Readers Insight
Publisher of open access books and journals
PJMLS
Print ISSN: 2707-4471. Online ISSN: 2707-448X

Research Article	Pak-Euro Journal of Medical and Life Sciences
DOI: 10.31580/pjmls.v6i3.2902	Copyright © All rights are reserved by Corresponding Author
Vol. 6 No. 3, 2023: 343-352	
www.readersinsight.net/pjmls	**Revised:** September 22, 2023 **Accepted:** September 28, 2023
Submission: August 09, 2023	**Published Online:** September 30, 2023

IN-SILICO IDENTIFICATION AND CHARACTERIZATION OF CHEMICAL STRESS RESPONDING GENES IN YEAST (*SACCHAROMYCES CEREVISIAE*)

Quratulain Qurban[1], Farrukh Bashir[1]*, Farida Bhelil[1], Ayesha Mushtaq[2], Sabeena Rizwan[2], Musarat Riaz[1], Zil-E-Huma[3], Huma Tareen[1], Ismail Mazhar[4], Muhammad Aamir Raza[5]

[1]**Department of Chemistry**, Sardar Bahadur Khan (SBK) Women's University, Quetta-87300, Balochistan, Pakistan

[2]**Department of Bio-Chemistry,** Sardar Bahadur Khan (SBK) Women's University, Quetta-87300, Balochistan, Pakistan

[3]**Department of Zoology,** Sardar Bahadur Khan (SBK) Women's University , Quetta-87300, Pakistan

[4]**Department of Medicine,** Combined Military Hospital Lahore Medical College and Institute of Dentistry-54590 Pakistan

[5]**Department of Mineral Testing,** Pakistan Council of Scientific and Industrial Research Laboratories Complex, Quetta-87300, Pakistan

***Corresponding Author:** Dr. Farrukh Bashir. Email: farrukh_chem@yahoo.com

Abstract

Saccharomyces cerevisiae (yeast) is treated as a model organism to study the life processes of all eukaryotes. Chemical stresses change the regulation of genes present in living organisms. To study the responses of genes at transcription level, yeast is found to be the best model. The information obtained from the responses of genes, under chemical stresses, provides a platform to formulate the mechanism and engineering strategies. These strategies will be helpful against the genes which are resistant to chemical stresses. Computational tools and data available on microarray are used to study the responses of genes in yeast under oxidative stresses, carbon dioxide and heme deficiency and hypoxia, and DNA damage stresses. 180 genes are identified out of 9335 genes of yeast under these chemical stresses. Out of these 180 genes, 131 expressed themselves whereas 49 were suppressed. Furthermore, these identified genes are characterized on the basis of their molecular function, biological process and cellular components.

Keywords: *Chemical stresses, Computational Tool, Genes, Microarray, Oxidative Stress, Saccharomyces cerevisiae*

INTRODUCTION

The word yeast has been emerged from 'gist' a Dutch word and in the German language "gischt" means fermentation (1). Yeast is found to be helpful in the production of different bioactive substances (2). Yeast comes in the category of eukaryotic organisms due to the presence of a single cell that contains all the genetic information. It has 1500 species and used as a model organism for all eukaryotes. These species are widely studied in genetics and cellular biology. Though it is single celled but one of its types known as 'fungi' is larger in size than bacteria (3).

Analysis of yeast pioneered the event of many post-genomic experimental approaches and procedure tools (4). Saccharomyces cerevisiae (S. cerevisiae) one in all the species of yeast (5), has positive effect on animal production, performance, nutrient degradation and internal microorganism population (6). It was completely sequenced in 1996 and studied to investigate eukaryotic cells and human beings. It has been discovered that S. cerevisiae has more than 6000 genes present on 16 chromosomes with diploid (two genomes) or haploid (one genome). It is used as a model to analyze the cell response, at genome, transcriptome, proteome and metabolism level, when exposed to any toxicants (7-9). On the basis of functional genomics studies, it was observed that S. cerevisiae showed different responses under chemical or

drug stresses (10-12). Like oxidative stress is observed under hydrogen peroxide and menadione stresses, toxic effect has been observed for ibuprofen and mefloquine whereas, its growth was observed to be effected under lithium chloride, tomatidine and lactic acid stresses (13).

Gene expression microarrays are stimulating new tools in biology (14) and utilized by researchers for the studies of genomic phenomenon in yeast under different stress conditions. Stress responding genes in different organisms like animals, human and yeast have been widely studied by using a well-known technique called as DNA microarray (15). Detailed data of yeast genes is available on the website "www.yeastgenome.org" with the name of "Saccharomyces Genome database (SGD)" (16).

Information available on National Center for Biotechnology Information Gene Expression Omnibus known as NCBI GEO correlates the gene expression pattern against different chemical stresses with the help of computer analysis. Gene expression data sets are stored on GEO database in the form of different series and platforms. Various bioinformatics tools are used to develop evidence of correlation between gene expression patterns under different chemical stresses). Different papers on S. cerevisiae are reported under different stresses by using different techniques (12, 17). On GEO datasets available on NCBI GEO information related genomic stress responses in *S. cerevisiae* is available on GPL90 platform (13). As *S. cerevisiae* is best model to understand the eukaryotic cells and human beings therefore, most common stresses like gene expression changes under stresses (i)- oxidative stress (reason to select it is, though oxygen is vital for life but its stress could damage cellular components), (ii)- carbon dioxide stress (change in industrial and environmental conditions changes the carbon dioxide level, therefore, it was selected to investigate the genes adaptation against this stress), (iii)- heme deficiency and hypoxia (as heme is cofactor for various proteins involved in respiration and transportation of oxygen, therefore, heme deficiency and low oxygen level or hypoxia could uncover the adaptation of gene expressions associated with these stresses), and (iv)- DNA damage (as DNA is also an important stress as gene expression involved in DNA repair and maintenance of genomic integrity could be studied). In present study common chemical stress responding genes in S. cerevisiae were identified by filtering data available on GPL90 and characterized on the basis of their cellular, biological and molecular functions with the help of Gene ontology (GO). Further, this data was graphically visualized by using a microarray tool known as Multi-experimental viewer (Mev) software (13). A total of 180 common chemical stress responding genes are identified under a minimum 4 stresses among oxidative stress, carbon dioxide, heme deficiency and hypoxia, DNA damage stresses. Out of these 180 genes, 131 genes expressed themselves whereas 49 genes were suppressed.

