

A microsatellite-based genetic linkage map of the waterflea, *Daphnia pulex*: On the prospect of crustacean genomics[☆]

Melania E.A. Cristescu^{a,*}, John K. Colbourne^b, Jelena Radivojac^b, Michael Lynch^a

^a Department of Biology, Indiana University at Bloomington, Bloomington, IN 47405, USA

^b Center of Genomics and Bioinformatics, Indiana University at Bloomington, Bloomington, IN 47405, USA

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Abstract

We describe the first genetic linkage map for *Daphnia pulex* using 185 microsatellite markers, including 115 new markers reported in this study. Our approach was to study the segregation of polymorphisms in 129 F₂ progeny of one F₁ hybrid obtained by crossing two genetically divergent lineages of *Daphnia* isolated from two Oregon populations. The map spanned 1206 Kosambi cM and had an average intermarker distance of 7 cM. Linkage groups ranged in size from 7 to 185 cM and contained 4 to 27 markers. The map revealed 12 linkage groups corresponding to the expected number of chromosomes and covers approximately 87% of the genome. Tests for random segregation of alleles at individual loci revealed that 21% of the markers showed significant transmission ratio distortion (primarily homozygote deficiency) likely due to markers being linked to deleterious recessive alleles. This map will become the anchor for the physical map of the *Daphnia* genome and will serve as a starting point for mapping single and quantitative trait loci affecting ecologically important phenotypes. By mapping 342 tentative orthologous gene pairs (*Daphnia/Drosophila*) into the *Daphnia* linkage map, we facilitate future comparative projects.

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Keywords: Crustacea; Transmission ratio distortion; Microsatellite DNA; Recombination; Genetic crosses; Comparative genomics; *Daphnia*; Linkage

The waterflea *Daphnia pulex* (Crustacea, Cladocera, Anomopoda) is an aquatic crustacean that has been central to ecological, toxicological, and evolutionary studies for several decades [1]. More recently, *Daphnia* has been advanced as the main nonclassical model organism for evolutionary and ecological genomics. Its genome consists of 12 pairs of chromosomes characterized by hypercondensation and minute size [2,3] and contains no sex chromosomes. A previous estimate of haploid *C* value of 0.24 pg [4] corroborates with subsequent genome size estimates from the *Daphnia* genome sequencing project of 199 Mb, which places the waterflea near the fruit fly (184 Mb) in terms of genome size.

Genetic linkage maps have become essential tools for many genetic and genomic studies. They are often used in the assemblage of physical maps and in genome-wide screenings for genetic variation. Recent progress in genetic mapping methodologies has made it feasible to localize and characterize single-gene traits or to dissect quantitative trait loci (QTL). However, rapid progress is impeded by practical difficulties associated with the lack of genetic markers for most species or with obtaining the large size segregating population that is required for mapping [5]. Many nonmodel organisms are very difficult to maintain and breed in the laboratory, and the number of progeny obtained in manipulated crosses is generally small and inadequate for searching for association between segregating markers and quantitative traits. *Daphnia* is not only well suited to mapping studies but also has the advantage of reproducing sexually as well as asexually. Therefore, the recombined progeny can be maintained clonally in the lab for a long time, which allows the mapping panel to be shared between laboratories and used in further QTL

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* Corresponding author. Fax: (812) 855 6705.

E-mail address: ecristes@indiana.edu (M.E.A. Cristescu).

studies. As part of the *Daphnia* Genome Project, the linkage map of *D. pulex* will soon become an essential tool for large-scale studies for localizing QTL that contribute to adaptation and speciation.

Broad-scale comparative gene mapping is an effective tool for the study of genome evolution in phylogenetically distant species by examining orthologous genes on interspecific homologous chromosome segments [6,7]. Presence of synteny could reflect the ancestral genomic organization and could also indicate the incidence of genomic regions resistant to linkage disruptions. Spatial comparative genomics can also aid in transferring genetic information from genetically well-characterized model species to less developed study organisms. However, large-scale comparative genomic studies depend heavily on the availability of extensive and transferable linkage maps in model as well as nonmodel species. This approach is impeded by the lack of a sufficiently diverse collection of genetic systems for most taxonomic groups. For example, with the exception of the preliminary linkage maps for the black tiger shrimp, *Penaeus monodon* [8] and the white shrimp, *Penaeus vannamei* [9], there are no genetic maps for crustaceans. Moreover, most genetic linkage maps are based on dominant markers (e.g., AFLP, RFLP, RAPD, RAPD-SSCP) that are not easily transferable across mapping populations or species. Microsatellites, in contrast to dominant markers, offer the advantage of being easily transferable. In addition, microsatellites have high levels of intraspecific and intrapopulation allele polymorphism, are ubiquitous in prokaryotes and eukaryotes, encompass both coding and noncoding regions of the genomes [10], and largely display a random distribution across genomes. All of these characteristics promote microsatellites as ideal markers.

In this paper we present the first genetic linkage map for *D. pulex* based on 185 markers (most of which are microsatellite loci) on 12 linkage groups. In addition to discussing the recombination landscape of the *Daphnia* genome we report the map location of 342 genes that show homology to *Drosophila* genes. We used these coding markers to search tentatively for conserved synteny between the two genomes and discuss the prospect of crustacean genomics.

Results

Linkage map

The total number of genotypes analyzed for this study was 21,546, including 185 loci and 129 individuals. The total number of individual genotypes analyzed per locus varied from 65 to 127, with an average of 115. A preliminary linkage map was constructed and instances of double crossovers were reexamined. We estimate that the data set contains less than 1% error. Overall, 97% of the markers tested showed detectable linkage to another marker at a lod threshold of 4.0. The final linkage map consisted of 12 linkage groups and spanned 1206 cM with an average marker

spacing of 7 cM and with few map segments being identified by multiple cosegregating markers. The size of the linkage groups ranged from 6.9 to 185.3 cM (mean: 100.5 cM) and the number of markers per linkage group varied from 4 to 27, with an average of 15 (Fig. 1).

Genome size and coverage

We estimated a total genome length of 1367 cM using the method of Fishman and colleagues [11], which accounts for the terminal parts of the linkage groups by adding twice the average spacing of markers to the lengths of each linkage group and summing across linkage groups. Using the method of Chakravarti and colleagues [12], in which the length of each linkage group is expanded by $(m + 1)/(m - 1)$, where m is the number of loci mapped, we obtained a corrected genome length of 1398 cM. The percentage of the genome covered by the linkage map based on these estimations of the genome length is 87.2%. Assuming a random distribution of markers and 12 linkage groups, we estimate that 95% of the genome is within 3.84 cM of a marker.

Marker distribution

Closer examination of marker distribution reveals clusters of markers on several linkage groups (Fig. 1). The clustered markers may not necessarily be closely spaced physically, but may appear aggregated due to the low recombination rate in particular regions [13,14]. Since most linkage groups contain only one region of recombination suppression, it is likely that these regions are associated with centromeres. There are a few large gaps within linkage groups (>30 cM), and it is difficult to determine at present whether these gaps represent false linkages or recombination hot spots. More extensive examination of recombination suppression will require typing markers in various crosses and the estimation of physical distance in these regions.

Transmission ratio distortion

Using tests for random segregation of alleles at individual loci, we determined that 21% of the 185 markers surveyed showed significant transmission ratio distortion (TRD) primarily due to homozygote deficiency and likely as a result of markers being linked to deleterious recessive alleles. Markers that showed TRD were clustered mainly in four linkage groups (II, V, VI, and X) with linkage group X containing almost exclusively markers that deviate significantly from the expected Mendelian ratio.

Comparative analysis

The availability of orthologous coding markers (type 1 markers) is critical to studies of synteny and colinearity [15]. We identified 342 putative orthologous genes between

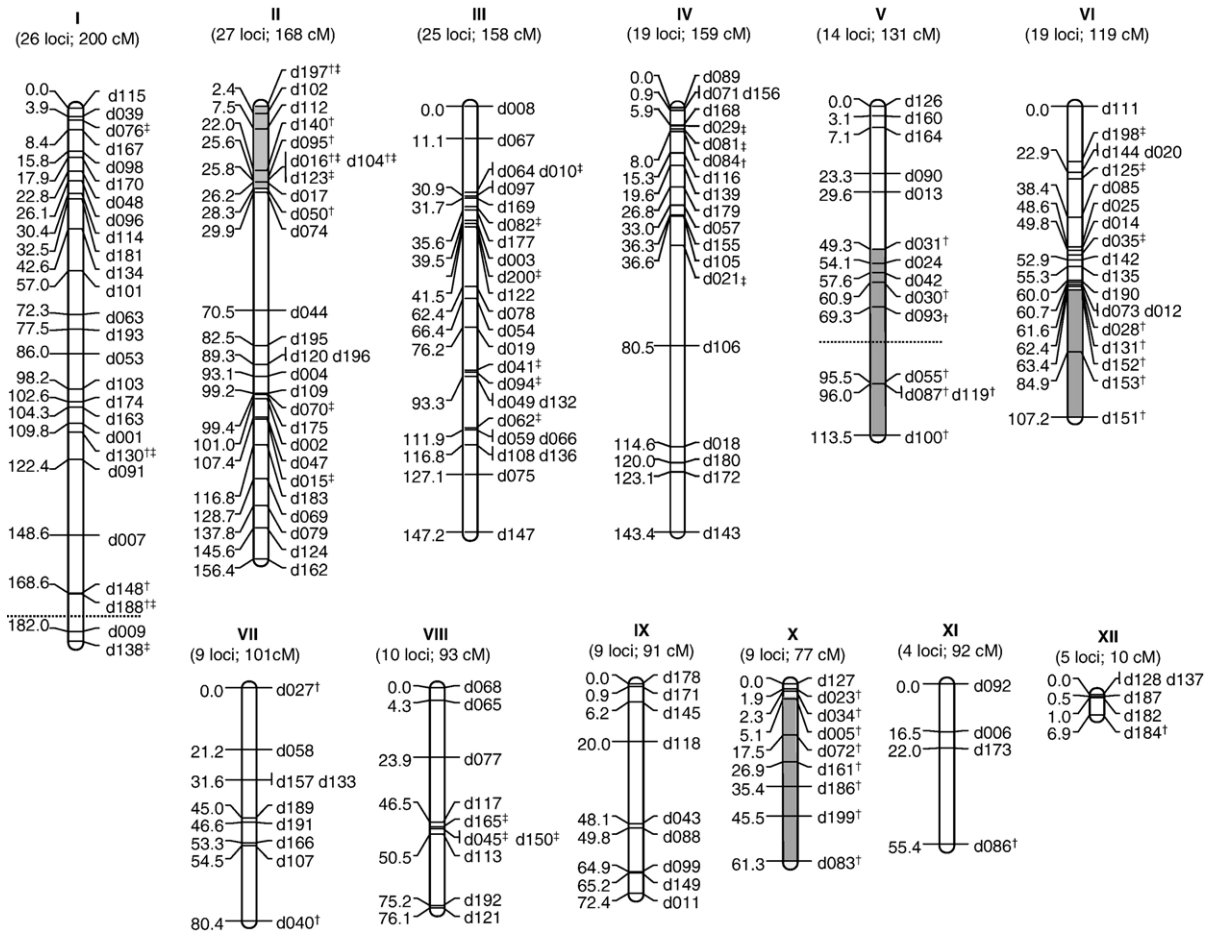


Fig. 1. Linkage map for the crustacean *D. pulex*, based on genotypes for 186 microsatellite DNA markers and two protein coding loci in 129 F_2 progeny. Numbers on the left of the map framework indicate cumulative genetic distance in centimorgans (Kosambi) between markers, while codes on the right indicate marker names as identified in Appendix A. The 12 linkage groups were arbitrarily ordered from largest to smallest and the number of loci and the corrected genetic length are indicated above every linkage group. Markers exhibiting significant deviation from expected Mendelian segregation ratio are denoted with † and corresponding regions exhibiting significant transmission ratio are shaded. Markers placed relative to the frame map at a log-likelihood threshold of 2.0 are denoted with ‡ and no distances are presented, that is, their distance from other markers is arbitrary. Markers appearing on the same line are markers that cosegregate and the order of the markers on the line is arbitrary. Horizontal interrupted lines point to specific regions of linkage groups that disassemble at a lod score greater than 6.

