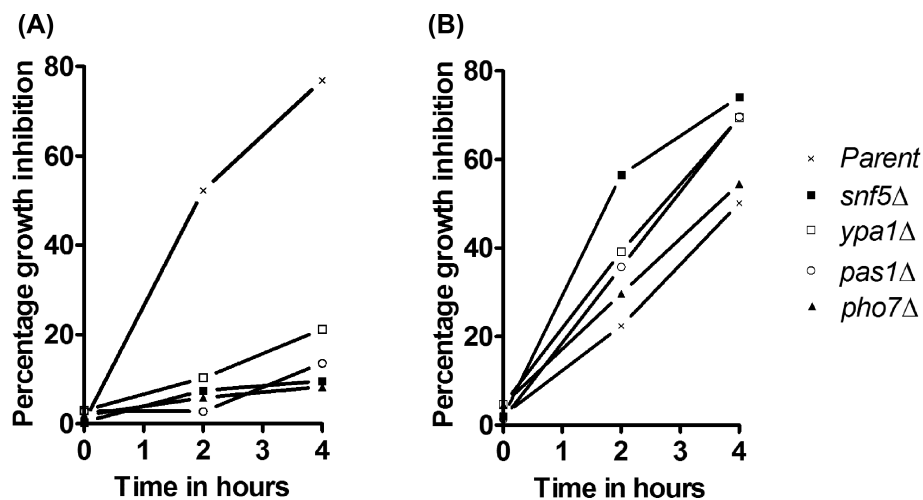
Four of these 14 strains identified in the screen exhibited moderate to strong resistance under glucose-repressing conditions on MM plates containing 1.0 mg/ml 2-DG. A fifth strain, *clr5Δ*, also caused 2-DG resistance, but we could not confirm the deletion by PCR genotyping (Supplementary Fig. 2, Supporting Information). The four PCR-verified strains were deleted for the following genes: *snf5*, *ypa1*, *pas1* and *pho7*. For all of these mutants, the kanamycin marker co-segregated with the 2-DG

resistance phenotype (data not shown) shows that the resistance is caused by the gene deletion. Examination of cell morphologies of the four resistant mutants did not reveal any evident differences to wild-type cells (data not shown). Except for the mutant *snf5Δ*, which has previously been reported to be 2-DG resistant (Monahan et al. 2008), the other four mutants also grew well under derepressing conditions on solid medium (Fig. 3). Growth tests of the four mutants in liquid medium exhibited strong 2-DG resistance under glucose-repressing conditions (Fig. 4A). On the other hand, these mutants did not show any 2-DG resistance under derepressing conditions, with most showing even higher sensitivity than the parental strain (Fig. 4B). We assume that osmotic stabilization effects acting in colonies but not in liquid medium may be responsible for the different growth behavior.

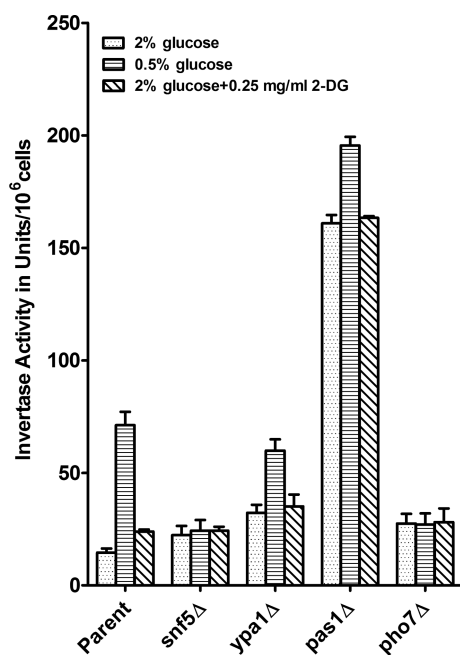
### 2-DG-resistant mutants exhibit altered invertase expression

The invertase *Inv1* of *Schizosaccharomyces pombe* is a glucose-repressible cell wall glycoprotein (Moreno et al. 1985). *Inv1* expression is partially diagnostic for the control of glucose metabolism and particularly for the state of glucose repression. We tested the *Inv1* activity in the 2-DG-resistant mutants grown under repressed and derepressed conditions. The mutant strains varied in their activity levels, both in the repressed and derepressed state, when compared to the parent strain, with the greatest upregulation observed in *pas1Δ*. The deletion mutants *snf5Δ* and *pho7Δ* were more affected in glucose derepression, whereas *ypa1Δ* was more affected under glucose repression (Fig. 5). In summary, comparing the ratios of the activities of cells grown under high- and low-glucose conditions, the mutants and the *odr1*-overexpressing strain featured a more constitutive invertase phenotype than the control strains (Table 2). Examination of the corresponding *odr1Δ* mutant revealed a hyperderepression (Table 2). These results indicate that the *odr1* gene, in its wild-type configuration, plays a role in glucose repression.

