

# Comprehensive Expression Analysis of Time-dependent Genetic Responses in Yeast Cells to Low Temperature

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Sahara, T., Goda, T., & Ohgiya, S. (2002). Comprehensive expression analysis of time-dependent genetic responses in yeast cells to low temperature. *Journal of Biological Chemistry*, 277(51), 50015-50021.

# Outline

- Introduction to cold shock and its effect on yeast
- Cold shock and microarray procedures of yeast samples
- Results of clustering analysis shows cooperative regulating
- How gene expression changed in areas of:
  - Transcription
  - Ribosomal proteins
  - Cell life
  - Metabolism & energy
  - Signal transduction
- What do previous studies say about these results?
- Summary of the response of yeast cells to cold shock

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# Background Information on Purpose of Experiment

- Low temperatures are known to have several effects on biochemical and physiological properties in various cells
  - Ex: low efficiency of protein translation, low fluidity of cellular membrane, slow folding of proteins
- Cold shock proteins are induced when cells are exposed to low temperatures in order to cope with the drastic change in environment
- In yeast, the **NSR1**, **TIP1**, and **OLE1** genes have been identified as important cold-inducible genes through past research, but their low temperature-dependent gene expression and response are still unclear
- **Purpose:** analyze global gene expression in low temperature-exposed yeast cells using a yeast cDNA microarray to obtain fundamental information on low temperature response and low temperature-dependent gene expression in yeast cells (Sahara et. al., 2002).

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# Flowchart of Overall Experimental Design

Yeast cells grown at 30°C

50 ml of culture collected for  
time reference 0

Remaining cells cold shocked at 10°C

Cells collected at 0.25, 0.5, 2, 4, and 8 hours after cold shock

Total RNA prepared and used for fluorophore-labeled cDNA probes for array hybridization

Microarray hybridization performed and data was scanned by laser microscope for analysis

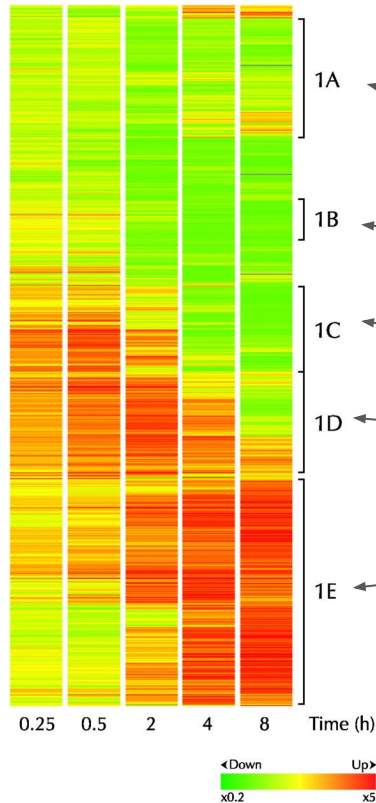
Fluorescence intensities were normalized and data was clustered

Referred to MIPS and other databases to determine functional relationship among clusters

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# Clustered genes showed similar expressions



- Genes close together were placed into clusters.
  - 1A: Unclassified proteins
  - 1B: Amino acid biosynthesis and metabolism
  - 1C: RNA polym. I & RNA processing
  - 1D: Ribosomal proteins
  - 1E: Not defined
- Clusters showed:
  - Similar functions
  - Cooperative regulation

