

Changes in gene expression in response to cold temperature in *Saccharomyces cerevisiae* grown in dextrose using microarrays



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Introduction

Saccharomyces cerevisiae is a model organism for eukaryotes. It is a favorable organism to study cellular responses to stress because it is unicellular and its genome has been sequenced. Microarrays are an excellent tool for identifying changes in gene expression in response to stress. Each yeast microarray contains 6,400 genes of distinct DNA sequences made with a simple robotic printing device (DeRisi, 1997). Previous studies using microarrays have examined the response of *S. cerevisiae* to cold shock at 4°C (Murata and other, 2005). In this research, we aimed to determine how gene expression changes in cells exposed to 10°C and to determine if there were differences in response to cold temperature between fermenting and respiring cells. *S. cerevisiae* cells were grown in dextrose, a media in which they ferment at 28°C. Control cells were collected and flash frozen in liquid nitrogen. Cold-treated cells were transferred into a 10°C shaking water bath and cells were harvested at 30 min., 2hr, and 8 hr. Gene expression was analyzed using Magic Tool software and compared to changes in gene expression in respiring cells grown in galactose. We hypothesized that *S. cerevisiae* grown in galactose at cold temperature would have higher levels of oxidative stress compared to cells grown in dextrose because oxygen is used in the electron transport chain during aerobic respiration. We concluded that yeast grown in dextrose and galactose have similar changes in gene expression in response to cold temperature.