We also tested the effect of 2-DG on the regulation of invertase activity under glucose-repressed conditions. In the parent strains, 2-DG enhanced *Inv1* activity, in contrast to the



**Figure 4.** Growth inhibition of deletion mutants by 2-DG in liquid medium. The mutants as indicated, along with the parent strain (*ade6-M210 ura4-D18 leu1-32 h<sup>+</sup>*), were grown at 30°C in MM medium containing 2% glucose (A) or 0.5% glucose (B) in the presence and absence of 2-DG (0.25 mg/ml). Growth was tested after 2 and 4 h and percentages of growth inhibition by 2-DG were plotted. The data represent the mean of two independent experiments.



**Figure 5.** Invertase activity of the 2-DG-resistant mutants. Cells from the 2-DG-resistant deletion mutants and the corresponding parent strains *ade6-M210 ura4-D18 leu1-32 h<sup>+</sup>* were grown in MM medium containing 2% or 0.5% glucose and in 2% glucose medium containing 2-DG as indicated. Invertase activity was determined and is given as activity per cells (Materials and Methods). The values given represent the mean of three measurements, with samples from each measured in five replicates, originating from three independent experiments. Error bars represent SEM ( $n = 3$ ).

**Table 2.** Ratios of invertase activity of 2-DG-resistant mutants under glucose-repressed and derepressed conditions and in the presence of 2-DG.

Strain	Fold increase of invertase activity from 2% to 0.5% glucose	Fold increase of invertase activity in 2% glucose containing 2-DG
pREP4X	3.9 ± 0.26	2.2 ± 0.19
pODR1	1.6 ± 0.06	1.3 ± 0.07
Parent	5.0 ± 0.44	1.7 ± 0.6
<i>odr1Δ</i>	6.9 ± 0.83	3.6 ± 0.61
<i>snf5Δ</i>	1.1 ± 0.01	1.2 ± 0.19
<i>ypa1Δ</i>	1.9 ± 0.22	1.1 ± 0.05
<i>pas1Δ</i>	1.2 ± 0.004	1.0 ± 0.03
<i>pho7Δ</i>	1.0 ± 0.08	1.0 ± 0.06

pREP4X: control strain for overexpressor strain pODR1.

Parent: parent strain of deletion strains (*ade6-M210 ura4-D18 leu1-32 h<sup>+</sup>*).

Different ratios of activities in pREP4X and parent strains are due to plasmid effects. Activity was measured in MM containing 2%, 0.5% or 2% glucose plus 0.25 mg/ml 2-DG (see Materials and Methods) and the ratios ±SEM ( $n = 3$ ) are indicated here.

situation in *S. cerevisiae* where 2-DG represses its activity (Randez-Gil, Prieto and Sanz 1995). Similar results were obtained for all tested strains, including control strains 972, *ura4-D18* and the pREP4X-containing strain (data not shown). These results suggest that 2-DG is mimicking glucose starvation. For the 2-DG-resistant mutants, the effects of 2-DG on Inv1 expression are qualitatively similar as for low glucose (Table 2).