Daphnia and *Drosophila*. The majority (86.6%) of the genes were located within 50 kb from the closest marker, with about 5% being placed 2 kb apart from the closest marker (Fig. 2). By examining the relative map location of *Drosophila/Daphnia* pairs of genes in the two genomes we identified a lack of synteny. The contingency table analysis found no relationship between the linkage groups of the two species (likelihood ratio $\chi^2 = 25.703$; $df = 264$; $P = 0.176$). The simple cluster analysis suggests that the null model of uniform random gene order could not be rejected ($\chi^2 = 8.53$; $df = 4$; $0.1 < P < 0.05$). Therefore, we could not reject the hypothesis that the observed clusters could have occurred by chance.

Discussion

This map represents the first step toward advancing genomic studies on *Daphnia*, which will conclude with the sequence of the whole genome in assembling stage at the Joint Genome Institute.

Genetic length

The map distance spanned approximately 1206 cM and included 185 loci and 12 linkage groups. It is therefore highly likely that all 12 chromosomes have been marked, although further assignment of actual chromosomes to linkage groups will be impeded by the very difficult cytogenetics of the *Daphnia* chromosomes, which are largely morphologically indistinguishable [2,3]. Considering a genome size of approximately 184 Mb and a genetic length of 1383 cM, it can be inferred that 1 cM spans a physical distance of about 133 kb. The physical distance of one map unit in *Daphnia* is 1 order of magnitude smaller than in human or mouse [16,17] and is more comparable with other invertebrates with small genome size such as *Bombus terrestris* (~255 kb/cM) [18] and the honeybee *Apis mellifera* (~44 kb/cM) [19]. The high magnitude of recombination per physical distance we found in *Daphnia* is consistent with the observation that the intensity of recombination scales negatively with genome size [20]. This is not unexpected given that chromosome

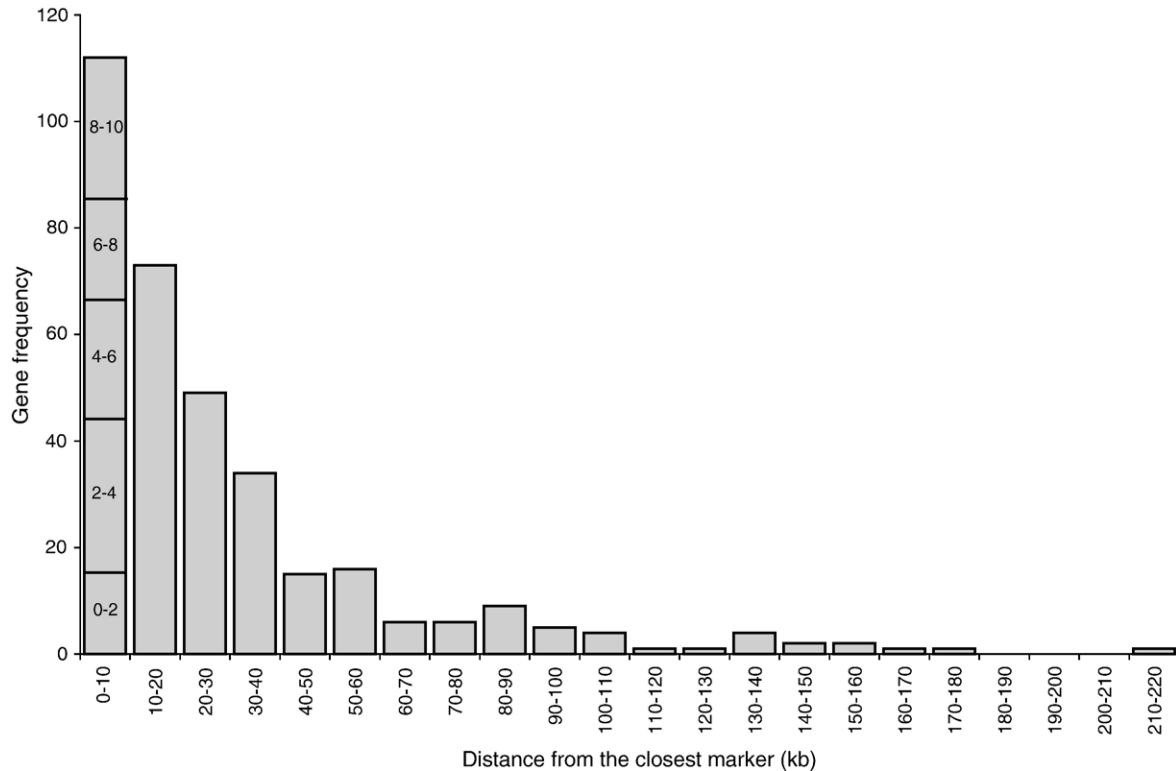


Fig. 2. Histogram of gene distribution based on distance from the closest marker.

number is not correlated with genome size and that most species experience one or two meiotic crossings over per chromosome [20].

Transmission ratio distortion

The segregation of genetic traits from parents to offspring is expected to conform to Mendel's rules. However, deviation of transmission ratios among offspring is often observed in interspecific crosses in animals and plants and occasionally in intraspecific crosses [21–23]. The mechanisms responsible for TRD are not completely understood but may result from altered chromosome segregation [24], differential viability of gametes, or differential survival of different genotypes [21]. Our tests for random segregation of alleles at individual loci revealed that 21% of the markers showed significant homozygote deficiency. These markers were clustered in four genomic regions that span between 30 and 70 cM. Since our recombinant lines experience low hatching success (~20%), low survivorship during first days of life (~30%), as well as a relatively high incidence of infertile progeny (~10%; excluded from the study) we suggest that the TRD was due mainly to the high genetic load of the parental lineages, reflected in the loss of alleles tightly linked to deleterious recessive genes or infertility recessive genes. The magnitude of inbreeding depression is in agreement with previous selfing experiments in *Daphnia pulicaria* and *Daphnia arenata* [25], *Daphnia magna* [26], and *Daphnia obtusa*

[27], which found 20–50% decrease of survivorship to maturity or egg survivorship.

Mapping crustacean genomes

The *Daphnia* linkage map serves several goals. First, the map is sufficiently dense to be used as an anchor for the construction of the physical map of the *Daphnia* genome by providing an ordered scaffold onto which “contigs” of overlapping clones can be assembled. Second, this map provides an effective tool for genetic analysis and manipulations and could be extended and used as an effective tool for identifying single loci or quantitative trait loci and for underpinning the genetic substrate of evolutionarily and ecologically significant traits such as sex determination, response to environmental stress, and reproductive isolation. Third, the map could be employed in comparative linkage mapping. Of the 183 microsatellite markers included in the map, 60 have been successfully amplified in *Daphnia* species outside the *D. pulex* complex (e.g., *D. obtusa*), and the majority of markers worked for species within the *D. pulex* complex (e.g., *D. pulicaria*, *D. melanica*). These homologous markers will make possible a comparative synteny analysis in the genus *Daphnia*. Furthermore, the enrichment of the linkage map with coding markers will enable comparative mapping with less related species for which high-density maps are available and will instigate comparative studies with other crustaceans for which full genomes remain to be characterized in the near future. The prospect of comparative genomics within Crustacea is

particularly appealing given that the subphylum Crustacea includes over 50,000 described species with immense variation in adaptations and body plans and includes many species of high economic importance. The explosive progress in the genomic field will likely transform small genomic projects that involve marine crustacean species (e.g., the blue crab *Callinectes sapidus*, the blue shrimp *Litopenaeus stylirostris*, the white shrimp *Litopenaeus vannamei*, the daggerblade grass shrimp *Palaemonetes pugio* [28]) into large-scale genome sequence projects.

Search for synteny

Comparative linkage mapping has provided evidence that genes in eukaryotic genomes are distributed nonrandomly. For example conservation of linkage relationships was found not only between closely related species of insects [29], mammals, fishes, and plants but also between different phyla. The search for residual synteny culminated with the discovery of a few ancient syntenic gene groups spanning vertebrates, invertebrates, and single-cell eukaryotic genomes [30]. In general, genome organization appears to be less conserved between distantly related species (e.g., outside of family level). As the genomes diverge progressively, the networks of synteny are often eroded by extensive gene duplication, gene loss, and horizontal gene transfer [31,32]. This degeneration of homology makes sorting between genuine remnants of ancestral gene order and simple coincidence very difficult [33]. It does not come as a surprise that our data suggest a lack of macrosynteny between *Daphnia* and *Drosophila* genomes. The estimated divergence time between Insecta and Crustacea is 666 ± 58 million years (Myr) [34], a long evolutionary history that led to an apparent randomization of gene order. Moreover, an extreme rate of internal chromosomal rearrangements of 0.9–1.4 chromosomal inversions fixed per million years was found within *Drosophila* [31]. Based on this rate, the authors suggest that for taxa that diverged more than 250 Myr ago information transferability will be useful only over

very short chromosomal distances (less than 100 kb). The full genome sequence of *Daphnia* will make possible the identification of residual synteny at a finer genomic scale.

Ecological, evolutionary, and toxicological studies on waterfleas extend back several hundred years. The advent of genomic advances will greatly accelerate traditional studies on *Daphnia* and will open the door for new genomic approaches and promote the establishment of emerging interdisciplinary research areas such as ecological genomics or toxicological genomics.

