SFB 960-/RCB – Colloquium

Tuesday, 9 May 2023, 13.00 h

H 53

Dr. Rafal Archacki

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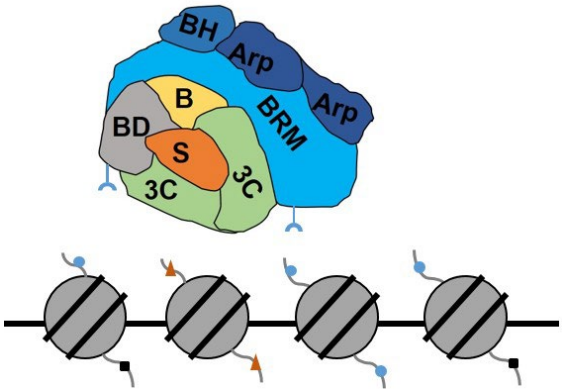
Understanding the activities of chromatin remodeler BRM in Arabidopsis

Eukaryotic nuclear DNA is packaged into chromatin, but must be accessible for critical genetic processes such as transcription, replication, recombination, and repair. Chromatin remodeling is one of the key activities that promote structural reorganization of chromatin during these processes. It depends on the activity of evolutionarily conserved multimeric complexes assembled around central ATPase that uses the energy from ATP hydrolysis to change interactions between histone octamers and the DNA. This regulatory system appears to be highly complicated, as dozens of different types of such complexes operate in the cell nucleus, and each type is further diversified . During the seminar, I will focus on the SWItch/Sucrose Non-Fermenting (SWI/SNF) class of complexes that are the most thoroughly studied in yeast, animals and plants. A number of genetic studies in Arabidopsis revealed that SWI/SNF complexes are critical for transcriptional control of developmental transitions, growth, and hormone-mediated responses. This is accompanied by binding and regulation of thousands of genes, as shown for BRM catalytic ATPase and some other subunits. However, how SWI/SNF complexes are recruited and how they work on these multiple genomic sites, only begins to be understood. We are especially interested in elucidating how different subunits, as well as particular motifs of the BRM protein contribute to the activity of the whole complex. I will describe our efforts to decipher the composition of native SWI/SNF complexes by using IP-MS approaches, as well as the role of particular subunits in the complex assembly and stability. Our data suggest a modular organization of the BRM-associated complexes, and I will discuss similarities of their composition with mammalian SWI/SNF. Furthermore I will show our work on generating new tools for more precise studies of BRM activities in vivo, including catalytic point mutant and Crispr-edited Arabidopsis lines, small inhibitors, and chemically-induced targeting.



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