Transcriptional regulation by histone modifications using yeast model

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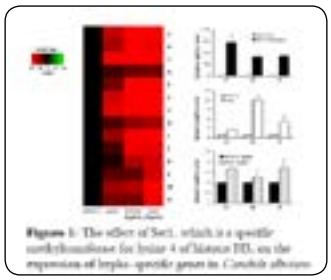
The methylation of the fourth lysine on histone H3 (H3K4me) is a well-known mark of transcription activation and the ubiquitination of the 123rd lysine of on histone H2B monoubiquitination (H2Bub1) is the prerequisite for H3K4 me in *Saccharomyces cerevisiae*. All three types of H3K4 methylation, including mono, di and tri-methylation, occur by sole H3K4 methyltransferase, Set1 in *S. cerevisiae*. We created the strain defective bulk level of H3K4me3 even when H2Bub1 signal is normal without any mutation of proteins. We found that some oxidation reduction related genes are less expressed in H3K4me3 defective strain comparing the strains bearing normal level of H3K4me3 by RNA-sequence analysis. Also, *Candida albicans*, which is the most common fungal pathogen in human has Set1 complex as its methyltransferase for the H3K4. It is previously described that Set1 deleted mutant shows attenuated virulence and pathogenesis in *C. albicans*. However, it is unclear why Set1 is important for virulence of *C. albicans*. In this study, we performed RNA sequencing of wild type and Δset1 strain to identify the role of Set1 in C. albicans pathogenesis. In Δset1, the 156 genes are down regulated more than 2-fold. The Gene Ontology (GO) enrichment analysis revealed that the significant number of these genes has oxidoreductase activity. Indeed, the Δset1 strain is more sensitive to hydrogen peroxide or menadione which induces oxidative stress. The survival assay in macrophages indicated that the survival rate of Δset1 in macrophages is less than wild type strain. These results show that the Set1 is required for the survival in host cells by regulating the expression of genes whose products defend against an oxidative stress.



Recent Publications:

1. Kim J, Lee J E and Lee J S (2015) Histone deacetylase-mediated morphological transition in *Candida albicans*. Journal of Microbiology 53(12):805-811
2. Lee J E, Oh J H, Ku M, Kim J, Lee J S and Kang S O (2015) Ssn6 has dual roles in *Candida albicans* filament development through the interaction with Rpd31. FEBS Letters 589(4):513-520.
3. Lee J S, Garrett A, Yen K, Takahashi Y H, Hu D, Jackson J, Seidel C, Pugh B F and Shilatifard A (2012) Co-dependency of H2B monoubiquitination and nucleosome re-assembly on Chd1. Genes and Development 26(9):914-919.
4. Lee J S, Smith E and Shilatifard A (2010) The language of histone crosstalk. Cell 142(5):682-685.
5. Lee J S, Shukla A, Schneider J, Floresn L, Swanson S K, Washburn M P, Bhaumik S R, and Shilatifard A (2007) Histone crosstalk between H2B monoubiquitination and H3 methylation mediated by COMPASS. Cell 131(6):1084-1096.

Biography

Jung Shin Lee is a Biochemist and Molecular Biologist studying to understand the molecular mechanism of the epigenetic regulation by histone modifications. She suggested the molecular mechanism of how the ubiquitination of histone H2B regulate the methylation of histone H3 lysine 4 when during her Post-doctorate. These two histone modifications are abundant within the actively transcribed genes and are considered to be important for the transcription. She started her own lab in 2012 and her group is studying mainly how histone modifications regulate epigenetically the gene expression and subsequently have effects on the physiological change.