Materials and methods

Crosses

We studied the segregation of 185 polymorphic loci in 129 progeny (F_2) obtained by selfing one *D. pulex* (F_1) interclonal hybrid (Fig. 3). To obtain recombinants from animals that reproduce by cyclical parthenogenesis, we first created a panel of outbred F_1 isolates and selected one line that regularly produced males and meiotic eggs under standard laboratory conditions and whose selfed embryos required both decapsulation of ephippia and strong stimuli to resume embryo development. The selected F_1 hybrid was clonally propagated within 10-L aquaria at 20°C under a 14 h light:10 h dark photoperiod. These populations were maintained at densities of approximately 1 individual per 5 ml of filtered lake water by feeding a concentrated monoculture of green algae (*Scenedesmus obliquus*). Under these conditions, *Daphnia* sexually produced resting eggs (ephippia), which were collected and decapsulated. The obtained embryos were incubated for a week in the dark at 5°C and then transferred to a 12 h light: 12 h dark photoperiod at 15°C to stimulate the breaking of diapause. In all, 129 progeny (F_2) were reared to maturity and individually cultured in 250-ml beakers.

Genomic DNA extraction

Total genomic DNA was extracted using a CTAB extraction method [35]. Whole adult individuals were ground with a plastic pestle in a microcentrifuge tube in CTAB DNA extraction buffer. Microcentrifuge tubes were placed in a water bath at 65°C for 1 h. The chloroform/isoamyl alcohol (24/1) extractions were followed by DNA precipitation, 70% ethanol washing, pellet drying, and DNA resuspension. Samples that had a low amount of tissue were extracted with a ProK extraction protocol [36].

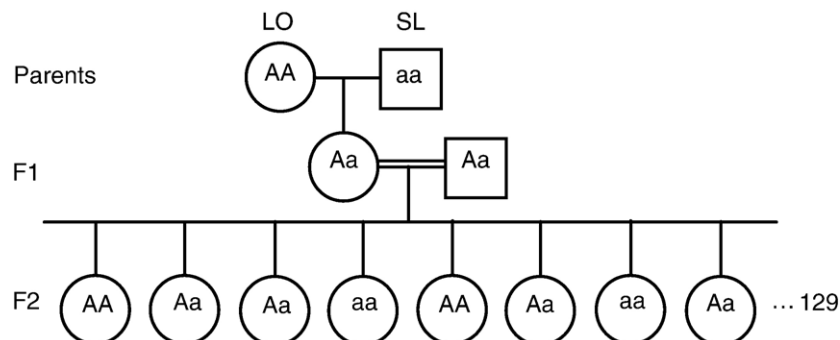


Fig. 3. Crosses performed to obtain segregated progeny for map construction. To obtain a heterozygous F_1 lineage, crosses were conducted with parental lineages of *D. pulex* (*arenata*) from two Pacific coastal ponds in Oregon (LO and SL) that showed marked genetic differentiation when screened at allozyme and microsatellite loci [50]. The recombinant F_2 progeny were obtained by selfing the F_1 hybrid.

Microsatellite markers and genotyping

The majority of the microsatellite markers consisted of simple or complex di- and trinucleotide repeats. Two additional markers consisted of protein-coding loci that show allelic length variation of more than 2 bases at one intron region. Primers were designed either by Colbourne and colleagues [37] or were created during this study using the programs Primer3 [38] and MicrosatDesign [39] and trace files obtained by the *Daphnia* Genome Sequencing Project (Appendix A). We employed the M13(-21) primer genotyping protocol [40]. The forward, sequence-specific primers were 5' extended with the M13(-21) oligonucleotide. The polymerase chain reactions (PCR) were performed in 12- μ l reactions with 10 ng of DNA template, 1 \times PCR buffer with 25 nmol of Mg²⁺, 0.5 units of *Taq* polymerase, 2.5 nmol of each dNTP, 1 pmol of the forward primer, 2 pmol of the reverse primer, and 2 pmol of the universal fluorescence-labeled M13(-21) primer. To reduce nonspecific amplification, we used a touchdown PCR. Thermal cycle programs included an initial denaturation step of 3 min at 95°C followed by 10 cycles of 35 s denaturation at 94°C, 35 s at final annealing temperature + 10°C (the annealing temperature was decreased by 1°C every cycle during each of the 9 following cycles), 45 s extension at 72°C followed by 30 cycles of 35 s denaturation at 94°C, 35 s annealing temperature at 48°C, and 45 s extension at 72°C, with a final extension at 72°C for 10 min. The amplified products were diluted 40- to 60-fold and combined in groups of four to six according to their size and fluorescent labels (NED, PET, FAM, VIC). Two microliters of the diluted PCR product was then mixed with 8.9 μ l of H₂O and 0.1 μ l of GeneScan-500 LIZ size standard (Applied Biosystems, Foster City, CA, USA). Samples were denatured for 5 min at 90°C, quickly cooled on ice, and genotyped using an ABI 3730 and GeneMapper software v3.0 (Applied Biosystems). One allele from each amplified locus was subsequently sequenced, to verify that the microsatellite DNA corresponded to the expected type of repeat. Sequences obtained in this study have been deposited with GenBank (Accession Nos. DQ249348–DQ249470).

Linkage analysis

To assemble linkage groups by maximum-likelihood we used MapMaker/Exp v3.00 [41]. Genotype data were entered in both phases to satisfy the requirements of the software (the absence of phase information does not impact the results of the software). All markers were tested for significant deviation from Mendelian segregation using a χ^2 test ($\alpha = 0.01$). Markers that showed significant TRD were double checked for genotyping errors and reliability. Marker clusters were initially identified using a LOD of 4 and after excluding TRD markers. To minimize the number of false linkage groups, the stability of each linkage group was further tested by gradually increasing the lod score to 8. For example, two large groups supported by LOD 4 were subsequently broken up by increasing the minimum LOD to 5 and 6, respectively. The most likely order of markers in each linkage group with nine or fewer markers was determined by calculating the maximum-likelihood map, and the corresponding map's likelihood for each possible order of markers using the "compare" command. For all other linkage groups with more than nine markers, the "order" command was used to obtain the sequence of markers with unique placement with the criteria for finding highly informative markers set to 4 maximum distance, 100 minimum individuals. The "try" command was used to determine the most likely placement of the orphaned markers, and subsequent orders were tested using the "ripple" command with "error detection" and "use three point" options enabled. The distances between neighboring markers were calculated using the multipoint analysis implemented in the "map" command. The Kosambi mapping function that incorporates the possibility of crossover interference was used to convert recombination frequencies into map distances [42]. The linkage map was drawn using MapChart software [43].

Dealing with genotyping errors

Since even small fractions of genotyping errors can artificially increase the total length and influence the marker order of the map, we employed

several different approaches to estimate and minimize genotyping errors. For example, 15 randomly chosen markers and six F₂ progeny were sequenced and genotyped twice. Based on the duplicated data, we estimated an average genotyping error to be less than 1%. The genotyping data were scored independently by two persons, and differences were compared and resolved. In general, discrepant data points were left as unscored. Moreover, the data were analyzed with the "error detection" algorithm enabled, and genotypes with LOD-error values of about 1.0 or greater were considered candidate mistyping errors [44] and were double checked.

Genome size and coverage

To calculate an estimate of the total map length (G_i) for the genome, we used the methods of Fishman and colleagues [11] and Chakravarti and colleagues [12]. These estimates were subsequently averaged and used to estimate the expected distance of a gene from the closest of n random markers, $E(m)$ [45,46].

Sequence comparisons between *Daphnia* and *Drosophila*

As a first attempt to identify conserved chromosomal regions between crustacean and insect genomes, we mapped the locations of putative *Drosophila* orthologous genes onto the *Daphnia* genetic map by first annotating the available genome sequence assembly provided by H. Shapiro and the Joint Genome Institute. This preliminary assembly—at the halfway point of the *Daphnia* Genome Sequencing Project—consisted of 3804 scaffolds (23,428 contigs) with a total length of 184 Mb. The length weighted average of the scaffold sizes (N50) was 776.2 kb. Putative *Daphnia* genes were identified by aligning the *Drosophila* proteome to the scaffolds using the tBLASTn program [47], with a grid-aware version of the NCBI software developed by P. Wang at Indiana University, implemented on the TeraGrid (<http://www.teragrid.org/>). This analysis was performed and archived by Don Gilbert at wFleaBase [48]. We required that a protein show a significant similarity (cutoff of E was 10^{-10}) to be considered an ortholog. We next positioned the microsatellite markers relative to the annotated genes using the BLASTn program on a local computer. For each of the markers mapped onto scaffolds, we then extracted the gene identities for the two best, nonoverlapping, matches to fly proteins flanking the microsatellite, for a maximum of four positioned genes. The relative placements of these genes on the *Daphnia* linkage groups and *Drosophila* chromosomes were compared to identify broad-scale syntenic relationship between the two genomes. First, we used a contingency table analysis to test for associations at the linkage group level between the two genomes. Test of significance were performed by a likelihood ratio χ^2 test in JMP IN 5.1 [49]. Second, we conducted simple cluster probabilities. We calculated the probability of finding a cluster association between genes linked to a particular marker in the focal species (*Daphnia*) and their orthologs in the reference genome (*Drosophila*) under the model of random gene order.

Acknowledgments

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Appendix A. List of primers used in the study

Accession Nos. AYxxxxxx correspond to primers developed by Colbourne and colleagues [37], while Accession Nos. DQxxxxxx correspond to primers developed during this study.

