Analysis of Expressed Sequence Tags of the Cyclically Parthenogenetic Rotifer *Brachionus plicatilis*

**Koushirou Suga**¹, **David Mark Welch**², **Yukari Tanaka**¹, **Yoshitaka Sakakura**³, **Atsushi Hagiwara**⁴

¹ Nagaoka Industrial Promotion Foundation, Omura, Japan, ² Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, Massachusetts, United States of America, ³ Faculty of Fisheries, Nagaoka University, Nagaoka, Japan, ⁴ Graduate School of Science and Technology, Nagaoka University, Nagaoka, Japan

**Background.** Rotifers are among the most common non-arthropod animals and are the most experimentally tractable members of the basal assemblage of metazoan phyla known as Gnathifera. The monogonont rotifer *Brachionus plicatilis* is a developing model system for ecotoxicology, aquatic ecology, cryptic speciation, and the evolution of sex, and is an important food source for finfish aquaculture. However, basic knowledge of the genome and transcriptome of any rotifer species has been lacking. Methodology/Principal Findings. We generated and partially sequenced a cDNA library from *B. plicatilis* and constructed a database of over 2300 expressed sequence tags corresponding to more than 450 transcripts. About 20% of the transcripts had no significant similarity to database sequences by BLAST; most of these contained open reading frames of significant length but few had recognized Pfam motifs. Sixteen transcripts accounted for 25% of the ESTs; four of these had no significant similarity to BLAST or Pfam databases. Putative up- and downstream untranslated regions are relatively short and AT rich. In contrast to bdelloid rotifers, there was no evidence of a conserved trans-spliced leader sequence among the transcripts and most genes were single-copy. Conclusions/Significance. Despite the small size of this EST project it revealed several important features of the rotifer transcriptome and of individual monogonont genes. Because there is little genomic data for Gnathifera, the transcripts we found with no known function may represent genes that are species-, class-, phylum- or even superphylum-specific; the fact that some are among the most highly expressed indicates their importance. The absence of trans-spliced leader exons in this monogonont species contrasts with their abundance in bdelloid rotifers and indicates that the presence of this phenomenon can vary at the subphylum level. Our EST database provides a relatively large quantity of transcript-level data for *B. plicatilis*, and more generally of rotifers and other gnathiferan phyla, and can be browsed and searched at gmod.mbl.edu.

Citation: Suga K, Mark Welch D, Tanaka Y, Sakakura Y, Hagiwara A (2007) Analysis of Expressed Sequence Tags of the Cyclically Parthenogenetic Rotifer *Brachionus plicatilis*. PLoS ONE 2(8): e671. doi:10.1371/journal.pone.0000671

**INTRODUCTION**

Rotiferá is one of the largest microinvertebrate phyla, in terms of both biomass and number of species. Its members are major components of freshwater and coastal marine ecosystems throughout the world, and are the chief non-arthropod component of most freshwater pelagic communities [1]. Most rotifers are smaller than 1 mm, but have ganglia; muscles; photo-, chemo-, and tactile sensory organs; structures for crawling, feeding, and swimming; digestive and secretory organs; and ovaries. The two major rotifer groups, Monogononta and Bdelloidea, are each significant for their unusual reproductive modes: bdelloids appear to be obligately asexual, reproducing only through mitotic division of germ cells; monogonont rotifers are facultatively sexual, generally reproducing through mitotic division of germ cells but entering a meiotic sexual phase in response to environmental cues [2].