MATERIALS AND METHODS

Different bioinformatics tools and databases available for gene expression like GEO:NCBI and GO were used to identify the chemical stress responding genes in *S. cerevisiae* (13). Steps involved for the accomplishment of this study are as follows:

MICROARRAY ANALYSIS

GEO-NCBI is an open and easily accessible storehouse where high throughput data related to gene expression, along with data generated from microarray analysis, is available. It is accessible at the website; www.ncbi.nlm.nih.gov/geo/. GEO dataset available on this website contains original submitter-supplied records in the form of series, samples and platforms. By using GEO dataset different attributes like keywords, organism, and platform can be searched. In the GEO dataset, each microarray platform is assigned a distinctive identifier like GPL90 contains extensive data related to *S. cerevisiae*. On this platform recorded data related to *S. cerevisiae* under different stresses are available (13). As sample should be analyzed by using uniform microarray platform and to fulfill the criteria all the data for chemical stresses was minded. In present research stresses like oxidative stress, carbon dioxide, heme deficiency and hypoxia, and DNA damage were minded for *S. cerevisiae* and finally one GPL90 platform consisting of 4 series was selected for the analysis. All the required data was downloaded and saved. A total of 9335 probes are available on this platform and each probe contains information about gene ontology and SGD accession number. Over-all 165 series with 2433 samples are available on this platform. In the present study, 4 series (GSE7645, GSE8900,

GSE9514, GSE5301) were selected for the above mentioned chemical stress. Data related to this platform, series and samples were downloaded and saved.

STUDY DESIGN

To obtain finest set of chemical stress responding genes, a broad, logical and to the point study design was made. The data available on GPL 90 for GSE7645, GSE8900, GSE9514, GSE5301 series was divided into four stages and assembled in the following 4 stages.

MINIMUM-1 STRESS STAGE

In the Minimum-1 stress stage, in all four series like data for oxidative stress for 3 minutes, carbon dioxide stress for glucose and nitrogen (each 79%), heme deficiency and hypoxia stress for aminolevulinic acid (ALA)/normoxia and DNA damage stress (calicheamicin, esperamicin, neocarzinostatin, gamma radiation) were considered.

MID-2 STRESS STAGE

In the Mid-2 stress stage the data for oxidative stress for 40 minutes, carbon dioxide stress for glucose and nitrogen (each 79%), heme deficiency and hypoxia stress for aminolevulinic acid (ALA)/ normoxia and DNA damage stress (calicheamicin, esperamicin, neocarzinostatin, gamma radiation) were selected.

MAXIMUM-3 STRESS STAGE

In the Maximum-3 stress stage the information for oxidative stress for 120 minutes, carbon dioxide stress for glucose 100% and nitrogen 79%, heme deficiency and hypoxia stress for 250 ◎M aminolevulinic acid (ALA)/ hypoxia, DNA damage stress (calicheamicin, esperamicin, neocarzinostatin, gamma radiation) were selected.

FINAL AVERAGE STRESS STAGE

In this stage the average of all the common analysis stresses were determined and used for further analysis.

FORMATION OF TAB-DELIMITED

For the platform identifiers (IDs), an excel sheet was created with the help of sample data. Under chemical stresses (oxidative stress, carbon dioxide stress, heme deficiency and hypoxia, DNA damage) the normalized log 2 intensities obtained from the GPL90 were entered and aligned. For all the four stages (Minimum, Mid, Maximum and average) separate excel sheets were created and saved as aligned tab delimited files containing platform IDs and log2 gene expression ratios (13).

MULTI EXPERIMENTAL VIEWER MEV

Mev is accessible publicly on the website (www.tm4.org/mev) and usually opened in JavaScript. It is the best software to view and analyze the normalized microarray data and identify the differentially expressed genes (18). This software was used for the analysis of tab-delimited aligned data (19).

COMMON STRESS RESPONDING GENES IDENTIFICATION

Response of genes under at least four stresses among oxidative stress, carbon dioxide, heme deficiency and hypoxia and DNA damage stresses with log 2 signal intensities (≥ / ≤ 2.0 fold) were identified and saved.

CHARACTERIZATION

With the help of GO, common chemical stress responding genes were characterized on the basis of molecular functions, biological categorization, cellular components (20). Annotation list and graphs of these genes remained were saved for comparison.

RESULTS

Overall 9335 genes of yeast were profiled and analyzed by microarray data mining tools. Following results are obtained by using microarray data mining.

MICROARRAY ANALYSIS

As 9335 probes are available on GEO platform GPL 90 at different stress stages. For present study, these genes were analyzed under four stresses by using microarray data mining. Out of 9335 genes 180 average of common chemical stress responding genes were selected having log2 signal intensities under a minimum of 3 stresses among the 4 chemical stresses (oxidative stress, carbon dioxide stress, heme deficiency and hypoxia, DNA damage) as depicted in Figure 1a and b. From 180 genes, 131 (72.8%) genes appeared to be expressed and 49 (27.2%) genes had shown suppressed responses. Common stress responding genes under different stages are shown in Fig. 1 (a, b).