Pr. code	Primer name	LG	Accession no.	Allele size	Left primer	Right primer
d001	Dp149	I	AY619162	457/462	ACACAGACCCGCCATCCATT	ACATGTGCCGGACTCGTGAT
d002	Dp321	II	AY619341	253/263	ACTCCAGATCGAGGTGTTGG	TAGCGAGAGGCGAAGAAGAG
d003	Dp24	III	AY619034	209/213	TGGCGGGCGGAATAGTTTG	ACTTTCCGACCGGTTTCTTCTTG
d004	Dp28	II	AY619038	379/387	GAAGGCGAAACATAAATAAACAC	AACCCCGCGTGAATCC
d005	Dp463	X	AY619486	302/307	TCGCCGATGAAAATACTCC	CAGCAAATAAGCCCGTGTG
d006	Dp70	XI	AY619081	272/278	ATGGGGCGGAATCAATCAC	GAGGCGCATCGGCTAAAAAG
d007	Dp74	I	AY619085	358/362	TGCGCCGCGATGTTTTCC	TGCGACCGACTTATGAACCAACTG
d008	Dp1498	III	DQ249470	215/241	CACGATACGGCGATTTTGT	TCAAAACGGCAACATGGAGA
d009	Dp48	I	AY619059	361/364	TCAATCCCATCATCCCATC	CCGCATCAATATCTTTTTCTG
d010	Dp71	III	AY619082	155/164	CGCGCAACTCTTCTATTATAC	AACGACCAGGCGCTCTAC
d011	Dp123	IX	AY619135	257/271	GGCATCCTCCAGTAATTGA	TTAGCCAGCCCTCAGAAAAA
d012	Dp146	VI	AY619159	388/393	GCATTGCAGGTGGCATTTC	ATGCCAAGCTTCCCCTCCA
d013	Dp91	V	AY619102	316/319	CGTACCGCAAGAGGATAGGA	ATCTCTCCCGAAAGGAAGA
d014	Dp126	VI	AY619138	173/178	TGCGTGAATCCGTATATTGA	TCGATTGGGATCCAGCCAGT
d015	Dp147	II	AY619160	429/433	AGAGGGAGACCCGCTTCGTT	ACAGCTCCGCCAAACAAACA
d016	Dp339	II	AY619359	174/178	CGCTCCCTCCGTCTATTCT	CCCAGCGTGTGACATCTCAAT
d017	Dp62	II		503/538	AGCAAATGGGGTGACTCG	ATGGCGTGAATAAAGAATGTT
d018	Dp143	IV	AY619156	376/388	CTCAGCAACAGGACCGTTG	ACCTGGAACCTGCAATGACG
d019	Dp337	III	AY619357	156/158	GGTACCTCTCTTCGCTCTCCTC	ACAAGTCGTGCGCATTTCCAATC
d020	Dp170	VI	AY619183	273/285	TTGTTGTCGGAAACGATGACG	ACCACCGGGGACAAGAGAA
d021	Dp295	IV	AY619313	212/216	CCGCGCTCTAACCGCTAAAT	GAGAAATCCTCCCGTTTGGG
d023	Dp460	X	AY619483	296/300	GCCAAAAGCCCAAGGTAAGG	GAGCGATGTACACGCACGAG
d024	Dp231	V	AY619247	232/235	CCCAAAACGATTGTAATAAATAAAGA	GACACGGCGGAGATGAAATC
d025	Dp298	VI	AY619316	347/352	TGCTGCTTCTTTTTGGGCAT	GGCCGACAGCCCTTATATCC
d026	Dp1486	Unlk	DQ249461	270/292	GTCAACGATCGAATCGGACT	TGACCCGAGGAAATAAATC
d027	Dp156	VII	AY619169	153/156	TATTGCCGGTTCGTCAGTCT	GATGCGCCAACAGCATATCA
d028	Dp385	VI	AY619408	318/320	CCTGTTTACCTAGCCCACG	CTTTTGCTTATGCCCTCCCC
d029	Dp430	IV	AY619453	198/203	AGAGTGGGCGAACGAACAAA	CGGAGAAAAACACGGACGAAG
d030	Dp319	V	AY619339	191/196	GGCCCCAGCAGTTCCTTATT	CATCATGGCATCAGCCAAAA
d031	Dp240	V	AY619257	266/268	CGCGAATACCCCTCTTTGTG	GTGCATTTCCCCTTTGGATGA
d033	Dp421	Unlk	AY619444	288/291	GCTCGACACACCGGTTAAGG	ACCCCAAAAATATGCTGCCA
d034	Dp304	X	AY619322	379/384	CGGCGTGCCAGGAGATCTAT	CCCAACCGCGATTATGCAAT
d035	Dp475	VI	AY619498	262/265	CGTAAATAAACCGAGGCGCA	GCTCAAATGGAGAAATGGCG
d039	Dp40	I	AY619051	404/409	CTATACAGCGGCTTCGGCAC	TGGCTGCTGCGATATCAAAA
d040	Dp1489	VII	DQ249462	169/174	TCAACACAACGGATTTGAA	ATTGTGCTGGGAGCTAGGTT
d041	Dp137	III	AY619149	232/234	AGCAAACGACGCAGCAAAAAT	TGCAAGGTATTCACGCGCA
d042	Dp208	V	AY619223	341/358	GGGACCGGACATGTGTTGT	ACCCCTCACAGCCCTTCTGT
d043	Dp330	IX	AY619350	152/156	GGGTTTTGGAGGCGAACTCT	AGTGTGTCCAGCCGCAACT
d044	Dp1494	II	DQ249466	343/346	CCACTCTGCGGAAATGAAC	TCACAGTTGTGATGGACGGC
d045	Dp1493	VIII	DQ249465	312/314	ACACAACCATCCGGCATCTT	CGAGCGAATAAGCGGTCTG
d047	Dp395	II	AY619418	224/225	GGAGACCAAAACCATGCTG	TCAATGCGAAATTCGAGACG
d048	Dp199	I	AY619214	316/320	ATTTCCCTGGGACGCTTGT	TCGATTGGCTTTGATCGCTT
d049	Dp144	III	AY619157	235/239	ATTGTTGTTTTCGTCGGAGG	AAAAGGGCGGAGTGTGTTGA
d050	Dp1491	II	DQ249464	184/187	GTAACGTGCGTGCATGTGTG	CGAAAAATACCGCAACGCTC
d051	Dp193	Unlk	AY619207	183/188	ACTCGACGGGAGCAGAATGA	AACCACAGCCGCTCAACTTC
d053	Dp300	I	AY619318	324/326	GTGGCGACTCTCTGCATT	CACCAGACTCTCGTTCGCT
d054	Dp115	III	AY619127	281/284	CGGACGTGTCAATGAACGAA	CGGTCGTAATCAACTCCGC
d055	Dp21	V	AY619031	238/242	GACGGAATTCATAGAGAGAAAAATG	GACACGGGAAGCGTTTGAAG
d057	Dp78	IV	AY619089	463/466	GCTGCAAAAGCGGAAAAATTG	ACCGGCTGGGTCAAACCTT
d058	Dp112	VII	AY619124	356/359	TTTGCCATTTTAGCGGTTG	CCTGCGAGGGTCAATATCCA
d059	Dp196	III	AY619210	268/275	CCAGCAGACGAGCCAAATTC	CGGAAGCTTGGGATTCCTT
d061	Dp1487	VI*		359/379	CCTCTTTGGCTCTGATTCG	GGCGACGTGTTGAGTTTCT
d062	Dp111	III	AY619123	443/457	TCTATTGAACGACCGAGACG	CGTGAGGTGGAACCAAAAAT
d063	Dp1495	I	DQ249467	420/426	GAAACTGGCTTGCAGCTGAT	ATTTCCATGGTGGCCATAA
d064	Dp1490	III	DQ249463	176/182	CAGCTGGTCCCCAAACCATATA	ACACCGGGGGAGATTACACC
d065	Dp142	VIII	AY619155	357/362	GCGACTTGACCAACAGAA	GGGAGATCGTGAGCGAACCT
d066	Dp1492	III		336/343	TGATGCGGGTCTCGAGTTTT	CCAGCAGACGAGCCAAATTC
d067	Dp308	III	AY619327	231/237	GTGACGATGTCCGCACCTTT	TCCGTCTTCTCCTCACGACG
d068	Dp53	VIII	AY619064	352/356	CGGTAGACGGCCAACAAGTC	GCTAAATTTCTCCGCTGGC

(continued on next page)

Appendix A (continued)

