

GENETICS

Supporting Information

<http://www.genetics.org/cgi/content/full/genetics.110.117614/DC1>

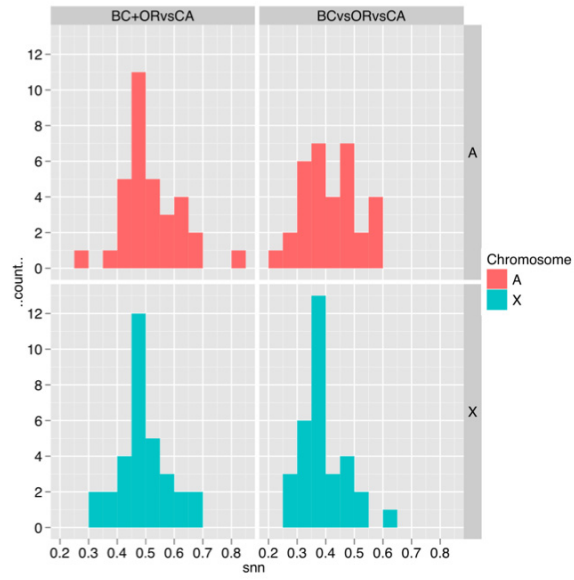
Estimating the Parameters of Selection on Nonsynonymous Mutations in *Drosophila pseudoobscura* and *D. miranda*

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(A)



(B)

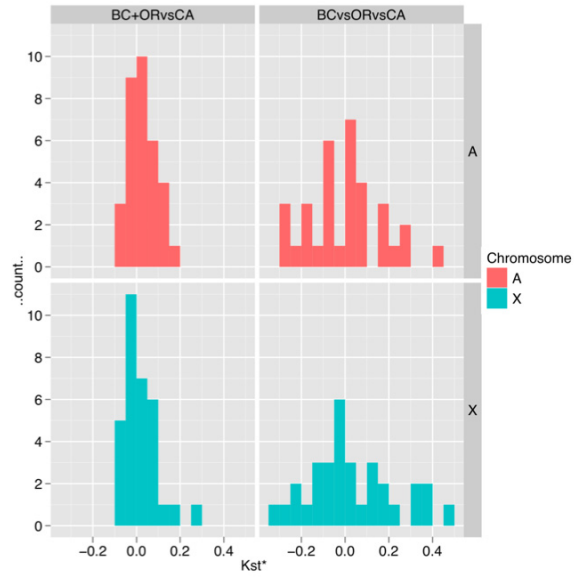


FIGURE S1.—Population subdivision between *D. miranda* lines measured by (A) *snn* and (B) *Kst**. The left hand side of each panel shows the results when the BC and OR lines are grouped together and compared to the CA lines, the right hand side shows the results when all three groups are considered separately (see main text for details).

FILE S1

Details and summary statistics for X-linked and autosomal loci in *D. pseudoobscura* and *D. miranda*, with divergence to *D. affinis*

File S1 is available for download as an Excel file at <http://www.genetics.org/cgi/content/full/genetics.110.117614/DC1>.

FILE S2

Population subdivision statistics for *D. miranda* data

File S2 is available for download as an Excel file at <http://www.genetics.org/cgi/content/full/genetics.110.117614/DC1>.

TABLE S1**Tajima's D values for subsets of the data divided by K_A/K_S values.**

	<i>D. miranda</i>		<i>D. pseudoobscura</i>	
	<i>X</i> chromosome	Autosome	<i>X</i> chromosome	Autosome
Nonsynonymous sites				
High K_A/K_S	-0.361 (0.374)	-0.687 (0.198)	-0.684 (0.172)	-0.728 (0.201)
Low K_A/K_S	-1.272 (0.113)	-0.168 (0.635)	-1.137 (0.025)	-1.266 (0.069)
Synonymous sites				
High K_A/K_S	-0.663 (0.243)	-0.415 (0.211)	-0.683 (0.169)	-0.739 (0.143)
Low K_A/K_S	-0.786 (0.260)	-0.743 (0.212)	-0.847 (0.177)	-0.961 (0.141)

Means with standard errors in parentheses.

TABLE S2

**Estimates of the distribution of fitness effects and the fraction of adaptive substitutions using the simplified LCBN method
on the dataset restricted to the two-thirds of loci with the highest K_A/K_S values**

Dataset	Neutrality index (\hat{m}_i)	c_{nc}	\hat{N}_{eSh}	α
Full dataset				
X chromosome	1.62 (0.57/1.81)	0.022 (0.005/0.046)	9.93 (4.78/infinity)	0.66 (0.31/0.92)
Autosomes	2.51 (1.29/3.40)	-0.003 (-0.018/0.011)	4.38 (2.80/8.36)	1.07 (0.78/1.34)
Restricted by K_A/K_S				
X chromosome	0.91 (0.42/1.63)	0.029 (0.005/0.046)	8.81 (3.63/infinity)	0.67 (0.32/0.97)
Autosomes	1.37 (1.18/3.40)	-0.023 (-0.025/0.020)	3.25 (2.06/6.56)	1.07 (0.70/1.32)

95% confidence intervals in parentheses (generated by bootstrapping across genes 1000 times).

Calculations were carried out as described by LOEWE *et al.* (2006).

TABLE S3

Estimates of the distribution of fitness effects and the fraction of adaptive substitutions using the Eyre-Walker and Keightley method on the dataset restricted to the two-thirds of loci with the highest K_A/K_S values

	$N2/N1$	Shape parameter (b)	Location parameter (mean/ b)	Proportion of mutations in different $N_e s$ categories:				α (fraction adaptive)
				0 – 0.5	0.5 – 5	5 – 50	50 – Inf	
X								
<i>mir</i>	8.79	0.090	-1.1 x 10 ⁹	0.102	0.023	0.029	0.847	0.122
	(0.1/10)	(0.033/99.999)		(0.000/0.459)	(0.000/0.389)	(0.022/1.000)	(0.000/0.891)	(-3.014/1.000)
<i>pse</i>	10	0.221	-5997.851	0.036	0.024	0.040	0.901	0.697
	(3.07/10)	(0.100/1.034)		(0.003/0.071)	(0.010/0.067)	(0.014/0.316)	(0.621/0.946)	(0.358/0.972)
A								
<i>mir</i>	2.79	0.229	-74.315	0.122	0.085	0.143	0.650	-0.361

	(0.1/10)	(0.060/99.999)		(0.000/0.213)	(0.016/0.790)	(0.021/0.958)	(0.000/0.885)	(-1.938/1.000)
<i>pse</i>	10	0.407	-111.884	0.016	0.024	0.062	0.899	0.833
	(3.07/10)	(0.105/0.992)		(0.002/0.074)	(0.010/0.047)	(0.015/0.188)	(0.762/0.946)	(0.10/0.981)

95% confidence intervals in parentheses.

mir / pse refer to data for *D. miranda* and *D. pseudoobscura*, respectively.

$N2/N1$ = estimated demographic model (relative difference between current and ancestral population size)

TABLE S4

Estimates of the fraction of adaptive substitutions using the Fay, Wycoff and Wu method on the dataset restricted to the two-thirds of loci with the highest K_A/K_S values

<i>D. miranda</i>		<i>D. pseudoobscura</i>	
X chromosome	Autosome	X chromosome	Autosome
-0.180	-1.112	0.398	0.534
(-1.434 / 0.550)	(-2.906 / -0.042)	(0.050 / 0.669)	(0.193 / 0.796)

90% confidence intervals in parentheses.