Recurrent Selection on the Winters Sex-ratio Genes in Drosophila Simulans

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FIGURE 1.

Regions sequenced of the genes of the Winters sex-ratio.

Chromosomal location of the distorter locus and suppressor locus are shown at the top. The two genes of the distorter are Distorter on the X (Dox) and Mother of Dox (MDox). The suppressor gene is called Not Much Yang (Nmy). Dox and MDox are separated by ~70 kb of DNA sequence on the X chromosome. Triangles indicate the location of the PCR primers used. Arrows indicate direction of transcription of the genes (Tao et al. 2007a; Tao et al. 2007b).

FIGURE 2.

Predicted exon structure of the loss-of-function mutants at Dox.

The allele name is followed by the frequency of the mutant in the total pooled sample. Exons are illustrated as grey boxes, deletions are shown as dashed lines.

FIGURE 3.

Pairwise HKA tests indicate selection acting on the derived form of the Winters SR genes.

Per-site level of polymorphism is shown above the x-axis (θW) and per-site average divergence in flanking sequence (DXY) between D. simulans and D. melanogaster is shown below the x-axis. Derived alleles are shown in dark grey, ancestral alleles are shown in light grey.

FIGURE 4.

Posterior distributions of the time since selection (in years) for a hitchhiking model.

SUPPLEMENTARY FIGURE 1.

Crossing scheme used to test for sex-ratio distortion of different Dox alleles.
In generation 1, X chromosomes of known *Dox* genotype were extracted from the Tremont lines. These were substituted into an isogenic background homozygous for a non-functional suppressor allele, “nmy[sim1247].” Males were mated to tester females (*w; e*) and sex ratios of their progeny were determined.

**SUPPLEMENTARY FIGURE 2.**

Posterior distributions of the time since selection (in units of N generations) for a hitchhiking model.