Pr. code	Primer name	LG	Accession no.	Allele size	Left primer	Right primer
d069	Dp224	II	AY619240	268/272	TCTCTGCCACCCCAACAAAT	TCATCACCGGTACATCGCAG
d070	Dp325	II	AY619345	184/192	GCACCGAAAAACCAATCAAA	TTTGTCCGCACCCATATTCC
d071	Dp311	IV	AY619331	134/136	TCCACCTCCTTCTCACC	GCGCGGCAGTAAAATAATC
d072	Dp1496	X	DQ249468	156/159	CCCATCTCACACCAGCAACA	AAAAGGCTGGTCCCATTGT
d073	Dp361	VI	AY619383	313/323	GGCGGCAACATCCTAAAGTAA	CCTGCTTCCAGTCCAAAACG
d074	Dp389	II	AY619412	129/133	GCGAAGAAAAGCTGGTGGTG	TCCATGGGAAAATCACTGCC
d075	Dp530	III	DQ249359	155/161	TCCTGTCAATTTCCCAAGAG	GCTGGAGATGGGTACTCAT
d076	Dp564	I	DQ249441	256/265	TGGGAGGATCGATAAAAACG	AACCGATCACGTAAGTTGGC
d077	Dp559	VIII	DQ249443	231/241	TGTGGAACAGATGGCGACTA	CACTCTCAACGATCCAAGCA
d078	Dp616	III	DQ249382	189/199	CGGAAACTTGTGAGTGGGTT	GACGGTTCATTTGCTGATT
d079	Dp557	II	DQ249361	156/163	GCTCTGTTCTCTGGGCAAAAC	TCAAACCAGCAACAGCAAG
d081	Dp605	IV	DQ249406	288/295	AGTCCGGAATTGACACCATC	CGAAAATTTCTCCCTCTCTC
d082	Dp581	III	DQ249391	323/327	AACTCAATTCGGAATCACGG	CCCACCGATTTTGTGTTTC
d083	Dp641	X	DQ249429	290/294	TTTTTCTCCGTGCTTTGGG	AGCTCATTTTGTGATGCGC
d084	Dp687	IV	DQ249455	208/211	AAAAACGGCCAAGAAAAGG	CACTCCACGGGAGAAGGATA
d085	Dp642	VI	DQ249364	318/320	CCGGGATATGAATGTTTCTCA	GACGACTGCTGATACAGGA
d086	Dp693	XI	DQ249353	164/176	AACAGATTTGTTGACGGGG	AGGAAAACCTGACCCGGAT
d087	Dp648	V	DQ249387	328/337	GGAAATGAAAAATGGGACGA	GATCCCTTAAGTCACCGTA
d088	Dp660	IX	DQ249372	124/129	TTTCAACAATCTTTGGCTG	TGCTGCGTGTGTTTATGTGA
d089	Dp675	IV	DQ249413	279/287	CGCGACATGACTCAAAACAC	TATAGTGCAGCTTTGTGCCG
d090	Dp11/87	V		233/236	GAGGGATTTGTGTAGGTGC	ATGAGCCAAAAGAGCTGC
d091	Dp655	I	DQ249403	262/271	CGTACTAGGCCACTTTTCGCT	ATTTCCCGAATCCTATCCG
d092	Dp808	XI	DQ249447	216/223	TGTTGTTGCATGACGAATCC	ACTGAGAGCAATGCCGAATC
d093	Dp721	V	DQ249408	236/244	TGAAATGATGATGTCGTCGC	CGAGCAGCAATGAGATGTGT
d094	Dp770	III	DQ249438	272/283	TTTGCCGAGTACCAGTAGGG	TGCAGCATATCCATCTCAGC
d095	Dp785	II	DQ249374	189/195	CAGAATCCTTTGCTTTTCGC	GCCACCCTTTAATAAGCCG
d096	Dp571	I	DQ249456	166/168	CTGGAGAGCGTCTGCTACT	CAAAACCTCCCTCAAGTCA
d097	Dp572	III	DQ249369	126/130	CGCTTGGAAAGAAAAGAAACG	AGTCCGGAGAAAAGGATGGAT
d098	Dp589	I	DQ249385	236/241	AAAAGGCCAGTCGAAATCT	ACTCCCTCGACTTCTGACCA
d099	Dp609	IX	DQ249442	250/285	CCCATCGGTTGTGTAGGTTT	CTTGTGGTCTTGTTCGGTT
d100	Dp775	V	DQ249394	141/148	GTAGCGTTGGTTGCTCATCA	ACCTGCAAAAAGACCCACATC
d101	Dp802	I	DQ249363	124/129	AGTGATGGGCTCCTTTGATG	CTCTTCCCTCGATCAGTTGC
d102	Dp725	II	DQ249418	261/264	ATCAGCATTACAGCACACAGC	CTTTTACAGAAATGCGACAA
d103	Dp729	I	DQ249439	134/138	GGCCAATAACAGCCGAAATA	AGTGAAGAAGACGACGCCAG
d104	Dp742	II	DQ249421	236/242	TGTATATCGCCGTGTGATGG	ATGTGTCTGTGCGTGCATG
d105	Dp779	IV	DQ249405	145/149	TTTACCCTTAGCTGACCCGC	TGCGTGTTTGGGTGTCTTA
d106	Dp830	IV	DQ249414	300/308	TGCTAATCATGTGGGCGATA	ATCAGCATTACGTCTGTGCTG
d107	Dp867	VII	DQ249426	218/224	TCGTGAGTGAGGTAAGTGCG	CCCGTCATCAAAGGAGAAA
d108	Dp813	III	DQ249404	240/252	GGGGTCCCTCGGTCAATATT	GGGTAATTACGACCCGTGTG
d109	Dp821	II	DQ249440	304/307	GCACACAACCAACACAAAAA	GACCTCAGCAATATAGCCCG
d111	Dp907	VI	DQ249409	268/288	CGCACACAGCGAAGGTAAT	GTCATCGTTGCTGTGTTGAC
d112	Dp848	II	DQ249400	175/181	TTTATCGCATTTTATGGGGC	ACAAGTTTCAAGAGCCACG
d113	Dp883	VIII	DQ249366	251/255	CCCCTTTTGTCTTTGTGTGT	CCTCCTGGTCCGATTACAGA
d114	Dp884	I	DQ249351	219/223	TCTGTGAAAACCTCTCGGCT	CACCTACCGGCTGAAATTGT
d115	Dp840	I	DQ249401	272/278	CATGCCGGTAAACGTCTCTT	GATTGCGAGTAGTTGCCAT
d116	Dp878	IV	DQ249355	317/323	ACGGAAAACAAGCCATTCTG	ACGACACAATGGGTCTAGC
d117	Dp887	VIII	DQ249362	220/227	TCATAGTCACAACGGCTCA	CACGCTTTCATTTCCAGGCT
d118	Dp621	IX	DQ249444	119/124	ACTCGACACAACCGGAAAAGT	AAAGGGAGGAGCTGAAATCC
d119	Dp632	V	DQ249420	287/289	ATGTCAGCCGAAAAGGCTA	GTCAAAGGGAAGATGACCGA
d120	Dp637	II	DQ249457	234/238	CAAAGATCCGAAAAGAACC	AGCAAGCCCCCTCTACTC
d121	Dp1485	VIII	DQ249460	397/416	TAGTTGTTGGCTTGCAGATG	CTTTAATAACAGGGTAGTATGC
d122	Dp50	III	AY619061	204/211	CGGTCAACAGCGATAAATG	AGTCCGATGATGCCACTG
d123	Dp1497	II	DQ249469	306/312	TCTCTTTCCCGTGTTC	CCTGCGAAATAGCAACCTG
d124	Dp117	II	AY619129	236/240	CGAAAAGAAGAAACGGCAGTC	AGGTCCTTCGTGACTCGTCT
d125	Dp815	VI	DQ249384	291/295	TCGCGTTTCAATCTCTTG	CAGGACCATAAAGTCCCGAA
d126	Dp838	V	DQ249396	256/259	TTGGCTCCTTCAAAATTC	ACACCGTGACCTTTTCGTTT
d127	Dp696	X	DQ249448	306/327	CGTGGCATTCTGTGAAGTA	CGTGAAGCAACAGAGGGAAT
d128	Dp726	XII	DQ249424	229/233	GAAAACGCTGCCAGAGAGAT	GAGGAGGAAAACGGGAGAAAC
d129	Dp746	II*	DQ249436	165/172	CCCATCATCTGTCGGTTTTT	CTTGTGTGATCGCTAGT
d130	Dp754	I	DQ249452	279/299	CTCAGGAGCTGTGGCTAAC	AGCACAAATATCTGACCCCG
d131	Dp612	VI	DQ249459	240/254	TATCGCATTATCCATTCGCA	ATAAGACCGTGACGATTCCG
d132	Dp895	III	DQ249454	258/263	ATTTGTTTTCGTGGGGTCTG	GCAAAGGCGAGAAAGAGAGA
d133	Dp786	VII	DQ249431	140/144	CCTATTTGCATCGTCCGTTT	GGCTTGGATGAACGTCAAAT
d134	Dp553	I	DQ249383	197/202	ATTGGTGAATGAGTCGAGC	GGCATGCCGTTACAAATTCT
d135	Dp985	VI	DQ249349	251/254	GCACTGCTCCTCTCCTCCTA	CGGGCGACAAACGATATAAT

Appendix A (continued)

Pr. code	Primer name	LG	Accession no.	Allele size	Left primer	Right primer
d136	Dp998	III	DQ249350	251/260	AGGTGCAATTACCGATCCAG	CAGCAGAAGGTGGAATGACA
d137	Dp936	XII	DQ249392	183/190	GCCAGGTCAGAAAATTGGAA	AGAGACGCCAAAAGTGAAGGA
d138	Dp957	I	DQ249399	310/313	ATTCTTTTGCCCCCTTTGAC	TGCTACCCGGGTTAAGAAGA
d139	Dp924	IV	DQ249419	133/140	GCAACCAGAAAAGGGAGAGTG	TCCAAATCTCCACCAACAGA
d140	Dp967	II	DQ249377	269/272	CTCGTCCAGCTCTCTGCTCT	CCTACGATAACAGGCCGAAA
d142	Dp1040	VI	DQ249370	176/180	CTGGCTCATCCACTCACTCA	TCCTCTATGCACACTGGTGG
d143	Dp1148	IV	DQ249453	325/333	AAAAGGGAAACGTTTCGAGGT	GGACGTTTCGAGAAAAGAG
d144	Dp1232	VI	DQ249380	296/304	TATGCACGCGTATCCTTGAA	GCGTCTTCTTCCGCTTATG
d145	Dp1325	IX	DQ249437	272/277	CCTGTAGGGAAAACACCCAA	ACAGCAGAGCACAGCACATC
d146	Dp1397	Unlk	DQ249433	196/113	TCGACAACATAACAACGCC	ATTTGAATTTTGCTGCCGAC
d147	Dp1041	III	DQ249371	286/292	GCACAGTCAGGAATGGGATT	TGATTCCACAAAGCCAACAA
d148	Dp1155	I	DQ249427	221/229	CGAGCACACGTTCTTTCTCA	CGCACGTTAATCACCGAATA
d149	Dp1236	IX	DQ249375	195/197	TATCGATCCCACCTTACGGC	CTGGCCACCATCAGACTTTT
d150	Dp1160	VIII	DQ249395	193/195	CGCTCTGCTTAATACGGTCC	AATGTCCCCCATGCATTA
d151	Dp1238	VI	DQ249348	266/269	TTCATAGGGGGTGAGACTGC	GGGTGACGCAAAAAGAAAGAG
d152	Dp1327	VI	DQ249445	299/301	TTGACCTCTATCCCCACTC	AGTCCAGCCACACAGGTAG
d153	Dp1350	VI	DQ249389	239/247	CGAAGCGGTGGAGAAAAATA	ACCAGTCCGAGATTTATGCG
d154	Dp1059	VI*	DQ249402	251/257	TGTGTCTGGGCTACCAACTG	TGAAGAAAACCCGGAGACGAC
d155	Dp1185	IV	DQ249354	199/201	TAATAATGGACCCTACGGGA	GGAAATGTCCGTCCTTTCA
d156	Dp1311	IV	DQ249390	217/223	ATCCCGTTTTGCTTCTCTCA	TATCTTCATCCATCTCCGC
d157	Dp1328	VII	DQ249446	243/251	ATTTTCGATGGTGAAGACGG	CAGTGTCCACAAGTGTCCG
d158	Dp1338	II*	DQ249415	299/302	TCTCTGCGGATGACACACTC	CGATGAATTGACGACGTGAC
d159	Dp1050	Unlk	DQ249434	215/217	GACCCTGGCTGTGCTGTAAT	CGCATGCAGTAATGGAGCTA
d160	Dp1123	V	DQ249410	156/158	GACGCGGTCAACCTGTTC	CTCATCCGCTGTCTCATTA
d161	Dp1302	X	DQ249358	210/214	TTTGTATCCTCGCGTAAAGG	TTCTATTCCAAATGGTCCG
d162	Dp1346	II	DQ249381	260/268	GCTTCGGTACACGACCAAT	ACTGTTTCGGTTGCTTCGAGT
d163	Dp1368	I	DQ249356	199/201	ACACGTTCCGCGAATCTAAC	GATGTGATGACCAACAACGG
d164	Dp1262	V	DQ249451	211/220	TCTCGACGAGGTGTTGACAG	TGGCCAGTAGAAAATGTTG
d165	Dp1404	VIII	DQ249450	190/202	GCCAGTAATTGAGCCTCCAG	CCGTTTCTGTCCAAAAGGAA
d166	Dp1300	VII	DQ249352	259/273	GGCGTTTGAATTAACCGAGA	CAAAGTGCCTGTCCACTCA
d167	Dp1354	I	DQ249398	232/251	AGCTTACCAAGGCAAAAGAA	GCTTGTGTTGCTGTTGTA
d168	Dp1372	IV	DQ249368	292/296	GCCTTTGAGAGAAGATCGGA	CCTTGAGGCAAATGAAAA
d169	Dp1058	III	DQ249393	194/198	AATCAATGAAATCCACGCC	CCATGACCATAAGTGGGTCC
d170	Dp1290	I	DQ249432	275/278	ACATTCCGAGGGTTCATGAAG	GGAGCCAGTTGAGAGCAAAG
d171	Dp1309	IX	DQ249360	213/219	AAGGACGACATCTGGCAATC	AATCGATCAGAACCAGCACCC
d172	Dp1396	IV	DQ249430	307/313	GTCTGCTGACCCAATTGCT	GCCGTAAAGGTTATACGCGA
d173	Dp1112	XI	DQ249388	259/282	CCACCAACCGACGCTATAAT	CGAACGACAAGCGAGTGATA
d174	Dp1266	I	DQ249386	137/140	CTCAAGGCTCACAGAGGAC	GGTCTCTCAAGTCGACCAGC
d175	Dp1363	II	DQ249407	259/261	CAATATTCGTCTTCTCCGC	AATGTGTCAATGCACAACAT
d177	Dp1276	III	DQ249357	289/294	TCACGCCACAAGATGTAAA	TCCTTCTGCTGCCGCTATT
d178	Dp1278	IX	DQ249376	255/259	CACGTGACCGTTGTTTGGAC	GTCTACATACAAGGGCGGGA
d179	Dp1376	IV	DQ249378	307/309	CCCTACACCCTACATGTCC	TAAGTTATCCGGTCCGATGC
d180	Dp1409	IV	DQ249435	199/206	ACGAGCTGCAGGTCAGAGAT	GCGTGTGTGTACCGGTGTAG
d181	Dp1073	I	DQ249367	209/214	CGGGCCAATACTTATGTCGT	GATGTGCCATCAGTTGAACG
d182	Dp1144	XII	DQ249423	304/316	GACTTGAACGAGTCTTGCCC	ACCTACGCCTGGTCAACAC
d183	Dp1056	II	DQ249412	302/304	ACGTCCAGTTTGCCTCAATC	GGATGACTAAATCCGCTCCA
d184	Dp1079	XII	DQ249422	212/215	TTCTAGCTAACCCGACGGTG	TCCGAGAGAGAAAACACACG
d186	Dp1057	X	DQ249416	313/316	GCAAAACCCCTACAAAACA	TACCCCAACCAAGAGATTCA
d187	Dp1080	XII	DQ249425	208/212	GTCGACGAGATGGGAATGTT	CGAAAATCCAGGAAATCAA
d188	Dp1195	I	DQ249379	151/162	GTGAACCAACCGAGACAGT	CCGGGGAATCAATGTTACAC
d189	Dp1347	VII	DQ249417	343/347	CCAACAGTGGAAAAGCCATT	CACGCAGAAAAGACATTCAA
d190	Dp1399	VI	DQ249449	272/277	TGCCATATATGTTGCTTGCG	AGGAAAGAGACAGACTGGCG
d191	Dp1391	VII	DQ249428	306/319	ATAGCCACCGGTGTAGATGG	ACGTAAGAAAGGGGATACGCA
d192	Dp1351	VIII	DQ249397	226/244	CAGACGCCATTTAGGAGGAG	GGCCGAGTTGCTTGTGTTT
d193	Dp1189	I	DQ249365	278/289	AATTTTCGATATGCTTTGGC	TTACAGTTGTGCCCTTTGA
d195	Dp969	II	DQ249373	308/312	TATCACGGACATCGTGTGGT	ATGGTTTCCCCTTTTGCTCT
d196	Dp1005	II	DQ249458	272/282	GGATTTCCCTTACCAAAA	GATTCAGCGGGAAAAATTA
d197	Dp1048	II	DQ249411	192/194	TCACCGGCTCTTTCTTTTC	CTGGACCATATGGGTTTTC
d198	AO5	VI		624/633	ATTGCTCTGGCCCTTACAAG	AACGGTCTCGGATTCTCCCT
d199	AO92	X		524/528	TCAAGTACAAAACCTCTTTCAA	CCACAATAGGTGTATTCTTGAAC
d200	P1N22	III		173/178	TCGTTATGGCAACAGTCGAG	AACTTTCCGACCGGTTTCTT

