

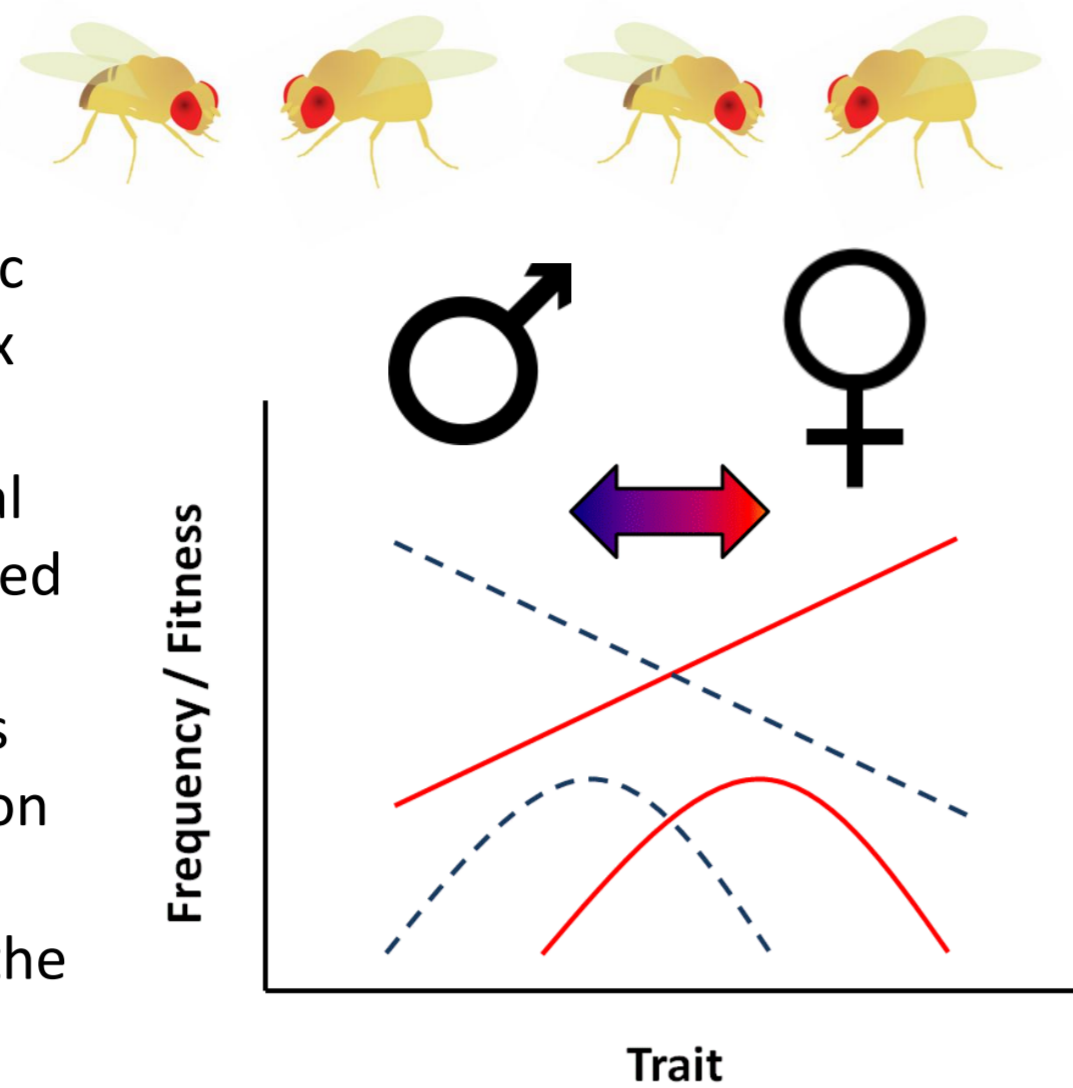


Using experimental evolution to investigate X-linked sexually antagonistic genetic variation in *Drosophila melanogaster*

