

Segregating Variation in the Transcriptome: *Cis* Regulation and Additivity of Effects

Kimberly A. Hughes,^{*,†,1} Julien F. Ayroles,^{‡,2} Melissa M. Reedy,^{*} Jenny M. Drnevich,^{*,3}
Kevin C. Rowe,^{*,4} Elizabeth A. Ruedi,[§] Carla E. Cáceres^{*} and Ken N. Paige^{*}

^{*}*School of Integrative Biology*, [†]*Institute for Genome Biology*, [‡]*Department of Natural Resources and Environmental Sciences*
and [§]*Program in Ecology and Evolutionary Biology*, University of Illinois, Urbana, Illinois 61801

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ABSTRACT

Properties of genes underlying variation in complex traits are largely unknown, especially for variation that segregates within populations. Here, we evaluate allelic effects, *cis* and *trans* regulation, and dominance patterns of transcripts that are genetically variable in a natural population of *Drosophila melanogaster*. Our results indicate that genetic variation due to the third chromosome causes mainly additive and nearly additive effects on gene expression, that *cis* and *trans* effects on gene expression are numerically about equal, and that *cis* effects account for more genetic variation than do *trans* effects. We also evaluated patterns of variation in different functional categories and determined that genes involved in metabolic processes are overrepresented among variable transcripts, but those involved in development, transcription regulation, and signal transduction are underrepresented. However, transcripts for proteins known to be involved in protein–protein interactions are proportionally represented among variable transcripts.

WITHIN-population genetic variability is a major source of phenotypic differences among individuals and is the raw material for evolution, yet very little is known about the characteristics of genes underlying this variation. Further, it is not clear what evolutionary processes maintain within-population variation in the face of natural selection and genetic drift (BARTON and TURELLI 1989; LYNCH *et al.* 1998; CHARLESWORTH and HUGHES 2000; TURELLI and BARTON 2004), and models to explain the maintenance of variation depend on parameters that have been difficult to estimate (CHARLESWORTH and HUGHES 2000).

Addressing these questions depends on measuring the effects and interactions of genes that segregate within natural populations (MACKAY 2001). However, reliable and unbiased data have been difficult to obtain because it is not usually possible to measure phenotypic effects of segregating alleles, except in rare cases of Mendelian segregation of discrete phenotypes. Quantitative trait loci (QTL) mapping studies can estimate allelic effects; however, most QTL have not been re-

solved to the level of individual loci, and most studies have investigated between- rather than within-population variation (GLAZIER *et al.* 2002).

Oligonucleotide microarrays provide a novel tool for investigating within-population variation because they allow the simultaneous sampling of large numbers of phenotypes (mRNA abundance of thousands of different transcripts). A high proportion of these phenotypes exhibit significant within-population variation, even when only moderate numbers of individuals are sampled (OLEKSIK *et al.* 2002; TOWNSEND *et al.* 2003; WAYNE *et al.* 2004). We therefore combined this technology with quantitative genetic experiments to measure patterns of genetic and phenotypic variation, *cis* and *trans* regulation, and dominance for >18,000 genes in adult male *Drosophila melanogaster*. We found that *cis*-regulatory effects predominate for transcripts with high levels of genetic variation and that variable transcripts tend to be involved in metabolic processes, but not in developmental or regulatory processes. We also found that most transcripts exhibited within-locus additivity or near additivity with respect to mRNA abundance, and few displayed dominance or overdominance.

MATERIALS AND METHODS

Experimental flies: We obtained third-chromosome substitution lines of *D. melanogaster* from J. Leips (University of Maryland, Baltimore County) for this experiment. Within each substitution line, flies were identically homozygous for all

¹*Corresponding author:* School of Integrative Biology, University of Illinois, 515 Morrill Hall, 505 S. Goodwin Ave., Urbana, IL 61801.
E-mail: kahughes@life.uiuc.edu

²*Present address:* Department of Genetics, North Carolina State University, Raleigh, NC 27695.

³*Present address:* Roy J. Carver Biotechnology Center, Keck Center for Functional Genomics, University of Illinois, Urbana, IL 61801.

⁴*Present address:* Department of Biological Science, Florida State University, Tallahassee, FL 32306.

genes on the third chromosome (C3), and each line contained a different wild-type C3 derived from a single natural population in Raleigh, North Carolina (DE LUCA *et al.* 2003). All other chromosomes were identical across lines and were derived from the highly inbred SAM stock (LYMAN *et al.* 1996). Thus, these isogenic lines differed only with respect to allelic variation of genes on C3. We checked homozygosity of the isogenic lines by typing each line for a set of seven variable microsatellite loci (four on C3 and three on C2). All were homozygous within each line.

We measured transcript abundance in equal-aged adult males from six different isogenic lines. We also intercrossed three of these lines (lines 33, 83, and 483) in all possible combinations to produce F₁ flies that were hybrids for alleles on C3. Because all lines contained identical sex chromosomes, reciprocal crosses (*e.g.*, 33 females × 83 males and 83 females × 33 males) produced flies that were identical for the nuclear genome. To eliminate differences between parental and F₁ lines due to maternal effects, we pooled offspring from reciprocal crosses and mixed them in equal numbers before extracting RNA. These pooled F₁ flies were designated as lines 33 × 83, 33 × 483, and 83 × 483.