Appendix B. List of putative homologs

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d076	Dp564a	I	190.5	8E-14	78	CG32770-PA	X
	Dp564b	I	202.5	1E-12	74	CG3367-PA	X
	Dp564c	I	-17,065	7E-17	64	CG11212-PA	2R
d098	Dp589a	I	9324.5	1E-31	137	CG4427-PA	2L
	Dp589b	I	9311	1E-26	121	CG3065-PA	2R
d170	Dp1290a	I	-8936.5	4E-13	75	CG17198-PA	3R
	Dp1290b	I	-9023.5	9E-17	87	CG17197-PA	3R
d048	Dp199a	I	27,065	1E-13	77	CG14780-PA	X
	Dp199b	I	25,031.5	3E-11	70	CG31873-PA	2L
	Dp199c	I	-17,445.5	9E-20	99	CG5411-PA	2R
	Dp199d	I	-23,100	1E-38	84	CG18104-PA	X
d096	Dp571a	I	25,700.5	4E-61	237	CG10952-PA	X
	Dp571b	I	-13,319	7E-24	100	CG32532-PA	X
d114	Dp884a	I	4669	3E-37	157	CG11202-PA	X
	Dp884b	I	4706.5	8E-30	132	CG6604-PA	2L
	Dp884c	I	-5988.5	2E-53	185	CG8003-PA	3L
	Dp884d	I	-8336	2E-53	122	CG9633-PA	3R
d181	Dp1073a	I	-26,589	7E-44	127	CG3045-PA	2R
	Dp1073b	I	-59,034.5	4E-80	300	CG3896-PA	2R
d134	Dp553a	I	32,439	9E-15	80	CG17029-PA	3L
	Dp553b	I	-2393	9E-30	131	CG4637-PA	3R
	Dp553c	I	-32,572.5	3E-18	93	CG32593-PA	X
	Dp553d	I	-83,360	7E-30	132	CG8376-PA	2R
d101	Dp802a	I	15,728	0	461	CG31671-PA	2L
	Dp802b	I	-9214	2E-11	70	CG1756-PA	X
	Dp802c	I	-16,655.5	7E-27	106	CG6391-PA	3L
d063	Dp1495a	I	2553	3E-65	231	CG11949-PA	2R
	Dp1495b	I	207	5E-40	144	CG1228-PD	3L
	Dp1495c	I	-2733.5	6E-17	87	CG8441-PA	2R
	Dp1495d	I	-8001	0	752	CG3725-PB	2R
d193	Dp1189a	I	-7020.5	8E-19	95	CG5590-PA	3R
	Dp1189b	I	-16,057	5E-18	92	CG7887-PA	3R
d053	Dp300a	I	22,026	2E-44	110	CG13348-PA	2R
	Dp300b	I	-53,458	2E-36	152	CG17187-PA	3R
	Dp300c	I	-107,243	2E-105	136	CG6137-PA	2L
d163	Dp1368a	I	18,981	2E-30	106	CG7831-PA	3R
	Dp1368b	I	15,315.5	2E-47	127	CG4212-PB	2L
	Dp1368c	I	-14,648.5	2E-53	211	CG12758-PA	2R
d001	Dp149a	I	3492.5	2E-25	90	CG33041-PA	2R
	Dp149b	I	8360	3E-11	66	CG14698-PA	3R
	Dp149c	I	-82,749	7E-50	156	CG32654-PC	X
	Dp149d	I	-89,930.5	3E-37	154	CG7359-PA	X
d130	Dp754a	I	25,450	9E-43	72	CG31860-PA	2L
	Dp754b	I	20,070	3E-45	185	CG8787-PA	2R
	Dp754c	I	-18,863	2E-141	197	CG5594-PD	2R
	Dp754d	I	-61,827	4E-19	95	CG7452-PA	3L
d091	Dp655a	I	15,999	5E-72	234	CG11870-PA	3R
	Dp655b	I	15,897	1E-35	104	CG6114-PA	3L
	Dp655c	I	-5332	1E-18	91	CG8627-PA	3L
d007	Dp74a	I	64,023.5	2E-11	70	CG7420-PA	2L
	Dp74b	I	45,856.5	5E-17	90	CG5155-PA	2L
	Dp74c	I	-3672	3E-34	146	CG5069-PA	3L
	Dp74d	I	-3651	2E-52	206	CG3668-PA	2R
d148	Dp1155a	I	135,223.5	1E-36	152	CG32072-PA	3L
	Dp1155b	I	133,927	2E-61	236	CG33110-PA	3R
d188	Dp1195a	I	6819	1E-18	93	CG2108-PA	3R
	Dp1195b	I	-11,925	3E-86	171	CG9318-PA	2L
	Dp1195c	I	31,409.5	2E-82	257	CG32592-PA	X
d138	Dp957a	I	19,149.5	2E-18	72	CG10237-PB	2L
	Dp957b	I	10,729	1E-14	65	CG7231-PB	2L

Appendix B (continued)