The phyllum is allied with other microinvertebrate groups such as Acanthocephala, Gnathostomulida, Micrognathozoa, and Cyclophora in the superphylum Gnathifera, a sister- or basal group to the Lophotrochozoa [3,4]. Unlike other gnathiferan fauna, many rotifer species can easily be cultured in axenic conditions in quantities suitable for large-scale biochemical and molecular genetic studies, making rotifers the optimal model system for studying this basal animal assemblage. Among rotifers, the most well-studied are the euryhaline rotifers of the *Brachionus plicatilis* species complex. Their widespread distribution and ease of culturing make this group a useful model system for studies of population dynamics [5–9], speciation [10–14], the evolution of sexual reproduction [15,16], and ecotoxicology [17–20]. The complex is also an important live food for the initial stage of larval rearing of marine fishes [21,22]. However, while the biology, ecology, and culture conditions of many rotifer species have been studied, molecular and genetic studies are scarce and there are few genomic resources [10,23]. Only genes used for phylogenetic analysis, such as those encoding ribosomal RNAs, cytochrome oxidase subunit I, and the 82kD heat shock protein have been widely sampled in Rotifera [11–14,24,25], and only a few others, such as those for the 70kD heat shock protein, a Mn-superoxide dismutase, and a ubiquitin-conjugating enzyme [26,27], have been reported for *B. plicatilis*.

To increase the amount of genetic information available and to develop tools for further genomic research of rotifers, we constructed an unnormalized cDNA library from a mixed (asexual females, sexual females, and males) culture of *B. plicatilis*. We partially sequenced over 2300 clones and acquired data on the

**Academic Editor:** Hans Ellegren, University of Uppsala, Sweden

**Received** May 16, 2007; **Accepted** June 29, 2007; **Published** August 1, 2007

**Copyright:** © 2007 Suga et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Funding:** This research was supported by the Nagaoka Prefecture Collaboration of Regional Entities for the Advancement of Technological Excellence, Japan Science and Technology Agency to KS, YT, YS and AH, and US NSF grants EF-0412674 and MCB-0544199 to DMW.

**Competing Interests:** The authors have declared that no competing interests exist.

*To whom correspondence should be addressed. E-mail: dmarkwelch@mbl.edu*
relative abundance, probable function, and sequence characteristics of more than 450 transcripts.

RESULTS

A rotifer culture is a complex microcosm of bacteria, protozoa, algae, fungi, and rotifers. A single rotifer may harbor as many as 10^6 bacterial colony forming units (cfu) and a culture typically contains 10^3–10^6 bacterial cfu/ml [28]. The fungal species *Atkinsonella parasitica* was isolated from eggs and body of *B. plicatilis* [29], and PCR with primers to small subunit ribosomal RNA (SSU rRNA) demonstrated the presence of bacteria including *Afishia, Bosea*, and *Delfia*, protozoa including *Hartmannella*, and fungi including *Catenaria* in seemingly axenic cultures (DMW, unpublished). To create a cDNA library with minimal xenic contamination we established an axenic rotifer culture method (KS, unpublished). The food source, the algae *Chlorella vulgaris*, was cultured axenically. To minimize contamination of the library from *Chlorella* mRNA, rotifer culture at log phase growth was harvested aseptically, kept in sterilize seawater to allow the rotifers to consume remaining *Chlorella* and excrete all the food in their gut, and then washed several times with sterilize sea water. This procedure appears to have produced a cDNA library largely free of xenic contamination: none of the clones we sequenced had a top BLAST score to a fungus, and the gene encoding ribulose bifosphate carboxylase/oxygenase, one of the most expressed genes in plants [30–32], was absent.

After removing sequences that were vector-only, low quality, or polyA-only reads, 2362 ESTs were recovered with an average read length of 770 bases. Clones corresponding to 166 of the ESTs were subsequently sequenced in the opposite direction. Assembly output consisted of 534 contigs and 473 potential transcripts (Table 1). Ninety-nine of the contigs contained forward and reverse reads, 122 represented 61 supercontig scaffolds of transcripts sequenced in both directions with sequencing gaps, and 313 contigs represented transcripts sequenced in one direction only, of which 236 were composed of a single EST. Rank-abundance and rarefaction curves are shown in Figure 1. The redundancy of the library, calculated as 2362 ESTs/473 potential transcripts, was 4.99. The total number of transcripts present in the library was estimated to be about 800 using the Chao1 nonparametric estimator of total species richness [33], calculated as $S_{\text{total}} = S_{\text{obs}} + \frac{(S_{1}^{2} - S_{2})}{2S_{2}}$ where $S_{1}$ and $S_{2}$ are the number of transcripts represented by 1 or 2 ESTs, respectively. Consensus contig sequences were deposited in DDBJ/EMBL/GenBank with accession numbers BJ979485 to BJ979996 and BJ999204 to BJ999251; individual ESTs were deposited in the dbEST division of GenBank with accession numbers ES466901-ES469274.