For each isogenic and F₁ line, we reared offspring from replicate vials produced from two independent sets of parents (block A and block B) to produce true biological replicates. We housed block A flies in one incubator and block B flies in another; both blocks were reared and collected at the same time. Parents of experimental flies were reared from constant-density vials (7 males and females per vial), and males used for expression analysis were reared at a constant larval density of 25 per vial. Over a 2-day period (days 0 and 1), we collected males within 8 hr of eclosion and kept them in single-sex vials at low density (10 males per vial) until day 4 when all males were 3–4 days posteclosion. Because we wanted to assay males with appropriate experience for their age, we housed males with females from a laboratory strain (*e/e* on Ives outbred background) beginning at day 4 and continuing until they were preserved for mRNA extraction on day 8. These mating vials were established at a density of 3 males and 3 females per vial, and four independent vials were maintained per genotype per block.

On day 8, we chose males from each genotype and block for extraction of mRNA, for a total of 18 extractions. For each extraction, we pooled six males chosen from the four mating vials in the appropriate block. Two males were chosen from each of two mating vials and one male from each of the two other vials. Males were flash frozen in random order between 13:00 and 15:00 hr CST. We extracted RNA from all block A flies on the same day and from all block B flies on the next day. Standard Trizol protocols were used for extraction and labeling with the MessageAmp aRNA kit. We hybridized labeled mRNA to Affymetrix Drosophila 2.0 GeneChips according to manufacturer's protocols and scanned them with an Affymetrix GeneArray Scanner at the University of Illinois Affymetrix Core Facility.

Transcript abundance and genetic variation: Affymetrix Drosophila 2.0 GeneChip contains probes for 18,769 transcripts with 14 probes per transcript. Probe-level intensity values were obtained for each array from MAS 5.0, and all probe intensity values were standardized to the mean value for the array. We determined that 14,298 transcripts were detectable in experimental flies by comparing signals from perfect-match (PM) probes to those from mismatch probes across all arrays using a Wilcoxon sign-rank test (*n* ranged from 162 to 213). This is probably a liberal test for transcript presence, but we deemed this appropriate because it includes more genes in the entire analysis than a more conservative test, so the false discovery rate (FDR, the expected proportion of significant results that are

false positives; BENJAMINI and HOCHBERG 1995) calculations for the remainder of the tests we applied are conservative. We used a cutoff of $P < 0.04$ for determining that a transcript was present, for an FDR of 0.05.

For subsequent analyses, we used only the mean-standardized PM intensity values from the 14,298 detectable transcripts (CHU *et al.* 2002). The consistency of probe-level measures from independent replicates of the same genotype was high (Pearson's $r = 0.94$), indicating high repeatability of expression measurements. We tested for significant variation in mRNA abundance among the C3 substitution lines, using gene-specific mixed linear models of the form $\text{Log}_2(\text{PM}) = \mu + L + P + L \times P + B(L) + \epsilon$, where L was the line effect, P the probe effect, and $B(L)$ the effect of block nested within line. L and P were fixed effects and $B(L)$ was random to provide the error term for L . These models were implemented in SAS PROC MIXED V. 9.1 (SAS INSTITUTE 2002). Probe-level values were deleted as outliers if they had external Studentized residuals > 3 . After outlier removal, 13,423 of the tested transcripts (94%) had residuals that were normally distributed (Shapiro–Wilk $P > 0.05$). For genes with significant among-line variation, we calculated genetic variance in transcript abundance (V_G) as the among-line variance component from a model that included the fixed effect of probe and random effects of line and block within line. To compare genetic variation among transcripts with different abundance levels, we calculated coefficients of genetic variation (CV_G) as $100\sqrt{V_G}/\bar{x}$, where \bar{x} was the mean abundance of the transcript.

Cis and trans regulatory effects: Because the only allelic differences between C3 substitution lines were attributable to genes on C3, all genetic variation in transcript abundance was due to sequence variation on C3. Variable expression of genes on other chromosomes must have been due to *trans*-acting effects of alleles on C3. This does not imply that the variable genes on other chromosomes have no *cis*-regulatory mechanisms, only that *cis* effects would not have contributed to genetic variation in our experiment. Variation in abundance of C3 transcripts could be caused either by *cis*- or by *trans*-acting sequence differences, but the proportion subject to *trans* regulation can be estimated from the number of variable transcripts on the other chromosomes. We therefore obtained chromosomal locations of genes producing each transcript with significant genetic variation, to determine the contributions of *cis*- and *trans*-regulatory effects. Chromosomal locations were obtained from the Affymetrix database on February 3, 2005 (LIU *et al.* 2003).

We used logistic regression to determine if the probability of a transcript occurring on C3 was significantly related to the magnitude of genetic variation as measured by CV_G . However, the logistic regression assumes that all transcripts are independent, so the test might be too liberal. We therefore applied a conservative contingency-table test (WAYNE *et al.* 2004), by dividing the 2329 variable transcripts into thirds (tertiles) on the basis of their CV_G values and using χ^2 -tests to determine if chromosomes were equally represented among tertiles (Table 1).

To determine the total number of *cis*- vs. *trans*-regulated transcripts, we also calculated the expected proportion of C3 genes that were *trans* regulated, assuming that the locations of *trans*-regulatory variants are randomly distributed relative to their target genes, which is consistent with data from yeast (BREM *et al.* 2002; YVERT *et al.* 2003). We based the estimate of *trans*-regulated C3 genes on the proportion of *trans*-regulated genes on the other major chromosomes in *D. melanogaster* (C2 and X).