## DISCUSSION

The genetics of 2-DG resistance is complicated as 2-DG and its metabolic products are involved in a variety of processes. This makes it difficult to understand mechanism of 2-DG actions or its resistance. We identified the *Schizosaccharomyces pombe odr1* gene causing strong 2-DG resistance when overexpressed. Despite examining many 2-DG resistant transformants, we could detect only one gene exhibiting this strong overexpression phenotype. In *Saccharomyces cerevisiae*, a similar screening yielded two genes, *DOG1* and *DOG2* (Randez-Gil et al. 1995). These findings suggest that the number of genes whose overexpression confers 2-DG resistance is limited. On the other hand, we uncovered several deletion mutants that render cells resistant to 2-DG. Among 14 initially selected mutants, four mutants conferred moderate to good resistance to 2-DG. By screening at a 2-fold lower 2-DG concentration, we isolated 59 resistant mutants (Supplementary Fig. 1, Supporting Information; Supplementary Table 1, Supporting Information). These findings suggest that control of 2-DG resistance is a complex process involving many genes, considering also that we have not tested any genes that are essential for growth. In a similar screen performed in *S. cerevisiae*, 19 deletion mutants that are resistant to 2-DG have been reported (Ralser et al. 2008), although it has later been suggested that 16 of these mutants are not actually causing 2-DG resistance (McCartney et al. 2014). Out of the three remaining genes, deletion of *HXX2* and *REG1* provides strong resistance on glucose-rich media, whereas deletion of *LSM6* is only weakly resistant (Neigeborn and Carlson 1987; Ralser et al. 2008; McCartney et al. 2014).

The transcription of the invertase gene is repressed by the presence of glucose (Tanaka et al. 1998). The deletion mutants are affected to different degrees in the control of invertase activity (Fig. 5). According to the invertase activity ratios in the repressed versus derepressed states, the mutants exhibit constitutive invertase activity (Table 2). The corresponding proteins could be directly or indirectly involved in this control. The invertase activity data also indicate that 2-DG induces a glucose starvation signal and thus derepresses the invertase activity, while the deletion mutants resistant to 2-DG show more constitutive invertase activities across different conditions (Fig. 5).

Decreased growth on glucose has been reported for mutants deleted for *clr5*, *ypa1* and *pho7*, consistent with these genes being defective in the control of glucose metabolism (Vachon et al. 2013; Doi et al. 2015). The genes *snf5*, *pas1* and *pho7* are involved in transcription (Table 3), raising the possibility that mutants of these genes prevent some changes in gene expression induced by 2-DG that could promote resistance to 2-DG. The *snf5*, *ypa1* and *pas1* genes show orthologs in *S. cerevisiae*, but the corresponding mutants have not been reported to be 2-DG resistant. The *S. cerevisiae* protein Snf1 is involved in controlling 2-DG sensitivity (O'Donnell et al. 2015), but its *S. pombe* ortholog, Ssp2, has neither been reported to be involved in resistance to 2-DG, nor did it come up in our screen.

Even though some molecular functions of the corresponding proteins have been described (Table 3), we do not have a straightforward explanation for how the genes identified affect 2-DG resistance and glucose repression when deleted. The protein Snf5 is a subunit of the SWI/SNF chromatin remodeling complex involved in transcription and chromatin-related processes. Interestingly, the human Snf5 ortholog is involved in cancer development (Roberts and Orkin 2004). Deletion of *snf5* leads to increased mRNAs encoding hexose transports (Monahan et al. 2008), which could explain the increased 2-DG resistance in the

**Table 3.** List of genes and their annotations identified in this study.

Gene standard name	Gene product	Molecular function	References
<i>snf5</i>	Chromatin remodeling (SWItch/Sucrose Non-Fermentable; SWI/SNF) complex subunit	Regulation of transcription and glucose import	Monahan et al. (2008)
<i>ypa1</i> <i>pho7</i>	Protein phosphatase type 2A regulator Transcription factor	Regulation of protein phosphatase activity Regulation of RNA polymerase II-mediated transcription	Goyal and Simanis (2012) Estill, Kerwin-Iosue and Wykoff (2015)
<i>pas1</i>	Cyclin	Regulation of G1/S transition of cell cycle	van Slegtenhorst, Mustafa and Henske (2005)

Only the most important annotations of the genes are given. For more details refer to *S. pombe* genome data and annotations database (Wood et al. 2012).

high-glucose condition only, where increased influx of glucose may titrate out 2-DG (Figs 3 and 4). This result is of interest in light of findings in *S. cerevisiae* that 2-DG acts by reducing the levels of hexose transporters by  $\alpha$ -arrestin-mediated endocytosis and degradation in vacuoles (O'Donnell et al. 2015). Deletion of *snf5* in *S. pombe* may thus counteract this effect of 2-DG. Except for the *snf5* deletion, the other four deletion mutants showed resistance to 2-DG in both high- and low-glucose conditions, suggesting that these gene deletions affect resistance by a different mechanism.