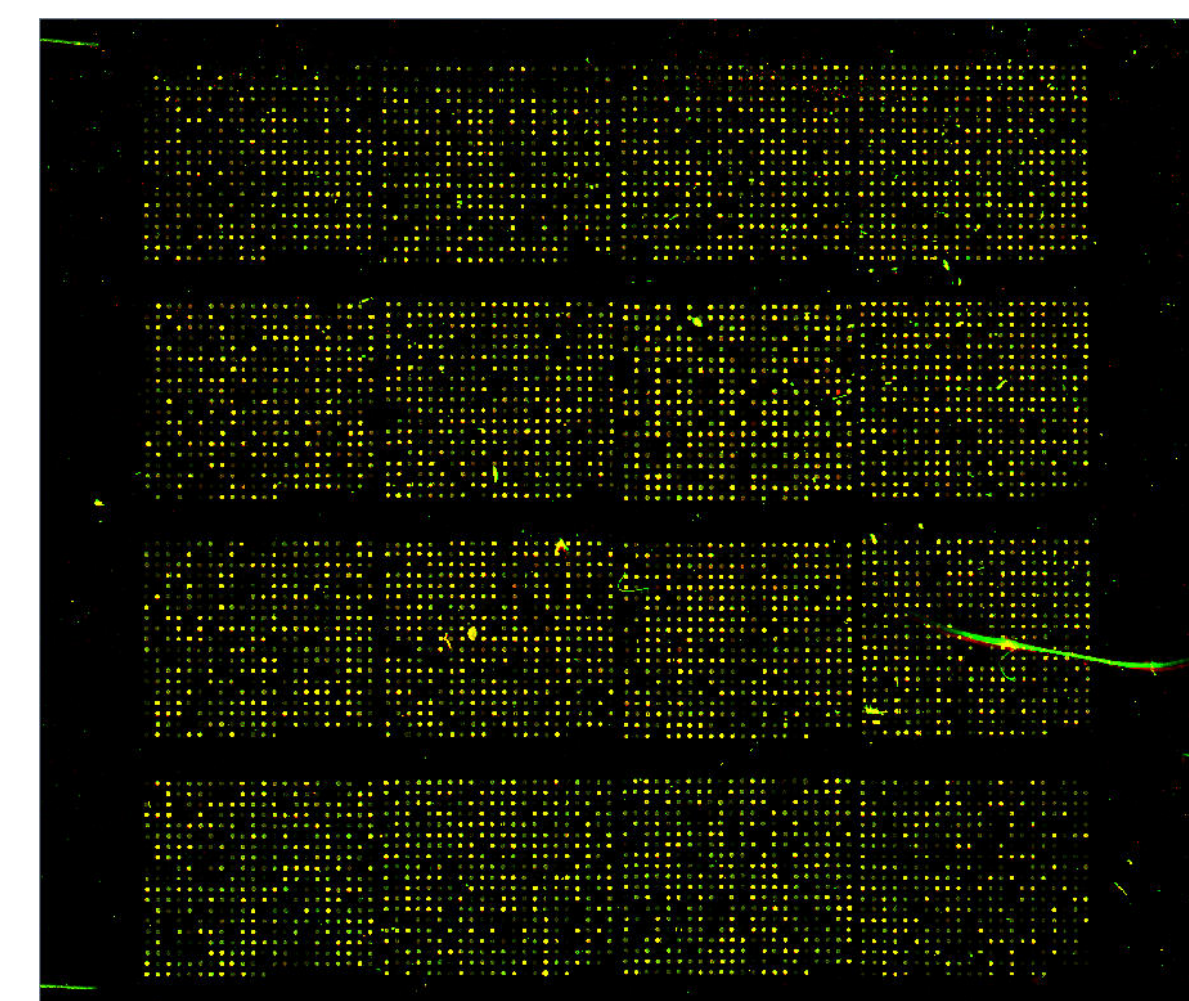
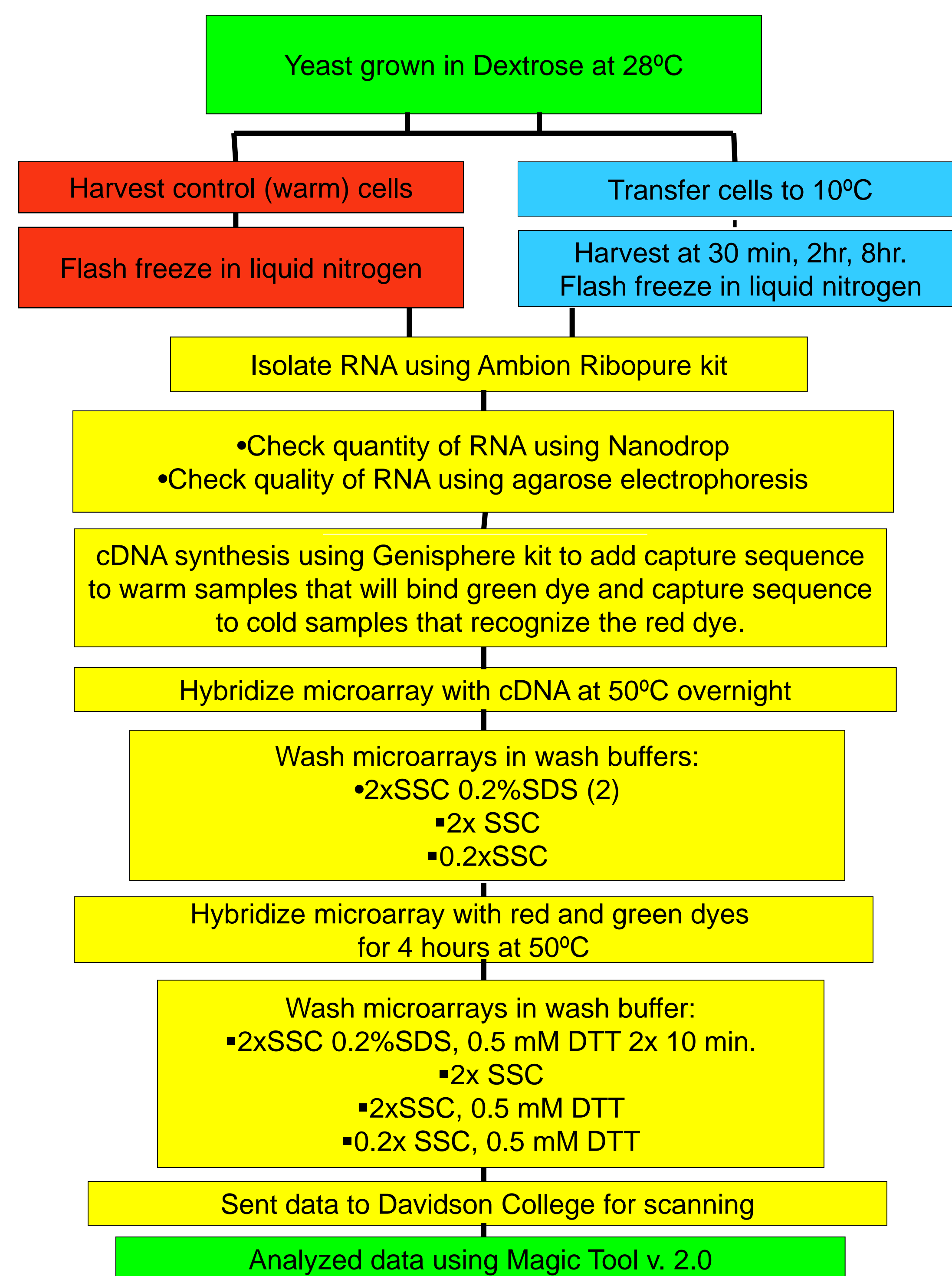


Fig. 1. Example of a microarray. Each spot represents a gene. **RED** indicates the gene has been induced. **GREEN** indicates it is repressed, and **YELLOW** indicates no change in expression in response to cold temperature exposure.