Functional classification and interacting transcripts: To test for under- or overrepresentation of functional categories among genetically variable transcripts, we used the Affymetrix gene

ontology (GO) mining tool (LIU *et al.* 2003). The database contains biological process annotation for 6895 genes, of which 1024 were variable among genotypes in our experiment; it contains molecular function annotation for 7240 genes, of which 1086 were variable. We tested the following GO functional categories for over- or underrepresentation among genetically variable genes: “development,” “regulation,” “metabolism,” and “cell communication” for biological process and “catalytic (enzymatic) activity,” “signal transduction,” “regulation of transcription,” and “structural molecule” for molecular function (RIKIN *et al.* 2003). We tested for disproportional representation of functional categories by comparing the frequency of each category among genetically variable transcripts to its expected frequency among all detectable transcripts. We used χ^2 -tests for this analysis, because of the potential for nonindependence among transcripts in the same functional category. A category was judged to under- or overrepresented if $P < 0.01$. Less than 1 false positive is expected under this criterion.

We also compared variable and nonvariable transcripts with respect to evidence for interactions among the protein products of the genes. GIOT *et al.* (2003) reported >20,000 interactions between 7048 proteins encoded in the *D. melanogaster* genome. They were able to ascribe high, intermediate, or low confidence to these interactions, with high confidence assigned to 4780 interactions involving 4679 proteins. We compared genetically variable and nonvariable transcripts to the entire list of interacting proteins and, separately, to the high-confidence list and tested for nonrandom associations using a two-by-two contingency table analysis.

Dominance: To calculate dominance effects, we compared mRNA abundance in isogenic lines with that of the F_1 hybrid offspring they produced. We first determined which transcripts were variable among the isogenic and F_1 lines that we used in crosses: 33, 83, 483, 33 \times 83, 33 \times 483, and 83 \times 483, using the linear model described above. We found that 905 transcripts were significantly variable among these lines at $P < 0.013$ (FDR of 0.2). For these 905 transcripts, we then determined if there was significant variation among lines that composed a cross (*e.g.*, pairwise differences between lines 33, 83, and 33 \times 83), using ESTIMATE statements in PROC MIXED and a P -value cutoff of 0.05. If there were pairwise differences, we calculated the dominance of transcript abundance as d/a , where a is half the difference in abundance between the isogenic parental lines and d is the difference between the F_1 hybrid and the mean of the parental lines (FALCONER and MACKAY 1996; GIBSON *et al.* 2004). If transcript abundance in the hybrid is exactly intermediate to that in the parental lines, $d = 0$; thus $d/a = 0$ indicates within-locus additivity and $|d/a| = 1$ indicates complete dominance. If $|d/a| > 1$, overdominance (heterosis) of transcript abundance is indicated, meaning the hybrid falls outside the range of phenotypes spanned by the parents.

We determine if mRNA abundance in the two parental lines was significantly different using ESTIMATE statements in PROC MIXED, equivalent to testing $2a > 0$. We also determined if the hybrid was significantly different from the mean of its parental lines, equivalent to testing $|d| > 0$ and indicating significant deviation from within-locus additivity. Type III F -tests for both effects had 2 numerator d.f. and 3 denominator d.f. This is an appropriate test for dominance if the dependent variable is linearly related to transcript abundance. Benchmark trials have shown that $\log_2(\text{PM})$ is linearly related to $\log_2(\text{abundance})$ (COPE *et al.* 2004) with slope estimates between 0.67 and 0.87. For the range of values we observed ($4.8 < \log_2(\text{PM}) < 11.6$), $\log_2(\text{PM})$ and abundance are nearly linearly related. We also calculated dominance by assuming a linear relationship between PM and abundance;

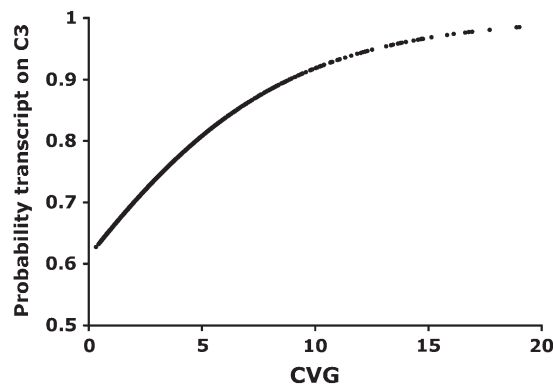


FIGURE 1.—Coefficient of genetic variation (CV_G) in transcript abundance, *vs.* the probability that the transcript is encoded by a gene on C3. The probabilities were calculated from a logistic regression analysis.

the results were nearly identical. We therefore report only results obtained on the log scale because of better distributional properties of all variables on this scale.

To determine if transcripts displayed significant overdominance, we calculated 80 and 95% confidence intervals for a and d using ESTIMATE statements within PROC MIXED. If upper and lower limits for d and a did not overlap, we concluded that there was statistical support for overdominance.

RESULTS

Cis and trans regulatory effects: Of the 14,298 detectable transcripts, 2329 (16.3%) showed significant variation among isogenic lines at $P < 0.01$ (FDR = 0.06, supplemental Table 1 at <http://www.genetics.org/supplemental/>). The CV_G values for these genes ranged from 19.0 to 0.3. Genes located on C3 were substantially overrepresented among genetically variable transcripts: C3 accounted for 44% (6338) of all detectable transcripts and for 72% (1683) of the genetically variable transcripts ($\chi^2_1 = 626$, $P < 10^{-5}$). This pattern is consistent with substantial *cis* regulation of genetically variable transcripts.

