SUPPLEMENTAL MATERIAL

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Support for the dominance theory in *Drosophila* transcriptomes

Table S1. Number of sequence reads (millions) and mapped Fragments Per Kb of transcript (median FPK) across the two technical replicates (14,687 transcripts)

Sample	R1 Reads	R1 FPK	R2 Reads	R2 FPK
D. yakuba Taï18E2 females	44.5	227	38.8	189
D. yakuba Taï18E2 males	55.1	384	28.6	194
D. santomea STO.4 females	48.5	201	36.1	168
D. santomea STO.4 males	51.7	333	27.6	178
F_1 females (Taï18E2 × STO.4)	45.6	263	29.4	176
F_1 males (Taï18E2 × STO.4)	45.7	232	35.8	185
F_1 females (STO.4× Taï18E2)	45.8	267	47.7	279
F_1 males (STO.4× Taï18E2)	43.2	186	35.9	146
D. yakuba C(1)RM females	51.3	247	23.8	113
D. santomea C(1)RM females	54.6	258	23.6	111
F_1 females (*D. yakuba* CRM × *D. santomea* CRM)	85.6	280	25.6	57
F_1 females (*D. santomea* CRM × *D. yakuba* CRM)	46.1	198	22.4	102

Note—In crosses, the genotype of the female parent is listed first; R1, replicate 1; R2, replicate 2; FPK was calculated with RSEM (Li and Dewey 2011).

Table S2. Genome-wide distribution of genes with different degrees of sex-biased expression across chromosomes

Sex-biased	*X*	*2L*	*2R*	*3L*	*3R*	*4*	All
Female/Male							
> 3	107	127	119	115	143	0	611
3 to 1.5	303	373	357	337	458	45	1,873
1.5 to 1.1	411	403	474	448	624	23	2,383
1.1 to 1	172	177	181	177	207	2	916
Male/Female							
> 3	278	431	399	359	487	2	1,956
1.5 to 3	194	219	210	251	321	2	1,197
1.5 to 1.1	365	435	410	438	561	4	2,213
1.1 to 1	121	150	158	160	210	1	800
All genes	1,951	2,315	2,308	2,285	3,011	79	11,949

Note—Sex-biased refers to the degree of sex-biased expression (i.e., fold change), which was calculated using DESeq2 (Love *et al.* 2014) and a multifactor design with two variables (~species + sex). Data based on the female and male transcriptomes of the *D. yakuba* Taï18E2 and the *D. santomea* STO.4 stocks.

Table S3. Spearman's correlations (ρ) between gene expression divergence and the magnitude of *cis*- and *trans*-regulatory divergence

Transcriptome -Chromosome	*Cis*	95%CI	*P*	*Trans*	95%CI	*P*	Number of genes
Female-*X*	0.46	0.41-0.50	1.26×10^{-78}	0.63	0.60-0.67	2.40×10^{-170}	1,504
Female-Auto	0.56	0.53-0.56	$< 1 \times 10^{-308}$	0.62	0.61-0.64	$< 1 \times 10^{-308}$	7,125
Male-Auto	0.49	0.47-0.51	$< 1 \times 10^{-308}$	0.64	0.63-0.66	$< 1 \times 10^{-308}$	6,922

Note—Gene expression divergence was estimated using species-specific reads; *cis*- and *trans*-regulatory divergence was estimated using hybrids from the cross between *D. santomea* STO.4 females and *D. yakuba* Taï18E2 males. *CI*, Confidence Intervals based on bootstrapping (10, 000 replicates); *X*, *X* chromosome; Auto, autosomes.

Table S4. Slower-X evolution for *cis*- and *trans*-regulatory divergence

	F_1 hybrids (*T*×*S*)			F_1 hybrids (*S*×*T*)		
	X	Auto	*P*	*X*	Auto	*P*
Cis-	0.26	0.28	4.9×10^{-3}	0.23	0.26	3.83×10^{-5}
Trans-	0.19	0.23	4.79×10^{-7}	0.19	0.21	3.61×10^{-5}

Note—*Cis*- and *trans*-regulatory divergence (median) was estimated using hybrid females from the cross between *D. yakuba* Taï18E2 females and *D. santomea* STO.4 males (*T*×*S*), or from the reciprocal cross (*S*×*T*). *X*, X-linked genes; Auto, Autosomal genes; *P*, Probability from Mann-Whitney tests.

