Data in Brief

Does gene length play a role? — Transient regulation of Gcn5 histone acetyltransferase under stress conditions

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ABSTRACT

Gcn5 is a histone modification enzyme that performs its function by global or locus-specific histone acetylation. It is known that Gcn5 involves in stress responses in yeast. Our previous data showed that Gcn5 relocalized to the long genes under IM KCl stress conditions in yeast. Here we use a stress adaptation and recovery model and performed 52 microarrays. By investigating the gene regulation pattern, genome-wide localization of Gcn5, as well as histone modification, we aim to understand the regulation mechanism. The data is available in Gene Expression Omnibus (GEO: SuperSeriesGSE 36601).

Specifications	
Organism/cell line/tissue	Yeast: *Saccharomyces cerevisiae*: By4742, *MATα*, *his3-1*, *leu2-0*, *lys2-0*, *ura3-0* Gcn5-MYC13-KanMX6
Sequencer or array type	Gene expression array: Affymetrix Yeast Genome 2.0 Array Tiling array: Affymetrix GeneChip *S. cerevisiae* Tiling 1.0R Array
Data format	Raw data: CEL file, normalized and processed data: BAR and TXT files. Analyzed data: TXT
Experimental factors	Time points during different phases in stress adaptation and recovery phase. Gene expression, genome-wide of *Gcn5*, histone acetylation marks *acH3K18*, *acH4K16* and histone *H3* density

Direct link to deposited data

The link to the whole superdata series can be found here: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36601.

The super data series include gene expression data and ChIP-on-chip tiling array data.

Direct link to the expression data: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36599.

Direct link to the ChIP-on-chip tiling array data: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36600.

Experimental design, strain, methods and data set description.

Experiment design

HAT family proteins are highly redundant at normal growth conditions. Here we utilize a KCl stress model so that Gcn5 performs its specific function. To study the transient regulation of Gcn5 during stress adaptation and recovery growth regime, samples are collected at 5 different time points, which represent different growth phases as shown in Fig. 1. For each sample, gene expression changes are measured by expression microarray. In parallel, genome-wide localization of Gcn5, histone H3 density, as well as acetylation level of relevant histone marks (H3K18 and acH4K16) are measured by ChIP-on-chip tiling array. For choice of histone acetylation marks, see reference [1].

Strain and methods

The Gcn5-myc tagged strain (By4742, *MATα*, *his3-1*, *leu2-0*, *lys2-0*, *ura3-0* Gcn5-MYC13-KanMX6) is used in the study [2]. Gcn5 protein level can be detected by anti-Myc antibody. Detailed method for sample collection, method for expression profile, ChIP-on-chip microarray and data analysis is described in [1].

Dataset description

Deposited Dataset overview is shown in Fig. 2. SuperSeriesGSE 36601 including subseries GSE36599 for expression array. And subseries GSE36600 for chip-on-chip tiling array.

For subseries GSE36599, 10 raw data file samples from 5 time points in replicates are uploaded as supplementary files related to the 10 normalized sample files (GSM987346–GSM987355).

For subseries GSE36600: 42 ChIP-on-chip tiling arrays — raw data in CEL format are uploaded as supplementary files. The bar files are normalized signals so that the medium values are the same for the 5 time points.

Each bar file is related to each sample file that has been further processed in TXT file format (GSM897356–GSM897375) showing the ChIP
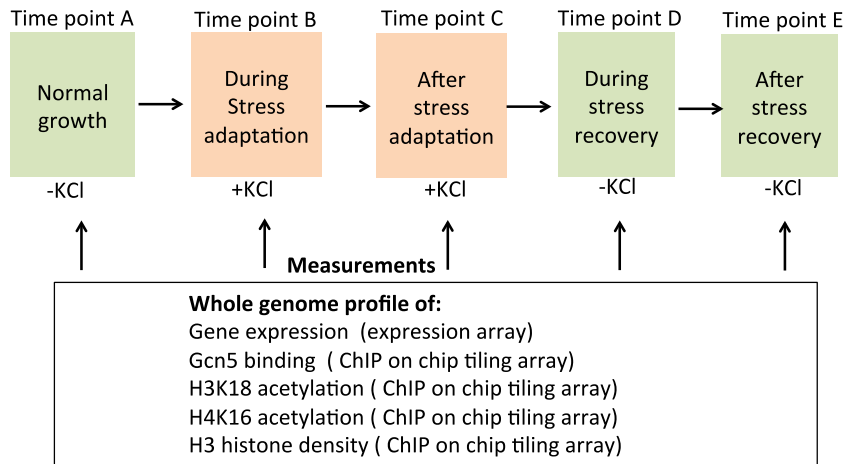
Fig. 1. Experiment design: For 5 different time phases of stress, gene expression, Gcn5 localization, histone acetylation marks (acH3K18, acH4K16) and histone H3 level are detected by expression array or ChIP-on-chip tiling array with duplicates.

signal at different regions, separating into 5′ IGR region, ORF region, and 3′ IGR regions. The JAVA codes for processing the files are in the supplementary files, provided by the author Johan Henriksson.