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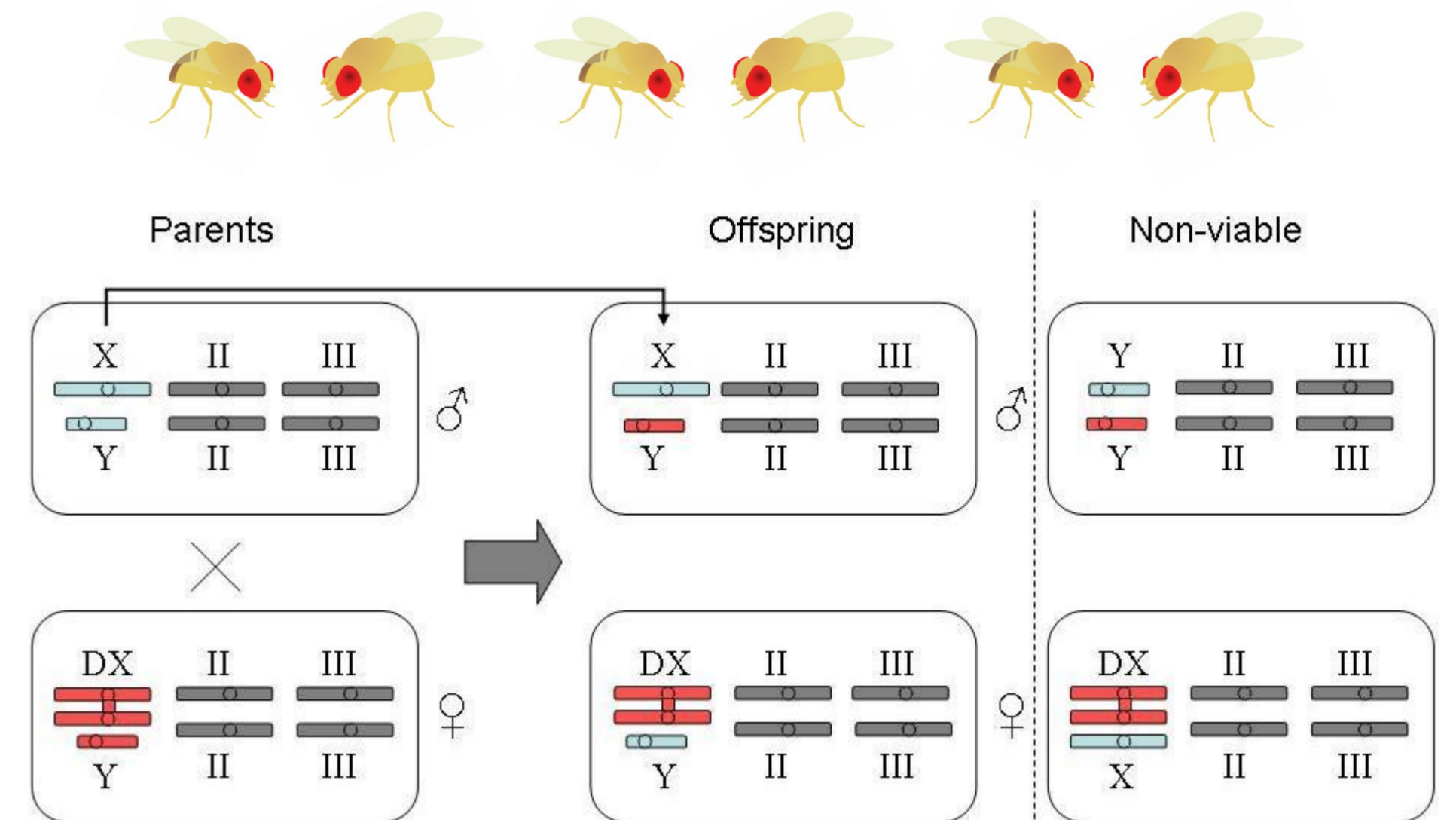
Introduction

Males and females often have different phenotypic optima, but share all of the genome except the sex chromosomes. 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*.