We speculate that the *S. pombe* Odr1 hydrolase might function in detoxifying toxic forms of 2-DG, similar to the *S. cerevisiae* Dog1/Dog2 proteins that encode haloacid dehalogenase-like (HAD-like) hydrolase enzymes exhibiting specific 2-DG-6-phosphatase activities and thus render cells 2-DG resistant when overexpressed. The physiological function of these enzymes is not known (Sanz, Rande-Gil and Prieto 1994; Rande-Gil, Prieto and Sanz 1995; Rande-Gil et al. 1995). An HAD-like hydrolase domain is also present in Odr1, besides a Cof-subfamily domain believed to be required for enzymes acting on phosphorylated sugars (Marchler-Bauer et al. 2015). It is therefore plausible that Odr1 detoxifies the toxic form of 2-DG. Notably, these proteins have opposite effects on invertase expression: overexpression of Odr1 causes derepression of *S. pombe* invertase, whereas overexpression of Dog1 causes repression of *S. cerevisiae* invertase (Rande-Gil, Prieto and Sanz 1995).

A BLAST search (Altschul et al. 1990) for Dog1/Dog2 orthologs in *S. pombe* yielded protein SPCC1020.07 (annotated as a pseudouridine 5' phosphatase), and a search for Odr1 paralogs in *S. pombe* revealed a protein (SPAC25B8.12c) with 45% identity. None of these proteins, however, did come up in our screen for genes causing 2-DG resistance during overexpression, but the deletion mutant of SPCC1020.07 renders the cells weakly 2-DG resistant (Supplementary data, screening at 0.5 mg/ml 2-DG, Supporting Information).

The *S. pombe* orthologs of genes conferring resistance when overexpressed or deleted in *S. cerevisiae* (DOG1/DOG2, REG1 and HXK2) did not come up in our screen. Moreover, the *odr1* gene, rendering *S. pombe* cells 2-DG resistant, shows the opposite effect on invertase activity to the DOG1 gene, rendering *S. cerevisiae* 2-DG resistant. Notably, the finding that 2-DG derepresses the invertase activity in *S. pombe*, unlike in *S. cerevisiae* where it is repressed (Rande-Gil, Prieto and Sanz 1995), suggests that control of 2-DG resistance in the two yeasts is achieved by at least partially different mechanisms. The mechanisms by which the identified genes affect 2-DG-induced gene expression, sensitivity and glucose repression in *S. pombe* require further studies.

## SUPPLEMENTARY DATA

Supplementary data are available at FEMSYR online.

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**Conflict of interest.** None declared.

## REFERENCES

- Altschul SF, Gish W, Miller W et al. Basic local alignment search tool. *J Mol Biol* 1990;215:403–10.
- Barbet N, Muriel WJ, Carr AM. Versatile shuttle vectors and genomic libraries for use with *Schizosaccharomyces pombe*. *Gene* 1992;114:59–66.
- Biely P, Z Krátký, Kovařík J et al. Effect of 2-Deoxyglucose on cell wall formation in *Saccharomyces cerevisiae* and its relation to cell growth inhibition. *J Bacteriol* 1971;107:121–9.
- Cairns RA, Harris IS, Mak TW. Regulation of cancer cell metabolism. *Nat Rev Cancer* 2011;11:85–95.
- Doi A, Fujimoto A, Sato S et al. Chemical genomics approach to identify genes associated with sensitivity to rapamycin in the fission yeast *Schizosaccharomyces pombe*. *Genes Cells* 2015;20:292–309.
- Entian KD, Zimmermann FK. Glycolytic enzymes and intermediates in carbon catabolite repression mutants of *Saccharomyces cerevisiae*. *Mol Gen Genet* 1980;177:345–50.
- Estill M, Kerwin-Iosue CL, Wykoff DD. Dissection of the PHO pathway in *Schizosaccharomyces pombe* using epistasis and the alternate repressor adenine. *Curr Genet* 2015;61:175–83.
- Forsburg SL. Comparison of *Schizosaccharomyces pombe* expression systems. *Nucleic Acids Res* 1993;21:2955–6.