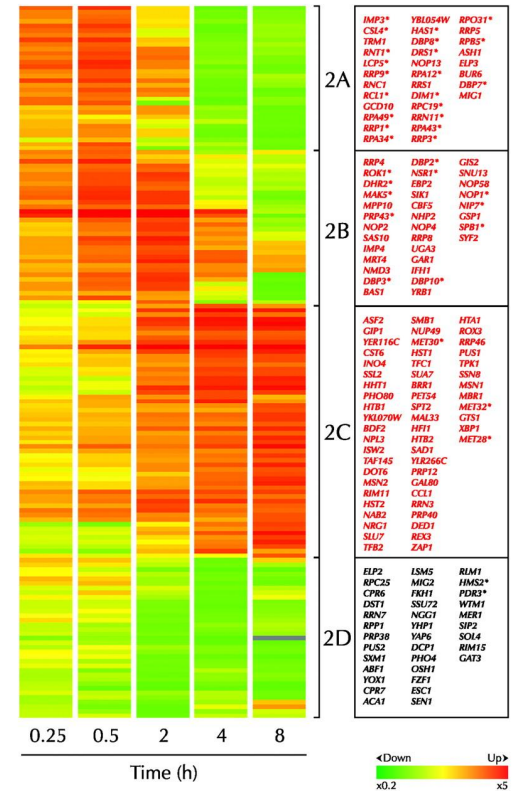


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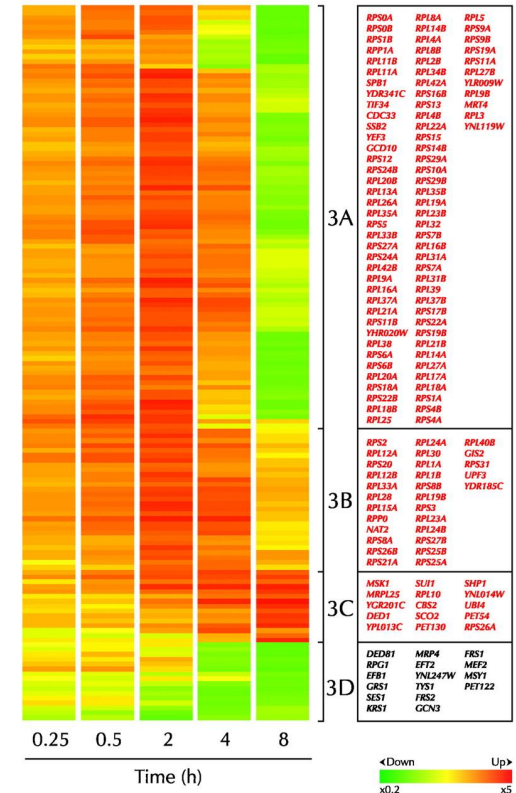
# Cluster of transcription genes changed expression

- Genes separated into different clusters:
  - 2A: RNA polymerase I & RNA processing
  - 2B: rRNA processing
  - 2C & 2D: mRNA transcription
- Factors essential to transcription and processing were up-regulated.
- Genes for synthesis and transcription regulation of mRNAs had mixed responses.



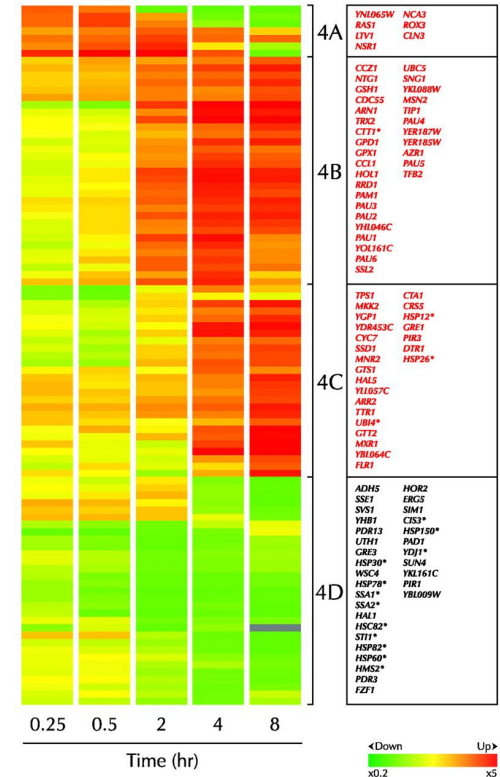
# Cluster of ribosomal protein genes changed expression

- Clusters:
  - 3A & 3B: cytosolic ribosome
  - 3C: translational control factors
  - 3D: tRNA synthetases
- Low temperature impairs translational ability.
- Yeast genes up-regulate to compensate.



