Abstract

CCCTC-binding factor (CTCF) can both activate as well as inhibit transcription by forming chromatin loops between regulatory regions and promoters. In this regard, Ctcf binding on the non-methylated DNA and its interaction with the Cohesin complex results in differential regulation of the *H19*/*Igf2* locus. Similarly, a role for CTCF has been established in normal hematopoietic development; however its involvement, despite mutations in CTCF and Cohesin complex were identified in leukemia, remains elusive. CTCF regulates transcription dependently on DNA methylation status and can if bound block interactions of enhancers and promoters.

Here, we show that in hematopietic cells CTCF binds to the imprinting control region of *H19*/*Igf2* and found that chromatin remodeller Smarca5, which also associates with the Cohesin complex, facilitates Ctcf binding and regulatory effects. Furthermore, Smarca5 supports CTCF functionally and is needed for enhancer-blocking effect at imprinting control region. We identified new CTCF-recognized locus near hematopoietic regulator SPI1 (PU.1) in normally differentiating myeloid cells together with members of the Cohesin complex. Due to DNA methylation, CTCF binding to the *SPI1* gene is reduced in AML blasts and this effect was reversible by DNA methylation inhibitor 5-azacitidine.