Materials and Methods



Results and Discussion

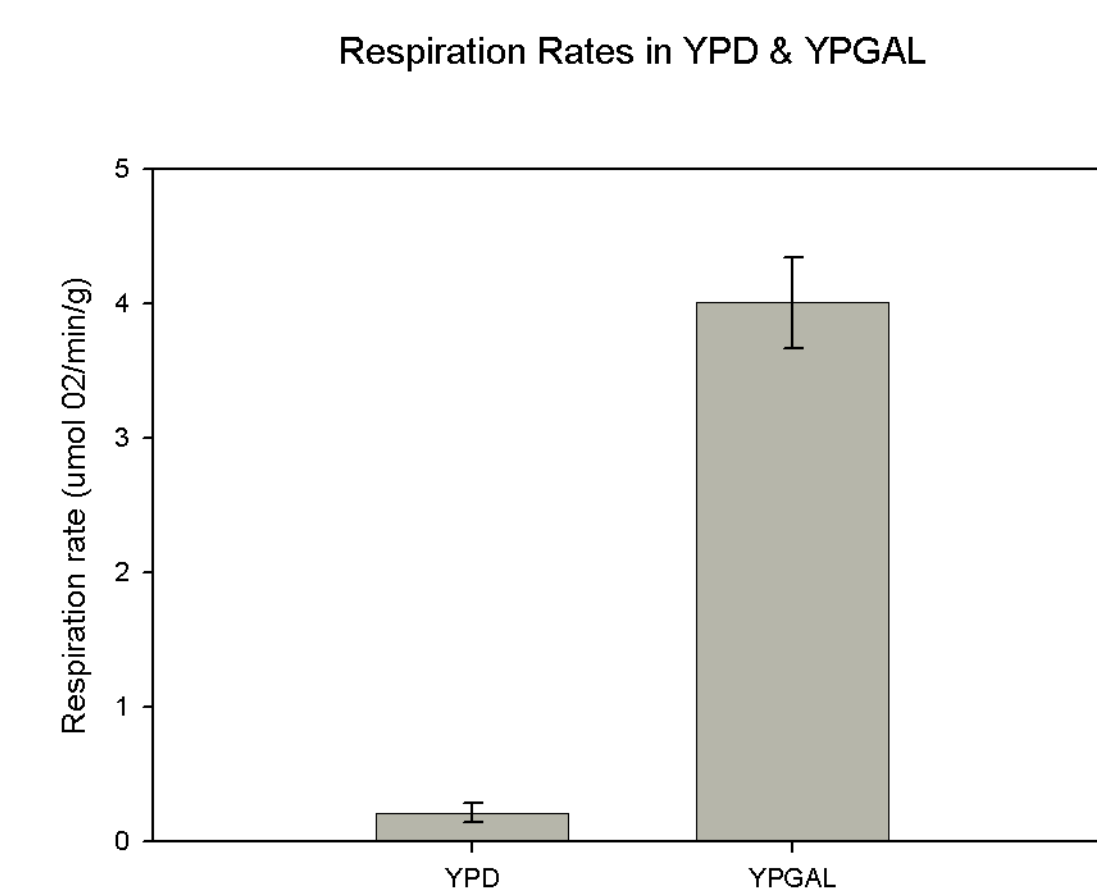


Fig. 2. Respiration rates of yeast cells grown in YPD (dextrose) & YPGAL (galactose).
• Respiration rates of cells grown in YPGAL were higher than cells grown in YPD.
• Cells grown in YPGAL obtain energy through cellular respiration. Cells grown in YPD obtain energy through fermentation.