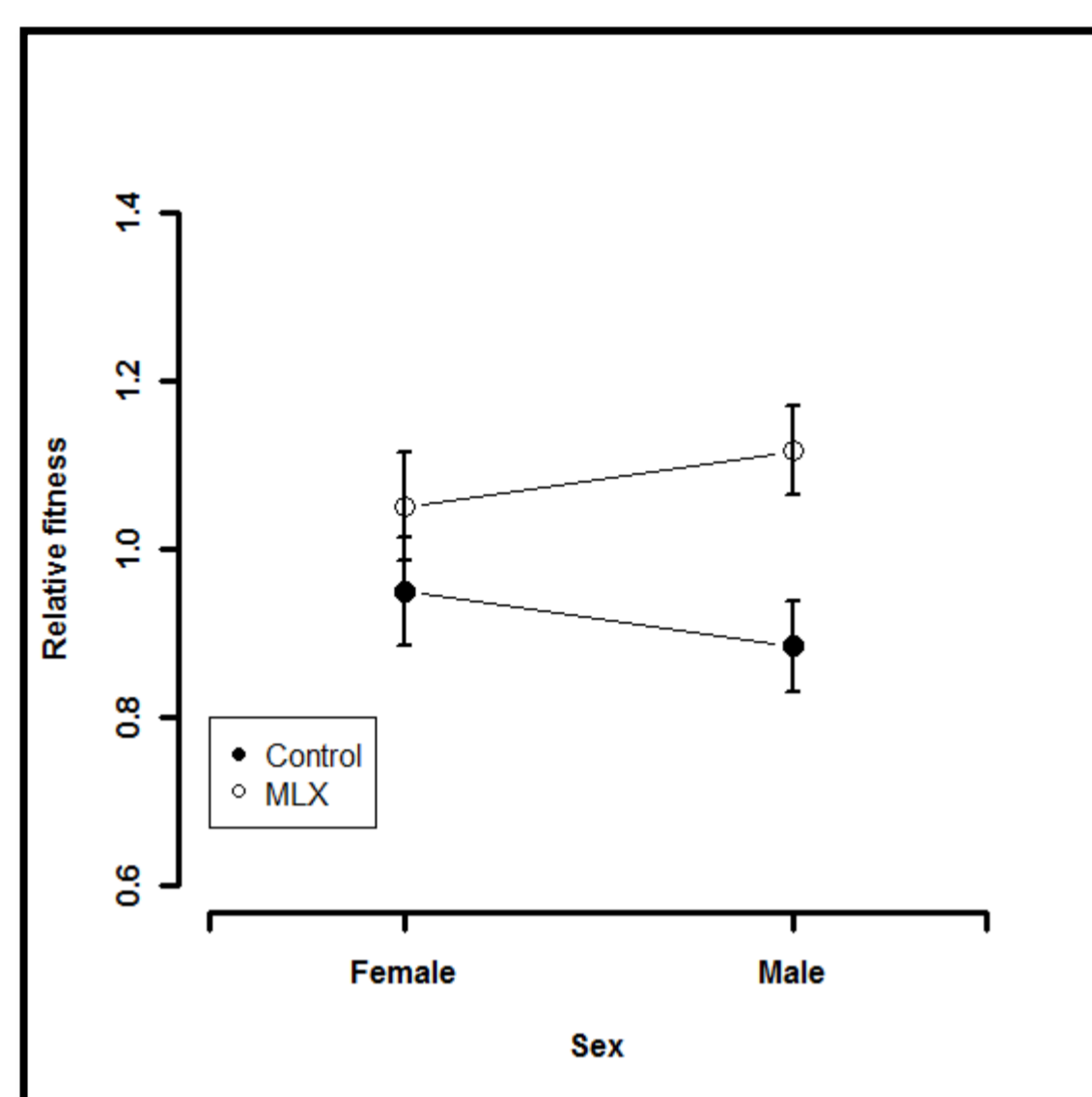


Methods

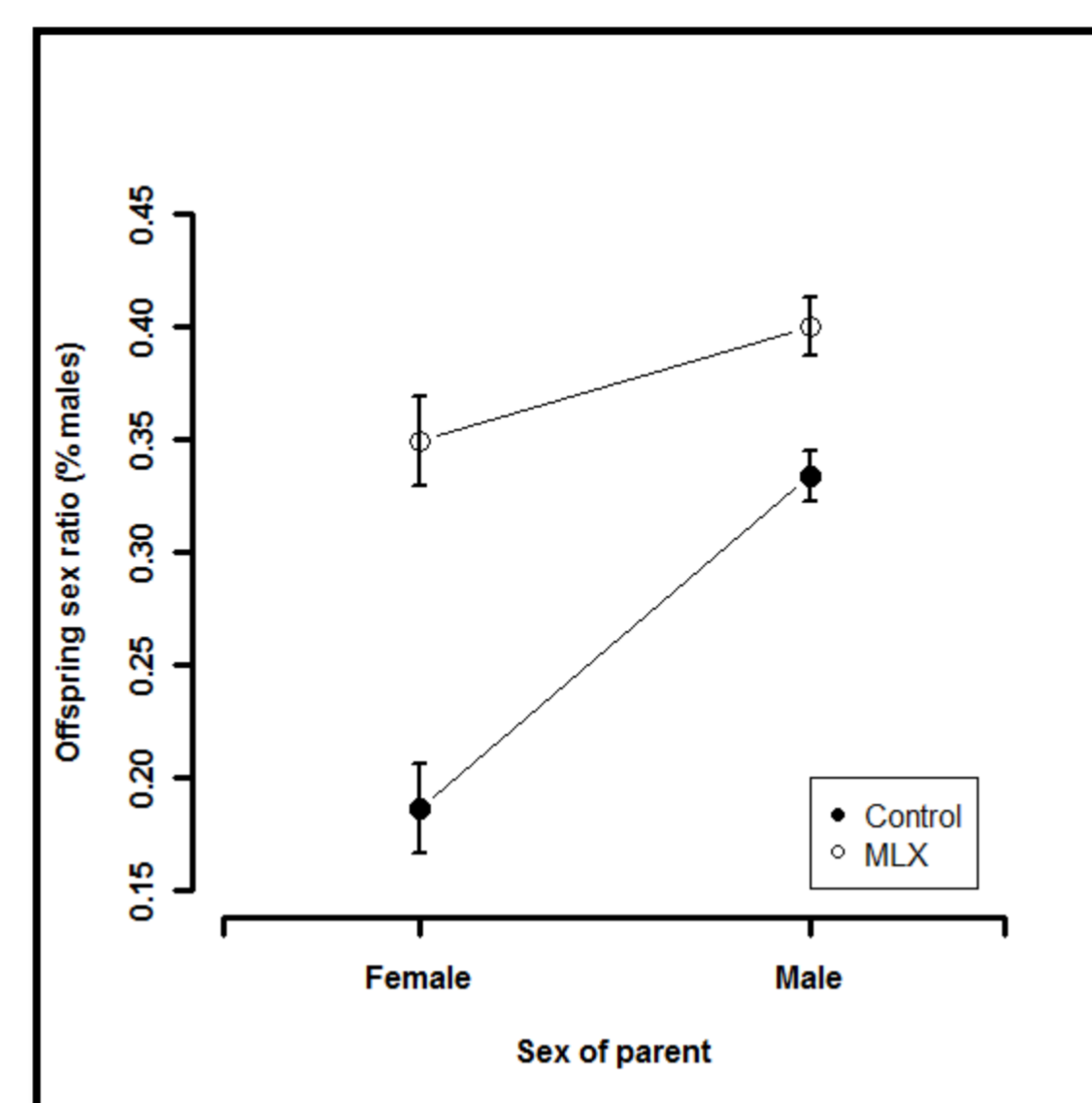
Males were crossed to females with a double X-chromosome. This causes in father-to-son transmission of the X (paternally inherited chromosomes in blue, maternally inherited in red). The X is never expressed in females, resulting in male-limited X-chromosome (MLX) evolution. Autosomes (gray) assort as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