### Transcript function and abundance

Contigs were compared to nucleotide and amino acid sequences in GenBank and to Pfam whole domain and fragment HMM databases. Of the 473 transcripts comprising the 534 contigs, 371 had matches to BLAST databases with E values <10^-10. Of the 103 transcripts that did not have significant similarity to BLAST databases, 53 had open reading frames of at least 300 bases and 22 had ORFs of at least 600 bases. However, only 12 had annotated Pfam motifs (as judged by an e-value <1e^-5). The most abundant transcript was an SSU rRNA not eliminated in the mRNA purification (EST BpA0300); other transcripts with more than 1% of the total ESTs are listed in Table 2. In addition to ribosomal proteins, tubulin, and DNA binding proteins, these include transcripts encoding proteins similar to the cysteine protease Cathepsin L, a glutathione S-transferase, acyl-CoA oxidase, and a sphingolipid activator protein (saposin). Contigs representing four of the most abundant transcripts, each accounting for more than 1% of ESTs, have no significant BLAST or Pfam matches. The most abundant such transcript (BpA0604) is more than 1700 nt in length but lacks an ORF of significant length; it includes a tandem array of ten 68 nt repeats with an average pairwise identity of 95%. Another abundant

---

**Table 1. cDNA Library and EST Database Properties**

| Property                                    | Value          |
|---------------------------------------------|----------------|
| Mean insert size in kb ± SD (n=40)          | 2.01 ± 1.1     |
| Recombinant efficiency                      | 83%            |
| Total reads                                 | 2678           |
| ESTs after quality screening                | 2362           |
| Total contigs                               | 534            |
| contigs with forward and reverse reads      | 99             |
| contigs with forward reads only             | 435            |
| supercontig scaffolds                       | 61             |
| contigs with one EST                        | 236            |
| supercontigs with 2 ESTs                   | 19             |
| Total inferred transcripts                  | 473            |
| rRNA transcripts                            | 4              |
| incompletely spliced transcripts            | 1              |
| Total inferred coding genes surveyed       | 468            |
| coding genes with 1 EST                    | 232            |
| coding genes with 2 ESTs                   | 84             |

DOI:10.1371/journal.pone.0000671.t001

---

**Figure 1. Transcript Abundance.** a) Transcript abundance by EST abundance; the most abundant transcript (BpA0300 with 139 ESTs) is SSU rRNA and is not shown. (b) Rarefaction curve of transcripts predicted by number of ESTs. doi:10.1371/journal.pone.0000671.g001
transcript (BpA0292), composed of an ORF of at least 591 bases before a short 3' UTR and a polyA tail, has no BLAST or Pfam similarity to database sequences, and is composed largely of serine-threonine repeats (none of the clones composing this contig contained an in-frame ATG near the 5’ end so the contig is probably an incomplete sample of the transcript).

Supplemental Table S1 lists all contigs in our EST database, the number of ESTs per contig, contig length, best BLAST hit, and the predicted functional category of the gene product when BLASTX to the nr database produced a match with a score >90 and E-value <1.0e-15. In addition to the SSU rRNA gene sampled in BpA0300, single-EST contigs BpA0284 and BpA0435 contained different regions of 28S ribosomal gene(s) and single-EST contig BpA0464 contained a region of a 5S ribosomal gene. As shown in Figure 2, the categories with the greatest abundance of ESTs were gene/protein expression (25.1%), metabolism (18.9%), unclassified (13.3%), and cell signalling/cell communication (10.6%).