C3 was also overrepresented among the transcripts exhibiting the most variation when the analysis is limited to the 2329 transcripts with significant genetic variation (Figure 1). The probability of a transcript occurring on C3 was positively related to CV_G (likelihood ratio $\chi^2_1 = 61.4$, $P < 0.0001$), while the probability of a transcript occurring on the other chromosomes was negatively related to CV_G (X chromosome $\chi^2_1 = 26.0$, $P < 0.0001$; chromosome 2 $\chi^2_1 = 43.8$, $P < 0.0001$) (Table 1). Using the tertile method, the representation of C3 was significantly heterogeneous ($\chi^2_2 = 94.2$, $P < 0.0001$), with 82% of transcripts in the highest tertile occurring on that chromosome, compared to 74% in the middle tertile and 60% in the bottom tertile (Table 1).

Of 5410 C2 transcripts that were detectable in our study, 81 (1.5%) were genetically variable and in the top tertile of all CV_G values, 153 (2.8%) were variable and in

TABLE 1
Chromosomal location of transcripts in each tertile of genetic coefficient of variation

Tertile ^a	C3 total	<i>Cis</i>	<i>Trans</i>	X	C2	Other	Total	Mean CV _G ^b
1	639	540	99	39	81	17	776	5.1
2	574	414	160	40	153	9	776	2.2
3	470	226	244	92	203	12	777	1.0
Total ^c	1683	1180	503	171	437	38	2329	3.0

^a Tertile 1 comprises transcripts with the most genetic variation in expression; tertile 3 comprises those with the least.

^b The mean standardized genetic variance for each tertile is the square of the mean CV_G.

^c Expected number of false positives is less than two in all categories.

the middle tertile, and 203 (3.8%) were variable and in the bottom tertile (supplemental Table 1 at <http://www.genetics.org/supplemental/>). The proportions were very similar for the 2250 detectable X chromosome transcripts: 39 (1.7%) were in the top, 40 (1.8%) were in the middle, and 92 (4.1%) were in the bottom tertile of all genetically variable transcripts. Taking the proportion of *trans*-regulated genes on X and C2 as the proportion of detectable transcripts that are expected to be *trans* regulated by genes on C3 and applying these proportions to the detectable C3 transcripts, we expect $0.0156 \times 6338 = 99$ C3 transcripts in the top tertile, $0.0125 \times 6338 = 160$ in the middle tertile, and $0.0385 \times 6338 = 244$ in the bottom tertile of genetically variable transcripts to be *trans* regulated by other genes on C3 (Table 1).

Over all tertiles, *cis* regulation thus accounts for $1180/2329 = 51\%$ of the genetically variable transcripts. However, it accounts for 70% of all transcripts in the top tertile of genetic variation, 53% of transcripts in the middle tertile, and 29% of those in the bottom tertile (Table 1). Because the mean standardized genetic variance (CV_G)² for transcripts in the top tertile is 5.4 times higher than that for transcripts in the middle tertile and 26 times higher than that for transcripts in the bottom tertile (Table 1), we conclude that *cis* effects are responsible for substantially more genetic variance in gene expression than are *trans* effects and consequently that *cis* effects are larger on average than are *trans* effects (MEIKLEJOHN *et al.* 2003; WAYNE *et al.* 2004).

To determine if variation in mRNA sequences among inbred lines was a potential source of bias in this analysis (HSIEH *et al.* 2003), we filtered the 2329 genetically variable transcripts on the basis of a measure of the average between-line correlation of hybridization signals within an individual probe: Cronbach's α (SAS INSTITUTE 2002). For each gene on each array, we sequentially deleted probes with the largest values of external Studentized residuals (r_s) from the original linear model until the value of Cronbach's α exceeded 0.90. We filtered all genes that did not achieve this level of α after deleting probes with $r_s \leq 1.0$. This left 1712 genes with known chromosomal locations, of which 112

were on C1, 327 were on C2, and 1273 were on C3. Thus, nearly the same proportion of genes occurs on C3 as on the unfiltered list of variable genes. Sequence variation at probe sites apparently did not bias our estimate of the proportion of *cis*- and *trans*-regulated transcripts.

Functional classification and interacting transcripts: Classification of genetically variable transcripts into biological process categories indicated that developmental, cell communication, and regulatory processes were significantly underrepresented, compared to their frequency among all transcripts in our sample (Table 2). Metabolic processes were overrepresented, but not significantly so. Two molecular function categories were also underrepresented: signal transduction and transcription regulation. Structural molecules were also underrepresented, but the deviation was nonsignificant by the conservative contingency-table analysis we used. Catalytic activity was the only molecular function category that was overrepresented.

When we compared variable and nonvariable transcripts with respect to the number of interacting proteins, we found no significant associations. Of the 2329 variable transcripts, 1115 are associated with proteins known to be involved in interactions, and 1214 are not. Of the 11,969 transcripts that were detectable in our sample but not genetically variable, 5533 were associated with interacting proteins, and 6436 were not. There is thus no evidence of association between variability and interaction ($\chi^2_1 = 2.13$, $P = 0.14$). When we restricted the analysis to high-confidence protein-protein interactions (GIOT *et al.* 2003), the results were similar: 731 variable transcripts were associated with high-confidence interacting proteins, and 1598 were not, while the numbers for nonvariable transcripts are 3690 of 8279, respectively. Again, there is no evidence of association ($\chi^2_1 = 0.28$, $P = 0.59$). Furthermore, the mean number of interactions per transcript is nearly identical for variable and nonvariable transcripts. Variable transcripts average 0.64 (SE = 0.03) interactions per transcript and nonvariable ones average 0.60 (SE = 0.01) interactions.