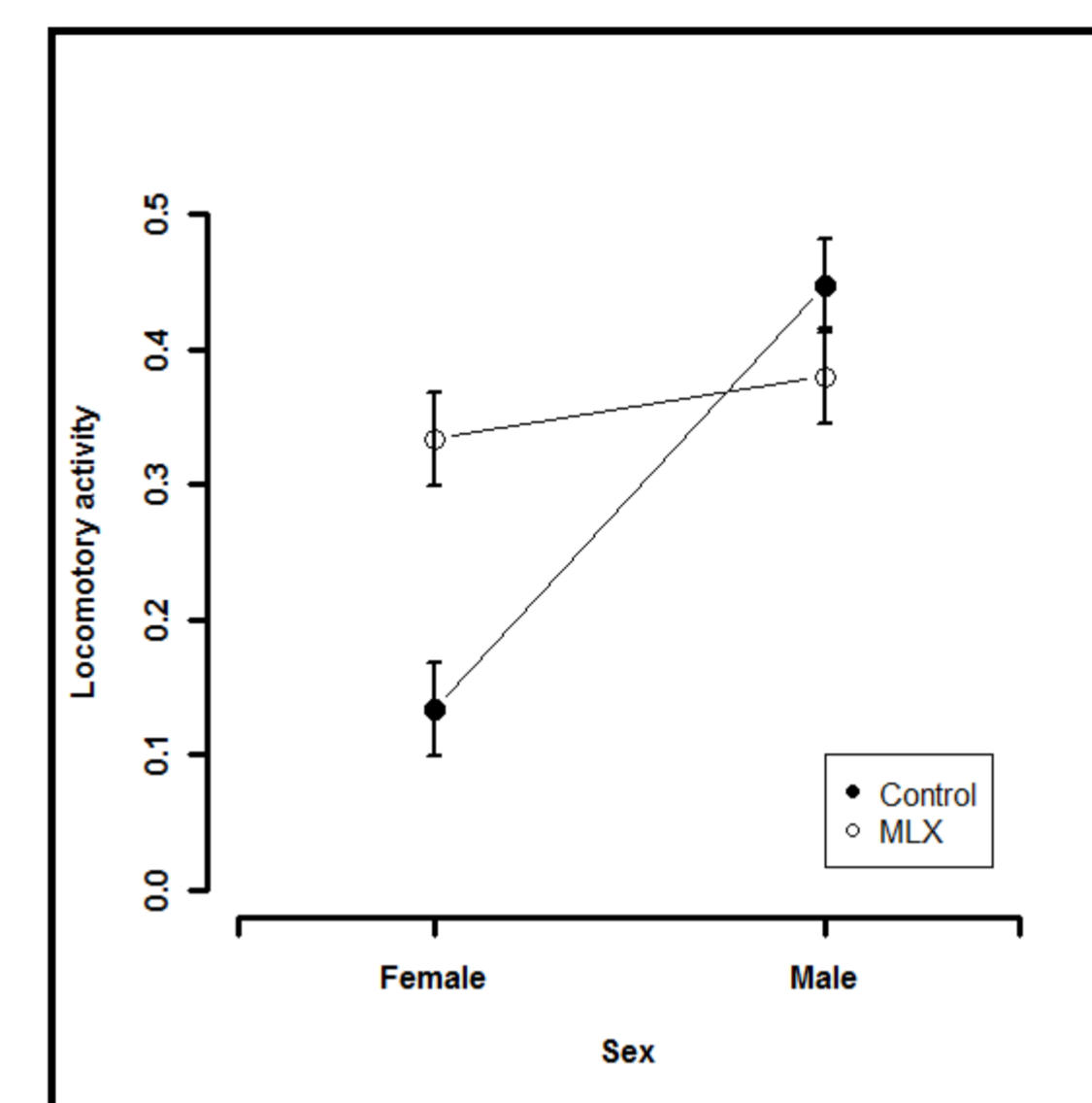
Phenotypic data



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

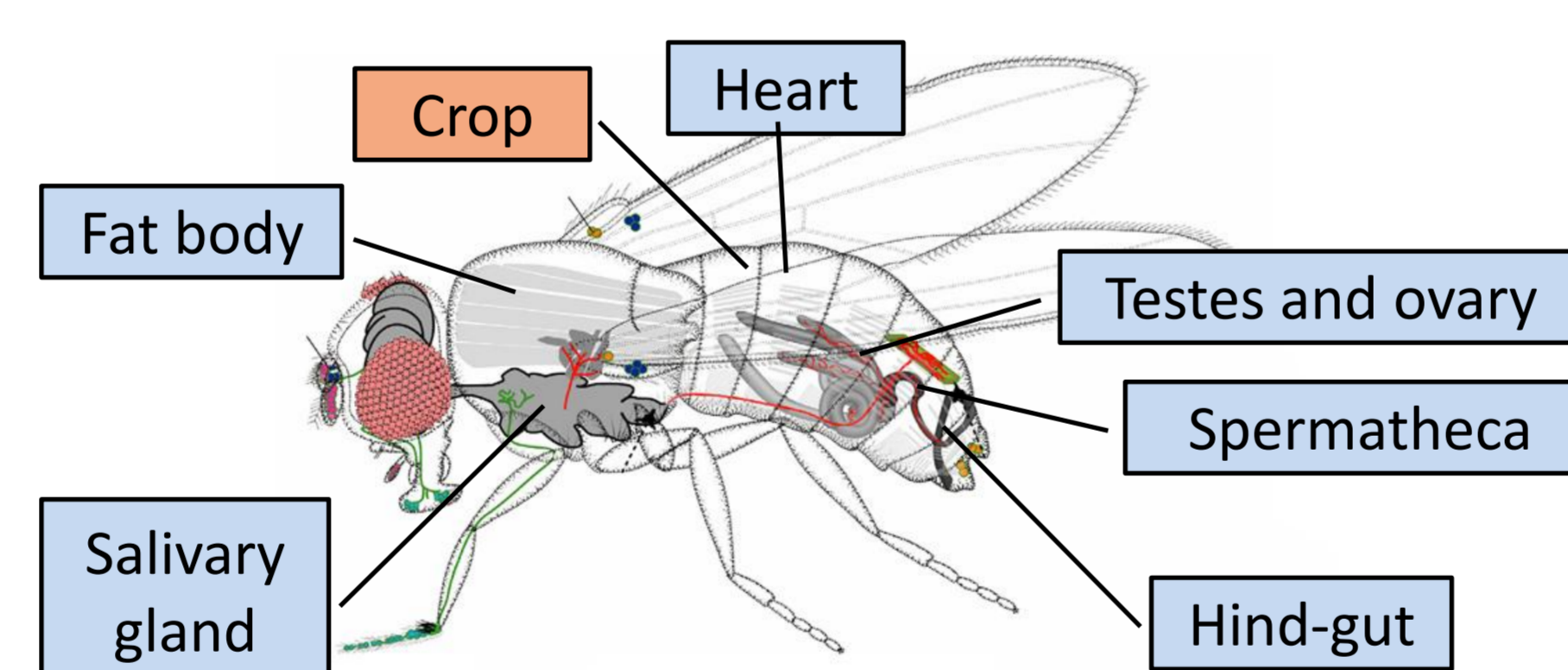
General information:

- 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.

Chromosome location:

Expected	Observed	
	Upregulated genes	Downregulated genes
X	X	X
2	2	2
3	3	3
4	4	4

Tissue specificity:



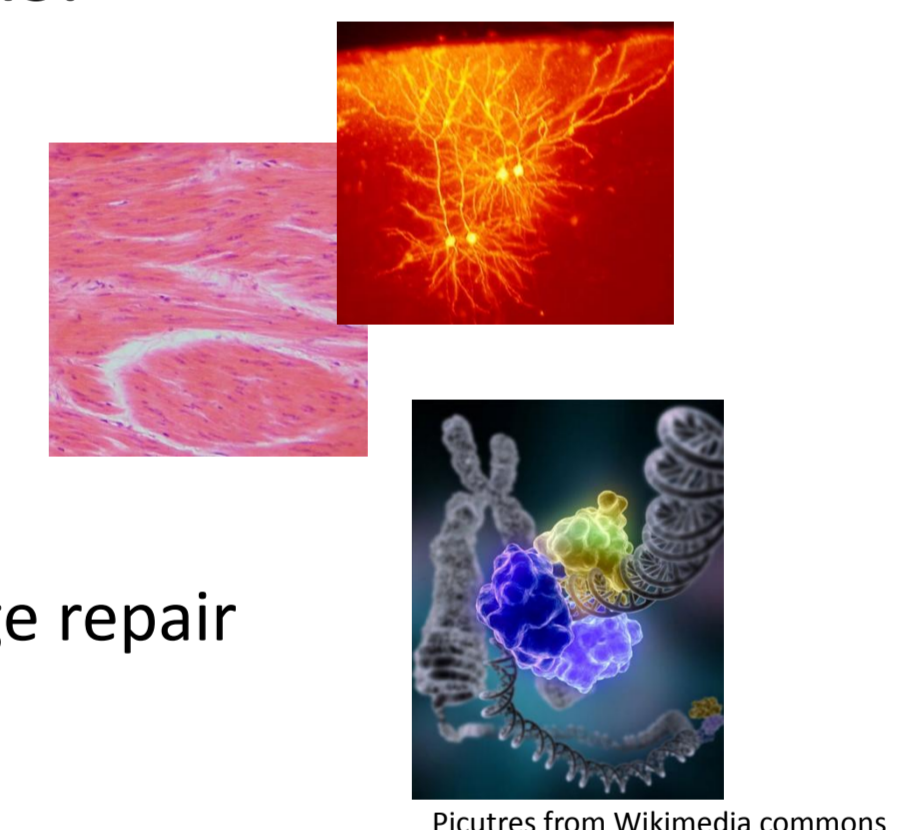
Overrepresentation of genes previously associated with fitness:

(From Innocenti & Morrow 2010)

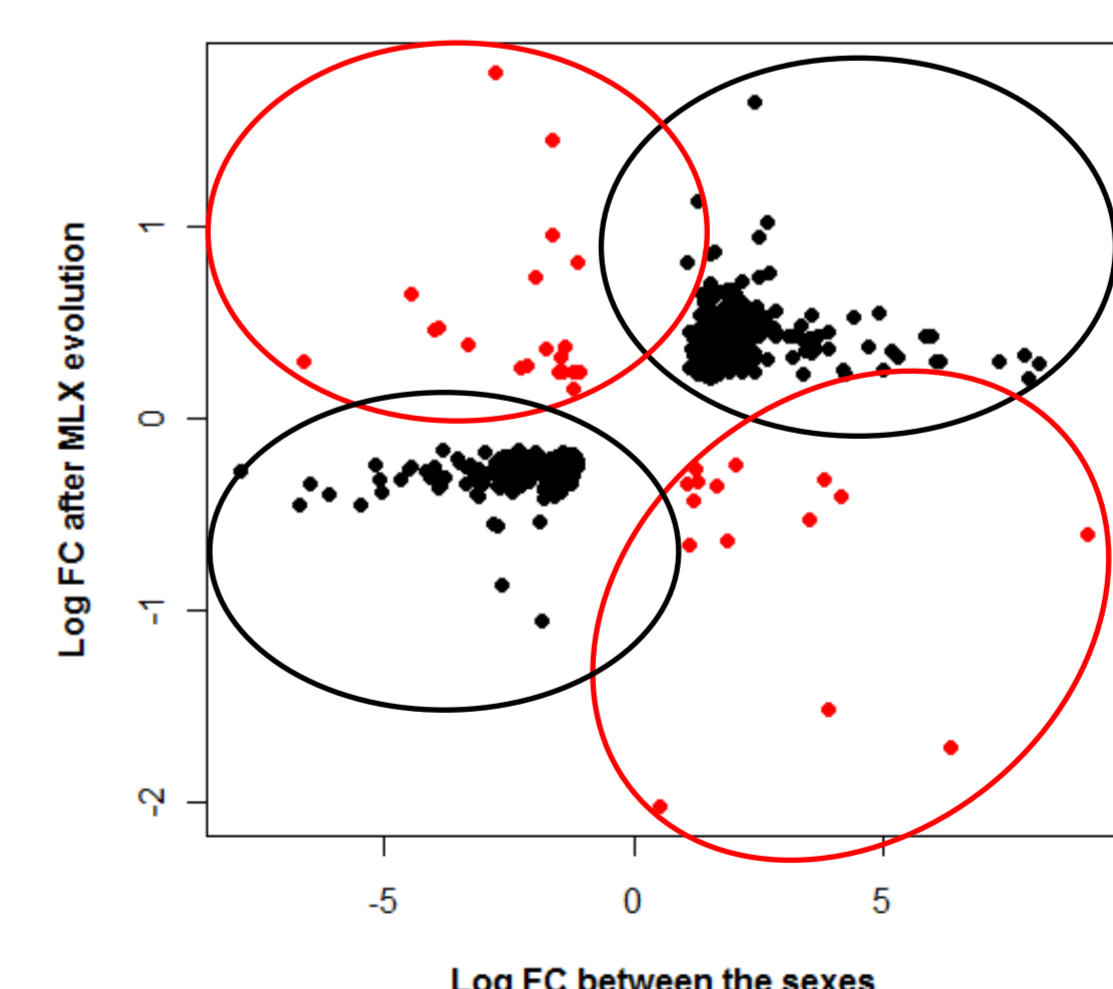
Genes associated with:	Relationship	
	Upregulated genes	Downregulated genes
Male fitness	+	-
Female fitness	-	+
Sexual antagonism	+	NS