Intragenomic comparisons
Every contig was compared to every other contig using BLASTN. One single pass read (BpA0008) was completely identical to another (BpA0417) except for a 351 base insertion. BpA0417 contains a complete ORF identified as ribosomal protein L11; BpA0008 has strong similarity to L11 by BLASTN, except for the 351 base insertion, which has no significant matches in BLAST or Pfam databases and does not contain an ORF of significant length. A genewise comparison of BpA0008 to the L11 protein of Danio rerio predicts an intron involving the insertion but not with exactly the same coordinates. The insertion begins with a GpT but does

Table 2. Highly abundant (>1%) non-SSU transcripts and their putative function. When two contigs make up a transcript scaffold both are listed; Score and E value are BLASTX to the nr database except for BpA0295 which is hmmpfam to Pfam.ps

| No. of ESTs (%) | Contig(s) | Acc. No.(s) | Gene product name or probable function | Score | E value |
|----------------|-----------|-------------|----------------------------------------|-------|---------|
| 56 (2.5)       | BpA0602   | BJ999206    | cathepsin L                            | 406   | 8.00E-112 |
| 49 (2.2)       | BpA0299   | BJ979768    | Peritrophin-A domain containing         | 53.6  | 5.90E-13  |
| 47 (2.1)       | BpA0294   | BJ979763    | saposin-like                           | 166   | 3.00E-39  |
| 45 (1.9)       | BpA0604   | BJ999208    | no significant BLAST or Pfam similarities | —     | —       |
| 39 (1.8)       | BpA0276, BpA0288 | BJ979746, BJ979757 | DNA binding, R3H domain containing       | 96    | 1.00E-18  |
| 38 (1.7)       | BpA0297   | BJ979766    | ribosomal protein L23                 | 219   | 3.00E-56  |
| 34 (1.5)       | BpA0296   | BJ979765    | Tubulin, beta, 2                       | 493   | 0       |
| 30 (1.3)       | BpA0295   | BJ979764    | no significant BLAST or Pfam similarities | —     | —       |
| 30 (1.3)       | BpA0284   | BJ979753    | no significant BLAST or Pfam similarities | —     | —       |
| 29 (1.3)       | BpA0601, BpA0610 | BJ999205, BJ999214 | DNA binding, similar to DEK oncogene | 73.2  | 2.00E-22  |
| 28 (1.2)       | BpA0292   | BJ979761    | no significant BLAST or Pfam similarities | —     | —       |
| 25 (1.1)       | BpA0291   | BJ979760    | acyl-CoA oxidase                       | 221   | 4.00E-56  |
| 25 (1.1)       | BpA0290   | BJ979759    | high-molecular-weight glutenin y-type subunit | 55.8  | 1.00E-06  |

Figure 2. Transcript Abundance by Functional Class of Predicted Protein Product
doi:10.1371/journal.pone.0000671.g002
not end in an ApG and may represent an incorrectly spliced gene product. The only other contigs with significant similarity to each other were examined to confirm that they were assembled correctly; comparison of BLAST hits showed these to be transcripts of different genes belonging to known gene families such as alpha- and beta- tubulins and low molecular weight heat shock proteins.

Untranslated regions
The distribution of untranslated region (UTR) length and %AT is shown in Figure 3. The average length of the putative 5’ and 3’ UTRs was 52 bases (SD 35) and 94 bases (SD 74.5), respectively. The length of the putative 5’ UTR was not negatively correlated with overall transcript length, suggesting that the estimate of 5’ UTR length was not biased by incomplete first strand synthesis of the cDNA library (not shown). The 5’ UTR was examined for the presence of trans-spliced leader (TSL) exons [34] by cluster analysis, multiple sequence alignment, and all-to-all BLASTN comparisons. No sequence conservation indicative of a TSL exon was found.

The average %AT of the putative 5’ and 3’ UTRs was 60.7% (SD 10.3%) and 63.4% (SD 6.5%). The %AT of both UTRs is significantly greater than the overall %AT of the transcripts from which they were extracted (59.7% and 63.6%, respectively, by Student’s T-test, p<0.01). While there is great variation in the length of the putative 3’ UTRs, there is little variation in %AT. The 19 transcripts with putative 3’ UTRs greater than 200 bases in length have an average %AT of 81.1%, indicating that their base composition is similar to shorter 3’ UTRs and unlike the rest of the transcript, suggesting that they have been properly identified.

