

We are family



“
...the JARID1 subfamily ... represent the first enzymes with specificity for H3K4me3.”



The methylation status of histones, which is essential for gene regulation and chromatin structure, is modulated by histone methylases and demethylases. Several proteins that contain a Jumonji C (JmjC) domain have recently been shown to be histone lysine demethylases. A flood of new studies now identify the JARID1 subfamily of JmjC-domain-containing proteins as histone demethylases with specificity for di- (me₂) and trimethylated (me₃) histone H3K4.

Christensen *et al.* showed that the retinoblastoma-binding protein-2 (RBP2, or JARID1A) is a H3K4me₃/me₂ histone demethylase that binds the promoters of certain Hox genes in undifferentiated embryonic stem (ES) cells. Binding is lost following ES-cell differentiation, which correlates with transcriptional repression and increased H3K4me₃ levels. The functional significance of RBP2 in development might be evolutionarily conserved, as mutation or knockdown of the *Caenorhabditis elegans* homologue *rbr-2* caused increased levels of H3K4me₃ and defective vulval formation. Incidentally, Secombe *et al.* identified the RBP2 *Drosophila melanogaster* homologue Lid, and Seward *et al.* and Liang *et al.* identified the JARID1B *Saccharomyces cerevisiae* homologue Yjr119C (or Jhd2) as H3K4me₃ demethylases. Lid regulates Myc-induced cell growth and binds to Myc, which negatively regulates its demethylase activity.

Methylation of H3K4 is normally associated with transcriptionally active genes. Indeed, Klose *et al.* showed that RBP2-knockout mouse cells displayed increased transcription of certain cytokine genes. This was accompanied by increased H3K4me₃ levels on the RBP2-responsive gene promoter compared with wild-type cells.

The X-linked mental retardation (XLMR) gene *SMCX* (or *JARID1C*) encodes another H3K4me₃/me₂ demethylase. Iwase *et al.* analysed point mutations that had been identified in patients with XLMR and found that several mutants had reduced enzymatic activity. To investigate whether abnormal *SMCX* demethylase activity contributes to the XLMR pathology, the authors knocked down *Smcx* in zebrafish and in primary mammalian neurons, which resulted in neuronal developmental defects. The mutational analysis also revealed that *SMCX* binds to H3K9me₃, which might have significance for establishing the local chromatin environment.

Lee *et al.* showed that JARID1D associates with the Polycomb-like protein Ring6a (or MBLR), which regulates its enzymatic activity. JARID1D and Ring6a/MBLR were enriched at the transcriptional start site of the *Engrailed-2* gene. Depletion of JARID1D led to the concurrent loss of Ring6a/MBLR at the *Engrailed-2* gene, enhanced levels of H3K4me₃ near the transcription start site and increased gene transcription.

Depletion of JARID1D also enhanced the recruitment of the chromatin-remodelling complex NURF and the basal transcription machinery to the target gene promoter — providing JARID1D with a possible mechanism for regulating transcription initiation.

Together, the JARID1 subfamily of JmjC-domain-containing proteins add an entire new group of evolutionarily conserved histone demethylases to the ever-growing list and represent the first enzymes with specificity for H3K4me₃.

Arianne Heinrichs, Chief Editor,
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ORIGINAL RESEARCH PAPERS

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FURTHER READING Klose, R. J. & Zhang, Y. Regulation of histone methylation by demethylation and demethylation. *Nature Rev. Mol. Cell Biol.* 7 Mar 2007 (doi:10.1038/nrm2143) | Klose, R. J. *et al.* The JmjC-domain-containing proteins and histone demethylation. *Nature Rev. Genet.* 7, 715–727 (2006)