

# Phenotypic Variation and Natural Selection at *Catsup*, a Pleiotropic Quantitative Trait Gene in *Drosophila*

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Table S1. Variance Components and Quantitative Genetic Parameters from ANOVA of Homozygous Chromosome 2 Substitution Lines

Parameter	Life Span	Starvation Resistance	Abdominal Bristles	Sternopleural Bristles	CV Abdominal Bristles
$\sigma_L^2$	39.927 <sup>a</sup>	139.132 <sup>a</sup>	5.283 <sup>a</sup>	0.913 <sup>a</sup>	134.719 <sup>a</sup>
$\sigma_{LS}^2$	2.178 <sup>b</sup>	26.065 <sup>a</sup>	1.576 <sup>a</sup>	0.039 <sup>b</sup>	35.231 <sup>a</sup>
$\sigma_E^2$	139.079	213.205	7.856	1.722	111.323
$\sigma_G^2$	42.105	165.197	6.858	0.953	169.949
$\sigma_P^2$	181.184	378.402	14.714	2.675	281.272
$H^2$	0.232	0.437	0.466	0.356	0.604

<sup>a</sup>  $p < 0.0001$ .

<sup>b</sup>  $p > 0.05$ .

Table S2. Variance Components and Quantitative Genetic Parameters from ANOVA of Locomotor Reactivity

Parameter	Estimate
$\sigma_L^2$	1.253 <sup>a</sup>
$\sigma_{LS}^2$	0.154 <sup>b</sup>
$\sigma_{LC}^2$	0.644 <sup>a</sup>
$\sigma_{LSC}^2$	0.138 <sup>b</sup>
$\sigma_E^2$	8.579
$\sigma_G^2$	2.190
$\sigma_P^2$	10.769
$H^2$	0.203

<sup>a</sup>  $p < 0.0001$ .

<sup>b</sup>  $0.001 < p < 0.01$ .

Table S3. *Catsup* Polymorphisms

Marker	Polymorphism <sup>a</sup>	Effect	Location	<i>q</i> ( <i>N</i> ) <sup>b</sup>
M1	In-522Del [29 bp]	Croc	Promoter	0.006 (1)
M2	T-470C	Zeste	Promoter	0.283 (47)
M3	Del-375In [7]	Elf-1	Promoter	0.295 (50)
M4	C-274T	Brcz-4	Promoter	0.145 (25)
M5	T-249G	Elf-1	Promoter	0.341 (57)
M6 <sup>c</sup>	A-226G	A/G	5'-UTR	0.042 (7)
M7 <sup>c</sup>	G-217A	G/A	5'-UTR	0.311 (52)
M8	G-197A	G/A	5'-UTR	0.392 (65)
M9	C10G	Gln(4)Glu	Exon 1	0.059 (10)
M10 <sup>c</sup>	T28G	Cys(10)Gly	Exon 1	0.018 (3)
M11	G109T	Ala(97)Ser	Exon 1	0.006 (1)
M12	G174A	Lys(58)Lys	Exon 1	0.018 (3)
M13	A194C	His(65)Pro	Exon 1	0.464 (77)
M14	A215G	His(72)Arg	Exon 1	0.097 (16)
M15 <sup>c</sup>	In270Del[57 bp]	aa (91–109)	Exon 1	0.061 (10)
M16	A366 G	Ala(122)Ala	Exon 1	0.117 (19)
M17	C518T	Leu(155)Leu	Exon 2	0.012 (2)
M18 <sup>d</sup>	G533T	Ala(160)Ser	Exon 2	0.012 (2)
M19 <sup>c</sup>	C599G	Leu(182)Val	Exon 2	0.037 (6)
M20	T625G	His(190)Gln	Exon 2	0.168 (28)
M21	C652T	His(199)His	Exon 2	0.084 (14)
M22	C731A	Leu(226)Met	Exon 2	0.042 (7)
M23	C757T	Ala(234)Ala	Exon 2	0.036 (6)
M24 <sup>c,d</sup>	C788A	Leu(245)ile	Exon 2	0.018 (3)
M25 <sup>d</sup>	A790G	Leu(245)Leu	Exon 2	0.341 (57)
M26	G835T	Lys(260)Asn	Exon 2	0.293 (49)
M27	C849T	Pro(265)Leu	Exon 2	0.006 (1)
M28 <sup>c</sup>	A876T	Glu(274)Val	Exon 2	0.012 (2)
M29 <sup>d</sup>	G907A	Lys(284)Lys	Exon 2	0.048 (8)
M30 <sup>c,d</sup>	T918C	ile(288)Thr	Exon 2	0.228 (38)
M31	In1411Del [38 bp]	38 bp InDel	3'-UTR	0.036 (6)
M32 <sup>d</sup>	Del1486In [CT]	2 bp InDel	3'-UTR	0.446 (74)
M33	A1492G	A/G	3'-UTR	0.325 (51)

<sup>a</sup> Markers are named according to their position in the aligned sequence, where +1 denotes the translation start site. The common variant is listed first.

<sup>b</sup> Frequency of rare allele (number of lines with rare allele).

<sup>c</sup> Markers exhibiting associations with quantitative traits at the Bonferroni-corrected experiment-wise significance threshold: M6 (environmental variance of abdominal bristle number), M7 (sternopleural bristle number), M10 (abdominal bristle number and environmental variance of abdominal bristle number), M15 (locomotor reactivity), M19 (life span), M24 (abdominal bristle number), M28 (locomotor reactivity), and M30 (sternopleural bristle number).

<sup>d</sup> Markers nominally ( $p < 0.05$ ) associated with starvation stress resistance.

Table S4. Genotype-Phenotype Associations at *Catsup*

Trait <sup>a</sup>	Marker	Effect <sup>b</sup>	Effect/ $\sigma_G$   <sup>c</sup>	Effect/ $\sigma_P$   <sup>c</sup>	$\sigma_M^2$ <sup>d</sup>	$\sigma_M^2/[\sigma_M^2+\sigma_E^2]$ <sup>e</sup>
LS	C599G	-7.53	1.16	0.56	28.70	0.32
LR	In270Del[57 bp]	1.27	0.86	0.39	0.80	0.24
	A876T	-1.82	1.23	0.55	1.70	0.39
SB	G-217A	-0.32	0.33	0.20	0.05	0.04
	T918C	0.38	0.39	0.23	0.07	0.05
AB	T28G	5.66	2.16	1.48	16.02	0.66
	C788A	2.86	1.09	0.74	4.05	0.32
CV <sub>E</sub> AB	A-226G	-13.97	1.07	0.83	93.71	0.25
	T28G	-25.11	1.93	1.50	295.62	0.52
SR	H <sub>ALL</sub> <sup>f</sup>	—	—	—	31.41	0.15

<sup>a</sup> LS, life span; LR, locomotor reactivity; SB, sternopleural bristle number; AB, abdominal bristle number; CV<sub>E</sub> AB, environmental variance in abdominal bristle number; SR, starvation resistance.

<sup>b</sup> Difference in means between common and rare allele.

<sup>c</sup> Absolute values of the effects, expressed in genetic ( $\sigma_G$ ) and phenotypic ( $\sigma_P$ ) standard deviation units.

<sup>d</sup> Variance attributable to the marker.

<sup>e</sup> Fraction of total variance attributable to the marker.

<sup>f</sup> Haplotypes derived from all 87 population haplotypes (H<sub>ALL</sub>).