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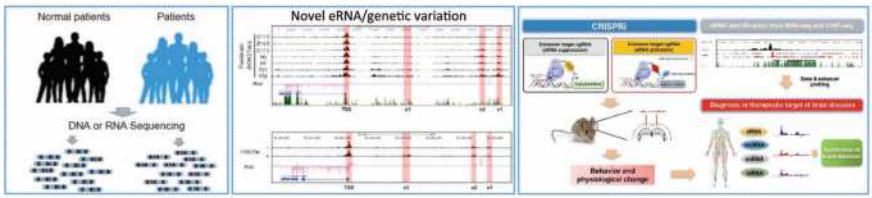
lncRNA(enhancer RNA) mediated gene expression and regulation in the brain diseases

In mammalian cells, transcription and gene expression are dynamically regulated by a variety of factors, and transcriptional controls are paramount for most genes. The central dogma of gene expression includes two main steps, namely, RNA transcription from the DNA sequence, followed by protein translation from the RNA sequence. Enhancer RNAs (eRNAs) are a class of long noncoding RNAs (lncRNAs) that are transcribed from DNA sequences upstream or downstream of active enhancer regions. In cortical neurons, eRNAs are synthesized in response to membrane depolarization, prior to the end of mRNA transcription. During neuronal development, various gene expression changes occur in the neurons, and such gene expression programs are necessary for synapse formation or maturation. Activity-regulated transcriptional programs are essential for the maturation or development of synapses, and transcription of gene contributes many cognitive disorders, which include Fragile X syndrome, Down syndrome, autism spectrum disorders or other rare genetic disorders. One of my interesting preliminary data indicated that endogenous eRNAs altered mouse behavior, and completely impaired the fear memory. Altogether, these evidences could imply that not only endogenous eRNAs directly regulates specific gene expression but also could be alter behavior *in vivo*. Therefore, high target gene specificity eRNAs may be useful therapeutic or diagnosis targets, and unique biomarkers of various diseases.

Aim	Enhancer RNA therapy : Genome editing in eRNA research
Tool	RNA-seq, ChIP-seq, CRISPRi, Chromosome conformation capture (3C), UV-RNA immunoprecipitation (UV-RIP)
TARGET	

Curriculum Vitae

2016.12~Present : Principal Investigator, KBRI
2012.04~2016.10 : Postdoctoral Fellow, University of Texas Southwestern Medical Center, TX, USA
2006~2007.03 : Researcher, The University of Tokyo, Graduate School of Medicine, Tokyo, Japan

Academic Credential

2012 : Ph.D., The University of Tokyo Graduate School of Medicine, Tokyo, Japan
2005 : M.S., Hanyang University, College of Medicine, Seoul, Korea
2003 : B.S., Hanyang University, Life Science, Seoul, Korea

Awards/Honors/Memberships

2008~2012 : The University of Tokyo Fellowship, Special full Scholarship (Excellence scholarship student, President Award)
2011 : KSBNS-MCCS Asia Conference, Takeda MCCS Travel Award
2014 : Association of Korean Neuroscientist (AKN), Research Award (Post-doc)
2008~Present : Member, Society for Neuroscience

Research keywords

Enhancer RNA, lncRNA, Transcriptome, Genome-wide association Study, Gene Expression, enhancer.

Key techniques

Genome-Wide technique (RNA-seq, ChIP-seq), CRISPRi, Chromosome conformation capture (3C), UV-RNA immunoprecipitation (UV-RIP), eRNA targeted AAV virus production, Stereotaxic injection, ChIP, FISH, Nascent RNA capture, Mouse behavior test. (Fear conditioning test, Rotarod test)

Research Interests/Topics

- Elucidation of function and mechanism for brain disease from novel enhancer RNA through transcriptome analysis and CRISPRi.

Research Publications (selected)

- **Joo JY**, Schaukowitch K, Farbiak L, Kilaru G, Kim TK. Stimulus-specific combinatorial functionality of neuronal c-fos enhancers. *Nature Neuroscience, 19(1):75-83, 2016.*
- Schaukowitch K*, **Joo JY***, Liu X, Watts JK, Martinez C, Kim TK. Enhancer RNA Facilitates NELF Release from Immediate Early Genes. *Molecular Cell, 56(1): 29-42,* 2014. *Co-first author. (This paper previewed by "eRNAs lure NELF from paused polymerases" *Molecular Cell, 56(1):3-4, 2014.)*
- Schaukowitch K, Reese A, Kim SK, Kilaru G, **Joo JY**, Kavalali E, Kim TK. An intrinsic transcriptiona program underlying synaptic scaling during activity suppression. *Cell Reports, 18(6):1512-1526, 2017.*
- Schaukowitch K*, **Joo JY***, Kim TK. UV-RNA Immunoprecipitation (UV-RIP) Protocol in Neurons. *Method's in Molecular Biology (Invited), 1468:33-38, 2017.* (*Equal contribution)