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d197	Dp1048a	II	56,229.5	3E–66	172	CG3335-PA	3L
	Dp1048b	II	48948	0	763	CG32659-PA	X
	Dp1048c	II	–80630	8E–31	135	CG4482-PA	2L
	Dp1048d	II	–87140.5	7E–24	95	CG30077-PA	2R
d102	Dp725a	II	52270	1E–25	97	CG2968-PA	X
	Dp725b	II	42399.5	5E–27	111	CG5586-PB	3R
d112	Dp848a	II	71981	9E–11	69	CG13338-PA	2R
	Dp848b	II	–8424	1E–85	317	CG10037-PA	3L
	Dp848c	II	–8578.5	3E–50	201	CG12287-PB	2L
d140	Dp967a	II	5339	4E–133	200	CG7729-PA	3L
	Dp967b	II	–2648	7E–88	327	CG9932-PA	2L
	Dp967c	II	–11117.5	3E–32	85	CG18735-PA	2R
d095	Dp785a	II	26949	2E–36	152	CG15455-PA	X
	Dp785b	II	11729.5	6E–145	309	CG1973-PA	3R
	Dp785c	II	–39510.5	7E–57	187	CG12287-PB	2L
d104	Dp742a	II	–152051	5E–33	134	CG4896-PC	2L
	Dp742b	II	–167340	2E–68	70	CG3057-PA	2L
d123	Dp1497a	II	21739.5	9E–21	62	CG16988-PA	3L
	Dp1497b	II	108988.5	2E–22	89	CG5708-PA	2L
d044	Dp1494a	II	1273.5	6E–47	186	CG13880-PA	3L
	Dp1494b	II	–157339	6E–17	60	CG7861-PA	2R
d109	Dp821a	II	21056	6E–21	50	CG3388-PA	2R
	Dp821b	II	17434.5	5E–26	119	CG8246-PA	2R
d070	Dp325a	II	16654	2E–11	72	CG31868-PA	2L
	Dp325b	II	4725.5	3E–53	160	CG11396-PA	3L
	Dp325c	II	–12084	8E–17	88	CG32843-PA	2R
d002	Dp321a	II	–4395	8E–108	394	CG11895-PA	2R
	Dp321b	II	–12581.5	2E–38	163	CG17941-PA	2L
	Dp321c	II	–36222.5	5E–39	164	CG6977-PA	3R
d047	Dp395a	II	219974.5	9E–28	82	CG7484-PB	3L
	Dp395b	II	217175	5E–32	88	CG32486-PD	3L
d015	Dp147a	II	–147333	2E–33	143	CG5893-PA	3L
	Dp147b	II	–147333	3E–22	107	CG18024-PA	2L
d183	Dp1056a	II	15914	9E–77	114	CG2248-PA	3L
	Dp1056b	II	8665	4E–30	115	CG32296-PA	3L
	Dp1056c	II	–10642.5	2E–11	70	CG6398-PA	X
	Dp1056d	II	–17949	2E–23	70	CG7058-PA	X
d069	Dp224a	II	762.5	2E–48	195	CG7245-PA	2L
	Dp224b	II	–23129.5	4E–54	213	CG13758-PA	X
	Dp224c	II	–23321.5	6E–19	95	CG12370-PA	2R
d079	Dp557a	II	9498	7E–39	83	CG4980-PA	3R
	Dp557b	II	5901.5	4E–39	162	CG5502-PA	3R
	Dp557c	II	–3713.5	3E–22	106	CG11324-PB	2L
	Dp557d	II	–21283.5	4E–13	77	CG4096-PA	X
d124	Dp117a	II	17754	9E–53	172	CG6661-PA	3L
	Dp117b	II	10235.5	4E–86	318	CG3576-PA	X
	Dp117c	II	–94337.5	3E–49	168	CG1316-PA	3L
	Dp117d	II	–96940	2E–58	113	CG4802-PA	2R
d162	Dp1346a	II	23530.5	4E–25	71	CG14435-PA	X
	Dp1346b	II	381	1E–53	144	CG8127-PB	3L
	Dp1346c	II	–8928.5	4E–73	276	CG6502-PA	3L
	Dp1346d	II	–12343.5	2E–15	62	CG4293-PA	X
d067	Dp308a	III	–11527.5	5E–20	101	CG31772-PA	2L
	Dp308b	III	–68392	5E–41	142	CG1147-PA	3R
d010	Dp71a	III	14823.5	1E–22	107	CG8882-PA	2L
	Dp71b	III	11127.5	4E–28	125	CG12524-PA	3L
	Dp71c	III	–20793.5	5E–15	79	CG32854-PA	3R
	Dp71d	III	–21960.5	8E–26	87	CG10447-PA	2L
d097	Dp572a	III	–11633.5	7E–38	159	CG33473-PB	2R
	Dp572b	III	–11639.5	3E–26	119	CG4427-PA	2L

(continued on next page)

Appendix B (continued)

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d169	Dp1058a	III	52101	6E–19	95	CG12096-PA	X
	Dp1058b	III	9846	2E–30	103	CG8913-PA	3R
	Dp1058c	III	–5671	3E–27	124	CG8967-PA	2R
	Dp1058d	III	–27067.5	4E–80	205	CG8274-PA	2R
d082	Dp581a	III	28718	8E–18	82	CG3738-PA	2L
	Dp581b	III	–7459	1E–38	164	CG9907-PA	X
d177	Dp1276a	III	12613	5E–19	98	CG9071-PB	2R
	Dp1276b	III	2226	2E–144	515	CG9907-PA	X
	Dp1276c	III	–8114.5	2E–26	72	CG6632-PA	X
	Dp1276d	III	–18421	2E–76	138	CG11093-PA	4
d003	Dp24a	III	3262	2E–51	156	CG7293-PA	3L
	Dp24b	III	3166	3E–54	162	CG10642-PA	3L
	Dp24c	III	–68468	1E–58	192	CG13567-PA	2R
d122	Dp50a	III	39212.5	8E–44	151	CG1099-PA	2L
	Dp50b	III	4067.5	0	275	CG32096-PB	3L
	Dp50c	III	–30719	6E–139	136	CG32823-PB	X
d078	Dp616a	III	38810	1E–26	121	CG14575-PA	3L
	Dp616b	III	41379	1E–17	91	CG9918-PC	3R
	Dp616c	III	–38333	2E–18	95	CG31643-PA	2L
d019	Dp337a	III	8886	6E–70	264	CG10160-PA	3L
	Dp337b	III	–11791	4E–143	308	CG8983-PA	2R
d041	Dp137a	III	34639	9E–24	112	CG10421-PA	3R
	Dp137b	III	–6913	2E–99	367	CG7749-PA	3L
d094	Dp770a	III	6447	2E–34	148	CG31690-PA	2L
	Dp770b	III	–17856	8E–47	190	CG6445-PA	3L
	Dp770c	III	–13992	6E–22	107	CG4509-PB	3R
d049	Dp144a	III	28708.5	3E–13	52	CG5454-PA	3R
	Dp144b	III	25622.5	6E–75	201	CG30421-PA	2R
	Dp144c	III	24421	1E–19	99	CG5798-PA	3R
d108	Dp813a	III	110323	3E–107	390	CG13900-PA	3L
	Dp813b	III	9902	5E–92	341	CG1449-PA	4
d075	Dp530a	III	13177	6E–14	64	CG12943-PA	2R
	Dp530b	III	7064	8E–31	136	CG32180-PB	3L
	Dp530c	III	–75127.5	4E–44	132	CG8070-PA	2R
	Dp530d	III	–78117.5	4E–20	63	CG13533-PA	2R
d147	Dp1041a	III	3800	3E–11	62	CG3251-PA	2L
	Dp1041b	III	1565	6E–65	249	CG1951-PA	3R
	Dp1041c	III	–4048	4E–11	70	CG5053-PA	3R
d089	Dp675a	IV	–72164.5	2E–58	206	CG1810-PA	X
	Dp675b	IV	–133679	8E–21	72	CG3026-PA	X
d071	Dp311a	IV	38474.5	5E–32	125	CG14885-PA	3R
	Dp311b	IV	3023	2E–38	108	CG33135-PA	2R
	Dp311c	IV	–8461	6E–29	125	CG7301-PA	3R
d156	Dp1311a	IV	26980	3E–13	49	CG11077-PA	4
	Dp1311b	IV	18589	8E–58	156	CG13188-PA	2R
	Dp1311c	IV	–46309.5	3E–102	276	CG3011-PA	X
d168	Dp1372a	IV	24744.5	5E–43	171	CG5177-PA	2L
	Dp1372b	IV	–3219.5	3E–32	140	CG3048-PA	2L
	Dp1372c	IV	–26742.5	4E–27	123	CG31794-PA	2L
d081	Dp605a	IV	17114.5	7E–54	211	CG1434-PA	X
	Dp605b	IV	–92654	7E–15	82	CG31392-PA	3R
	Dp605c	IV	–92628.5	6E–40	165	CG3956-PA	2L
d084	Dp687a	IV	13888.5	2E–12	50	CG31251-PA	3R
	Dp687b	IV	10037.5	0	474	CG7908-PA	3R
	Dp687c	IV	–33502.5	7E–30	132	CG33227-PB	2R
d116	Dp878a	IV	79044	5E–53	124	CG9601-PA	3R
	Dp878b	IV	28568.5	1E–94	348	CG12630-PA	2L
	Dp878c	IV	–24207.5	5E–51	203	CG31612-PA	2L
	Dp878d	IV	–32396.5	0	424	CG11579-PA	X
d139	Dp924a	IV	13882	2E–24	115	CG3291-PA	X
	Dp924b	IV	8373	6E–25	115	CG7404-PB	3L
	Dp924c	IV	–16436	1E–47	98	CG12908-PB	2R

Appendix B (continued)

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d179	Dp1376a	IV	-3973	4E-58	147	CG7323-PA	3L
	Dp1376b	IV	-28672	1E-122	316	CG31729-PB	2L
d057	Dp78a	IV	38541	9E-30	89	CG8201-PA	2R
	Dp78b	IV	33408.5	9E-41	101	CG11376-PA	2L
	Dp78c	IV	-8539.5	2E-14	82	CG8949-PA	X
d155	Dp1185a	IV	40877	1E-38	162	CG31304-PA	3R
	Dp1185b	IV	-12647.5	9E-98	182	CG7913-PB	3R
	Dp1185c	IV	-11501	2E-25	94	CG32568-PA	X
d105	Dp779a	IV	13615	2E-42	124	CG7619-PA	3L
	Dp779b	IV	9052.5	3E-126	452	CG2017-PA	3R
	Dp779c	IV	-22483.5	1E-18	85	CG31842-PA	2L
	Dp779d	IV	-30722	1E-18	94	CG6530-PA	2R
d106	Dp830a	IV	8076	6E-44	138	CG10733-PA	3L
	Dp830b	IV	-7733.5	1E-29	131	CG6187-PA	2L
	Dp830c	IV	-34552.5	2E-12	56	CG8407-PA	2R
	Dp830d	IV	-36094	6E-21	71	CG9705-PA	3L
d018	Dp143a	IV	37275.5	0	233	CG2637-PA	2L
	Dp143b	IV	-126653	2E-45	71	CG11236-PA	2L
d180	Dp1409a	IV	18790	4E-31	135	CG7383-PA	3L
	Dp1409b	IV	-3003.5	9E-29	128	CG4717-PA	3L
	Dp1409c	IV	-42284.5	6E-31	93	CG5352-PA	2L
d172	Dp1396a	IV	16648	3E-92	196	CG6388-PA	2L
	Dp1396b	IV	13223.5	1E-139	218	CG7415-PC	3R
	Dp1396c	IV	-29271.5	3E-32	116	CG3756-PA	2L
d126	Dp838a	V	52613.5	5E-16	87	CG16932-PA	2R
	Dp838b	V	17672.5	0	195	CG2999-PB	4
d013	Dp91a	V	55597	4E-43	143	CG15218-PA	2L
	Dp91b	V	3088.5	4E-28	126	CG13287-PA	3L
	Dp91c	V	-5328.5	0	550	CG5033-PA	2R
	Dp91d	V	-11690	1E-27	125	CG11798-PA	2R
d031	Dp240a	V	2597.5	1E-18	95	CG32137-PB	3L
	Dp240b	V	-9348	6E-84	108	CG6969-PA	3R
	Dp240c	V	-13927.5	2E-65	123	CG5585-PA	3L
d024	Dp231a	V	35164	5E-98	205	CG9191-PA	3L
	Dp231b	V	-62561.5	6E-21	104	CG16779-PA	3R
	Dp231c	V	-137939	3E-30	100	CG9717-PA	3R
	Dp231d	V	25412	4E-14	79	CG15553-PA	3R
	Dp231e	V	3396.5	6E-40	166	CG31721-PA	2L
	Dp231f	V	-7972	2E-104	304	CG10639-PA	2L
d030	Dp319a	V	-63727	3E-17	55	CG8383-PA	3R
	Dp319b	V	-109689	1E-96	152	CG1598-PA	2R
d093	Dp721a	V	10441	1E-17	67	CG10198-PA	3R
	Dp721b	V	7425.5	1E-63	246	CG10198-PA	3R
	Dp721c	V	-33049	7E-17	89	CG31646-PA	2L
d087	Dp648a	V	34072.5	4E-18	89	CG31779-PA	2L
	Dp648b	V	-9844	3E-16	87	CG4853-PA	2R
	Dp648c	V	-28493	3E-69	198	CG7369-PA	3L
d119	Dp632a	V	85367.5	3E-61	176	CG2864-PA	X
	Dp632b	V	35435	2E-13	75	CG14469-PA	2R
	Dp632c	V	-3190	2E-72	181	CG2316-PA	4
	Dp632d	V	-18027	1E-119	163	CG2845-PA	X
d020	Dp170a	VI	47966	3E-139	310	CG10080-PA	2R
	Dp170b	VI	4888.5	5E-84	129	CG10754-PA	3L
d085	Dp642a	VI	8130	1E-38	119	CG2061-PA	X
	Dp642b	VI	-1233.5	1E-138	306	CG6335-PB	X
d025	Dp298a	VI	23948	2E-69	154	CG2827-PA	2R
	Dp298b	VI	19955.5	1E-24	102	CG8965-PA	2L
d142	Dp1040a	VI	-2428.5	7E-61	110	CG9379-PA	3R
	Dp1040b	VI	-11258	4E-28	125	CG10075-PA	3L
d135	Dp985a	VI	39883.5	9E-136	301	CG8344-PA	2R
	Dp985b	VI	29575	5E-19	96	CG6476-PA	3R
	Dp985c	VI	-6196.5	2E-14	80	CG5810-PA	3R
	Dp985d	VI	-7143	0	716	CG8896-PA	2R

