

Correlation between Methylation and Acetylation within the Cell due to Environmental Factors

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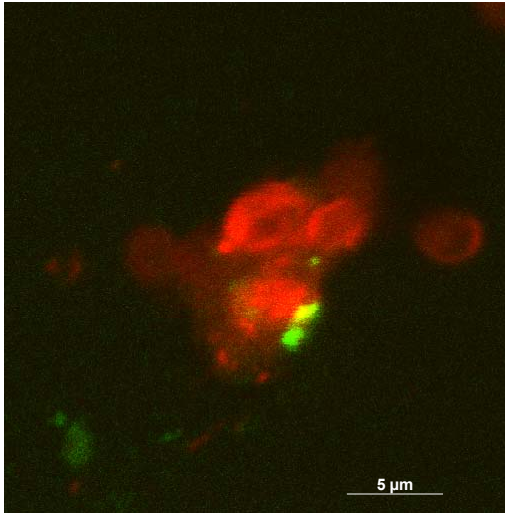
The inner works of the genome involve the integration of various processes within the cell, such as DNA methylation, chromatin remodeling and histone modification. These components allow the cell to maintain its stability with different chromatin conformations that ensure proper genetic expression. The genome of an organism is constructed in such a way that its expression can be correlated with the effects of the outside environment. Functions within a cell are uniform but become heterogeneous when outside factors are introduced and genes are expressed.

Using immunohistochemical analysis, the effects of environmental stress on the epigenetic state of the genome is observed through phenotypic and genetic expression. It was determined that a correlation between methylation and acetylation of the histones is caused by environmental stimuli. Wild-type strains of the yeast, *saccharomyces cerevesiae*, were employed to study genetic reaction to outside components such as copper. Copper causes the induction of the *CUP1* gene which creates activity within the cell, thus acetylation occurs and methylation ceases.

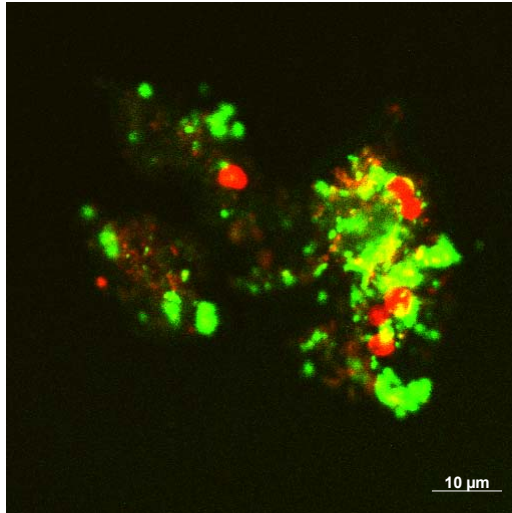
A continuation in outside factors affecting reactions within the genome will be studied along with the stimulus of hydroxyurea and ultra-violet light. This study should reveal molecular mechanisms used by the cell to sustain unsuitable conditions.

References:

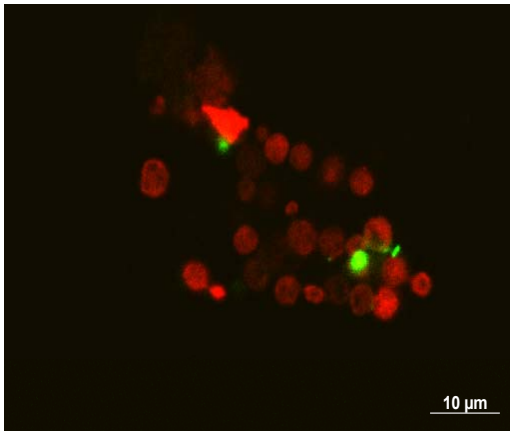
- [1] R. Jaenisch, A. Bird. *Nature Genetics* 33 (2003): 245.



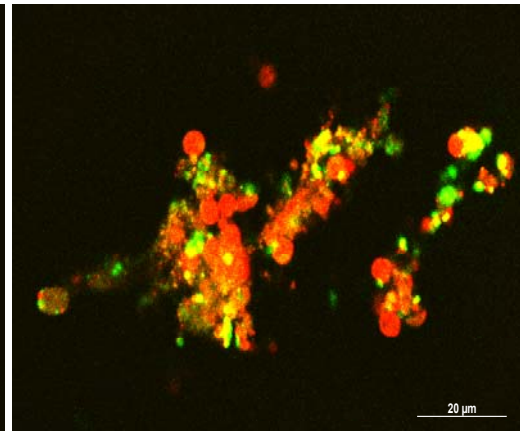
Wild Type No Cu



Wild Type with Cu
Increased acetylation



Wild Type +Cu



Wild Type No Cu
Increased methylation