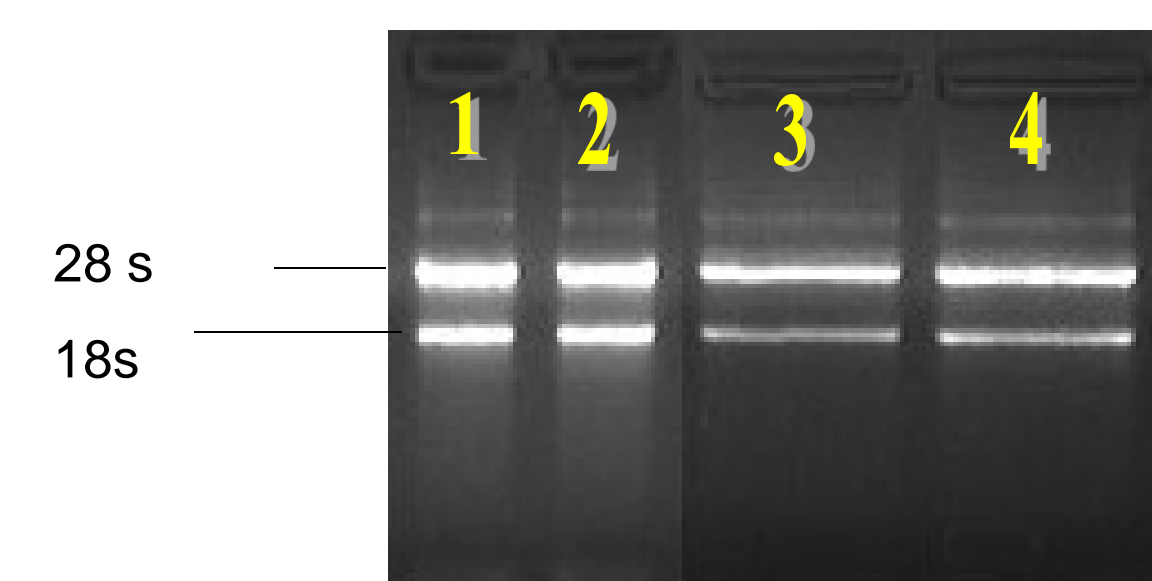


Fig. 3. Agarose Gel
1. warm YPD 28°C
2. 30 min. YPD 10°C
3. 2hr YPD 10°C
4. 8hr YPD 10°C

• Quality check of RNA using agarose gel electrophoresis.

Table 1: Expression change of yeast genes at each time point in 10° C in YPD

A. Genes that are induced in response to cold temperature ≥ 3-fold

Biological Process	Total # of genes	30 min	%	2hr	%	8hr	%
Biogenesis	229	22	10%	25	11%	0	0%
Cell Cycle	50	5	10%	5	10%	0	0%
Chaperone	84	9	11%	6	7%	0	0%
DNA Repair	53	2	4%	3	6%	0	0%
DNA Replication	42	4	10%	3	7%	0	0%
Folding	41	1	2%	1	2%	0	0%
Heat Shock	24	2	8%	3	13%	0	0%
Metabolism	206	16	8%	12	6%	0	0%
Modification	37	5	14%	7	19%	0	0%
Oxidative Phosphorylation	3	1	33%	1	33%	0	0%
Oxidative Stress	28	5	18%	3	11%	0	0%
Protein	770	70	9%	58	8%	0	0%
Respiration	48	3	6%	4	8%	0	0%
Signal	56	4	7%	2	4%	0	0%
Stress	142	17	12%	15	11%	0	0%
Transcription	289	27	9%	25	9%	0	0%
Translation	65	6	9%	4	6%	0	0%
Transport	396	39	10%	30	8%	0	0%
Unknown	2258	193	9%	181	8%	0	0%

• Genes involved in protein processes, metabolism, and stress were found to be significantly up regulated

B. Genes that are repressed ≥ 3-fold in response to cold temperature

Biological Process	Total number of genes	30 min	%	2 hr	%	8 hr	%
Biogenesis	229	3	1%	3	1%	0	0%
Cell Cycle	50	1	2%	0	0%	0	0%
Chaperone	84	3	4%	1	1%	0	0%
DNA Repair	53	1	2%	0	0%	0	0%
DNA Replication	42	3	7%	1	2%	0	0%
Folding	41	2	5%	0	0%	0	0%
Heat Shock	24	1	4%	1	4%	0	0%
Metabolism	206	4	2%	5	2%	0	0%
Modification	37	2	5%	0	0%	0	0%
Oxidative Phosphorylation	3	0	0%	0	0%	0	0%
Oxidative Stress	28	4	14%	0	0%	0	0%
Protein	770	19	2%	19	2%	0	0%
Respiration	48	2	4%	0	0%	0	0%
Signal	56	0	0%	0	0%	0	0%
Stress	142	7	5%	2	1%	0	0%
Transcription	289	11	4%	3	1%	0	0%
Translation	65	4	6%	0	0%	0	0%
Transport	396	4	1%	2	1%	0	0%
Unknown	2258	53	2%	37	2%	2	0%

