The first mitochondrial genome for the wasp superfamily Platygastroidea: the egg parasitoid *Trissolcus basalis*

Meng Mao, Alejandro Valerio, Andrew D. Austin, Mark Dowton, and Norman F. Johnson

Abstract: The nearly complete mitochondrial (mt) genome of an egg parasitoid, *Trissolcus basalis* (Wollaston), was sequenced using both 454 and Illumina next-generation sequencing technologies. A portion of the noncoding region remained unsequenced, possibly owing to the presence of repeats. The sequenced portion of the genome is 15 768 bp and has a high A+T content (84.2%), as is typical for hymenopteran mt genomes. A total of 36 of the 37 genes normally present in animal mt genomes were located. The one exception was *trnR*; a truncated version of this gene is present between $trnS_1$ and *nd5*, but it is unclear whether this gene fragment could code for the entire *trnR* gene. The mt gene arrangement of *T. basalis* is different from other Proctotrupomorpha mt genomes, with a number of *trn* genes in different positions. However, no shared derived gene rearrangements were identified in the present study. Bayesian analyses of mt genomes from 29 hymenopteran taxa and seven other orders of holometabolous insects support some uncontroversial evolutionary relationships, but indicate that much higher levels of taxonomic sampling are necessary for the resolution of family and superfamily relationships.

Key words: mitochondrial, Hymenoptera, Proctotrupomorpha, *Trissolcus*, gene rearrangement, phylogenetic relationship.

Résumé : Le génome mitochondrial (mt) presque complet d'un parasitoïde des œufs, *Trissolcus basalis* (Wollaston), a été séquencé au moyen des technologies de séquençage 454 et Illumina. Une portion de la région non-codante demeure non séquencée, possiblement en raison de la présence de répétitions. La portion séquencée du génome totalise 15 768 pb et présente un contenu élevé en A+T (84,2 %), chose typique chez les génomes mitochondriaux des hyménoptères. Trente-six des 37 gènes normalement présents au sein des génomes mt chez les animaux ont été localisés à l'exception de *trnR*. Dans ce cas, une version tronquée de ce gène est présente entre $trnS_1$ et *nd5*, mais il n'est pas clair si ce fragment de gène peut coder pour un gène *trnR* complet. L'agencement des gènes chez le *T. basalis* est différent de ce qu'il est chez d'autres génomes mt chez les Proctotrupomorpha, plusieurs gènes *trn* occupant des positions différentes. Cependant, aucun réarrangement génique partagé n'a été identifié dans ce travail. Des analyses bayesiennes des génomes mt chez 29 taxons au sein des hyménoptères et sept autres ordres d'insectes holométaboles supportent certaines relations évolutives peu controversées, mais indiquent qu'un échantillonnage taxonomique beaucoup plus important sera nécessaire pour résoudre les relations au niveau de la famille et de la superfamille.

Mots-clés : mitchondrial, Hymenoptera, Proctotrupomorpha, *Trissolcus*, réarrangement génique, relation phylogénétique.

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Introduction

Mitochondrial (mt) genomes have been widely used for the reconstruction of phylogenetic relationships at different taxonomic levels (Miya et al. 2003; Cameron et al. 2007; Kim et al. 2009; Li et al. 2011). In insects, mtDNA is typically a double-stranded circular molecule of about 16 kb. It contains 13 protein-coding genes, 2 ribosomal RNA (*rrn*) genes, and 22 transfer RNA (*trn*) genes (Boore 1999). Additionally, there is a major noncoding region, known as the AT-rich region or control region, which plays a role in initiation of transcription and replication (Zhang and Hewitt 1997).