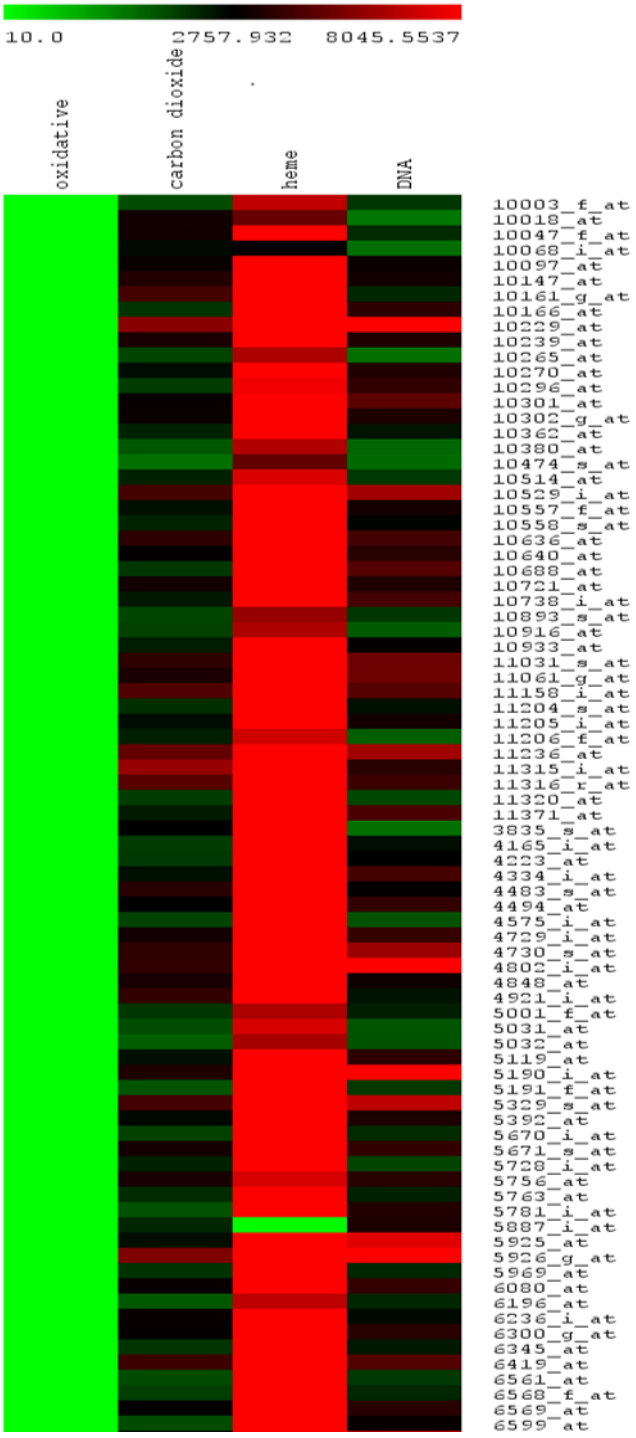

Fig.1 (a). (Mev) average of common chemical stress responding genes for up-regulated expression under at least four stress condition among oxidative stress, carbon dioxide, heme deficiency and DNA damage

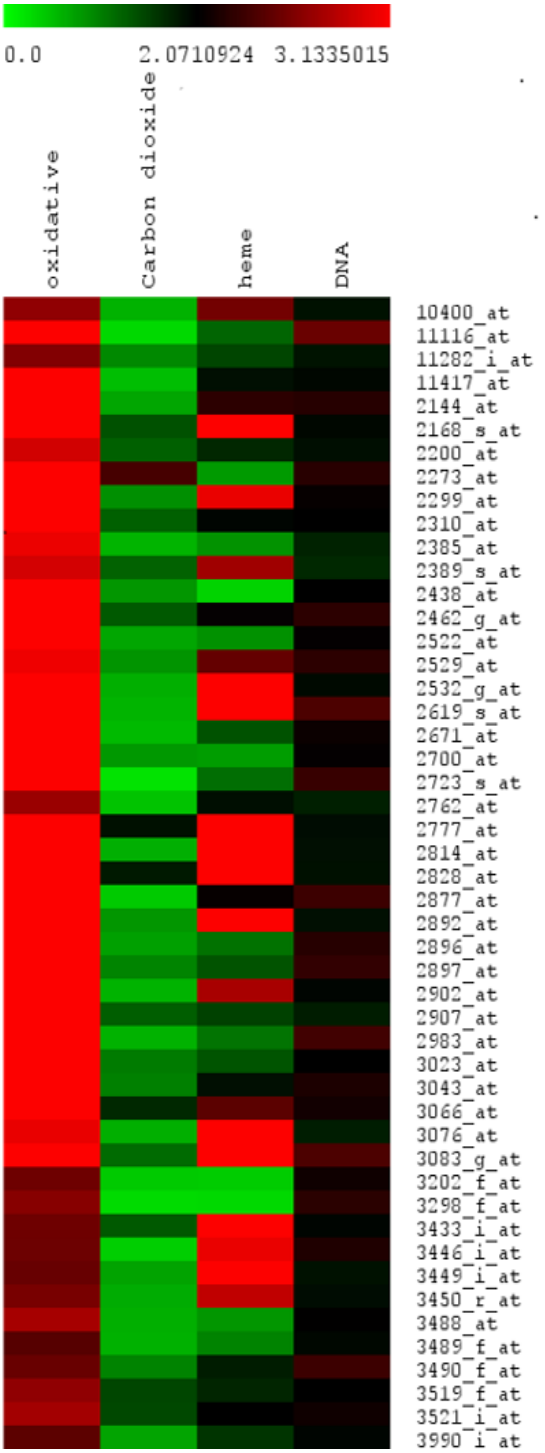

Fig. 1 (b). (Mev) average of common chemical stress responding genes for down-regulated expression under at least four stress condition among oxidative stress, carbon dioxide, heme deficiency and DNA damage