Dominance of transcript abundance: We detected at least one pairwise difference between the parental and

TABLE 2
Gene ontology (GO) categories under- or overrepresented among genetically variable transcripts

Gene ontology category	Genetically variable	Present in adult males	χ^2_1	P^a
Biological process				
All genes annotated for biological process	1024	6248		
Underrepresented categories				
<i>Development</i>	<i>180</i>	<i>1568</i>	<i>17.4</i>	<i>< 0.0001</i>
<i>Cell communication</i>	<i>172</i>	<i>1446</i>	<i>13.5</i>	<i>0.0002</i>
<i>Regulation of biological process</i>	<i>120</i>	<i>1069</i>	<i>13.9</i>	<i>0.0002</i>
Overrepresented categories				
Metabolism	706	4007	1.9	0.17
Molecular function				
All genes annotated for molecular function	1086	6517		
Underrepresented categories				
<i>Signal transduction</i>	<i>113</i>	<i>890</i>	<i>6.7</i>	<i>0.01</i>
<i>Transcription regulator</i>	<i>79</i>	<i>760</i>	<i>15.1</i>	<i>0.0001</i>
Structural molecule	87	656	3.7	0.05
Overrepresented categories				
<i>Catalytic activity</i>	<i>632</i>	<i>3285</i>	<i>7.0</i>	<i>0.009</i>

Significant categories (two-sided $P < 0.0001$) are indicated in italics.

^a Calculated by contingency-table analysis, comparing the representation of a category among genetically variable transcripts to its representation among all annotated transcripts present in our sample.

F₁ lines in 1589 cases (646 in cross 33 × 83, 620 in cross 33 × 483, and 323 in cross 83 × 483). Parental lines were significantly different from each other (*i.e.*, $a > 0$) in 1549 of these cases. The hybrid was significantly different from the mean of the parental lines (*i.e.*, $|d| > 0$) in only 205 cases. This disparity was not due to differential power of the tests, because they had the same degrees of freedom, median standard errors were not strikingly different (SE[d] = 0.04; SE[a] = 0.03), but medians of the estimates themselves were quite different (median d = 0.06, median a = 0.19). Distributions for a and d are shown in Figure 2, A and B, and all values of standard errors are provided in supplemental Table 2 at <http://www.genetics.org/supplemental/>.

Distributions of dominance values are shown in Figure 2C. Median values were -0.03 (Wilcoxon test, $P > 0.50$), 0.08 ($P < 0.001$), and 0.14 ($P < 0.001$) for the three crosses, respectively. In each cross, $>66\%$ of values fell between -0.5 and $+0.5$, indicating additivity or intermediate dominance. Overall, 1128 transcripts had d/a values consistent with additivity or intermediate dominance ($0 < |d/a| < 0.5$), 330 had values consistent with intermediate-to-complete dominance ($0.5 < |d/a| < 1$), and 131 had values consistent with overdominance ($|d/a| > 1$).

Of the apparently overdominant transcripts, seven were significantly overdominant using a stringent criterion of nonoverlap of the 95% confidence intervals of d and a ; 30 were significant using 80% confidence intervals. A previous study of dominance of mRNA abundance phenotypes used a cutoff of $|d/a| > 1.32$ on the $\log_2(\text{PM})$ scale, instead of confidence limits, to indicate overdominance (GIBSON *et al.* 2004). This ap-

proach protects against underestimation of the number of overdominant transcripts because of low statistical power. Using this criterion, 88 (3.7%) transcripts displayed overdominance, in broad agreement with the results of GIBSON *et al.* (2004). There were few transcripts with $|d/a| > 3$, and all were associated with small values of a (Figure 3). Excluding values of $a < 0.1$, there were no significant associations between a and $|d/a|$ (cross 33 × 83, Pearson's $r = -0.04$, $P = 0.39$, $N = 546$; cross 33 × 483, $r = 0.007$, $P = 0.87$, $N = 552$; crosses 33 × 83 and 83 × 483, $r = -0.03$, $P = 0.62$, $N = 265$).

DISCUSSION

Over 16% of the transcripts present in adult males demonstrated significant genetic variance in expression within a single population when only C3 (~40% of the genome) varied among genotypes. This is only slightly smaller than the proportion of genes showing within-population phenotypic variation in *Fundulus* (18%, OLEKSIK *et al.* 2002) and/or the proportion of genes varying between inbred lines from different source populations in *D. melanogaster* (25%, GIBSON *et al.* 2004). This comparison suggests that quantitative genetic variation for mRNA abundance is at least as prevalent within populations as it is between populations of *D. melanogaster*. Our results indicate that within-population variation in gene expression is due largely to the segregation of many nearly additive alleles, that, numerically, *cis* effects account for about half the genetically variable transcripts, and that *cis* effects contribute substantially more to genetic variance in