- Goyal A, Simanis V. Characterization of *ypa1* and *ypa2*, the *Schizosaccharomyces pombe* orthologs of the peptidyl prolyl isomerases that activate PP2A, reveals a role for Ypa2p in the regulation of cytokinesis. *Genetics* 2012;**190**:1235–50.
- Gupta DR, Paul SK, Oowatari Y et al. Complex formation, phosphorylation, and localization of protein kinase A of *Schizosaccharomyces pombe* upon glucose starvation. *Biosci Biotech Bioch* 2011;**75**:1456–65.
- Harkness TA, Arnason TG. A simplified method for measuring secreted invertase activity in *Saccharomyces cerevisiae*. *Biochem Pharmacol* 2014;**03**, DOI: 10.4172/2167-0501.1000151.
- Hoffman CS. Glucose sensing via the protein kinase A pathway in *Schizosaccharomyces pombe*. *Biochem Soc T* 2005;**33**:257–60.
- Hoffman CS, Wood V, Fantes PA. An ancient yeast for young geneticists: a primer on the *Schizosaccharomyces pombe* model system. *Genetics* 2015;**201**:403–23.
- Jaspers HTA, van Steveninck J. Transport-associated phosphorylation of 2-deoxy-d-glucose in *Saccharomyces fragilis*. *BBA-Biomembranes* 1975;**406**:370–85.
- Johnson BF. Lysis of yeast cell walls induced by 2-deoxyglucose at their sites of glucan synthesis. *J Bacteriol* 1968;**95**:1169–72.
- Kanter-Smoler G, Dahlkvist A, Sunnerhagen P. Improved method for rapid transformation of intact *Schizosaccharomyces pombe* cells. *BioTechniques* 1994;**16**:798–800.
- Kato H, Kira S, Kawamukai M. The transcription factors Atf1 and Pcr1 are essential for transcriptional induction of the extracellular maltase Agl1 in fission yeast. *PLoS One* 2013;**8**:e80572.
- Kig C, Turkel S, Temizkan G. Isolation and characterization of glucose derepressed invertase mutants from *Schizosaccharomyces pombe*. *Biosci Biotech Bioch* 2005;**69**:2475–8.
- Kim D-U, Hayles J, Kim D et al. Analysis of a genome-wide set of gene deletions in the fission yeast *Schizosaccharomyces pombe*. *Nat Biotechnol* 2010;**28**:617–23.
- Krátký Z, Biely P, Bauer Š. Mechanism of 2-Deoxy-d-glucose inhibition of cell-wall polysaccharide and glycoprotein biosyntheses in *Saccharomyces cerevisiae*. *Eur J Biochem* 1975;**54**:459–67.
- Lobo Z, Maitra PK. Resistance to 2-deoxyglucose in yeast: a direct selection of mutants lacking glucose-phosphorylating enzymes. *Mol Gen Genet* 1977;**157**:297–300.
- Madrid M, Fernández-Zapata J, Sánchez-Mir L et al. Role of the fission yeast cell integrity MAPK pathway in response to glucose limitation. *BMC Microbiol* 2013;**13**:34.
- Madrid M, Soto T, Franco A et al. A cooperative role for Atf1 and Pap1 in the detoxification of the oxidative stress induced by glucose deprivation in *Schizosaccharomyces pombe*. *J Biol Chem* 2004;**279**:41594–602.
- Madrid M, Soto T, Khong HK et al. Stress-induced response, localization, and regulation of the Pmk1 cell integrity pathway in *Schizosaccharomyces pombe*. *J Biol Chem* 2006;**281**:2033–43.
- Marchler-Bauer A, Derbyshire MK, Gonzales NR et al. CDD: NCBI's conserved domain database. *Nucleic Acids Res* 2015;**43**:D222–6.
- McCartney RR, Chandrashekarappa DG, Zhang BB et al. Genetic analysis of resistance and sensitivity to 2-deoxyglucose in *Saccharomyces cerevisiae*. *Genetics* 2014;**198**:635–46.
- Megnet R. Effect of 2-deoxyglucose on *Schizosaccharomyces pombe*. *J Bacteriol* 1965;**90**:1032–5.
- Mehta SV, Patil VB, Velmurugan S et al. Std1, a gene involved in glucose transport in *Schizosaccharomyces pombe*. *J Bacteriol* 1998;**180**:674–9.