MINIMUM-1

In the present research over-all 258 genes out of 9335 genes were identified as common chemical stresses responding genes in Minimum-1 (M-1) stage, under the stress period of 3 minutes for oxidative stress, glucose (79%) and nitrogen (79%) for carbon dioxide stress, aminolevulinic acid (ALA) and normoxia for heme deficiency and hypoxia, (calicheamicin, esperamicin, neocarzinostatin, gamma radiation) DNA damage. Out of 258 genes, 131 genes expressed themselves (Figure.2). Among these genes like ribosomal protein L22A (RPL22A), Histone H2A1 and Histone H2A2 protein (HTA1 & HTA2), Hypusine-containing protein P2 (HYP2) ribosomal protein L14A (RPL14A), Fructose-1,6-Bisphosphate Aldolase A1 (FBA1), ribosomal protein S25A (RPS25A) and ribosomal protein S30A (RPS30A) are involved in biological methods like translation and protein-transporting (ATP) synthase complex biogenesis and translational initiation, translation termination, translation frame shifting and cytoplasmic translation and gluconeogenesis and the glycolytic process. However, 127 genes were observed to be suppressed (Fig. 2). Among these genes like benign prostatic hyperplasia (BPH), epithelial cell line (BPH-1), nuclear migration (NUM1) and super killer SKI2-like helicase (SLH1) remained the significant ones and found to be involved in the biological processes like, fungal-type-cell wall group intracellular protein transport response to pH mitochondrial fission, nuclear migration along microtubule, and cytoplasmic translation, regulation of translation.

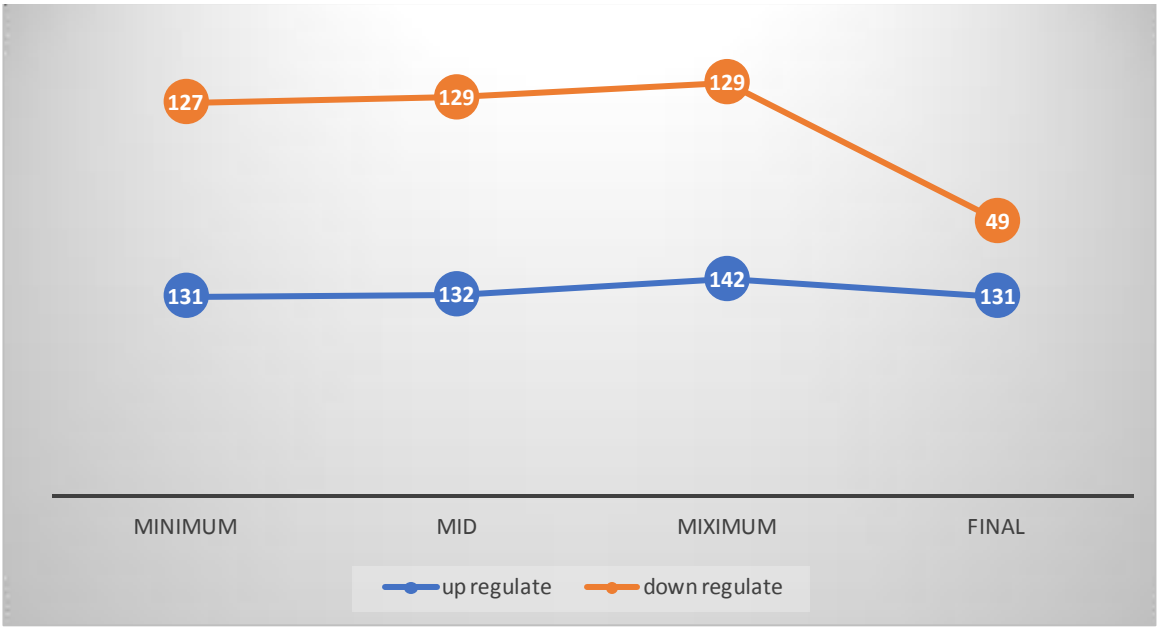

Fig. 2. Comparative analysis of identification average common stress responding genes at different stress stage

MID-2

As a result of the study in Mid-2 (Mid-2) the stress periods at four chemical stresses were 40 minutes for oxidative stress, 79% glucose and 79% nitrogen for carbon dioxide, aminolevulinic acid (ALA) and normoxia for heme deficiency and hypoxia and (calicheamicin, esperamicin, neocarzinostatin , gamma radiation) for DNA damage. A total of 261 genes were found out of which, 132 genes expressed themselves (Figure.2). Among these genes like ribosomal protein S26A (RPS26A), Cell surface protein (ECM33), Enolase 2 (ENO2), Histidine triad nucleotide-binding (HNT1), S8A and S8B ribosomal protein (RPS8A, RPS8B) and Glycerate PhosphoMutase (GPM1) are the significant genes as they are involved in biological methods like cytoplasmic translation, ribosome assembly, rRNA export from nucleus and Fungal-type cell wall, organization and re-entry, mitotic cell cycle, nucleotide metabolic process, maturation of SSU- RNA from tricistronic, RNA transcript, gluconeogenesis and Glycolytic process. However, 129 genes showed suppressed responses (Fig. 2). Among these genes like Secretory (SEC16), Ras GTPase activating protein (IRA2) and Establishes Silent Chromatin protein (ESC1) are some important genes as they are involved in the biological processes like, COPII vesicle coating, macroautophagy protein, localization to endoplasmic reticulum and negative regulation of Camp biosynthetic process, negative regulation of Ras protein, signal

transduction, positive regulation of Ras, GTPase activity response to stress and Chromatin silencing at telomere.