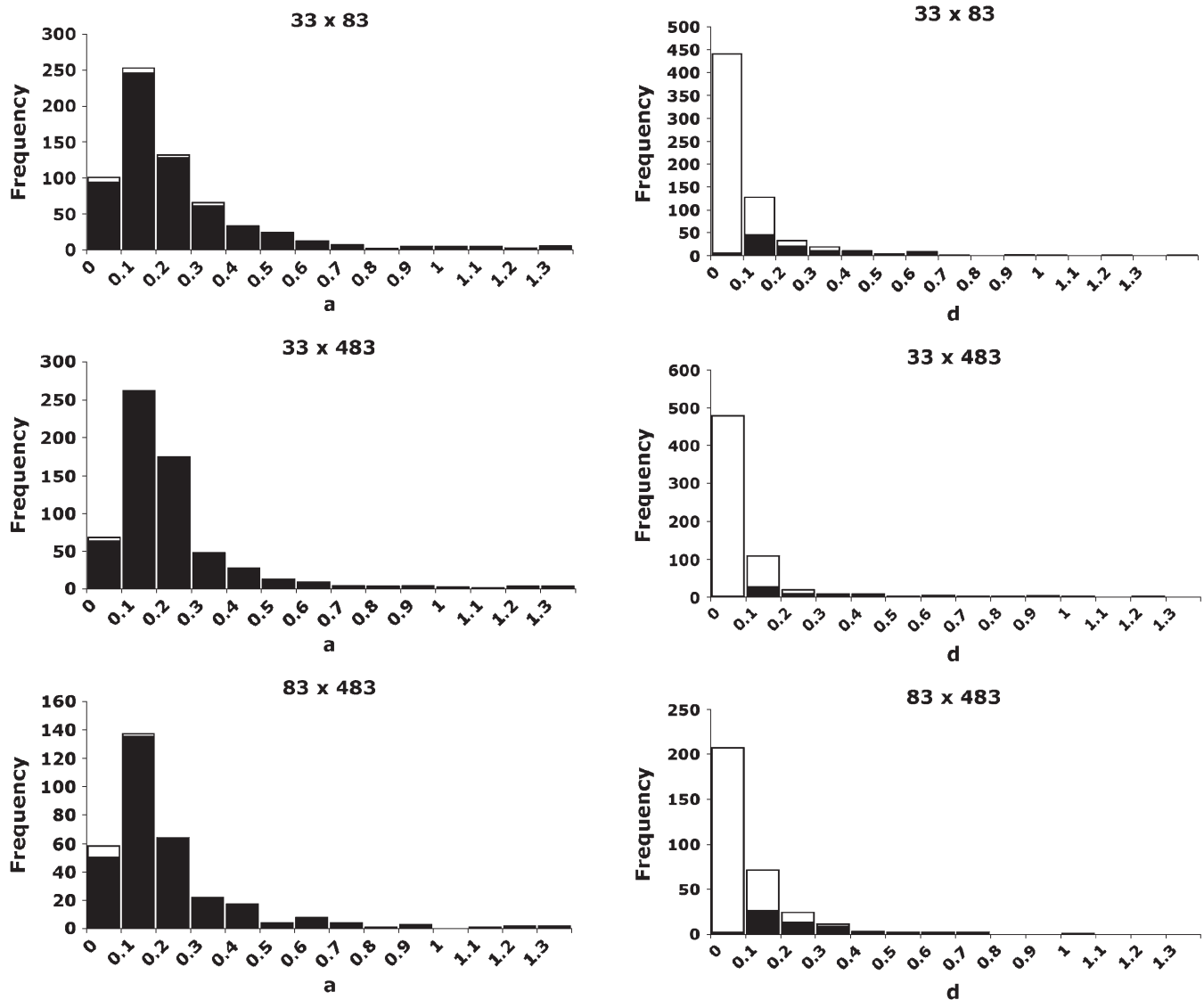


FIGURE 2.—Values of a (A), d (B), and dominance, d/a (C), for transcripts that had at least one pairwise difference in expression between members of a cross. The results for three crosses are shown. Solid areas indicate values for which the parameter was significantly different from 0 ($P < 0.05$), and open areas indicate nonsignificant estimates. Note the difference in vertical scale for cross 83×483 .

expression that do *trans* effects. Previous studies of modes of regulation have yielded mixed results, with some reporting a high proportion of *trans* regulation (MONTTOOTH *et al.* 2003; YVERT *et al.* 2003; WAYNE *et al.* 2004; HARBISON *et al.* 2005) and some reporting mostly *cis* (WITTKOPP *et al.* 2004). However, most of these studies evaluated regulation by using between-population or between-species crosses. *Trans* effects may be more typical of between- than of within-population variation, since selection acting within populations may strictly limit variation in *trans*-acting genes with multiple downstream effects (DENVER *et al.* 2005).