The Hymenoptera is one of the most species-rich and biologically diverse insect orders (LaSalle and Gauld 1993). Although much progress has been made to investigate the phylogeny of the Hymenoptera (Dowton and Austin 1994, 2001; Ronquist et al. 1999; Castro and Dowton 2006; Heraty et al. 2011; Sharkey et al. 2011), there are also many relationships remaining unresolved. For example, the monophyly of the Proctotrupomorpha (sensu Rasnitsyn 1988) is well

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supported by recent studies, but the relationships among the proctotrupomorph families are still controversial (Dowton and Austin 2001; Castro and Dowton 2006; Rasnitsyn and Zhang 2010; Heraty et al. 2011). Several analyses have demonstrated that the whole mt genome is a useful tool to resolve hymenopteran evolutionary relationships (Castro and Dowton 2007; Cameron et al. 2008; Dowton et al. 2009*a*; Wei et al. 2010*a*). To date, 18 complete mt genomes and 15 nearly complete mt genomes have been successfully sequenced in the Hymenoptera, with 18 taxa added in the last 3 years. This large amount of data holds promise to improve phylogenetic analysis. Notwithstanding, there remain shortcomings with this dataset, with only 11 superfamilies represented. For approximately half of the hymenopteran superfamilies, there is no mt genome data available.

In this paper, we provide the mt genomic sequence of *Trissolcus basalis* (Wollaston) from the superfamily Platygastroidea, the third largest of the parasitic superfamilies after the Ichneumonoidea and Chalcidoidea (Austin et al. 2005). No mt genome sequences for the Platygastroidea have previously been published. The characteristics of this mt genome, with respect to genome composition, nucleotide content, and codon usage, were compared with other hymenopteran mt genomes. We conducted phylogenetic analyses of mt genomes from 29 hymenopteran taxa and seven other orders of holometabolous insects. Bayesian analyses were performed using nucleotide sequences (including and excluding the third codon position). The performance of two alignment methods (Clustal W and Muscle) was also compared. Another goal of this research was to further explore the evolution of mt gene rearrangement. The hymenopteran mt genome has been reported to rearrange more frequently than those from other insect orders (Crozier and Crozier 1993; Dowton and Austin 1999; Dowton et al. 2009*b*). Here we compared the genome structures of four Proctotrupomorpha taxa.

Materials and methods

DNA extraction, PCR amplification, and sequencing

454 sequencing

Genomic DNA was extracted from whole bodies of 25 adult male specimens of *T. basalis* from a laboratory culture maintained by F. Bin at the Università di Perugia. The extract was sent to the DNA Sequencing Facility at the University of Pennsylvania Perelman School of Medicine. Five full plates were run on a Roche/454 GS FLX sequencer (454 Life Sciences, Branfort, Conn., USA) using Titanium chemistry. This resulted in 5 080 113 reads and a total of 1 535 920 544 bases. These reads were assembled using gsAssembler 2.5.3 with a minimum overlap of 30 bases and the complex genome assembly option.

Illumina sequencing

To address the issue of possible homopolymer errors in 454 sequencing, genomic DNA was extracted from an additional five female specimens from the same culture. The extract was processed using the Nextera DNA sample preparation kit from Epicentre Biotechnologies (Madison, Wis., USA) following the manufacturer's instructions. The sample was submitted to the Nucleic Acid Shared Resource of the College of Medicine at The Ohio State University. A single lane of 51 base reads was run on an Illumina Genome Analyzer IIx (Illumina, San Diego, Calif., USA) resulting in 29 780 645 reads and a total of 1 518 812 895 bases. These reads were assembled using VCAKE 1.5 into repetitive and nonrepetive contigs, and short contigs (<70 base) were then removed. The remaining contigs were then assembled together with the final 454 assembly using gsAssembler 2.5.3. Nesoni 0.42 software was used to correct errors in the hybrid assembly.

Contigs of mt origin from the entire assembly were identified by a BLAST search using known hymenopteran mt proteins. Two contigs emerged from the search, with lengths of 8067 and 7719 bases.