MAXIMUM-3

The investigation of common chemical stress responding genes in Maximum-3 (M-3), the stress periods remained, the oxidative stress 120 minutes, glucose 100% and nitrogen 79% for carbon dioxide, 250 μM aminolevulinic acid (ALA)/hypoxia for heme deficiency and hypoxia, and (calicheamicin, esperamicin. neocarzinostatin, gamma radiation) for DNA damage. A total of 271 common chemical stress responding genes were identified. Among these identified genes, 142 genes expressed themselves (Fig. 2). Among these genes like, (RPP1B) ribosomal protein P1 beta, Translation machinery associated (TMA19) and ribosomal protein S22A (RPS22A), ribosomal protein L26A and L26B (RPL26A $ RPL26B), ribosomal protein of the small subunit S5 (RPS5), ribosomal protein 31A (RPL31A) and Hyperosmolarity-responsive (HOR7) are important as they are present in the biological developments such as cytoplasmic translation, Positive regulation of protein, kinase activity and cellular reply to oxidative stress, cytoplasmic translation, regulation of translation, RNA export from nucleus and plasma membrane. Meanwhile, 129 genes showed suppressed responses (Fig. 2). Among these genes like Polymerase II Protein (POL2), Cyclic AMP requirement (CYR1), Target of rapamycin (TOR1) and RNA exonuclease (REX3), remain the significant genes as they are present in biological methods such as DNA replication present in S-phase, DNA combination present in DNA reparation, double-strand break repair via nonhomologous end connection, chromatid cohesion, nucleotide-excision repair, Adenylate cycle-modulating G protein-coupled, receptor and cellular reply to DNA damage stimulus, cellular reply to oxidative stress, chronological cell gang, fungal-type cell wall, meiotic cell cycle, mitochondria- nucleus, negative regulation of protein kinase, phosphorylation, nucleolar large RNA transcription and rule of the cell cycle, ribosome biogenesis, TOR signaling, translation initiation, exonucleolytic trimming to generate, RNA transcript and RNA processing.

CHARACTERIZATION

The common identified genes were characterized by using Gene ontology (GO) annotation to express the processes involved in the biology, cell component and molecular function. Similarly, characterization of chromosome number was done by using browser UCSC genome.

BIOLOGICAL CATEGORIZATION

Categorization based on biological processes of genes showed that 3.97% of genes expressed and 2.60% suppressed themselves in protein. However, 1.59% expressed and 7.79% suppressed genes were involved in biosynthetic processes followed by 2.60% suppressed and 2.12% expressed genes in oxide stress, 1.85% expressed and 1.30% suppressed genes in endo-nucleotide, 1.85% expressed and 3.90% suppressed genes in the cell wall, 8.47% expressed and 7.79% suppressed genes in genetic interaction, 16.67% expressed and 2.60% suppressed genes in translation while 20.90% expressed and 15.58% suppressed genes were involved in mutant phenotype (Fig. 3a).

CELLULAR COMPONENTS

In this category the genes response under common chemical stresses were explained on the basis of cellular components. It is found that 1.63% of genes expressed and 0% suppressed them in extracellular region. The 1.89% expressed and 44.12% suppressed genes showed unknown cellular components, 13.75% genes expressed and 4.41% genes suppressed themselves in the intercellular regions. In mitochondria, 5.36% expressed and 7.35% genes suppressed themselves whereas, 25.41% expressed and 11.76% suppressed genes were involved in the cytoplasm, ribosome and the membranes (Fig. 3b).

MOLECULAR FUNCTIONS

This category explained the genes response under common chemical stresses on the basis of molecular functions. It is found that 0% of genes expressed and 55.56% suppressed themselves in unknown molecular function whereas, 8.84% expressed and 12.96% suppressed genes were engaged in phenotype, while 22.79%

expressed and 16.67% suppressed genes were found in enzyme A, 33.02% expressed and 14.81% suppressed genes were involved in binding. The structure cellular function was performed by 35.35% expressed and 0.00 suppressed genes (Fig. 3c).

