doi: http://dx.doi.org/10.7124/bc.0009FB

S-7. Life time of some products of human rDNA intergenic spacer.

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In human cells, ribosomal genes are interspersed by 30 kb long intergenic spacers (IGS). Recently it has been found that all, or almost all, parts of IGS may be transcribed, and at least some of them play important role in the regulation of rDNA transcription, maintenance of nucleolar architecture and reaction of the cell nucleus to the stress. But, since each cell contains hundreds not quite identical copies of IGS, the structure and functions of this locus remain poorly understood, dynamics of its products has not been studied specially. In this study we used qPCR to measure expression levels of various ribosomal and spacer regions at different times after inhibition of the transcription by ActD. This approach allowed us to measure real or extrapolated half-life times of some IGS loci. Our study reveals characteristic dynamic patterns suggestive of various pathways of RNA utilization and decay.

doi: http://dx.doi.org/10.7124/bc.0009FC

S-8. Mechanisms of telomere instabilit*y in the D*rosophila female germline

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Telomeres are nucleoprotein complexes that protect the ends of eukaryotic linear chromosomes from degradation and fusion. Telomere dysfunction leads to developmental disorders, oncogenesis and aging. A telomere consists of DNA repeats and their bound proteins, as well as a telomeric RNA that is transcribed from telomeric repeats. Transcription of telomeric repeats is a conserved feature of telomeres in all studied species. Telomeric transcripts are maintained at a low level but their significant fraction is retained near telomeres. The telomeres of *Drosophila* are maintained in the absence of telomerase, by the transpositions of the specialized telomeric non-LTR retrotransposons; the HeT-A element being the most abundant. Here, we address a question on the factors of telomere instability in the *Drosophila* female germline. The level of HeT-A RNA in the germline is regulated by Piwi-interacting (pi) RNAs, the nuclear RNA surveillance system and transcription factors. Depletions of any of these components leading to the upregulation of HeT-A expression cause early embryonic lethality. It is suggested that accumulation of chromatin-bound telomeric RNA can destabilize telomeric DNA, leading to DNA lesions and recombination events. To find out more about a link between telomeric RNA abundance and telomere instability, we performed a study of the telomere integrity when the telomeric RNA biogenesis was impaired, which led to HeT-A overexpression. Moreover, abundant telomeric transcripts were revealed in a specific RNA fraction associated with chromatin. We detected the presence of

H2Av, the main marker of DNA breaks, on telomeres after HeT-A derepressing, suggesting that HeT-A overexpression could cause DNA breaks in telomeres. Moreover, the presence of DNA breaks in telomeres was accompanied by the appearance of R-loops, the DNA-RNA hybrid structures associated with DNA damage. Chromatin immunoprecipitation was done to prove the accumulation of R-loops in telomeres. The formation of R-loops is most likely caused by retention of HeT-A transcripts in chromatin. Thus, telomere-associated RNA is an essential factor of telomere stability during normal oogenesis and early development.

Program for Molecular and Cellular Biology of Presidium of Russian Academy of Sciences

doi: http://dx.doi.org/10.7124/bc.0009FD

S-9. PEV-induced HP1a propagation does not correlate with the expression of the genes located near the eu-heterochromatin breakpoint

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Position effect variegation (PEV) is a disturbance of the expression of euchromatic genes transferred into the heterochromatin vicinity caused by the changes in its chromatin organization (heterochromatinization). Little is known about the molecular mechanisms of interactions between gene transcription machinery and the large-scale chromatin structures like heterochromatin, and the chromosomal rearrangement In(2)A4 provide a convenient model to study PEV. The aim of our work was to track the changes in chromatin organization of euchromatin in the vicinity of In(2)A4 new eu-heterochromatin borders and analyze the possible correlations between chromatin changes and the functional organization of the affected regions. Methods: We've performed analysis of genome-wide HP1a distribution in In(2)A4/In(2)A4 homozygous flies and in the control wild type flies by ChIP-Seq with qPCR verification and bioinformatic analysis of the received data. Results: In(2)A4 rearrangement is an inversion in the left arm of chromosome 2 with a breakpoint in the satellite block in the 2L pericentromeric heterochromatin. This results in two new eu-heterochromatin boundaries – one near the main block of 2L heterochromatin and another one near the separated small heterochromatin block. ChIP-Seq data on HP1a distribution shows an enrichment for HP1a in the euchromatin regions near the new eu-heterochromatin borders. HP1a spreads up to 200 kb from the main pericentromeric block and up to 50 kb from the small block. No apparent correlation between HP1a enrichment and genes expression levels (studied in [1]) or gene amenability to PEV were detected. The unusual enrichment in HP1a immediately near the small separated heterochromatin block was observed. Conclusions: In In(2)A4, HP1a propagates at a distance of up to 200 kb from the breakpoints and there is no apparent correlation between HP1a enrichment and expression levels of genes in the affected region as well as no correlation between HP1a binding and sensitivity of any particular gene to heterochroma-