Gene ontology terms:

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



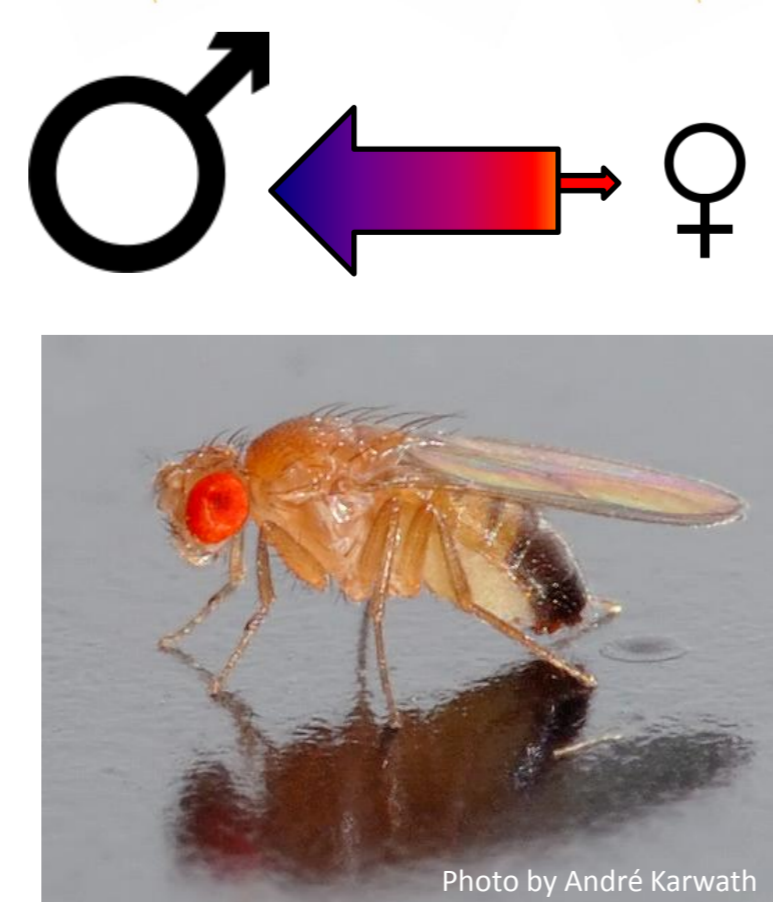
Change in expression relative to ancestral sexual dimorphism:



Same direction = 483
Opposite direction = 35

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

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