The role of chromatin dynamics in DNA damage response

Tsuyoshi Ikura[1], Ryo Matsuda[1], Satoshi Tashiro[2], and Masae Ikura[1]

[1]Department of Mutagenesis, Division of Chromatin Regulatory Network, Radiation Biology Center, Kyoto University, Yoshidakonoe, Sakyo-ku, Kyoto 606-8501, Japan. [2]Department of Cellular Biology, Research Institute for Radiation Biology and Medicine, Hiroshima University, 1-2-3 Kasumi, Minami-ku, Hiroshima 734-8553, Japan.
e-mail: ikurat@house.rbc.kyoto-u.ac.jp

Chromatin is a dynamics structure that can be regulated by epigenetic code involving DNA methylation, histone modifications, ATP-dependent chromatin remodeling and histone variant eviction/exchange. By developing proteomics approach or gemone wide screening, a large number of protein modules and networks, which were not previously linked to DNA damage response were identified and new interconnections between DNA repair, replication and transcription have led us to expand our knowledge regarding the signaling of DNA damage response. We have previously shown that TIP60 histone acetyltransferase complex, which is involved in DNA damage response signaling, regulates the eviction of histone H2A variant, H2AX after DNA damage. To investigate the role of the eviction of histone H2AX in DNA damage response, we purified histone H2AX as a protein complex from HeLa cells. We identified the functional module for the eviction of histone H2AX through the TIP60 and H2AX complexes interaction network. In this time, focusing on these complexes, we will discuss current knowledge on chromatin dynamics and epigenetic regulation with respect to the cellular response to DNA damage.