DISCUSSION
We obtained 2220 non-rRNA ESTs from our B. plicatilis cDNA library, which assembled into 530 unique contigs, 98 of which contained reads in forward and reverse orientation. A limited amount of bidirectional sequencing allowed us to determine that 122 contigs were forward and reverse pairs from a total of 61 transcripts. Some fraction of the remaining 310 contigs may also be forward and reverse pairs, particularly those containing a large and similar number of ESTs, but we have conservatively treated each as a separate transcript (with the exception of Bp0008, which we interpret as an incompletely spliced product of the same gene as Bp0417). The redundancy of the library (which decreases to 4.7 without the rRNA transcripts and incompletely spliced EST), is higher than libraries of other invertebrate metazoans, such as the copepod Tigriopus japonicus (2.62 [35]), the cladoceran Daphnia magna (2.44 [36]), the cnidarian Cyanea capillata (2.11[37]), and the nematode Nippostrongylus brasiliensis (1.66[38]). The reason for such high redundancy is unclear; however, we hypothesize that the expression of many genes may have been depressed during starvation. This is supported by the low estimation of total transcript diversity in the library estimated by rarefaction and by the Chaol nonparametric estimator of total species richness, which both predict a total diversity of fewer than 1000 transcripts (Figure 1).

About 20% of the transcripts have no significant similarity to database sequences by BLAST, a lower fraction than in many EST studies, perhaps due to the starvation regime. Most of these transcripts contain identifiable ORFs but no recognized Pfam motifs, and represent genes of unknown function. Because there is little genomic data for Gnathifera the transcripts we found with no known function may represent genes that are species-, class-, phylum- or even superphyllum-specific. These genes include four of the most abundant transcripts, which combined account for nearly 6% of the sequenced ESTs. Further study of these genes, of obvious importance to rotifers, will no doubt greatly expand our understanding of the biology and evolution of rotifers and other gnathifera.

Although this library is far from complete, our database provides a large amount of information about the transcriptome of rotifers, including the predicted products of the highly expressed transcripts of B. plicatilis (Table 2). The most abundant non-SSU rRNA transcript encodes a cathespin L-like cysteine peptidase. Cathespin L has been identified in several arthropods, but the role of cathespinns in invertebrates is not known. The next most abundant transcript (BpA0299) contains a complete 1593 nt ORF with weak BLASTX matches (E>=0.01) to insect chitinas and has three chitin binding Peritrophin-A domains identified by hmmpfam. In insects, proteins with these domains are associated with the peritrophic matrix lining the midgut and play a role in partitioning digestive enzymes, and in defence against ingested bacterial pathogens [39]. Both of these processes are important to understanding rotifer ecology and to aquaculture, and this gene provides a potential avenue to their study. Gamma-aminobutyric acid (GABA) has been shown to enhance population growth of B. plicatilis cultures, particularly in stressful conditions such as low food concentration and high free ammonia levels [40,41], suggesting the existence of a GABA receptor and its importance for rotifer aquaculture. We found a transcript for a GABA receptor associated protein (BpA0418), which now allows the action of GABA in rotifers to be explored at the molecular level. Finally, one of our transcripts (BpA0140) has significant similarity to trehalase-6-phosphate synthase (tps) in BLAST and hmmpfam searches. This gene encodes the enzyme used in the first step of trehalose synthesis in most eukaryotes. The three ESTs that represent this transcript are similar to 5’ portion of tps containing the glycosyltransferase domain GT-20 (pfam00982, E value 2.6 x 10^(-5)) associated with trehalose synthase activity, but the whole transcript has not been isolated. Trehalase has been detected in the resting eggs of B. plicatilis [42] but not in several bdelloid species [42,43]. Unsuccessful PCR screens for tps in bdelloids have suggested that bdelloids are unable to synthesize trehalose [43]. Our discovery of a potential tps in B. plicatilis suggests that non-bdelloid rotifers use the tps pathway to synthesize trehalose and that bdelloids secondarily lost tps and the ability to synthesize trehalose.