• Fewer genes were repressed than induced during cold acclimation

Table 2: Metabolic genes that are induced in response to cold temperature ≥ 3-fold

Gene Name	Alias	Biological Process	Molecular Function
30 Minutes			
YAL044C	GCV3	one-carbon compound metabolism	glycine dehydrogenase (decarboxylating) activity
YPL273W	SAM4	sulfur amino acid metabolism	homocysteine S-methyltransferase activity
YOL011W	PLB3	phosphonitride metabolism	lysophospholipase activity
YER091C_rep2	MET6	methionine metabolism	5-methyltetrahydropteroylglutamate-homocysteine S-methyltransferase activity
YPL038W	MET31	sulfur amino acid metabolism	specific RNA polymerase II transcription factor activity
YDR204W	COO4	ubiquinone metabolism	molecular_function unknown
YJR139C	HOM6	methionine metabolism	homocysteine dehydrogenase activity
YER024W	VAT2	alcohol metabolism	carbamoyl-O-acetyltransferase activity
YJR101W	MET3	methionine metabolism	sulfate adenylyltransferase (ATP) activity
YDR287W		myo-inositol metabolism	myo-inositol-(1-or 4)-monophosphatase activity
YKR080W	MTD1	one-carbon compound metabolism	methyltetrahydrofolate dehydrogenase (NAD+) activity
YDR502C	SAM2	methionine metabolism	methionine adenylyltransferase activity
YOR125C	CAT5	ubiquinone metabolism	molecular_function unknown
YKL038W	RG11	glucose metabolism	DNA binding activity
YOL109C		lipid metabolism	lipase activity
YMR170C	ALD2	aldehyde metabolism	aldehyde dehydrogenase activity
2 hr Up			
YPL170W	DAP1	sterol metabolism	molecular_function unknown
YOL011W	PLB3	phosphonitride metabolism	lysophospholipase activity

• Genes involved in amino acid biosynthesis and lipid metabolism were up regulated in response to the cold

Table 4: Genes involved in stress that are induced in response to cold temperature ≥ 3-fold

Gene Name	Alias	Biological Process	Molecular Function
30 minutes			
YMR175W	SIP18	response to osmotic stress	phospholipid binding activity
YBL075C	SSA3	response to stress	heat shock protein activity
YLL039C_rep11	UBI4	response to stress	protein tagging activity
YML100W_rep2	TSL1	response to stress	enzyme regulator activity
YIR037W	HYR1	response to oxidative stress	glutathione peroxidase activity
YLL039C_rep14	UBI4	response to stress	protein tagging activity
YER103W_rep17	SSA4	response to stress	chaperone activity
YDL166C	FAP7	response to oxidative stress	molecular_function unknown
YLL026W_rep15	HSP104	response to stress	heat shock protein activity
YKL062W	MNS4	response to stress	transcription factor activity
YDR258C	HSP78	response to stress	chaperone activity
YPL091W	GLR1	response to oxidative stress	glutathione reductase (NADPH) activity
YLL039C_rep15	UBI4	response to stress	protein tagging activity
YLL039C_rep16	UBI4	response to stress	protein tagging activity
YGR209C	TRX2	response to oxidative stress	thiol-disulfide exchange intermediate activity
YBR244W	GPX2	response to oxidative stress	glutathione peroxidase activity
YLL039C_rep17	UBI4	response to stress	protein tagging activity

• Cold temperature induces the expression of chaperones

Conclusions

• Overall, cells grown in YPD and YPGAL had similar changes in gene expression in response to cold temperature. Thus, our data do not support our hypothesis that cells grown in YPGAL would experience more oxidative stress compared to cells grown in YPD.

• Our analysis shows that in response to cold temperature, there are more genes induced than repressed.

• For more definitive conclusions the experiment should be repeated.

