Using experimental evolution to investigate X-linked sexually antagonistic genetic variation in *Drosophila melanogaster*

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**Introduction**

Males and females often have different phenotypic optima, but share all of the genome except the X chromosome. This results in an intralocus sexual conflict which can constrain the evolution of sexual dimorphism (Rice & Chippindale 2001). Male-limited experimental evolution of haploid genotypes has successfully been used in the past to look for traits whose evolution is constrained by counter-selection in females (Prasad et al. 2007). Here I extend this method to specifically look at the contribution of the X-chromosome to intralocus sexual conflict in the fruit fly *Drosophila melanogaster*.

**Methods**

Males were crossed to females with a double X-chromosome. This causes in father-to-son transmission of the X (paternally inherited chromosomes in blue, maternally inherited in red). The X is never expressed in males, resulting in male-limited X-chromosome (MLX) evolution. Autosomes (gray) assort as usual.

**Phenotypic data**

- Male fitness had increased by about 20% relative to controls after approximately 30 generations of experimental evolution. There was no significant change in female fitness, consistent with a previous study by Rice (1998).
- MLX individuals of both sexes had an increased production of adult sons. Note that the difference in son production between males and females is an experimental artefact; female data was collected two days later due to time constraints.
- MLX females had higher locomotory activity than control females. There was no significant difference in males. This is consistent with previous data which suggests that locomotory activity is a sexually antagonistic trait which is partly X-linked (Long & Rice 2007).

**Gene expression data**

- 6286 transcripts retained after filtering.
- 518 transcripts showed a significant change in expression after more than 40 generations of MLX evolution; 342 were upregulated and 176 were downregulated.
- Only 4 transcripts showed a significant interaction.

**Gene ontology terms:**

- Muscle activity
- Locomotory activity
- Synaptic function
- Metabolism
- Chromosomal damage repair

**Conclusions**

- Although only the X chromosome experienced male-limited evolution, changes in gene expression could be seen throughout the genome.
- Changes in expression were consistent with an increase in male fitness, mediated by increased metabolic activity.
- Changes in expression were almost always in the direction predicted from the pattern of ancestral sexual dimorphism.
- There was no evidence of any effect of imprinting. This is significant because imprinting is suggested to be one of the ways of resolving intralocus sexual conflicts (Day & Bonduriansky 2005).
- This study confirms that changes seen on the level of gene expression mirror those seen on a phenotypic level.

**References**