Significantly, none of the genes we identified are related to the production of collagen, although collagens are very abundant proteins in most animals; other genes encoding proteins involved in cell structure, particularly laminin as well as actins, filamin, connectin, and tubulins, are present in our database. Biochemical assays have found no evidence of fibrous or non-fibrous collagens in B. plicatilis [44] and this is supported by the absence of collagen gene transcripts in our database. While acanthocephalans are

Figure 3. Distribution of UTRs by Length and %AT
doi:10.1371/journal.pone.0000671.g003
known to contain collagen [45], the distribution of collagen in other rotifers and in other gnathifera phyla is unknown. The presence of collagen genes may thus be a useful cladiastic marker [4] and the morphological and physiological response over evolutionary time to the loss of collagen may be of interest.

We found no evidence of alternately spliced genes, although our survey was too small to rule out alternate splicing in rotifers. We found one transcript that appeared to be an incorrectly spliced version of another; if this interpretation is correct it would imply that the introns of the monogonont B. plicatilis are much larger than those found in several bdelloid rotifers (~350 nt vs ~60 nt, [46]; DMW unpublished). Other than genes belonging to known gene families (primarily, alpha- and beta-tubulins) we found no evidence of multiple divergent gene copies in B. plicatilis, whereas this appears to be the norm in bdelloid rotifers ([47]; DMW unpublished). This provides additional evidence that the unique multiple-copy genome of bdelloids is related to their uniquely asexual evolution.

Another difference between monogonont and bdelloid rotifers apparent from our results is that monogonont rotifers appear to lack a conserved trans-spliced leader sequence. In contrast, bdelloid rotifers from two species belonging to different families were shown to have the same 23 nt exon sequence trans-spliced from ~100 nt spliced leader (SL) RNAs to the 5’ end of more than 50% of their transcripts [48]. Searches of putative 5’ UTRs from our library revealed no similarity to the bdelloid SL exon, or any similarity among 5’ UTR sequences themselves. While our library was not enriched for 5’ ends, we did identify likely upstream regions in 68 transcripts. As our criteria were rather stringent, requiring identifiable similarity with the 5’ end of the coding sequence of a BLAST ortholog, this is no doubt an underestimate of the 5’ UTRs present in our database. If premature termination of first-strand synthesis had created these 5’ UTRs to be incomplete, we would expect an inverse relationship between 5’ UTR length and total transcript length. No such relationship was observed, so most or perhaps all of the 5’UTRs we identified are probably full length. As TSL sequence was easily identified in the introns of the monogonont species, this is probably a conserved trans-spliced leader sequence. In contrast, bdelloid rotifers examined thus far lack SL RNA, bdelloids and monogononts would be the most closely related groups that are known to differ in this phenomenon, and may thus provide a useful model system in which to study the evolution of SL RNA.

MATERIALS AND METHODS
cDNA library construction and sequencing
Brachionus plicatilis Muller 1856 strain NH1L [49], a member of the B. plicatilis sensu strictu clade of the B. plicatilis species complex [11], was cultured at 25°C in Allen’s artificial seawater [50] (diluted to 17 ppt salinity) inoculated with 3–7×10^6 cells/ml Chlorella vulgaris strain K-73122 in a Jarfermentor (MBS, Japan). The algal food source C. vulgaris was cultured in bacteria-free medium, harvested by centrifugation, suspended in deionized, filtered water to a density of 8.6×10^8 cells/ml supplemented with 800 ng/ml vitamin B12 (which is essential for rotifer growth [51,52]) prior to introduction to the rotifer culture.

Rotifers were harvested by filtration onto a plankton net (45 micron mesh) that was washed with sterilized artificial seawater; rotifers were resuspended in 400 ml seawater that was exchanged every 2–3 hours over 12 hours to allow the rotifers to consume any remaining Chlorella and excrete their gut contents. The washed and starved rotifers were collected by plankton net and suspended in ISOGEN (Nippon Gene, Japan). The rotifers were homogenized with 0.8 mm glass beads using a vortex mixer and total RNA was isolated from the homogenate according to the manufacturer’s instructions. Poly(A)+ RNA was purified from total RNA using MagExtractor (Toyobo, Japan). About 2.8 µg of poly(A)+ RNA was used to construct the cDNA library. Double-stranded cDNA was prepared using a cDNA Synthesis Kit (Amersham Bioscience, USA). The blunt-ended cDNA was ligated to the EcoRI/VNl adaptor, then ligated into EcoRI-predigested lambda-ZAPII arms (Stratagene, USA), and packaged in vivo by using Gigapack III gold packaging extract (Stratagene).