Table 3: Genes involved in protein processes that are induced in response to cold temperature ≥ 3-fold

Gene Name	Alias	Biological Process	Molecular Function
30 Minutes			
YGL038C	OCH1	N-linked glycoprotein maturation	alpha-1,6-mannosyltransferase activity
YLR106C	MDM1	protein complex assembly	ATPase activity
YDR394W	RPT3	ubiquitin-dependent protein catabolism	ATPase activity
YDR117W	RPT5	ubiquitin-dependent protein catabolism	ATPase activity
YHR135C	YCK1	protein amino acid phosphorylation	casein kinase I activity
YGL095C	VPS45	protein complex assembly	chaperone activity
YOR056C	NOB1	ubiquitin-dependent protein catabolism	chaperone activity
YDL239W	SSB1	protein biosynthesis	chaperone activity
YNL064C	YDJ1	protein-mitochondrial targeting	chaperone regulator activity
YPL106C	SSE1	protein folding	co-chaperone activity
YML112W	CTK3	protein amino acid phosphorylation	cyclin-dependent protein kinase activity
YBR160W	CDC28	protein amino acid phosphorylation	cyclin-dependent protein kinase activity
YOR085W	OST3	protein complex assembly	dibethyl-lipidophospho-oligosaccharide-protein glycosyltransferase activity
YPR054W	SMK1	protein amino acid phosphorylation	MAP kinase activity
YDR231W	MKK1	protein amino acid phosphorylation	MAP kinase kinase activity
YPL140C	MKK2	protein amino acid phosphorylation	MAP kinase kinase activity
YLR362W	STE11	protein amino acid phosphorylation	MAP kinase kinase activity
YPL084W	BR01	ubiquitin-dependent protein catabolism	molecular_function unknown
YAL058W	CNE1	ER-associated protein catabolism	molecular_function unknown
YLR119W	SRN2	protein-vacuolar targeting	molecular_function unknown
YNL297C	MON2	protein-vacuolar targeting	molecular_function unknown
YJL053W	PEP6	protein-Golgi retention	molecular_function unknown
YGL295C	MTG1	protein biosynthesis	molecular_function unknown
YIL147C	SLN1	protein amino acid phosphorylation	osmosensor activity
YOR253W	NAT5	protein amino acid acetylation	peptide alpha-N-acetyltransferase activity
YMR264W	CUE1	ER-associated protein catabolism	protein binding activity
YPR185W	APG13	protein-vacuolar targeting	protein binding activity
YNL298W	CLA4	protein amino acid phosphorylation	protein serine/threonine kinase activity
YLR248W	RCK2	protein amino acid phosphorylation	protein serine/threonine kinase activity
YOR351C	MEK1	protein amino acid phosphorylation	protein serine/threonine kinase activity
YPL203W	TPK2	protein amino acid phosphorylation	protein serine/threonine kinase activity
YKL123C	SRP21	protein-ER targeting	protein signal sequence binding activity
YKR014C	YPT52	protein-vacuolar targeting	RAB small monomeric GTPase activity
YLR417W	VPS36	protein-vacuolar targeting	regulator of G-protein signaling activity
YBR181C_rep15	RPS6B	protein biosynthesis	structural constituent of ribosome
YBR181C_rep17	RPS6B	protein biosynthesis	structural constituent of ribosome
YLR355C	RPL38	protein biosynthesis	structural constituent of ribosome
YPL143W	RPL33A	protein biosynthesis	structural constituent of ribosome
YMR142C	RPL13B	protein biosynthesis	structural constituent of ribosome
YMR242C	RPL20A	protein biosynthesis	structural constituent of ribosome
YPL079W	RPL21B	protein biosynthesis	structural constituent of ribosome
YGL147C	RPL9A	protein biosynthesis	structural constituent of ribosome
YDR132C	RPL26B	protein biosynthesis	structural constituent of ribosome
YDR509C	RPL37B	protein biosynthesis	structural constituent of ribosome
YBL092W_rep16	RPL32	protein biosynthesis	structural constituent of ribosome
YER117W	RPL23B	protein biosynthesis	structural constituent of ribosome
YGL076C	RPL7A	protein biosynthesis	structural constituent of ribosome
YNL162W_rep2	RPL42A	protein biosynthesis	structural constituent of ribosome
YLR406C	RPL31B	protein biosynthesis	structural constituent of ribosome
YDR064W	RPS13	protein biosynthesis	structural constituent of ribosome
YLR048W	RPS0B	protein biosynthesis	structural constituent of ribosome
YDL121C	RPS19A	protein biosynthesis	structural constituent of ribosome
YOR182C	RPS30B	protein biosynthesis	structural constituent of ribosome
YHL015W	RPS20	protein biosynthesis	structural constituent of ribosome
YJR123W	RPS5	protein biosynthesis	structural constituent of ribosome
YLR333C	RPS5B	protein biosynthesis	structural constituent of ribosome
YNL185C	MRPL19	protein biosynthesis	structural constituent of ribosome

• In response to the cold temperature genes involved in protein synthesis are induced

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