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Appendix B (continued)

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d190	Dp1399a	VI	-1017.5	1E-20	101	CG31543-PC	3R
	Dp1399b	VI	-1271	6E-26	118	CG30036-PA	2R
d073	Dp361a	VI	5524.5	8E-62	239	CG4125-PA	X
	Dp361b	VI	5499	5E-68	259	CG3653-PA	X
d028	Dp385a	VI	21330	9E-19	94	CG14305-PA	3R
	Dp385b	VI	21321	9E-31	136	CG3105-PA	2R
	Dp385c	VI	-26501.5	3E-14	81	CG6324-PA	X
	Dp385e	VI	-27266.5	1E-10	68	CG8994-PA	2R
d152	Dp1327a	VI	36898	7E-49	196	CG9650-PB	X
	Dp1327b	VI	-50400.5	5E-19	67	CG3817-PA	3R
	Dp1327c	VI	-100573	3E-44	101	CG3633-PA	2R
d153	Dp1350a	VI	37195.5	5E-32	139	CG2977-PA	X
	Dp1350b	VI	29528	1E-78	138	CG7035-PA	X
d157	Dp1328a	VII	17411.5	4E-38	144	CG32920-PB	3R
	Dp1328b	VII	-719.5	7E-13	75	CG2851-PA	2L
	Dp1328c	VII	-23947.5	0	355	CG2747-PA	3R
d058	Dp112a	VII	5916.5	2E-63	157	CG8282-PA	2L
	Dp112b	VII	-3182.5	1E-61	207	CG17923-PA	4
d107	Dp867a	VII	1371.5	4E-81	171	CG9738-PA	3R
	Dp867b	VII	-4314.5	5E-61	119	CG33304-PA	2L
d166	Dp1300a	VII	-4460.5	1E-62	102	CG1100-PA	3R
	Dp1300b	VII	-6004.5	1E-14	80	CG32147-PA	3L
d189	Dp1347a	VII	-3925	1E-43	179	CG32577-PA	X
	Dp1347b	VII	-55154.5	6E-21	73	CG32578-PA	X
d027	Dp156a	VII	27339.5	3E-20	100	CG5488-PA	X
	Dp156b	VII	25583.5	2E-12	73	CG6545-PA	3R
	Dp156c	VII	-52957.5	1E-20	102	CG5488-PA	X
d068	Dp53a	VIII	-1204	6E-22	77	CG7902-PA	3R
	Dp53b	VIII	-50894	5E-81	132	CG10220-PA	2R
d065	Dp142a	VIII	88658	8E-34	145	CG6488-PA	2L
	Dp142b	VIII	40984	1E-39	104	CG3373-PA	3R
d077	Dp559a	VIII	53796.5	7E-26	118	CG9428-PA	2R
	Dp559b	VIII	53780	3E-26	120	CG6898-PA	3R
	Dp559c	VIII	-2070.5	2E-32	140	CG7535-PA	3R
	Dp559d	VIII	-2067.5	6E-16	83	CG6112-PA	3L
d117	Dp887a	VIII	92744.5	2E-48	151	CG5970-PA	2R
	Dp887b	VIII	15464	2E-50	201	CG2102-PA	3R
	Dp887c	VIII	-24426	2E-84	313	CG3157-PA	2L
d045	Dp1493a	VIII	7055.5	2E-27	120	CG9344-PA	2R
	Dp1493b	VIII	6111.5	2E-25	57	CG5846-PA	2L
d192	Dp1351a	VIII	72150	2E-21	104	CG7121-PA	2L
	Dp1351b	VIII	-6458	5E-40	167	CG3228-PA	X
	Dp1351c	VIII	-6479	2E-89	282	CG3225-PA	2L
d178	Dp1278a	IX	2824.5	2E-23	107	CG6870-PA	2L
	Dp1278b	IX	2818.5	2E-13	73	CG3566-PB	X
	Dp1278c	IX	-19811	1E-46	187	CG9175-PA	2L
	Dp1278d	IX	-24238.5	1E-45	134	CG8400-PA	2R
d171	Dp1309a	IX	35445	5E-11	68	CG3672-PA	3L
	Dp1309b	IX	-16322.5	1E-125	453	CG15288-PB	2L
	Dp1309c	IX	-25927.5	2E-54	164	CG7269-PA	2L
d145	Dp1325a	IX	6561.5	2E-42	175	CG14120-PA	3L
	Dp1325b	IX	3599	9E-47	189	CG11887-PA	2R
	Dp1325c	IX	-2632.5	1E-17	90	CG15604-PA	X
	Dp1325d	IX	-9520	5E-75	199	CG9163-PA	X
d043	Dp330a	IX	34298.5	2E-26	84	CG4787-PA	3R
	Dp330b	IX	3722	1E-56	199	CG10693-PB	3R
	Dp330c	IX	-14486	7E-28	127	CG10693-PB	3R
	Dp330d	IX	-31731.5	2E-32	140	CG32423-PB	3L
d088	Dp660a	IX	32427	6E-16	62	CG9109-PA	2L
	Dp660b	IX	19668	3E-14	81	CG12290-PA	3R
	Dp660c	IX	-16563.5	9E-54	138	CG6551-PA	X
d127	Dp696a	X	-1916.5	1E-75	142	CG8205-PD	2R
	Dp696b	X	-15365	2E-20	101	CG4713-PA	2L

Appendix B (continued)

<i>Daphnia</i>				<i>E</i> value	Bit score	<i>Drosophila</i>	
Marker	Gene ID	Lk	Distance from closest marker			Gene ID	Cytology
d023	Dp460a	X	51284.5	2E–19	58	CG4210-PA	3R
	Dp460b	X	7620.5	4E–21	103	CG17117-PC	3R
	Dp460c	X	–86107.5	3E–14	79	CG5646-PA	3R
d034	Dp304a	X	13685	7E–19	48	CG33088-PA	3L
	Dp304b	X	12564.5	9E–12	70	CG10365-PA	3R
d072	Dp1496a	X	38824.5	9E–76	285	CG8833-PA	3L
	Dp1496b	X	20675	1E–12	77	CG10122-PA	2R
d161	Dp1302a	X	–7307	7E–18	94	CG5406-PB	3L
	Dp1302b	X	–34144	1E–73	200	CG5406-PB	3L
d186	Dp1057a	X	49005	7E–66	253	CG17209-PA	X
	Dp1057b	X	48972	6E–97	357	CG10122-PA	2R
	Dp1057c	X	–5131	7E–32	138	CG2328-PA	2R
	Dp1057d	X	–10203.5	8E–28	73	CG6009-PA	3R
d083	Dp641a	X	39475.5	2E–38	124	CG6643-PB	3R
	Dp641b	X	5580	4E–25	115	CG18769-PA	3L
	Dp641c	X	–15435.5	5E–25	113	CG14145-PA	3L
	Dp641d	X	–20074	1E–60	212	CG6378-PA	3R
d092	Dp808a	XI	40318	1E–84	315	CG9355-PA	X
	Dp808b	XI	40274.5	5E–71	269	CG15013-PA	3L
	Dp808c	XI	–11911.5	7E–31	136	CG9333-PA	2L
	Dp808d	XI	–14853.5	2E–155	168	CG4063-PA	2L
d006	Dp70a	XI	82401	0	222	CG11337-PA	3R
	Dp70b	XI	46862.5	8E–133	475	CG5685-PA	3R
	Dp70c	XI	–33190	3E–81	303	CG1119-PA	3R
	Dp70d	XI	–46643.5	5E–138	233	CG5222-PA	3L
d173	Dp1112a	XI	24553.5	9E–59	230	CG7050-PA	3R
	Dp1112b	XI	9834	7E–86	178	CG8200-PB	2R
	Dp1112c	XI	–16578	2E–21	102	CG14270-PA	X
d137	Dp936a	XII	–52736	5E–103	375	CG32281-PA	3L
	Dp936b	XII	–54685	4E–71	182	CG1837-PA	X
d182	Dp1144a	XII	5402.5	4E–15	84	CG10421-PA	3R
	Dp1079b	XII	22188	2E–22	104	CG1319-PA	3L
	Dp1079c	XII	10770.5	6E–91	338	CG11895-PA	2R
	Dp1079d	XII	–4970	1E–112	410	CG11895-PA	2R

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