

Epigenetics, Chromosomes and Chromatin**Oral Presentation****Monday November 7****2.00pm – 2.15pm****O-30****BALANCED EXPRESSION BETWEEN THE X CHROMOSOME AND AUTOSOMES IN GERM CELLS AND IN EARLY MOUSE DEVELOPMENT**D K Nguyen, [C M Disteché](#)

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Monosomy of the X chromosome due to divergence between the sex chromosomes caused by degeneration of the Y lead to dosage compensation mechanisms to restore balanced expression between the X and the autosomes. In *Drosophila*, up-regulation of the male X achieves dosage compensation. Likewise, we have previously shown that mammals up-regulate their active X chromosome in adult somatic tissues. Together with X inactivation, this mechanism would maintain balanced expression between the X and autosomes and between the sexes. Presently, we have used microarray data to show that the X chromosome is expressed but not up-regulated in spermatids and secondary oocytes, preserving balanced expression of the genome in these haploid cells. Furthermore, similar expression levels between the X chromosome and autosomes were observed as early as the zygote and 2-cell stage; this doubling of global transcription from the X in diploid cells was maintained throughout development. Our results imply that upon fertilization, up-regulation of the active X, probably mediated by either removal or onset of epigenetic modifications, must rapidly occur to achieve the observed dosage compensation.

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A DRAFT METHYLATION MAP AT 4000 *NotI* SITES IN THE C57BL/6J GENOMEH Nagase¹, F Song¹, M T Kimura¹, K Fujiwara¹, E Kitamura², W A Held¹¹ Roswell Park Cancer Institute, Buffalo, NY, United States, ² Nihon University, Tokyo, Japan

DNA methylation is an important epigenetic modification in mammals. In order to understand the significance of DNA methylation, we utilized a method for global DNA methylation analysis using Restriction Landmark Genomic Scanning (RLGS) coupled with Virtual image RLGS software (ViRLGS) (Nucleic Acids Res. 31, 4490-4496, 2003). When using a methylation sensitive enzyme such as *NotI* as the restriction landmark, the comparison between real and *in silico* RLGS profiles of the genome provides a methylation map of genomic *NotI* sites. *Mus musculus* (C57BL/6J) RLGS patterns (*NotI-PstI-PvuII* and *NotI-PvuII-PstI* enzyme combinations using adult testis, brain, colon, kidney, liver, and muscle genomic DNAs) were compared with an *in silico* image pattern estimated from published genome sequences using the Vi-RLGS software. *NotI* sites of RLGS spots which were present in a Vi-RLGS pattern but absent in real RLGS patterns were considered methylated sites due to the influence of 5'-methylcytosine on *NotI* landmark detection. Approximately 1,000 constitutively methylated genomic *NotI* sites, 3,000 constitutively unmethylated sites and 150 tissue-specific methylated sites, have been plotted in the C57BL/6J genome and created a methylation map with a chromosome banding pattern. We will also present the similar methylation status in the human genome confirmed at several conserved CpG islands. The application of a quantitative whole-genome methylation analysis by Vi-RLGS and real RLGS to the mouse genomes provides a novel method for identifying specific differences in DNA methylation associated with alterations in chromatin structure that are associated with important biological phenomena such as differentiation, proliferation, aging, and diseases.