

Differential analysis of drosophila chromatin structure during spermatogenesis

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Spermatogenesis is a complex process in which germ cells undergo dynamic changes in chromatin conformation to facilitate highly diverse gene expression. However, it remains unknown how germline chromatin is organized to promote the complex transcriptomes of spermatogenesis. Here, we establish the interrelation between chromatin structure and gene regulation in the course of spermatogenesis.

Chromatin structure is established using the Hi-C method [1], which provides insight into patterns of chromatin interactions on both local and global scales. The Hi-C technology has revealed that chromatin is packaged into cell-type invariant, evolutionarily conserved topologically associating domains (TADs). To determine the genome-wide organization of chromatin we performed Hi-C for two *D. melanogaster* mutants, Vas and Bam, corresponding to the early and late stage of spermatogenesis. We developed a protocol for stable TAD calling and filtering by optimizing parameters of the Armatus algorithm [2]. We then zoomed in on TAD borders to estimate the levels of testis-specific gene enrichments [3] in TADs, interTADs and TAD borders. Using three separate methods for gene enrichment evaluation we consistently proved that testis-specific genes are enriched on TAD borders for the Bam mutant and predominantly located in interTAD regions for the Vas mutant.

This is joint work with Sergey Ulianov¹, Sergey Razin² and Mikhail Gelfand³ (¹ Faculty of Biology, Moscow State University, ² Institute of Gene Biology, Russian Academy of Sciences, ³ Institute for Information Transmission Problems, Russian Academy of Sciences).

Источники и литература

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Иллюстрации

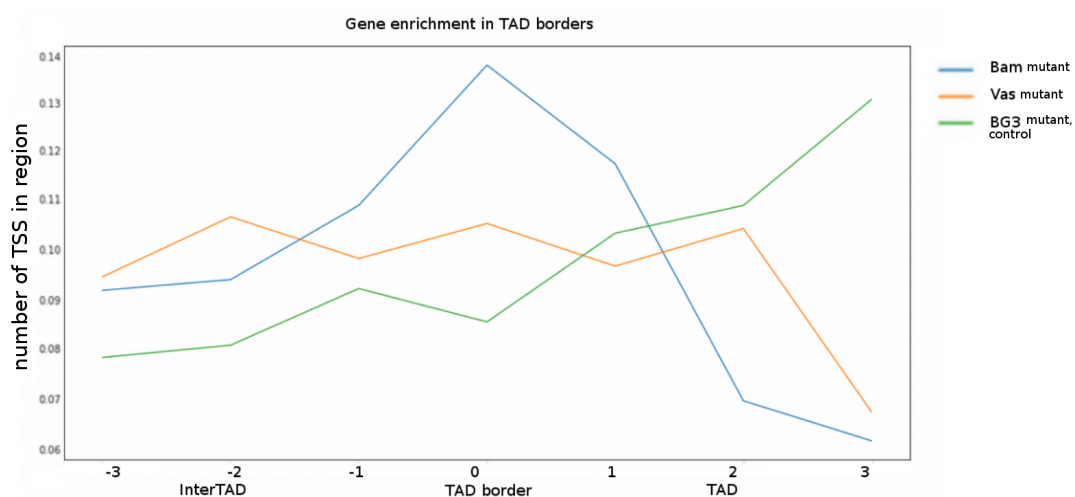


Рис. 1. Enrichments in testis-specific genes on TAD borders for 3 fruit fly mutants - Vas (early), Bam (late) and BG3 (control).