One previous study of within-population variation in *D. simulans* also reported evidence for both *cis* and *trans* regulation, and found that *trans* effects were more numerous than *cis* effects (WAYNE *et al.* 2004), but that

cis effects were larger than *trans* effects (a result also reported by MEIKLEJOHN *et al.* 2003). Thus there are both intriguing differences and similarities between the two studies. We detected a higher proportion of available transcripts on the Affymetrix chip (76% *vs.* 56%), a difference that could be explained by our use of a more liberal statistical threshold for transcript presence or by a loss of detectability in the *D. simulans* study due to hybridizing a different species to *D. melanogaster* chips or to a difference between first and second-generation Affymetrix arrays (we used the newly available second-generation arrays). We also found a larger proportion of genetically variable transcripts overall (16% *vs.* 8%). Our lines varied only for C3, which accounts for $\sim 40\%$ of the *D. melanogaster* genome, meaning that we would have detected an even higher proportion of variable

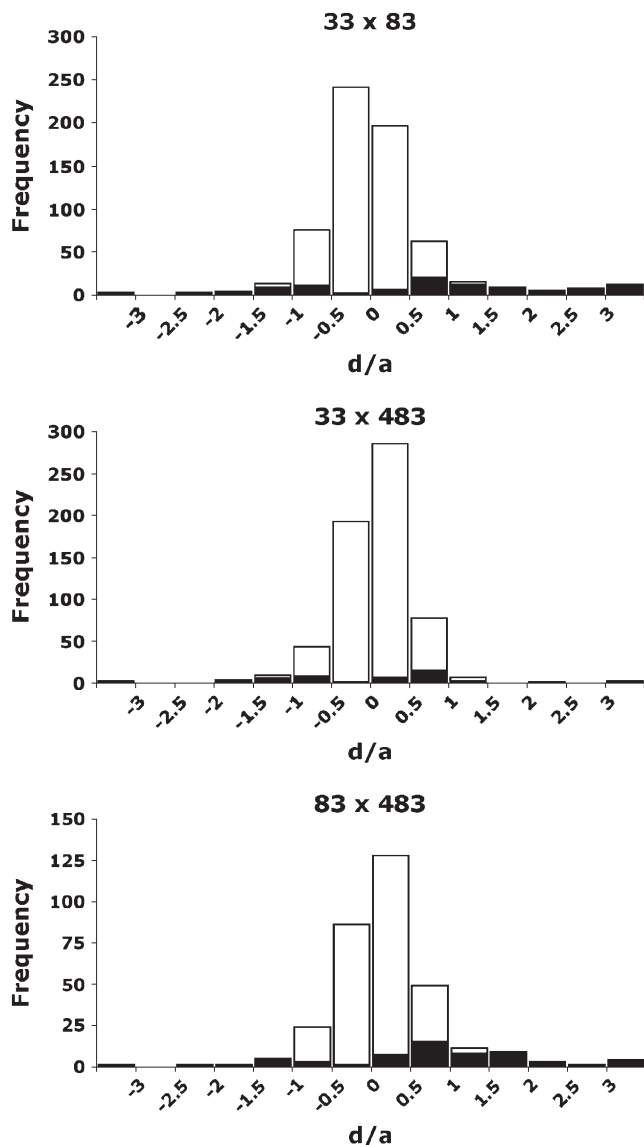


FIGURE 2.—Continued.

transcripts had our lines differed for all chromosomes. However, a likely explanation of this difference is that different genetic components of variation were measured in the two studies (additive variance in the previous study *vs.* variation among homozygous lines in ours). Homozygous genetic variance is expected to exceed additive variation within populations (CHARLESWORTH and HUGHES 1996), and experiments confirm this expectation (HUGHES 1995a,b; HUGHES *et al.* 2002). Thus our observation of more genetically variable transcripts might simply reflect higher power to detect the larger variances associated with inbred lines.

We also detected an approximately equal numerical representation of *cis*- than of *trans*-acting variation in contrast to the study of within-population variation in *D. simulans*, but like that study, ours indicates that *cis* effects are on average larger than *trans*. We could detect only

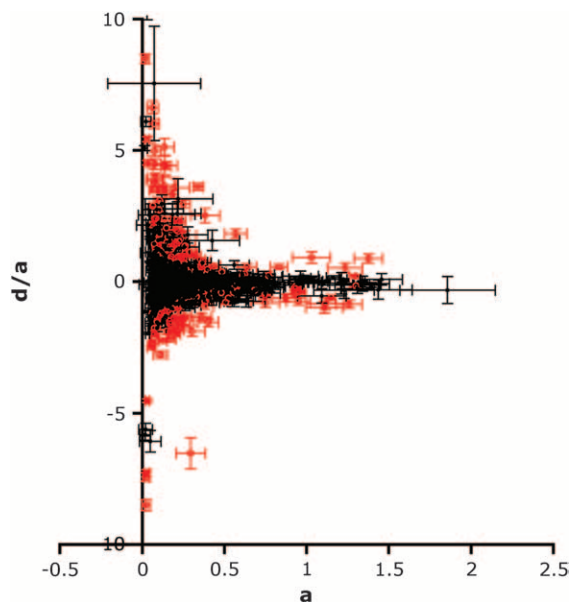


FIGURE 3.—Values of d/a *vs.* a . Five points are not shown to retain reasonable detail in the graph. These points are, for cross 33×83 , a , d/a pairs, 0.002, 154; 0.002, 86.8; 0.014, 42.4; 0.004, 40.3; and for cross 33×483 , a , d/a pairs, 0.012, 22.7. Red symbols indicate transcripts for which d was significantly different from 0; black symbols indicate transcripts for which d was not significant. Horizontal bars show standard errors for a ; vertical bars show standard error for d/a (calculated by propagating of error). Note the different scales for a and d/a .

transcript variation that was caused by sequence variation on C3. If patterns of *cis* and *trans* regulation differ between chromosomes, and particularly if they differ between sex chromosomes and autosomes, our results would not be representative of sex-linked variation. We know of no direct evidence for such differential patterns of regulation, however. Further, genetic variation on other chromosomes would be likely to induce some additional *trans* effects on C3, although interchromosomal epistatic interactions could also increase the level of *cis*-acting variation. Studies comparing chromosome extraction lines directly to whole-genome inbred lines from the same population could be used to address this issue. Finally, the two sets of results are reconcilable if genes that are highly variable within *D. melanogaster* (mostly *cis* regulated) are also characterized by greater sequence divergence between species and are therefore less likely to be detected in cross-species hybridizations. Evidence for a positive correlation of within-species variation and between-species divergence has come from studies of genes involved in reproduction (BEGUN *et al.* 2000) and cell-surface proteins (LAZZARO 2005); evaluation of the genomewide pattern awaits genome sequencing of other *Drosophila* species.

