MS109.O06

Structural studies of Rhino protein in piRNA biogenesis

Y. Huang[1,2], B. Yu[1,2]

[1]*National Center for Protein Science Shanghai, Shanghai, China,* [2]*Shanghai Institute of Biochemistry and Cell Biology, CAS, Shanghai, China*

Small-RNA-guided gene regulation is a common biological process in eukaryotic cells. Animal germ cells are characterized by an intriguing small-RNA-mediated gene-silencing mechanism known as PIWI pathway. PIWI-interacting RNAs (piRNAs) are small, 21-30 nt single-stranded RNAs that associate with PIWI proteins. The function of piRNA is silencing transposon elements in germ line cells to keep the genome integrity since germ line cells are the only source for transmitting genetic information to the next generation. For a long time the biogenesis of piRNA and the mechanism of how it functions remains unclear. The biogenesis of piRNAs is quite different from that of other small-RNA pathways, which is independent of Dicer. piRNA biogenesis occurs through both primary and secondary pathway (or called ping-pong cycle). In drosophila transcripts from heterochromatic clusters are processed into primary piRNAs. A particularly fast evolving homologue of heterochromatin protein 1 (HP1) called Rhino binds to dual-strand piRNA clusters and is required for their production. But how does Rhino recognize histone H3 trimethylated on lysine 9? What's the difference between Rhino and other HP1 proteins? Here we show the crystal structure of Rhino both in apo form and complex form with H3K9me3. We observed a unique dimer interface in Rhino and a domain-swapping in conformational change. These findings provide insights into the molecular mechanism of the specificity of Rhino recognizing histone H3K9me3 and its function in piRNA biogenesis.

Keywords: Rhino, piRNA biogenesis, transposon silencing