Sequence analyses

The two contigs were imported into Bioedit (version 7.0.5; Hall 1999). Visual inspection revealed that the same dinucleotide repeat, $(TA)_n$, was present at one end of each of the contigs. When the contigs were oriented in the ancestral orientation (i.e., with protein-coding genes oriented on the same strand and direction as the ancestral pancrustacean), the shorter contig had a $(TA)_{13}$ repeat at the 3′ end, while the longer contig had a $(TA)_9$ repeat at the 5′ end. We interpret this as indicating that a dinucleotide repeat that varies in length is situated between these two contigs. Joining these, the ancestral orientation of all protein-coding and *rrn* genes is maintained. The dinucleotide repeat is situated in the intergenic space, between the *trnH* and *nd4* genes.

Nineteen *trn* genes were identified by tRNA-Scan SE (version 1.21; lowelab.ucsc.edu/tRNAscan-SE/) (Lowe and Eddy 1997), specifying mitochondrial/chloroplast DNA as the source and choosing the invertebrate mt genetic code for tRNA isotype prediction. The cove cutoff score was set to 5 to avoid missing *trn* genes with lower cutoff scores. Two *trn* genes (*trnN* and $trnS_1$) failed to be detected by tRNA-Scan SE, but they were identified by visually comparing unassigned regions of the genome with previously determined tRNA counterparts from the Hymenoptera. Thirteen protein-coding genes were identified using an open reading frame (ORF) finder (www.ncbi.nlm.nih.gov/gorf/orfig.cgi), specifying the invertebrate mt genetic code. The initiation and termination codons of some genes were identified according to the boundaries of *trn* genes and comparison with other insect mt sequences. The precise boundaries of *rrn* genes are difficult to define. They were assumed to be bounded by the neighboring *trn* genes (Beckenbach 2011; Beckenbach and Stewart 2009; Dowton et al. 2009*a*). However, the boundary between *rrnL* and *rrnS* was difficult to define in *T. basalis*, as the *trnV* that is usually between the two *rrn* genes is not present here. Instead, we determined this boundary by aligning the *rrn* regions from *T. basalis* with other closely related insect *rrnL* and *rrnS* genes.

Sequence alignment

Mitogenomic sequences from 29 hymenopteran taxa and 7 taxa from other holometabolous insects were obtained from GenBank (Table 1). Nucleotide sequences for each of the 13 protein-coding genes and the 2 *rrn* genes were imported into separate files using MEGA (version 5.05; Tamura et al. 2011) and aligned using Clustal W (Thompson et al. 1994)

Table 1. List of taxa used in phylogenetic analyses.

