Arnab Nayak, J Clin Epigenet 2017, 3:4
DOI: 10.21767/2472-1158-C1-002

Interplay of actin remodeler and SUMO pathway govern epigenetic regulation and cellular programming

Arnab Nayak
Hannover Medical School, Germany

The discovery of SUMO (Small Ubiquitin-like Modifier) system is relatively new in biology; however, studies from last decade established a crucial role of SUMO in the control of cellular signaling pathways, particularly in the context of gene regulation. Categorical demonstration of the relationship between epigenetic regulators and the SUMO system in the broader context of transcription, however, is not well established. I will present our newfound evidence that shows the SUMO-specific isopeptidase SENP3 controls epigenetic landscape of the homeobox genes by regulating histone-modifying SET1/MLL complexes and thus determining the fate of human mesenchymal stem cells. Detailed molecular mechanisms that regulate histone methyltransferase complex assembly and its chromatin recruitment are contentious and vigorously pursued questions in the field of transcription regulation. We have investigated molecular events on the involvement of the SUMO system in these regulatory processes that fine-tune epigenetic events and further downstream phenomenon such as recruitment of active elongating RNA polymerase II. These observations link SUMO-mediated regulation with evolutionary conserved epigenetic processes. Besides, our very recent work on SENP (SENtrin-specific Protease) proteomics approach unraveled a cohort of novel interactome consists of chromatin remodelers and epigenetic modifiers. The outcomes from the large-scale quantitative proteomics screen strengthen our argument of a global role of SUMO system in modulating transcriptional mechanisms. I will also discuss how these studies established a platform to understand many key questions in developmental biology such as the less-understood mechanism of temporospatial expression of homeobox genes.

Recent publications

1. Arnab Nayak, Anja Reck, Christian Morsczeck and Stefan Müller (2017) Flightless-I governs cell fate by recruiting the SUMO isopeptidase SENP3 to distinct HOX genes. Epigenetics & Chromatin 10:15.
2. Stefan Muller and Arnab Nayak (2016) Inhibition of MLL1 histone methyltransferase brings the developmental clock back to naïve pluripotency. Stem Cell Investigation. 3:58.
3. Arnab Nayak, Sandra Viale-Bouroncle, Christian Morsczeck and Stefan Müller (2014) The SUMO-specific Isopeptidase SENP3 Regulates the MLL1/2 Methyltransferase Complex and Controls Osteogenic Differentiation. Molecular Cell. 55(1): 47-58.
4. Arnab Nayak and Stefan Müller (2014) SUMO-specific proteases/isopeptidase: SENPs and beyond. Genome Biology 15:422.
5. Arnab Nayak, Judith Glöckner-Pagel, Martin Vaeth, Julia E. Schumann, Mathias Buttmann, Tobias Bopp, Edgar Schmitt, Edgar Serfling and Friederike Berberich-Siebelt (2009) Sumoylation of the transcription factor NFATc1 leads to its subnuclear relocalization and interleukin-2 repression by histone deacetylase. J Biol Chem. 284(16):10935-46.

Biography

Arnab Nayak has expertise in the field of SUMO modification of protein in the context of epigenetic regulations during cellular programming. He has shown how addition of SUMO moiety can alter a transcriptional activator to a genomic site-specific repressor to modulate immune response. His recent work established a new SUMO-mediated mechanism that is required to govern function of evolutionary conserved epigenetic regulators such as MLL histone methyltransferase complex. Besides, he is currently engaged in single molecule biophysical studies to understand how molecular motor protein function. This unique approach is indispensable to understand mechanisms underlying human diseases such as familial hypertrophic cardiomyopathies at an individual molecule level.

nayakarnab@yahoo.com