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Title: Role of mitochondrial genome in sexual conflict in Drosophila melanogaster

Authors: Bhatt, Karan (/jspui/browse?type=author&value=Bhatt%2C+Karan)

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Abstract:

Earlier Mitochondrial genome variations were considered to be neutral. Now many of the studies have shown the mitochondrial and cytoplasmic variation in life history and fitness traits.Mitochondrial genome interacts with the nuclear genome and form enzyme complexes(oxidative phosphorylation) which leads to ATP production. Genetic variation in the cytoplasmic gene can hence affect the metabolism and aging. From mitochondrial aging hypothesis, we know that reactive oxygen species plays a major role in senescence of the individuals. From these all studies we know that the Mt-DNA are not selectively neutral. Positive selection is there in the mitochondrial genome, and Fitness consequences arise from the mt-DNA variation. The production of high-quality sperm is itself energetically demanding. There are many other studies suggesting mitochondrial genome's role in sperm competition theory. Mitochondrial variation can be maintained within/between the population as Mito-nuclear genotype where the nuclear genome is common in all population. Here using laboratory adopted populations of Drosophila melanogaster selected for the different level of sexual conflict were used to create these mitochondrial-nuclear lines where different mitochondrial genome was expressed in a common nuclear genome background. Now, these different families were used to check the role of the mitochondrial genome and see how the same has evolved under the sexual conflict. Different reproductive traits(sperm competitive ability and mating behavior) were measured between the two population. We do not find any difference in the sperm competitive ability between the families of two different population in all three blocks, the same pattern can be observed for the copulation duration. However, there is a difference in copulation duration in one block where F regime has higher copulation duration than M regime.

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