School of Life Sciences

Seminar Series

No. 2019-26

Thu., **14 November**, 4:00pm

Jukhyun Bio Auditorium(RM.121)

English

3D chromatin structure in cancer genome

Speaker | Inkyung Jung

Affiliation | KAIST

Host | Prof. Sung-Gyoo Park

광주과학기술원 생명과학부

Gwangju Institute of Science and Technology School of Life Sciences

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Inkyung Jung, Ph.D.

Education/Experience

2002.03-2006.02	B.S. in Biosystems, KAIST, Daejeon, Korea
2006.03-2011.01	Ph.D. in Bioinformatics, KAIST, Daejeon, Korea
2009.01-2009.02	Visiting Researcher, Lab. Of Chemical Genetics, RIKEN, Saitama, Tokyo, Japan(Minoru Yoshida, Ph.D.)
2011.02-2012.06	Postdoctoral Researcher, Dept. of Bio and Brain eng., KAIST, Daejeon, Korea(Dongsup Kim, Ph.D.)
2012.07-2016.09	Postdoctoral Researcher, Lab. Of Gene Regulation, Ludwig Institute for Cancer Research, San Diego, California(Bing Ren, Ph.D.)
2016.10-present	Assistant Professor, Dept. of Biological Sciences, KAIST, Korean

Abstract

A large number of structural variations including deletion, inversion, and translocation are often found in cancer genome, but delineating their effect in gene regulation during cancer development and progression has been challenging because they are mostly non-coding. We postulate that structural variations may disorganize higher-order chromatin structure, resulting in abnormal gene regulation by exposing genes to inappropriate regulatory cis-regulatory elements. To test our hypothesis, we generate genome-wide chromatin contact maps with 40 colorectal cancer patients' samples and reveal extensively disorganized higher-order chromatin structure largely explained by structural variations. These changes frequently rewire or disrupt super-enhancer and target gene relationships, which is correlated with either activation of proto-oncogenes or inhibition of tumor-suppressor genes. Unexpectedly, we reveal chromosome-wide disorganized higher-order chromatin structure that may represent a massive chromosomal rearrangement in cancer genome, associating with widespread abnormal gene expression changes without coding sequence mutations. Our study highlights the effect of non-coding structural variations on cancer-specific gene expression. In this talk, I will discuss how investigating 3D genome organization provides a new mechanistic insight to understand abnormal gene regulation mechanisms underlying cancer development and progression.