An aliquot of the cDNA library was incubated with E. coli XL1-Blue MRF to allow in vivo mass excision by ExAssist helper phage. The incubated solution was transfected into E. coli SOLR strain and plated on LB ampicillin plates containing X-Gal and IPTG to recover pBluescript SK (-) plasmids. Based on blue/white selection, the recombinant efficiency of the cDNA library was 83%. The average insert length from 40 randomly picked clones was estimated by restriction enzyme analysis to be approximately 2 kb (SD 1 kb).

Plasmid DNA was purified using a QIAGEN plasmid kit or a Genomic Solutions RevPrep robot, sequenced with ABI Big Dye 3.1 chemistry using standard M13 forward and reverse primers, and eluted on ABI PRISM 310, 3100, or 3730xl Genetic Analyzers (Applied Biosystems).

Sequence analysis
All sequence data was examined independently using either DNAsIS Pro software (Hitachi software, Japan) or unix shell scripts developed at the Josephine Bay Paul Center combining plprph [53-55], lucy [56] trimseq, and trinem [57] and available from the corresponding author on request. Assemblies were compared and discrepancies examined and reconciled by hand. Contigs and unique sequences from singletons were compared to NCBI databases using BLASTN and BLASTX [58] and to Pfam databases using estgene [59] and hmmfam [60]. Putative function was assigned based on best BLAST hit to a well-annotated sequence, and scored as similar if the top hit had a score greater than 50, and as highly similar if the top hit had a score greater than 90.

Sequences with significant similarity to database sequences by BLASTN were, when necessary, reoriented to match the subject sequence. All forward open reading frames greater than 150 bp were found, translated, and compared to databases by BLASTP. If an ORF began with an ATG, its set of top blast hits were similar to those found when blasting the entire transcript, and the ATG of the ORF was within 60 bases of the start site of at least one top blast hit, that ORF was considered the likely translation start site and all positions upstream to be part of the 5’ untranslated region. Similarly, if a sequence contained a polyA tail and had an ORF with a set of top blast hits similar to those found when blasting the entire transcript, the stop codon of the ORF was considered the likely translation termination site, and all positions downstream but before the polyA tail were considered to be the 3’ untranslated region.

SUPPORTING INFORMATION
Table S1 Table S1 is a tab delimited ASCII text file containing Accession, # of ESTs, length, best BLAST hit information, predicted function, and predicted functional class for each contig. Found at: doi:10.1371/journal.pone.0000671.s001 (0.10 MB TXT)
ACKNOWLEDGMENTS

We thank Susan Huse for importing and formatting our database at gmod.mbl.edu and Hillary Smith and two anonymous reviewers for helpful comments on the manuscript.