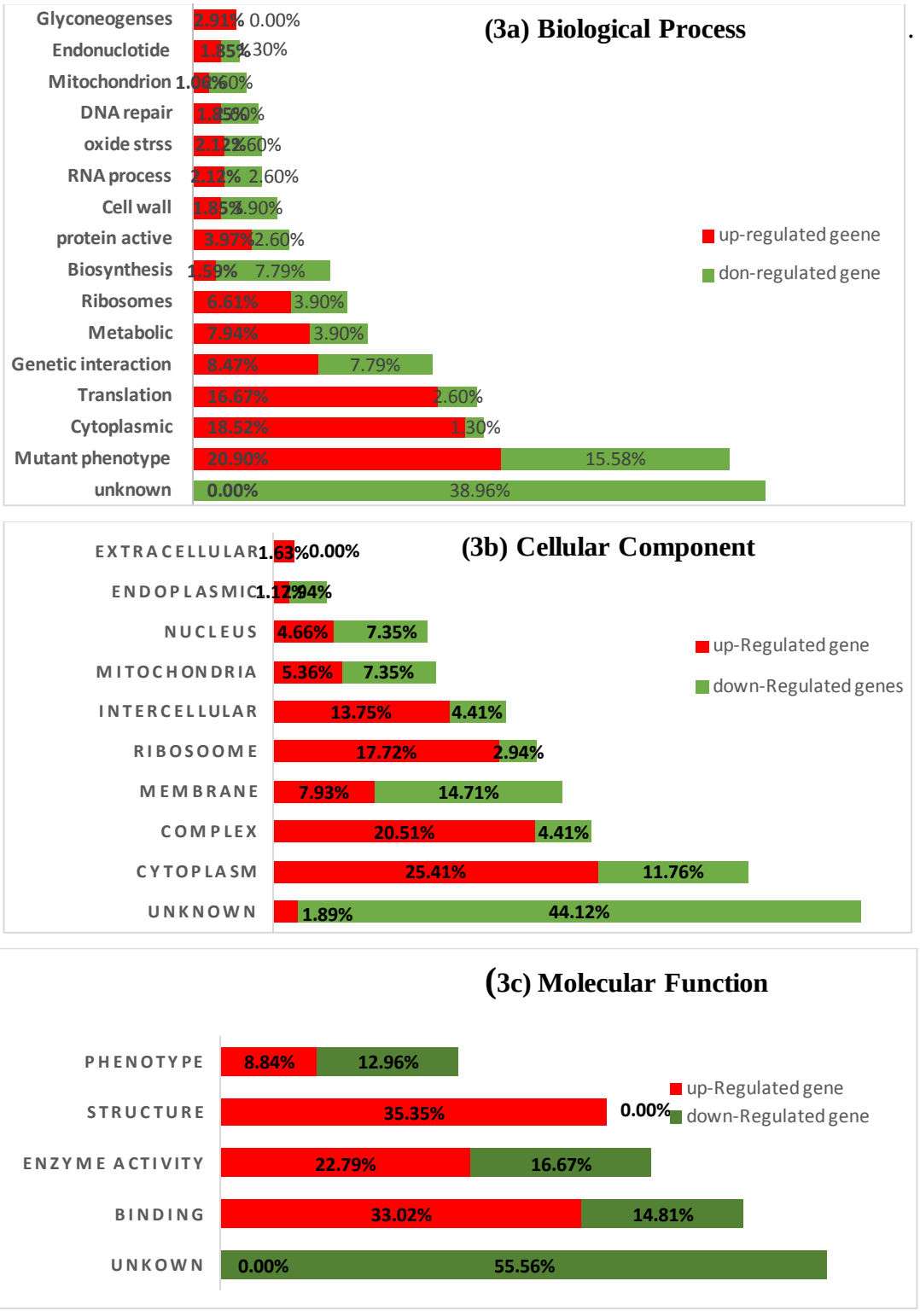

Fig. 3. Distribution of identified and characterized genes via gene Ontology (GO) under three principle GO categories; (3a) Biological processes, (3b) Cellular components, (3c) Molecular function

YEAST CHROMOSOMES AND RESPONDING GENES

The 31% of suppressed genes revealed the unknown chromosomal location while that of expressed genes were known. For example, at chromosome 12, 24% expressed and 1% suppressed genes were observed. At chromosomes 10, 11% genes expressed and 7% suppressed themselves, at chromosome number 4, 17% expressed and 0% suppressed, at chromosome number 5, 11% expressed and 2% suppressed, at chromosome number 2, 12% expressed and 1% suppressed, whereas, 10% expressed and 2% suppressed genes were found at chromosome number 13 with 11% expressed and 0% suppressed genes at chromosome

number 11. The remaining chemical stress responding genes have shown their presence on rest of the chromosomes of yeast (Fig. 3d).

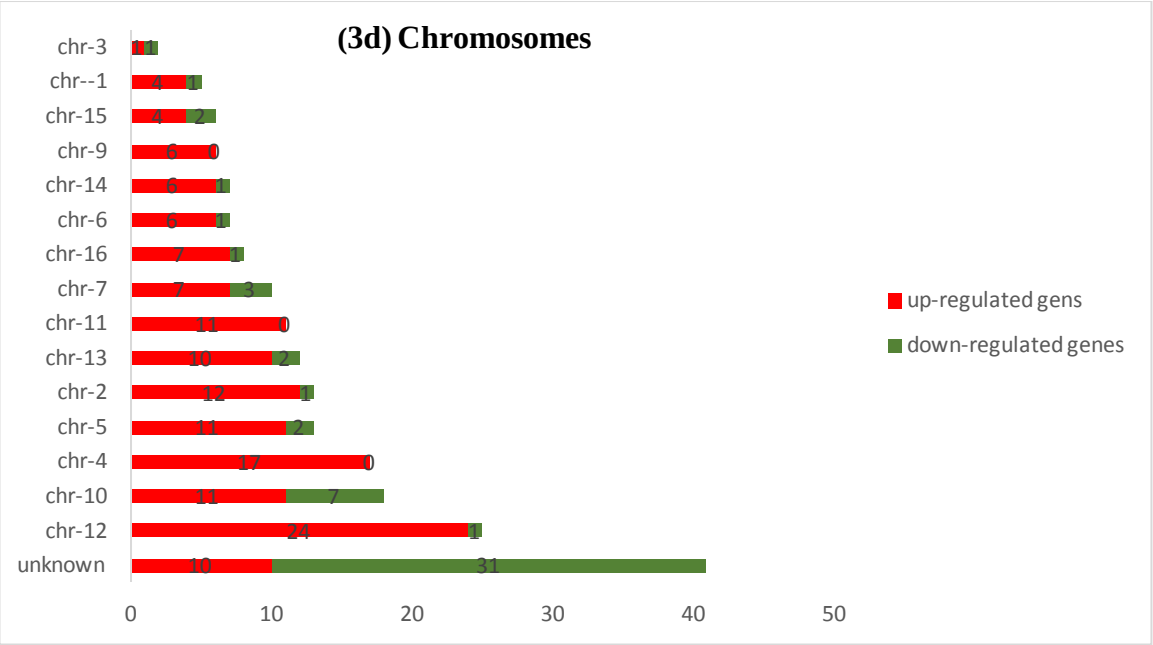

Fig. 3 (d). In yeast chemical stress responding genes identification and characterization by UCSC genome browser. The bar chart showed the distribution of average common chemical stress responding genes in yeast according to Chromosome numbers

DISCUSSION

In-silico identifications and characterizations are playing very important role in the development of pharmacology and testing due to the increased data bases available for different organisms under different stresses (21). Different computer tools like data bases, data mining, data analysis and homology models were used in this technique (22). A lot of research has been done and much more is in processing to unwrap the hidden characteristics of yeast (*S. cerevisiae*) genes as it is treated as a model organism for the human being studies.

