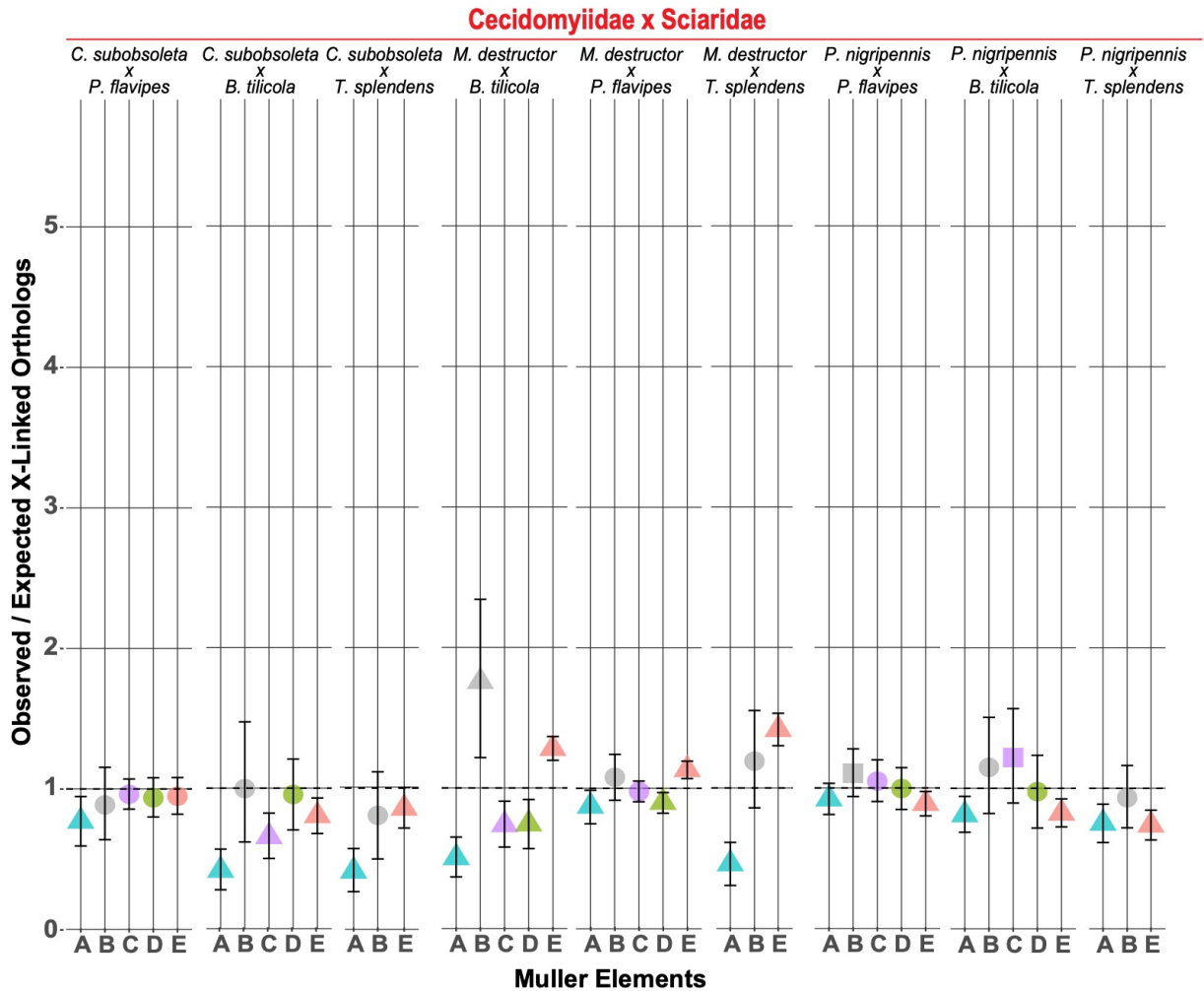


**Fig. S2.** Male DNA coverage distributions for *Exechia fusca* (sister to *Gnoriste bilineata*) and the Cecidomyiid *Lestremia cinerea*. The distribution of *E. fusca* shows indistinct peaks, negatively skewed toward the autosomal center, likely due to poor genome assembly quality (See Fig. S1). Three distinct read coverage peaks were found in *L. cinerea*, present across all Muller elements. Our method is not designed to accommodate such multi-peak situations, and unsurprisingly breaks down on the F element in *L. cinerea*, where the two right peaks are classified as autosomal despite the middle peak centering on -1 (the expected peak value for X-linked genes), because the F has very few (6) likely true autosomal genes in the far right peak. Our current methods assign a majority of the *L. cinerea* genome as X-linked (71%), though because of the unknown identity of the far left peak, this estimate may be unreliable. This unusual distribution could be indicative of partial genome duplication, as suggested by the BUSCO results, but more investigation is needed.



**Fig. S3.** Pairwise comparison of the number of mutually X-linked orthologs between Sciaridae and Cecidomyiidae gPGE species pairs to the expected X-linked ortholog abundance. Between-family comparisons are shown here, while within-family comparisons are shown in Figure 3. Color indicates Muller element. Muller elements for which species do not share X-linked orthologs are excluded, as is the F element. Shapes indicate significance via Chi square: triangle  $p < 0.01$ , square  $p < 0.05$ , circle nonsignificant based on  $p > 0.05$ . Error bars represent 95% CIs computed from 10,000 bootstrap replicates.