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A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis (Article)

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Abstract

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PRDM9 binding localizes almost all meiotic recombination sites in humans and mice. However, most PRDM9-bound loci do not become recombination hotspots. To explore factors that affect binding and subsequent recombination outcomes, we mapped human PRDM9 binding sites in a transfected human cell line and measured PRDM9-induced histone modifications. These data reveal varied DNA-binding modalities of PRDM9. We also find that human PRDM9 frequently binds promoters, despite their low recombination rates, and it can activate expression of a small number of genes including CTCFL and VCX. Furthermore, we identify specific sequence motifs that predict consistent, localized meiotic recombination suppression around a subset of PRDM9 binding sites. These motifs strongly associate with KRAB-ZNF protein binding, TRIM28 recruitment, and specific histone modifications. Finally, we demonstrate that, in addition to binding DNA, PRDM9's zinc fingers also mediate its multimerization, and we show that a pair of highly diverged alleles preferentially form homo-multimers. © Altemose et al.

Indexed keywords

EMTREE drug terms: zinc finger protein

EMTREE medical terms: amino acid sequence, Article, cell culture, cloning, controlled study, cytolysis, DNA purification, female, fluorescence microscopy, gene activation, gene control, gene expression, histone methylation, human, human tissue, immunoprecipitation, male, meiosis, mouse, nonhuman, position weight matrix, protein binding, protein DNA interaction, RNA extraction, spermatogenesis, telomere, tissue culture, Western blotting

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