For example, a group of researchers studied the responses of gene expression in *S. cerevisiae* under organic and inorganic chemical stresses and found 388 responding genes, out of 9335 genes, as the average of common chemical stresses (13). In this study they observed that 231 genes expressed whereas 157 genes suppressed themselves. In another research on *S.cerevisiae*, under different abiotic stresses like pH and change in temperature, researcher found the higher number (62%) of suppressed genes as compared to the expressed (38%) ones (20). Over all the responses of genes, in *S. cerevisiae*, towards various parameters available on NCBI website, are required to be explored. Present research is also a step forward in this queue focused on *S. cerevisiae*, under four different chemical stresses which commonly influence the human genes as well. These genes were categorized on the basis of their developments and functions. In biological processes, the study was focused on mutant phenotype (as organism's phenotype is changed when genetic mutation occurs and it helps in understanding the function/role of specific genes in biological processes), cytoplasmic translation (as translation of genetic information takes place in ribosome that is located in the cytoplasm, therefore it is an important process for gene expression and production of functional proteins), genetic interaction (as genes are present in the form of networks and they influence each other either by enhancing each other's influence or by reducing the influence or remain neutral), metabolic, ribosomes, biosynthesis, protein active, cell wall, RNA process, oxide stress, DNA repair, mitochondrion, endo-nucleotide, and gluconeogenesis. However, cellular components were grouped as unknown, cytoplasm, complex, membrane, ribosome, intercellular, mitochondria, nucleus, endoplasmic reticulum, and extracellular components. Moreover, molecular functions remained grouped as unknown, binding, enzyme activity, structure, and phenotype.

Based on the chromosome number, genes were characterized under chemical stresses with the help of the chromosomal integration method provided in the literature (23). In present research, most of the expressed ribosomal proteins (RPs) genes were found to be present on chromosome numbers 2, 4, 5, 7, 10, 11, 12, 13 and 14 whereas in human most of them were observed on chromosome number 19 (13). RPs being significant for protein synthesis causes various diseases like cancer susceptibility, anemia, and cardiovascular disease that involve in carcinogenesis (24).

Some important genes like GPM-1 phosphoglycerate mutase 1 (involved in the interconversion of 3 and 2 phosphoglycerate with 2,3 bisphosphoglycerate, a crucial step in glycolysis) found at chromosome number 11, PDC1 pyruvate decarboxylase (involved in the non oxidative conversion of pyruvate to acetaldehyde and CO2, main step of alcoholic fermentation) and EGR3 early growth response protein 3 (present in human as well and involved in transcriptional regulation of genes) found at chromosome number 12, FBA-1 fructose bisphosphate aldolase (involved in glycolysis and gluconeogenesis) found at chromosome number 11, ribosomal proteins like RPL22A and RPS26A found at chromosome number 7 and 10 respectively and RPS-5 found at chromosome number 10 expressed themselves under applied chemical stresses. Up-regulations/expression of these genes show their involvement in different modes like GPM-1, which may redirect the metabolic flux under applied stresses, PDC1, under applied stresses may indicate the activation of alternative energy production pathways, EGR3, may show the adaptation and survival of genes under these stresses. Conversely, genes like polymerase 1 (POL-1, involved in DNA replication and repair) present on chromosome number 14, CYR-1 (involved in adenylate cyclase) found on chromosome number 10, BPH-1 (related to heat shock responses) found on chromosome number 3, SLH-1 helicases present on chromosome number 7 suppressed themselves under the applied stresses. It shows that under the applied stresses, these genes downregulated the pathways of specific signaling like cAMP signaling, heat shock response, or RNA processing.

Huge data is available on *S. cerevisiae* under separate stresses however, unique gene expression patterns, identification of potential metabolic regulators, understanding of the cellular adaptations, hypoxic adaptations and understanding of DNA damage induced gene expression were observed in present study under 4 collective stresses. It may be suggested that regulation of genes under oxidative stress are involved in superoxide dismutase (SODs), and catalases and they activate the repairing mechanisms of oxidative damage to proteins, lipids or DNA. Changes in carbon dioxide level changes the metabolic pathways and those changes are observed by the regulation of genes. Similarly, regulation of genes under DNA damage either show the involvement of genes in the DNA repair pathways or arrest the cycle in order to stop the propagation of damaged DNA. Present study helps us to identify regulatory elements and stress specific adaptations that contribute to the novelty and significance of findings.

CONCLUSION

Computational tool was used for the profiling and characterization of genes in *S. cerevisiae* under oxidative, carbon dioxide, heme deficiency and hypoxia, DNA damage. Out of 9335 genes 180 genes were identified on the basis of common chemical stresses. From 180 genes, 131 genes were involved to be expressed meanwhile 49 were found to be suppressed. High similarity between *S. cerevisiae* and human allows functional genomics study of *S. cerevisiae* to be used to identify human genes involved in different diseases so their expression should be suppressed to reduce/minimize the chances of diseases/disadvantages caused under the above stresses. The present study may help pharmacologists in developing novel therapeutic strategies by identifying the potential drug targets for modulating cellular responses to stress. Similarly, these findings have potential to shape the biotechnological processes under optimized stress tolerance that leads to improve the yields of bio based products.