# Stress response genes changed expression

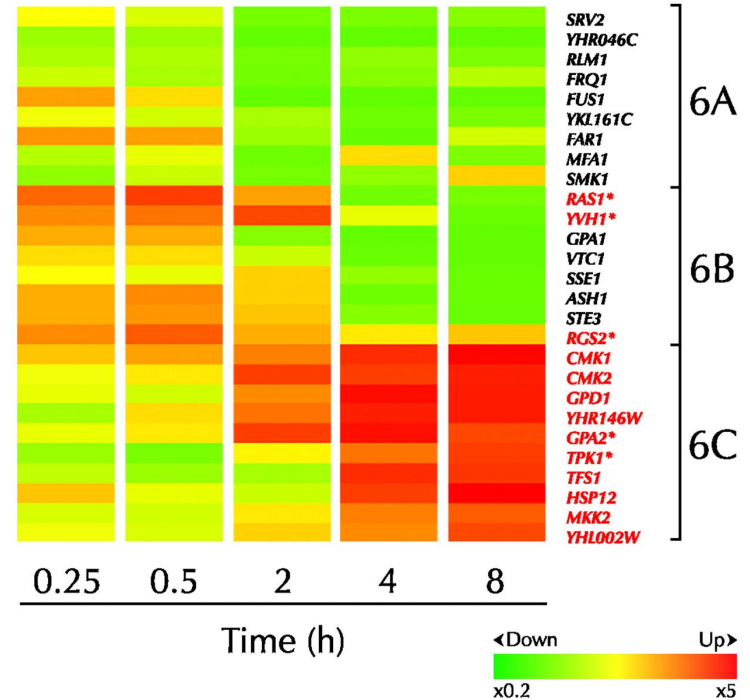
- Clusters:
  - 4A: not defined
  - 4B & 4C: stress response
  - 4D: stress response and chaperone
- Heat shock protein genes down-regulated (EXCEPT for HSP12 and HSP26).
- Protein folding genes up-regulated.





# Signal transduction genes changed expression

- Clusters were not defined in article.
- Genes related to cAMP-PKA pathway and Msn2p/4p were up-regulated.
- Increased
  - Signaling
  - Metabolism control
  - Stress resistance



# Overall changes show trend in cold shock response

- Microarray and clustering analysis shows three separate phases:
  - Early phase
  - Middle phase
  - Late phase
- Transcriptional genes up-regulated first to help transcription and translation.
- Ribosomal proteins up-regulated in the middle phase to further assist maintenance of translation.
- Stress response induced genes up-regulated in the late phase.

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- **What do previous studies say about these results?**
- Concluding remarks about the response of yeast cells to cold shock



# Similar findings on changes in gene expression

- This article is one of the first to analyze the time-dependent genetic responses in yeast cells to low temperature
- Translational efficiency is dramatically reduced by low temperature, because of the formation of secondary structure in RNA molecules and the increase of inactivated ribosome (Jones and Inouye, 1996).
- **NSR1**, **TIP1**, and **OLE1** were confirmed as being important genes in the response of cold shock (Sahara et. al., 2002).
- Other cells exposed to environmental stresses such as heat, salinity, hydrogen peroxide, and osmotic stresses undergo similar changes in gene expression

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- **Summary of the response of yeast cells to cold shock**

# Summary

- Cold shock proteins are induced when cells are exposed to low temperatures in order to cope with the drastic change in environment
- Microarray Hybridization was performed in order to analyze the effects of cold shock on yeast cells
- Clustering analysis shows trends of gene expression changes
- Gene expression changed to maintain transcription and translation and to adapt a tolerance to the colder temperature
- Other organisms show similar responses in gene expression when exposed to environmental stresses

# Conclusion

- Yeast cells respond to cold shock by altering expressions of genome for survival.
- This article provides us with information about the effects of cold shock on gene expression in yeast cells
- Application to GRNsight project:
  - Understand what information scientists may want when looking at yeast genes

# Acknowledgments

Biological Databases

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# References

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- LMU BioDB 2017. (2017). Week 12. Retrieved November 14, 2017, from [https://xmlpipedb.cs.lmu.edu/biodb/fall2017/index.php/Week\\_12](https://xmlpipedb.cs.lmu.edu/biodb/fall2017/index.php/Week_12)
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