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# Re-analysis of the larval testis data on meiotic sex chromosome inactivation revealed evidence for tissue-specific gene expression related to the drosophila X chromosome

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## Abstract

**Background:** Meiotic sex chromosome inactivation (MSCI) during spermatogenesis has been proposed as one of the evolutionary driving forces behind both the under-representation of male-biased genes on, and the gene movement out of, the X chromosome in *Drosophila*. However, the relevance of MSCI in shaping sex chromosome evolution is controversial. Here we examine two aspects of a recent study on testis gene expression (Mikhaylova and Nurminsky, *BMC Biol* 2011, **9**:29) that failed to support the MSCI in *Drosophila*. First, Mikhaylova and Nurminsky found no differences between X-linked and autosomal genes based on the transcriptional profiling of the early testis development, and thus concluded that MSCI does not occur in *D. melanogaster*. Second, they also analyzed expression data from several *D. melanogaster* tissues and concluded that under-representation on the X chromosome is not an exclusive property of testis-biased genes, but instead, a general property of tissue-specific genes.

**Results:** By re-analyzing the Mikhaylova and Nurminsky's testis data and the expression data on several *D. melanogaster* tissues, we made two major findings that refuted their original claims. First, the developmental testis data has generally greater experimental error than conventional analyses, which reduced significantly the power to detect chromosomal differences in expression. Nevertheless, our re-analysis observed significantly lower expression of the X chromosome in the genomic transcriptomes of later development stages of the testis, which is consistent with the MSCI hypothesis. Second, tissue-specific genes are also in general enriched with genes more expressed in testes than in ovaries, that is testis-biased genes. By completely excluding from the analyses the testis-biased genes, which are known to be under-represented in the X, we found that all the other tissue-specific genes are randomly distributed between the X chromosome and the autosomes.

**Conclusions:** Our findings negate the original study of Mikhaylova and Nurminsky, which concluded a lack of MSCI and generalized the pattern of paucity in the X chromosome for tissue-specific genes in *Drosophila*. Therefore, MSCI and other selection-based models such as sexual antagonism, dosage compensation, and meiotic-drive continue to be viable models as driving forces shaping the genomic distribution of male-related genes in *Drosophila*.

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