

THE MYST-FAMILY OF ACETYLTRANSFERASE COMPLEXES IN EPIGENETIC MECHANISMS LINKED TO GENE REGULATION, GENOME STABILITY AND ONCOGENESIS

Jacques Côté, Ph.D.

Laval University Cancer Res Ctr, Quebec City, Canada

Chromatin dynamics associated with gene regulation, DNA repair and replication implicate protein complexes that control acetylation and methylation of histones, and the composition of chromatin. These are central in the molecular mechanisms of epigenetics, in which signals to chromatin mark different genomic loci and are read by effectors to translate a biological response. Histone acetyltransferases complexes contain reader domains that recognize other histone marks enabling intricate epigenetic cross-talk. In some cases, they also contain additional enzymatic activities like chromatin remodelers. These stable molecular assemblies are truly multi-functional and implicated in most DNA-based mechanisms. Our work on the MYST-family of HAT complexes (TIP60/NuA4-KAT5, HBO1-KAT7, MOZ/MORF-KAT6, MOF-KAT8) highlighted these functional characteristics and recent data will be presented on their action during gene regulation, DNA repair and how they can be hijacked during oncogenic mechanisms driven by recurrent chromosomal translocations.