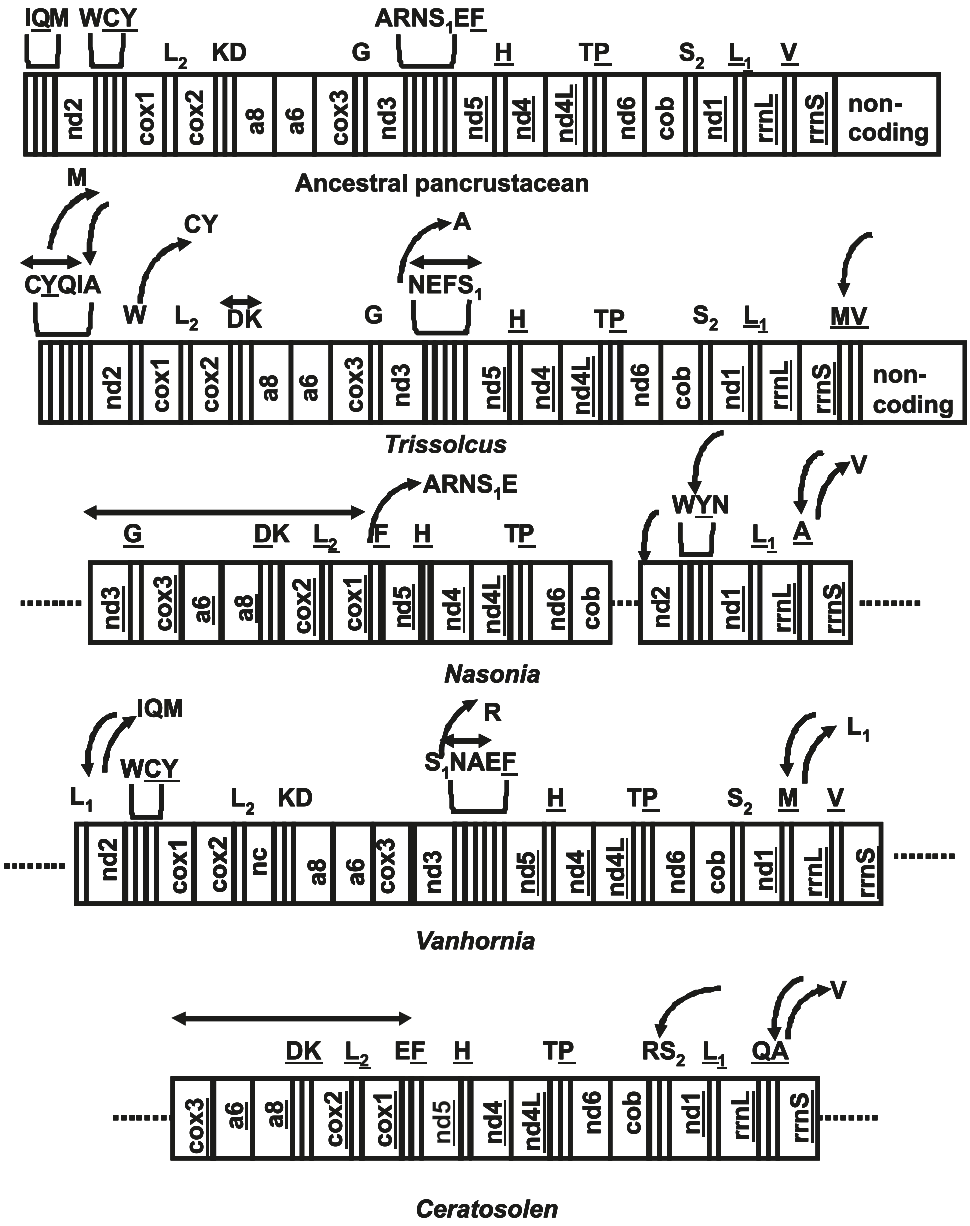
Order	Family	Genus	GenBank accession	Reference
Coleoptera	Tenebrionidae	*Tribolium*	AJ312413	Friedrich and Muqim 2003
Diptera	Ceratopogonidae	*Culicoides*	AB361004	Matsumoto et al. 2009
Mecoptera	Bittacidae	*Bittacus*	HQ696578	Beckenbach 2011
Megaloptera	Sialidae	*Sialis*	FJ859905	Cameron et al. 2009
Neuroptera	Ascalaphidae	*Ascaloptynx*	FJ171324	Beckenbach and Stewart 2009
Lepidoptera	Tortricidae	*Adoxophyes*	NC_008141	Lee et al. 2006
Raphidioptera	Raphidiidae	*Mongoloraphidia*	FJ859902	Cameron et al. 2009
Hymenoptera				
Suborder				
Symphyta				
Cephoidea	Cephidae	*Cephus*	NC_012688	Dowton et al. 2009*a*, 2009*b*
Orussoidea	Orussidae	*Orussus*	NC_012689	Dowton et al. 2009*a*, 2009*b*
Tenthredinoidea	Pergidae	*Perga*	AY787816	Castro and Dowton 2005
Apocrita				
Apoidea	Apidae	*Apis*	NC_001566	Crozier and Crozier 1993
	Apidae	*Bombus*	DQ870926	Cha et al. 2007
	Apidae	*Melipona*	NC_004529	Silvestre et al. 2008
Chalcidoidea	Agaonidae	*Ceratosolen*	AH016005	Chen et al. unpublished
	Pteromalidae	*Nasonia*	NW_001815691	Oliveira et al. 2008
Chrysidoidea	Bethylidae	*Cephalonomia*	FJ823227	Wei et al. unpublished
	Chrysididae	*Primeuchroeus*	AH015389	Castro et al. 2006
Evanioidea	Evaniidae	*Evania*	NC_013238	Wei et al. 2010*b*
Ichneumonoidea	Braconidae	*Aphidius*	GU097658	Wei et al. 2010*a*
	Braconidae	*Cotesia*	NC_014272	Wei et al. 2010*a*
	Braconidae	*Diachasmimorpha*	GU097655	Wei et al. 2010*a*
	Braconidae	*Macrocentrus*	GU097656	Wei et al. 2010*a*
	Braconidae	*Meteorus*	GU097657	Wei et al. 2010*a*
	Braconidae	*Phanerotoma*	GU097654	Wei et al. 2010*a*
	Braconidae	*Spathius*	NC_014278	Wei et al. 2010*a*
	Ichneumonidae	*Diadegma*	NC_012708	Wei et al. 2009
	Ichneumonidae	*Enicospilus*	FJ478177	Dowton et al. 2009*a*, 2009*b*
	Ichneumonidae	*Venturia*	FJ478176	Dowton et al. 2009*a*, 2009*b*
Platygastroidea	Scelionidae	*Trissolcus*	JN903532	Present study
Proctotrupoidea	Vanhorniidae	*Vanhornia*	NC_008323	Castro et al. 2006
Stephanoidea	Stephanidae	*Schlettererius*	FJ478175	Dowton et al. 2009*a*, 2009*b*
Vespoidea	Formicidae	*Pristomyrmex*	NC_015075	Hasegawa et al. 2011
	Formicidae	*Solenopsis*	NC_014669	Gotzek et al. 2010
	Mutillidae	*Radoszkowskius*	NC_014485	Wei and Chen unpublished
	Vespidae	*Abispa*	NC_011520	Cameron et al. 2008
	Vespidae	*Polistes*	EU024653	Cameron et al. 2008

