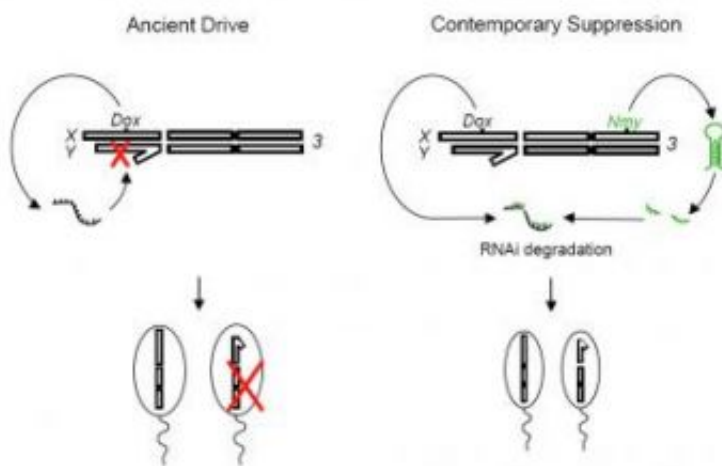


A sex-ratio meiotic drive system in *Drosophila simulans*

November 6 2007



The X-linked *Dox* gene first evolved to target an unknown component of the Y chromosome, so that Y-bearing sperm fail to develop. This leads to an increased transmission frequency of the *Dox*-bearing X chromosome and a female-biased sex ratio. It remains unclear whether *Dox* is an RNA or protein-coding gene. Later, a transposition of *Dox* to Chromosome 3 created the *Nmy* gene. siRNAs produced from the doublestranded hairpin of *Nmy* target the homologous region of *Dox* for degradation via the RNAi pathway. As a result, Y-bearing sperm develop normally, and X-chromosome meiotic drive is suppressed. The model depicts a pre-meiotic germ cell, but the cellular manifestation of distortion occurs during nuclear condensation and maturation of sperm. Only the sex and third chromosomes are shown. Credit: Ferree et al.

If you met a person who had 10 children, all of whom were girls, you

would probably find this surprising. Yet this kind of distorted sex ratio does occur in groups as diverse as mammals, insects, and plants, where some parents consistently produce litters in which the sex ratio is dramatically skewed. For the first time, Yun Tao and colleagues report, in this week's issue of the open-access journal *PLoS Biology*, the identification of both a fly gene that can create these skewed ratios and the counter-gene, found in most of the fly population, which suppresses such distortion.

Skewed sex ratios, such as the one investigated by Tao and colleagues at Harvard and Emory Universities, have been known to evolutionary biologists for a long time. They usually occur because genes on the X chromosome “prefer” an individual to have female offspring, as daughters will have two copies of X chromosome genes compared to one in sons, and more copies of a gene mean evolutionary success for that gene.

This sets up a conflict within the genome, as genes on the other chromosomes may lose out through being passed on to an all female litter. When there is a skew towards one sex, being a gene in a member of the other sex is very advantageous, as the rare sex will have lots of opportunities to reproduce. This makes finding a gene on the non-sex chromosomes that counters the distortion evolutionarily likely.

The mystery of the sex ratio skew was in how it worked on a molecular and genetic level. This paper is the first to map a distorting gene, *Dox*, found on the X chromosome in *Drosophila simulans*, and *Nmy*, the suppressor gene found on a non-sex chromosome that “fights back” for an equal sex ratio. Interestingly, the new paper reports that *Dox* and *Nmy* are very similar in terms of their sequence. This provides Tao et al. with a clue towards how *Nmy* may defeat *Dox*—a mechanism called RNA interference (RNAi).

RNAi can “turn off” a gene—just like Nmy does to Dox—when one gene produces RNA that is complementary in sequence to that of another. On a physiological level, Tao et al. showed that males who have offspring with a distorted sex ratio do so because their Y-bearing sperm fail to mature successfully. The findings in this paper also suggest that the evolution of the genome will one day be explained as adaptations to limit sex ratio distortion.

Citation: Tao Y, Masly JP, Araripe L, Ke Y, Hartl DL (2007) A sex-ratio meiotic drive system in *Drosophila simulans*. I: An autosomal suppressor. *PLoS Biol* 5(11): e292. doi:10.1371/journal.pbio.0050292

Citation: Tao Y, Araripe L, Kingan SB, Ke Y, Xiao H, et al. (2007) A sex-ratio meiotic drive system in *Drosophila simulans*. II: An X-linked distorter. *PLoS Biol* 5(11): e293. doi:10.1371/journal.pbio.0050293

Source: Public Library of Science, www.plosbiology.org

Citation: A sex-ratio meiotic drive system in *Drosophila simulans* (2007, November 6) retrieved 23 April 2024 from <https://phys.org/news/2007-11-sex-ratio-meiotic-drosophila-simulans.html>

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