Supplemental I

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Review

Sharing marks: H3K4 methylation and H2B ubiquitination as features of meiotic recombination and transcription

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Abstract: Meiosis is a specialized cell division that gives raise to four haploid gametes from a single diploid cell. During meiosis, homologous recombination is crucial to ensure genetic diversity and guarantee accurate chromosome segregation. Both the formation of programmed meiotic DNA double-strand breaks (DSBs) and their repair using homologous chromosomes are essential and highly regulated pathways. Similar to other processes that take place in the context of chromatin, histone posttranslational modifications (PTMs) constitute one of the major mechanisms to regulate meiotic recombination. In this review, we focus on specific PTMs occurring in histone tails as driving forces of different molecular events, including meiotic recombination and transcription. In particular, we concentrate on the influence of H3K4me3, H2BK123ub, and their corresponding molecular machineries that write, read, and erase these histone marks. The Spp1 subunit within the Complex of Proteins Associated with Set1 (COMPASS) is a critical regulator of H3K4me3-dependent meiotic DSB formation. On the other hand, the PAF1c (RNA polymerase II associated factor 1 complex) drives the ubiquitination of H2BK123 by Rad6-Bre1. We also discuss emerging evidence obtained by cryo-electron microscopy (EM) structure determination that has provided new insights into how the "cross-talk" between these two marks is accomplished.

Keywords: meiosis, recombination, DSB, transcription, COMPASS, histone, PAF1c, methylation, ubiquitination.

Supplemental II

***Table S1* List of proteins analysed in interaction network plots.** Each protein includes its name and a brief description. In red, Mog1 and the five subunits of PAF1c.

Name	Description
Bre1	E3 ubiquitin ligase that catalyze H2Bub
Bur1	Phosphorilates Ser2 CTD
Cdc14	Phosphorilates Spc110 and stimulates DSB
Cdc73	Component of the PAF1 complex
Cnm67	SPB component
Cse4	centromeric histone H3-like protein
Ctf19	Blocks DSB in centromeric regions
Ctk1	Phosphorilates Ser2 CTD
Ctr9	Component of the PAF1 complex
Ddc2	Recruits Mec1
Dmc1	Facilitates homologous region search
Dot1	Histone H3K79 methylation
Hop1	DSB formation and spindle detachment, in axis
Ime1	Regulates sporulation, induct early genes
Ime4	RNA methyltransferase, Ime1 inductor
Jhd2	De-methylase
Kin28	Phosphorilates Ser5 CTD
Leo1	Component of the PAF1 complex
Lge1	Regulatory cofactor Rad6/Bre1
Mec1	DNA damage response kinase. DSB checkpoint
Mei4	RMM complex, involved in DSB formation
Mek1	Control Rec8
Mer2	RMM complex, involved in DSB formation
Mog1	Ran-binding protein required for Rad6, Bre1 and Rtf1 recruitment to H2Bub
Mre11	MRX complex, involved in DSB formation
Mre4	Control Rec9
Ndt80	Regulates sporulation, induct middle genes
Nej1	Encodes non-homologous end-joining process
Paf1	Component of the PAF1 complex
Rad50	MRX complex, involved in DSB formation
Rad51	Facilitates homologous region search
Rad6	E2 ubiquitin ligase that catalyze H2Bub
Rec102	Required for meiotic DSB
Rec104	Required for meiotic DSB
Rec114	RMM complex, involved in DSB formation

Rec8	Cohesin
Red1	Component of the synaptonemal complex axial elements
Rme1	Repressor of meiosis I
Rtf1	Component of the PAF1 complex
Set1	From COMPASS required for H3K4me/H2Bub
Set2	Histone H3K36 methylation
Sgf73	From the SAGA complex, related with IME1
Ski8	Subunit of hPAF1c, in yeast is required for meiotic DSB
Soh1	Subunit of the RNA polymerase II Mediator complex
Spc110	SPB component
Spc42	SPB component
Spc72	SPB component
Spo11	Topoisomerase-like protein which programs DSB
Spp1	From COMPASS complex, opens the chromatin, interacts with Mer2
Spt4	Elongation control during transcription
Spt5	Elongation control during transcription
Sus1	From SAGA complex, related to mRNA export
Tel1	DNA damage response kinase. DSB checkpoint
Ubp8	Cse4 deubiquitination
Xrs2	MRX complex, involved in DSB formation