Table S5. Faster-male c*is*- and *trans*-regulatory divergence for autosomal genes

	F_1 hybrids (*T*×*S*)			F_1 hybrids (*S*×*T*)		
	Females	Males	*P*	Females	Males	*P*
Cis-	0.28	0.30	1.26×10^{-3}	0.26	0.28	7.01×10^{-7}
Trans-	0.23	0.24	7.70×10^{-4}	0.21	0.23	2.65×10^{-7}

Note— *Cis*- and *trans*-regulatory divergence (median) was estimated using hybrids from the cross between *D. yakuba* Taï18E2 females and *D. santomea* STO.4 males (*T*×*S*), and from the reciprocal cross (*S*×*T*). *P*, Probability from Mann-Whitney tests.

Table S6. Classification of autosomal genes into the different classes of regulatory evolution based on the transcriptome of hybrid females

Sex-biased	Con.	*Cis* only	*Trans* only	*Cis*+*trans*	*Cis*×*trans*	Comp.	Amb.	Total
Female/Male								
> 3 to 1.1	2,274	176	137	32	35	37	433	3,124
Male/Female								
> 3 to 1.1	1,462	126	70	24	15	21	219	1,937
FSGs	48	10	3	2	1	3	8	75
All	4,627	386	263	76	59	77	851	6,339

Note—The number of genes with *cis*- and *trans*-regulation was estimated using hybrids from the cross between *D. santomea* STO.4 females and *D. yakuba* Taï18E2 males. Con., conserved; Comp., compensatory; Amb., Ambiguous; FSGs, genes with female-specific expression; All, all analyzed genes.

Table S7. Classification of autosomal genes into the different classes of regulatory evolution based on the transcriptome of hybrid males

Sex-biased	Con.	*Cis* only	*Trans* only	*Cis*+*trans*	*Cis*×*trans*	Comp.	Amb.	Total
Female/Male								
> 3 to 1.1	2,128	113	93	27	30	32	277	2,700
Male/Female								
> 3 to 1.1	1,459	152	126	35	37	39	321	2,169
MSGs	451	72	46	30	8	12	227	846
All	4,894	405	324	112	97	106	984	6,922

Note—The number of genes with *cis*- and *trans*-regulation was estimated using hybrids from the cross between *D. santomea* STO.4 females and *D. yakuba* Taï18E2 males. Con., conserved; Comp., compensatory; Amb., Ambiguous; MSGs, genes with male-specific expression; All, all analyzed genes.

Table S8. Misexpression (median $\log_2$ fold change) of autosomal genes in standard hybrid females, attached-X hybrid females and hybrid males

Sex-biased	*f*	*att-X f*	*m*	*P* (*f vs. af*)	*P* (a*f vs. m*)
Female/Male:					
> 3	0.21	0.33	0.39	9.7×10^{-13}	0.011
3 to 1.5	0.20	0.25	0.38	6.4×10^{-7}	5.6×10^{-31}
1.5 to 1.1	0.17	0.17	0.31	0.87	3.0×10^{-65}
Male/Female:					
> 3	0.29	0.30	0.64	0.63	8.2×10^{-15}
1.5 to 3	0.21	0.36	0.34	2.2×10^{-26}	0.29
1.5 to 1.1	0.19	0.24	0.23	1.6×10^{-15}	0.041
NBGs	0.17	0.17	0.25	0.98	8.3×10^{-26}
FSGs/MSGs	0.41	0.66	0.89	4.5×10^{-6}	2.5×10^{-6}
All	0.19	0.22	0.34	4.0×10^{-33}	4.2×10^{-156}

Note—Data from hybrids from the cross between *D. santomea* females [STO.4 or C(1)RM] and *D. yakuba* males [Taï18E2 or C(1)RM]. To be able to compare the same set of genes across genotypes, only genes expressed in both sexes were included. *f*, standard hybrid females; *att-X f*, attached-X hybrid females; *m*, males. NBGs, genes with nonsex-biased expression; FSGs, genes with female-specific expression; MSGs, genes with male-specific expression. *P*, Probability from Mann-Whitney tests.