References:

1. Anusha S, Sundar S, Williams P. Studies on the isolation and characterisation of marine yeast, β-glucan production and immunostimulatory activity on Carassius auratus. International Journal of Current Microbiology and Applied Sciences. 2014;3(9):230-40.

2. Zaky AS, Tucker GA, Daw ZY, Du C. Marine yeast isolation and industrial application. FEMS Yeast Research. 2014;14(6):813-25.
3. Aitman TJ, Boone C, Churchill GA, Hengartner MO, Mackay TF, Stemple DL. The future of model organisms in human disease research. Nature Reviews Genetics. 2011;12(8):575.
4. Botstein D, Fink GR. Yeast: an experimental organism for 21st Century biology. Genetics. 2011;189(3):695-704.
5. Teixeira MC, Mira NP, Sá-Correia I. A genome-wide perspective on the response and tolerance to food-relevant stresses in Saccharomyces cerevisiae. Current opinion in biotechnology. 2011;22(2):150-6.
6. De Ondarza M, Sniffen C, Dussert L, Chevaux E, Sullivan J, Walker N. Case study: Multiple-Study analysis of the effect of live yeast on milk yield, milk component content and yield, and feed efficiency. The Professional Animal Scientist. 2010;26(6):661-6.
7. Lorrine OE, Rahman RNZRA, Tan JS, Khairuddin RFR, Salleh AB, Oslan SN. Determination of Putative Vacuolar Proteases, PEP4 and PRB1 in a Novel Yeast Expression Host Meyerozyma guilliermondii Strain SO using Bioinformatics Tools. Pertanika Journal of Science & Technology. 2022;30(1).
8. Zelinsky AA, Rubel AA, Ryabinina MV. Identifying novel amyloid candidates using bioinformatics algorithms and a yeast model approach. Ecological genetics. 2023;21:45-.
9. Sun Y, Huang J, Wang Z, Pan N, Wan C. Identification of Microproteins in Saccharomyces cerevisiae under Different Stress Conditions. Journal of Proteome Research. 2022;21(8):1939-47.
10. dos Santos SC, Teixeira MC, Cabrito TR, Sá-Correia I. Yeast toxicogenomics: genome-wide responses to chemical stresses with impact in environmental health, pharmacology, and biotechnology. Frontiers in genetics. 2012;3:63.
11. Li B, Liu N, Zhao X. Response mechanisms of Saccharomyces cerevisiae to the stress factors present in lignocellulose hydrolysate and strategies for constructing robust strains. Biotechnology for Biofuels and Bioproducts. 2022;15(1):28.
12. Zhao X, Lian X, Liu Y, Zhou L, Wu B, Fu YV. A peptide derived from GAPDH enhances resistance to DNA damage in Saccharomyces cerevisiae cells. Applied and Environmental Microbiology. 2022;88(4):e02194-21.
13. Barozai MYK, Bashir F, Muzaffar S, Afzal S, Behlil F, Khan M. In-silico identification and characterization of organic and inorganic chemical stress responding genes in yeast (Saccharomyces cerevisiae). Gene. 2014;550(1):74-80.
14. Brown PO, Botstein D. Exploring the new world of the genome with DNA microarrays. Nature genetics. 1999;21(1s):33.
15. Duggan DJ, Bittner M, Chen Y, Meltzer P, Trent JM. Expression profiling using cDNA microarrays. Nature genetics. 1999;21(1s):10.
16. Cherry JM, Adler C, Ball C, Chervitz SA, Dwight SS, Hester ET, et al. SGD: Saccharomyces genome database. Nucleic acids research. 1998;26(1):73-9.
17. de Fátima Alves L, Bortolucci J, Reginatto V, Guazzaroni M-E, Mussatto SI. Improving Saccharomyces cerevisiae acid and oxidative stress resistance using a prokaryotic gene identified by functional metagenomics. Heliyon. 2023;9(4).
18. Saeed AI, Bhagabati NK, Braisted JC, Liang W, Sharov V, Howe EA, et al. [9] TM4 microarray software suite. Methods in enzymology. 2006;411:134-93.
19. Quayum N, Kutchma A, Sarkar SA, Juhl K, Gradwohl G, Mellitzer G, et al. GeneSpeed Beta Cell: an online genomics data repository and analysis resource tailored for the islet cell biologist. Experimental diabetes research. 2008;2008.
20. Barozai MYK, Wahid HA. Insilico identification and characterization of cumulative abiotic stress responding genes in Potato (Solanum tuberosum L.). Pak J Bot. 2012;44:57-69.
21. Aceituno FF, Moseyko N, Rhee SY, Gutiérrez RA. The rules of gene expression in plants: organ identity and gene body methylation are key factors for regulation of gene expression in Arabidopsis thaliana. BMC genomics. 2008;9(1):438.
22. Ekins S, Mestres J, Testa B. In silico pharmacology for drug discovery: methods for virtual ligand screening and profiling. British journal of pharmacology. 2007;152(1):9-20.
23. Zhang T, Sun L, Xin Y, Ma L, Zhang Y, Wang X, et al. A vaccine grade of yeast Saccharomyces cerevisiae expressing mammalian myostatin. BMC biotechnology. 2012;12(1):97.
24. Narla A, Ebert BL. Ribosomopathies: human disorders of ribosome dysfunction. Blood. 2010;115(16):3196-205.