

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Histone codes

ArticleInfo		
ArticleID	:	4019
ArticleDOI	:	10.1186/gb-spotlight-20010319-01
ArticleCitationID	:	spotlight-20010319-01
ArticleSequenceNumber	:	90
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-03-19 OnlineDate : 2001-03-19
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

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The [histone code](#) hypothesis posits that distinct combinations of histone modifications can recruit chromatin-modifying enzymes and exert epigenetic control over heterochromatin assembly. In the March 15 [ScienceXpress](#), Nakayama *et al.* describe a role for [histone methylation in heterochromatin assembly](#) in the fission yeast *Schizosaccharomyces pombe*. The [Clr4 protein](#) methylated lysine 9 of histone H3 (H3Lys9) preferentially within heterochromatin-associated regions. H3Lys9 methylation led to the recruitment of the chromodomain protein [Swi6](#), a homolog of *Drosophila* HP1. Both methylation and recruitment were dependent on activity of the histone deacetylase Clr3. Chromatin assembly by Swi6/Clr4 at the mating-type locus results in silencing. Hence, sequential deacetylation and methylation of histone tails leads ultimately to epigenetic inheritance patterns.

References

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5. The chromodomain protein Swi6: a key component at fission yeast centromeres.