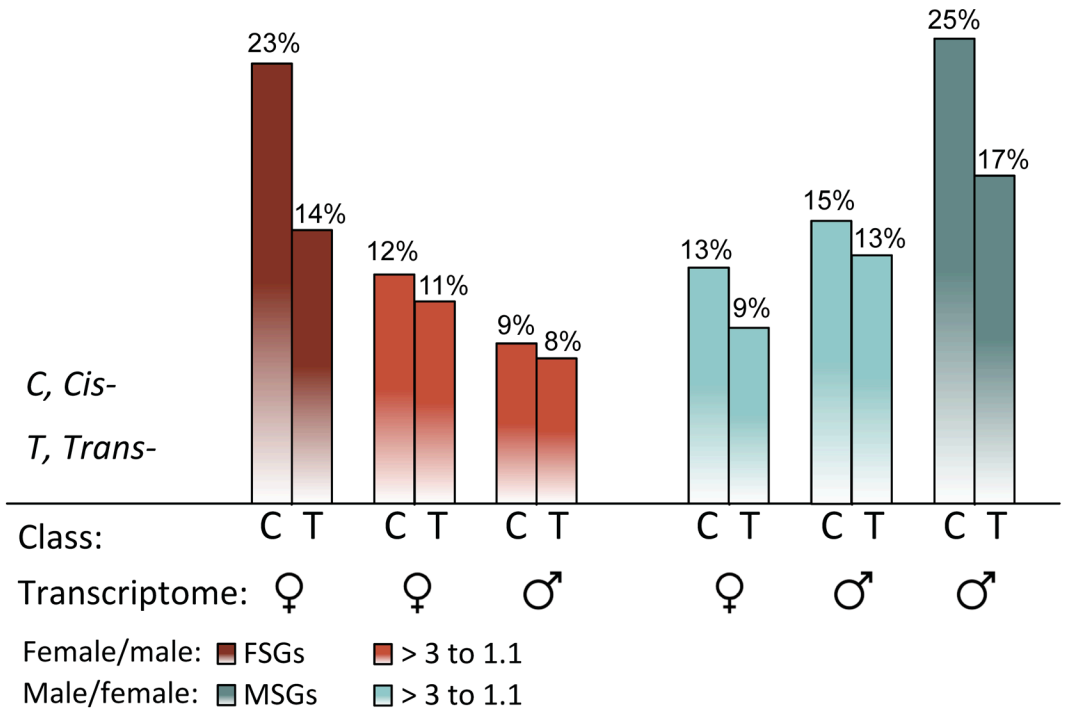

Figure S1. **Percentage of autosomal genes with significant *cis*- or *trans*-regulatory divergence for classes of genes with sexually dimorphic expression**. The percentages of *cis*-regulatory divergence reflect the combination of genes showing *cis* only, *cis* + *trans*, *cis* × *trans*, and compensatory regulatory evolution (genes with ambiguous classification were excluded). Equivalently, the percentages of *trans*- reflect *trans* only, *cis* + *trans*, *cis* × *trans*, and compensatory regulatory evolution. Data based on first generation female or male hybrids from the cross between *D. yakuba* Taï18E2 females and *D. santomea* STO.4 males. To equalize the statistical power to detect significant *cis*- and *trans*-regulatory divergence, we used the same number of total stock-specific mapped reads in all comparisons (10,738,987 stock-specific mapped reads; 2.6 million reads per allele and per genotype). FSGs, female-specific genes; MSGs, male-specific genes.

Supplemental references

Li, B., and C. N. Dewey, 2011 RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics 12**:** 323. https://doi.org/10.1186/1471-2105-12-323

Love, M. I., W. Huber and S. Anders, 2014 Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 15**:** 550. https://doi.org/10.1186/s13059-014-0550-8