REFERENCES

1. Hutchinson GE (1957) A Treatise on Limnology. New York: Wiley.
2. Wallace RL, Snell TW (2001) Rotifera. In: Thorp JH, Covich AP, eds. Ecology and Classification of North American Freshwater Invertebrates. New York: Academic Press, pp 167–248.
3. Girbet G, Dutet DL, Polz M, Sturier W, Wheeler WC (2000) Triplastoblastic relationships with emphasis on the acelomates and the position of Gnathostomulida, Cyclophorida, Phylommatinidae, and Chaerogastia: a combined analysis of 18S rDNA sequences and morphology. Systematic Zoology 49: 539–562.
4. Mark Welch DB (2001) Early contributions of phylogenetics to understanding the evolution of Rotifera. Hydrobiologia 446/447: 313–329.
5. Ortelli R, Gomez A, Serra M (2003) Coexistence of cryptic rotifer species: ecological and genetic characterisation of Brachionus plicatilis. Freshwater Biology 48: 2194–2202.
6. Serra M, Snell TW, King CE (2002) The tuning and proportion of sex in monogonont rotifers. In: Moya AE, Font E, eds. Evolution From Molecules to Ecosystems. Oxford: Oxford University Press, pp 135–146.
7. Ortelli R, Snell TW, Gomez A, Serra M (2000) Patterns of genetic differentiation in resting egg banks of a rotifer species complex in Spain. Arch Hydrobiol 149: 259–299.
8. Yoshinaga T, Haigawa A, Tsukamoto K (2003) Life history response and age-specific tolerance to starvation in Brachionus plicatilis O.F. Muller (Rotifera). Journal of Experimental Marine Biology and Ecology 267: 261–271.
9. Gomez A, Adcock GA, Lunt DH, Carvalho GR (2002) The utility of the 16S rDNA in investigating cryptic speciation within the Brachionus plicatilis species complex. Marine Biology 147: 1129–1139.
10. Campillo S, Garcia-Roger EM, Martinez-Torres D, Serra M (2005) Morphological traits of 24 species belonging to the Lophomorpha in the Brachionus plicatilis species complex. Hydrobiologia 546: 161–187.
11. Snell TW, King CE (2004) Effect of growth hormone and γ-aminobutyric acid on Brachionus plicatilis (Rotifera) reproduction at low food or high ammonia levels. Journal of Experimental Marine Biology and Ecology 280: 179–191.
12. Suen CW, Nakamura K, Hatai K (1994) Life history response and body size of the marine rotifer, Brachionus plicatilis. New York: Taylor and Francis. pp 169–185.
13. Lohan MJ (1997) Peritrophic matrix structure and function. Annual Review of Entomology 42: 525–550.
14. Mark Welch DB, Meselson M (2001) A survey of introns in three genes of the Rotifera. Hydrobiologia 446/447: 333–336.
15. Cain GD (1970) Collagen from the giant acanthocephalan Macrocephalucha hirudinacea. Archives of Biochemistry and Biophysics 141: 264–270.
16. Hatagaya A, Hamada K, Nishii A, Imazumi K, Hirayama K (1993) Mass production of rotifer Brachionus plicatilis resting eggs in 50 m³ tanks. Nippon Suisan Gakkaishi 59: 93–98.
17. Allen E, Nelson EW (1910) On the artificial culture of marine plankton organisms. Journal of the Marine Biological Association of the UK 8: 412–474.
18. Scott JM (1983) Rotifer nutrition using supplemented monoculture. Hydrobiology 104: 155–166.
19. Hirayama K, Funamato H (1988) Supplementary effect of several nutrients on nutritive deficiency of baker’s yeast for population growth of the rotifer Brachionus plicatilis. Bulletin of the Japanese Society of Fisheries 49: 505–510.
20. Ewing B, Green P (1998) Base-calling of automated sequencer traces using phred. II. Error probabilities. Genome Research 8: 186–194.

Author Contributions

Conceived and designed the experiments: KS AH. Performed the experiments: DM KS YT. Analyzed the data: DM KS YS YT AH. Contributed reagents/materials/analysis tools: DM KS AH. Wrote the paper: DM KS.
54. Ewing B, Hillier L, Wendl MC, Green P (1998) Base-calling of automated sequencer traces using phred. I. Accuracy assessment. Genome Research 8: 175–185.
55. Gordon D, Abajian C, Green P (1998) CONSED: a graphical tool for sequence finishing. Genome Research 8: 195–202.
56. Chou H-H, Holmes MH (2001) DNA sequence quality trimming and vector removal. Bioinformatics 17: 1093–1104.
57. Rice P, Longden I, Bleasby A (1999) EMBOSS: The European Molecular Biology Open Software Suite. Trends in Genetics 16: 276–277.
58. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, et al. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Research 25: 3389–3402.
59. Birney E, Clamp M, Durbin R (2004) GeneWise and Genomewise. Genome Research 14: 988–995.
60. Eddy SR (1998) Profile hidden Markov models. Bioinformatics 14: 755–763.