Functional analysis of genetically variable transcripts provides insight into the selective constraints that operate on within-population variation. Transcripts involved in

metabolic/catalytic processes tend to be genetically variable, while those involved in development, transcriptional regulation, and signal transduction do not. Metabolic transcripts may be more variable than developmental and regulatory ones because they are subject to weaker purifying selection or because variation is actively maintained in metabolic enzymes by heterozygote advantage, genotype–environment interaction, or other forms of balancing selection. Strong purifying selection on developmental and regulatory transcripts may be common if small deviations in transcript abundance disrupt highly integrated developmental and regulatory pathways. Conversely, balancing selection mediated by a variable environment could be particularly relevant to metabolic enzymes, which mediate interactions directly between the organism and its environment.

Genetic variation is not disproportionately represented among transcripts that produce proteins that interact with other proteins. Because transcriptional, translational, and metabolic proteins are all enriched among those engaged in protein–protein interactions (GROT *et al.* 2003), and metabolic genes are likely to be genetically variable, but regulatory genes are not, this result is not too surprising. However, our results do suggest that protein interaction itself does not constrain or enhance within-population genetic variation.

Dominance patterns indicate that overdominance is rare, and within-locus additivity is typical of segregating variation in transcript abundance. Over 97% of variable transcripts had significant expression differences between two homozygous parents, but only 13% had F_1 values that deviated significantly from the midpoint of parental values. There is no obvious relationship between $|d/a|$ and a , as might be expected if genes with large differences between parental lines tend to be dominant or overdominant. This preponderance of additivity contrasts with results from a recent study of crosses between inbred lines derived from different source populations (GIBSON *et al.* 2004). In our study, 71% of dominance values fell between -0.5 and $+0.5$, while only 15% of values fell in that range in the previous study (calculated from supplemental information for males in GIBSON *et al.* 2004). It might be argued that this difference derives from pooling of reciprocal crosses in our experiment, since Gibson *et al.* detected differences between F_1 reciprocal males in 9% of transcripts tested. However, that study crossed inbred lines that differed at all chromosomes. Male flies from reciprocal crosses thus had different X (and Y) chromosomes, and this could account for differential expression in reciprocal males and for some cases of apparent dominance in males in that experiment. In our study, all lines had the same X, C2, and Y chromosomes, so males from reciprocal crosses had identical genotypes and should have identical expression patterns, aside from maternal effects.

Another possible contributor to different dominance patterns in the two studies is that different filtering criteria were used. GIBSON *et al.* (2004) included a transcript in all dominance calculations if at least one significant pairwise difference was detected among their 12 genotype/sex categories, even though any given dominance value was calculated from only 3 of the 12 categories. We used a more stringent criterion and calculated dominance values only for transcripts showing significant differences among the three genotypes actually used in the dominance calculation.

Because these experimental differences are unlikely to completely account for the large differences in dominance patterns in the two studies, we believe that the discrepancy reflects real differences in the genetic architecture of the lines used. The most obvious difference is that we investigated a random sample of within-population variation, while Gibson *et al.* used crosses between inbred lines derived from two different source populations (Ore-R and 2b). Although there appears to be limited molecular population structure in *D. melanogaster* outside of Africa (DIERINGER *et al.* 2005), substantial population differentiation has been found among non-African populations for many quantitative traits (DE JONG and BOCHDANOVITS 2003; SCHMIDT *et al.* 2005), even on a microgeographic scale (WAYNE *et al.* 2005). In addition, neutral markers have been shown to drastically underestimate population structure for adaptive traits in other species (KARHU *et al.* 1996). We therefore suggest that differences in the genetic architecture of nonneutral quantitative traits might depend critically on the level at which the variation is investigated (*i.e.*, between *vs.* within populations).

Alternately, the process of inbreeding itself might lead to different genetic architectures. The lines used by Gibson *et al.* were produced by many generations of brother–sister mating, which provides an extended opportunity for selection to operate. Furthermore, one of the lines, 2b, underwent selection for low male mating ability during the course of inbreeding. Our lines were produced by sampling third chromosomes directly from a natural population using balancer chromosomes. Third chromosomes that were homozygous lethal or that had very low homozygous fitness would have been removed by this process, but selection was otherwise minimized, and most genetic variation would have been preserved in these lines.

Characterizing effects and interactions of alleles that segregate in natural populations is critical for understanding the genetic basis of phenotypic variation. Our results indicate that the genetic architecture of within-population variation might be different from that observed between populations and that there is a real need for more information on within-population variation. Ultimately, accurate descriptions of variation at both levels will be required for a complete understanding of the causes of genetic and phenotypic diversity.

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