- Milbradt B, Höfer M. Glucose-transport-deficient mutants of *Schizosaccharomyces pombe*: Phenotype, genetics and use for genetic complementation. *Microbiology* 1994;**140**:2617–23.
- Monahan BJ, Villén J, Marguerat S et al. Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. *Nat Struct Mol Biol* 2008;**15**:873–80.
- Moreno S, Klar A, Nurse P. Molecular genetic analysis of fission yeast *Schizosaccharomyces pombe*. *Method Enzymol* 1991;**194**:795–823.
- Moreno S, Ruíz T, Sánchez Y et al. Subcellular localization and glycoprotein nature of the invertase from the fission yeast *Schizosaccharomyces pombe*. *Arch Microbiol* 1985;**142**:370–4.
- Neugeborn L, Carlson M. Mutations causing constitutive invertase synthesis in yeast: genetic interactions with *snf* mutations. *Genetics* 1987;**115**:247–53.
- O'Donnell AF, McCartney RR, Chandrashekarappa DG et al. 2-Deoxyglucose impairs *Saccharomyces cerevisiae* growth by stimulating Snf1-regulated and  $\alpha$ -arrestin-mediated trafficking of hexose transporters 1 and 3. *Mol Cell Biol* 2015;**35**:939–55.
- Pelicano H, Martin DS, Xu R-H et al. Glycolysis inhibition for anticancer treatment. *Oncogene* 2006;**25**:4633–46.
- Raez LE, Papadopoulos K, Ricart AD et al. A phase I dose-escalation trial of 2-deoxy-d-glucose alone or combined with docetaxel in patients with advanced solid tumors. *Cancer Chemoth Pharm* 2013;**71**:523–30.
- Rallis C, López-Maury L, Georgescu T et al. Systematic screen for mutants resistant to TORC1 inhibition in fission yeast reveals genes involved in cellular ageing and growth. *Biol Open* 2014;**3**:161–71.
- Ralsler M, Wamelink MM, Struys EA et al. A catabolic block does not sufficiently explain how 2-deoxy-D-glucose inhibits cell growth. *P Natl Acad Sci USA* 2008;**105**:17807–11.
- Randez-Gil F, Blasco A, Prieto JA et al. DOGR1 and DOGR2: two genes from *Saccharomyces cerevisiae* that confer 2-deoxyglucose resistance when overexpressed. *Yeast* 1995;**11**:1233–40.
- Randez-Gil F, Prieto JA, Sanz P. The expression of a specific 2-deoxyglucose-6P phosphatase prevents catabolite repression mediated by 2-deoxyglucose in yeast. *Curr Genet* 1995;**28**:101–7.
- Roberts CWM, Orkin SH. The SWI/SNF complex — chromatin and cancer. *Nat Rev Cancer* 2004;**4**:133–42.
- Roux AE, Leroux A, Alaamery MA et al. Pro-aging effects of glucose signaling through a g protein-coupled glucose receptor in fission yeast. *PLoS Genet* 2009;**5**:e1000408.
- Sanz P, Randez-Gil F, Prieto JA. Molecular characterization of a gene that confers 2-deoxyglucose resistance in yeast. *Yeast* 1994;**10**:1195–202.
- Schweingruber ME, Edenharter E. Thiamin regulates agglutination and zygote formation in *Schizosaccharomyces pombe*. *Curr Genet* 1990;**17**:191–4.
- Tanaka N, Ohuchi N, Mukai Y et al. Isolation and characterization of an invertase and its repressor genes from *Schizosaccharomyces pombe*. *Biochem Bioph Res Co* 1998;**245**:246–53.
- Vachon L, Wood J, Kwon E-JG et al. Functional characterization of fission yeast transcription factors by overexpression analysis. *Genetics* 2013;**194**:873–84.
- van Slegtenhorst M, Mustafa A, Henske EP. Pas1, a G1 cyclin, regulates amino acid uptake and rescues a delay in G1 arrest in Tsc1 and Tsc2 mutants in *Schizosaccharomyces pombe*. *Hum Mol Genet* 2005;**14**:2851–8.
- Wood V, Harris MA, McDowall MD et al. PomBase: a comprehensive online resource for fission yeast. *Nucleic Acids Res* 2012;**40**:D695–9.
- Zimmermann FK, Scheel I. Mutants of *Saccharomyces cerevisiae* resistant to carbon catabolite repression. *Mol Gen Genet* 1977;**154**:75–82.