

University of Massachusetts Medical School

eScholarship@UMMS

Open Access Articles

Open Access Publications by UMMS Authors

2013-04-08

Expression of the repeat genome and aberrant epigenetic factors in cancer

Dawn M. Carone

University of Massachusetts Medical School

Et al.

Let us know how access to this document benefits you.

Follow this and additional works at: <https://escholarship.umassmed.edu/oapubs>



Part of the [Cancer Biology Commons](#), [Genomics Commons](#), [Neoplasms Commons](#), and the [Oncology Commons](#)

Repository Citation

Carone DM, Hall LL, Byron M, Lawrence JB. (2013). Expression of the repeat genome and aberrant epigenetic factors in cancer. Open Access Articles. <https://doi.org/10.1186/1756-8935-6-S1-P110>.

Retrieved from <https://escholarship.umassmed.edu/oapubs/2453>

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in Open Access Articles by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.

POSTER PRESENTATION

Open Access

Expression of the repeat genome and aberrant epigenetic factors in cancer

Dawn M Carone^{*}, Lisa L Hall, Meg Byron, Jeanne B Lawrence

From *Epigenetics & Chromatin: Interactions and processes*
Boston, MA, USA. 11-13 March 2013

Nearly half of the human genome consists of noncoding repetitive DNA elements, including tandem satellite repeats in large blocks at the pericentric regions of chromosomes and intergenic repetitive elements. While both repeat types were long thought to remain mostly silent, recent evidence indicates that repeats can be expressed, but the extent and regulation of their expression or their potential function(s) remain to be elucidated. Due to their critical location within regions vital for cell division, it is expected that tight regulation of pericentric satellite sequences is essential for both epigenetic and genetic stability. Our data suggests aberrant expression of pericentric satellite RNA is tightly linked to epigenetic misregulation in cancer. It is well known that epigenetic changes can be important in cancer initiation and progression, but studies have focused primarily on the inappropriate silencing and methylation of tumor suppressor genes. While pathologists have long noted the loss of heterochromatic organization in cancer nuclei, and hypomethylation of satellite DNA has been observed, the misregulation of repeat RNAs has only recently been described. Our results provide a link between overexpression of repeat RNAs and aberrant distribution of epigenetic factors in cancer. Our data suggests regulation of the repeat genome has potentially important roles in both normal and neoplastic cells in their ability to affect distribution and recruitment of epigenetic factors.

Published: 8 April 2013

doi:10.1186/1756-8935-6-S1-P110

Cite this article as: Carone *et al.*: Expression of the repeat genome and aberrant epigenetic factors in cancer. *Epigenetics & Chromatin* 2013 **6**(Suppl 1):P110.

Department of Cell Biology, University of Massachusetts Medical School,
Worcester MA, USA



© 2013 Carone *et al.*; licensee BioMed Central Ltd. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Submit your next manuscript to BioMed Central
and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