Discussion

The experiment design is based on our previous interesting observation that histone acetylatransferase Gcn5 recruited to the longer genes in a genome-wide level under the stress conditions (1 M KCl treatment) [3]. We try to find out the answers for the following questions: 1) If the recruitment of Gcn5 to longer genes is a reversible process when the stress withdraws? and 2) what is the regulation mechanism?

The whole genome-wide data includes gene expression, Gcn5 localization and histone modification. As published in [1], gene length, gene abundance, as well as different gene regulation patterns under stress adaptation and recovery regime are considered and tested in the data analysis. In conclusion, Gcn5 plays a genome-wide role to increase the transcription elongation of long genes under stress conditions; this process is reversible. Interestingly, by looking into ORF regions and the promoter regions separately, we found that Gcn5 interacts with histones close to the transcription start site by acetylating H3K18, therefore leading to histone depletion and active gene transcription initiation.

This is valuable data to understand the mechanisms of epigenetic regulation for the yeast researchers as well as non-yeast researchers, considering the function of Gcn5 is evolutionarily highly conserved.
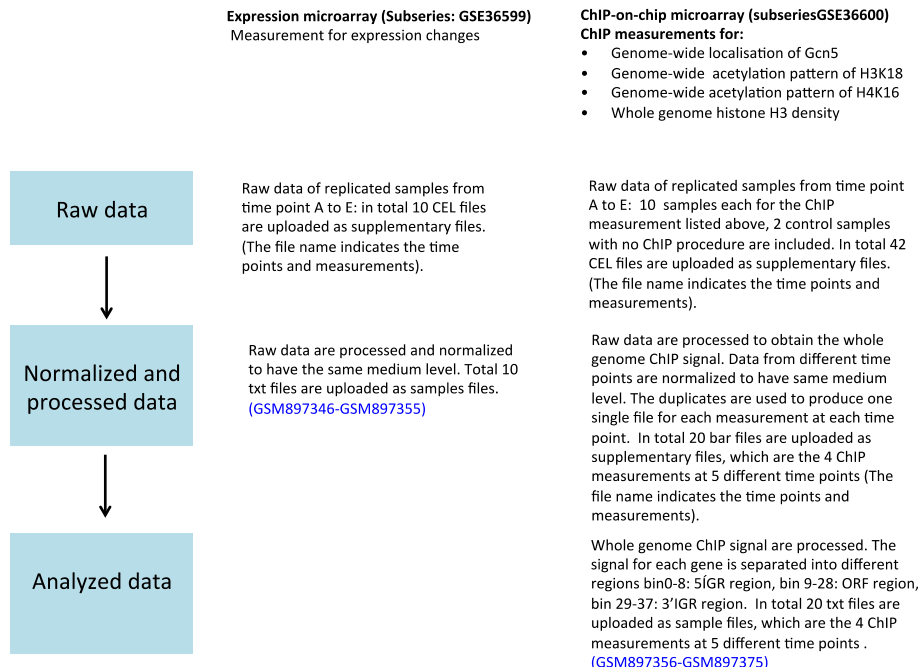
Fig. 2. Overview of the data structure submitted. The relation among the raw data, normalized/processed data and analyzed data is presented.

Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.gdata.2014.09.001.

References

[1] Y. Xue-Franzén, J. Henriksson, T.R. Bürglin, A.P.H. Wright, Distinct roles of the Gcn5 histone acetyltransferase revealed during transient stress-induced reprogramming of the genome. BMC Genomics 14 (2013) 479.

[2] L.E. Rosaleny, A.B. Ruiz-Garcia, J. Garcia-Martinez, J.E. Perez-Ortin, Tordera V: the Sas3p and Gcn5p histone acetyltransferases are recruited to similar genes. Genome Biol. 8 (2007) R119.

[3] Y. Xue-Franzén, A. Johnsson, D. Brodin, J. Henriksson, T.R. Büglin, A.P.H. Wright, Genome-wide characterisation of the Gcn5 histone acetyltransferase in budding yeast during stress adaptation reveals evolutionarily conserved and diverged roles. BMC Genomics 11 (2010) 200.