

Heritable Variation in Courtship Patterns in *Drosophila melanogaster*

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DOI: [10.1534/g3.114.014811](https://doi.org/10.1534/g3.114.014811)

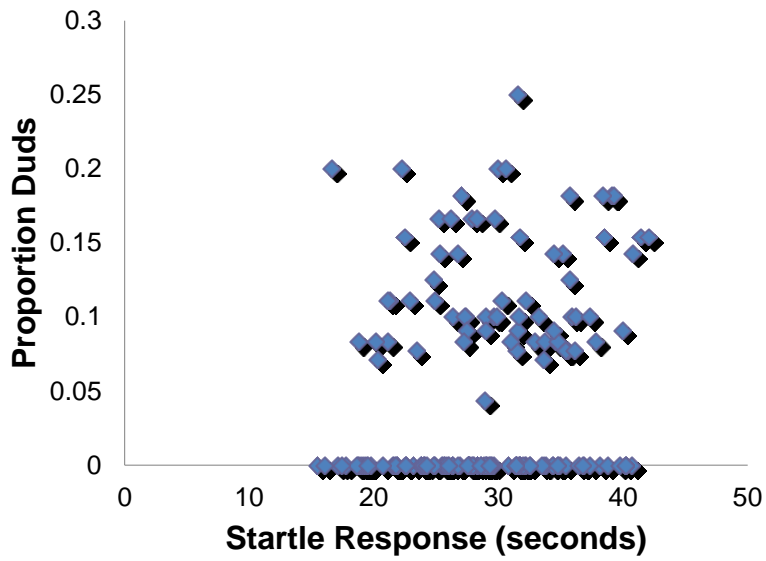


Figure S1. Low correlation between the proportion of ‘dud’ males and a measure of general locomotor activity, startle response. $r^2 = 0.0383$.

Table S1 Top SNPs from the GWAS for E-A transition probability. Location is noted by both chromosome and genomic location. The minor allele frequency (MAF) was obtained by dividing the number of lines with the frequent allele by the total number of lines tested at that locus. The effect is one-half the difference in mean between lines containing the major and minor allele (Falconer and Mackay, 1996). The *P*-value is from a mixed model analysis that takes *Wolbachia* infection status and relatedness due to shared inversion karyotypes as well as cryptic genetic relatedness into account. Probable gene as well as effect the polymorphism has on that gene is noted as derived from Flybase (Marygold *et al.* 2013). * indicates significant after Bonferroni correction ($\alpha = 0.05$, $P = 2.08 \times 10^{-8}$).

Genomic Location	MAF	Effect	<i>P</i>-value	Gene	Site Class
3R_23010872	0.075	-0.0062	6.97E-09*	<i>Ser</i>	Intron
3R_21296904	0.054	-0.0075	9.89E-09*	<i>Fur1</i>	Intron
3L_3706152	0.086	-0.0051	1.31E-07	Intergenic	N/A
3R_23009915	0.061	-0.0061	2.03E-07	<i>Ser</i>	Intron
X_20318587	0.129	-0.0044	3.10E-07	<i>CG42578</i>	Downstream
3R_22864199	0.0556	-0.0065	4.46E-07	<i>NepYr</i>	Intron
3R_23003275	0.067	-0.0056	5.04E-07	<i>Ser</i>	Synonymous
3R_22998908	0.073	-0.0056	5.54E-07	<i>Ser</i>	Synonymous
3L_15807977	0.058	-0.0067	5.92E-07	<i>fwe</i>	Intron
3L_3706141	0.097	-0.0047	6.65E-07	Intergenic	N/A
3R_24359687	0.068	-0.0057	7.41E-07	<i>Ppn</i>	Intron
3R_23004871	0.100	-0.0047	8.85E-07	<i>Ser</i>	Intron
3R_22864182	0.061	-0.0060	1.21E-06	<i>NepYr</i>	Intron
3R_12558223	0.150	-0.0042	1.50E-06	<i>Ubx</i>	Intron
3R_23006864	0.055	-0.0061	2.03E-06	<i>Ser</i>	Intron
2R_3790141	0.095	-0.0047	2.42E-06	<i>CG30377</i>	Intron
3R_23005060	0.067	-0.00523	2.79E-06	<i>Ser</i>	Intron
2R_9824749	0.200	-0.0035	2.93E-06	<i>shot</i>	Intron
3R_6210960	0.342	-0.0029	2.93E-06	<i>mun</i>	Intron
X_800458	0.085	-0.0053	3.12E-06	<i>e(r)</i>	Upstream
3R_8624797	0.490	-0.0026	3.29E-06	Intergenic	N/A

Genomic Location	MAF	Effect	P-value	Gene	Site Class
3R_3007818	0.059	-0.0058	3.70E-06	<i>Ser</i>	Intron
3L_706240	0.072	-0.0048	3.73E-06	Intergenic	N/A
3L_6821987	0.094	-0.0048	4.07E-06	<i>CG13024</i>	Start gained
3R_2999273	0.061	-0.0056	4.53E-06	<i>Ser</i>	Synonymous
3R_3001738	0.0549	-0.0057	4.86E-06	<i>Ser</i>	Intron
2L_3477359	0.237	-0.0033	5.49E-06	<i>CG42784</i>	Intron
3L_3766554	0.198	-0.0036	6.12E-06	<i>bru-3</i>	Intron
3R_2925879	0.063	-0.0059	6.20E-06	<i>eater</i>	Upstream
3R_3012273	0.069	-0.0055	6.21E-06	<i>Ser</i>	Intron
2R_312457	0.385	-0.0025	6.26E-06	<i>CG42321</i>	Intron
3R_2864293	0.158	-0.0039	7.03E-06	<i>NepYr</i>	Intron
X_1066955	0.115	-0.0038	7.24E-06	Intergenic	N/A
2R_586976	0.106	-0.0041	7.26E-06	<i>wuc</i>	Upstream
3R_2999769	0.067	-0.0053	7.46E-06	<i>Ser</i>	Synonymous
X_1067153	0.114	-0.0038	7.65E-06	Intergenic	N/A
3R_3002423	0.105	-0.0042	8.10E-06	<i>Ser</i>	Intron
2R_9337098	0.106	-0.0037	8.37E-06	<i>cnn</i>	Intron
3R_23009365	0.062	-0.0054	8.74E-06	<i>Ser</i>	Intron
X_21066980	0.110	-0.0039	8.75E-06	Intergenic	N/A
3R_24360681	0.055	-0.0058	8.77E-06	<i>Ppn</i>	Intron
3R_18106804	0.288	0.0030	8.79E-06	<i>SKIP</i>	Intron
2R_7000740	0.110	-0.0041	9.08E-06	Intergenic	N/A
3L_13938151	0.269	0.0027	9.10E-06	<i>CG32137</i>	Intron
2R_9312454	0.394	-0.0024	9.31E-06	<i>CG42321</i>	Intron
3L_13766585	0.195	-0.0035	9.49E-06	<i>bru-3</i>	Intron
2R_6301231	0.200	-0.0034	9.80E-06	<i>CG42732</i>	Intron
3L_2799032	0.354	0.0027	9.99E-06	<i>CG43444</i>	Intron

File S1

Raw data used in the analyses.

Available for download as an Excel file at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.014811/-/DC1>