or Muscle (Edgar 2004) as implemented within MEGA 5. For the protein-coding genes (excluding the stop codons), the nucleotide sequences were translated into the amino acid sequences using the invertebrate mt genetic code, and the amino acid sequences were aligned using Clustal W or Muscle. MEGA 5 then creates a nucleotide alignment using the amino acid sequences as a guide. The alignment parameters were the default settings for all genes. The Clustal W alignment parameters were as specified in Cameron et al. (2008). The MUSCLE alignment parameters for the *rrn* genes were gap open penalty = –400, gap extend penalty = 0; and for the protein-coding genes were gap open penalty = –2.9, gap extend penalty = 0. For both types of gene, the maximum memory allocated was 2047 MB, with a maximum of eight iterations. The clustering method used for all iterations was UPGMB, with the length of the minimum diagonal set to 24. Following alignment, individual genes were concatenated prior to phylogenetic analysis.

Phylogenetic analysis

Previous phylogenetic studies using hymenopteran mt genome sequences indicated that nucleotide data analyses were superior to amino acid data analyses, and that Bayesian analyses were superior to parsimony analyses (Castro and Dowton 2007; Dowton et al. 2009*a*). For this reason, we employed Bayesian analyses in this study. The analyses were conducted using MrBayes (version 3.1.2; Ronquist and Huelsenbeck 2003) at the freely available Bioportal server (www.bioportal.uio.no). The two datasets (one aligned using Clustal W, the other aligned using Muscle) were divided into four partitions: the first, second, and third codon positions and *rrn* genes. The GTR+G+I model (nst = 6, rate = invgamma) was chosen as the best-fit model for all of the partitions (MrModelTest 2.3; Nylander et al. 2004). Two analyses (all codon positions included or the third codon positions excluded) were performed for the two alignment datasets. The Markov chain Monte Carlo (MCMC) process was set so that

Fig. 1. Mitochondrial genome organizations of four Proctotrupomorpha taxa, compared with the ancestral pancrutacean mt genome organization (Crease 1999; Cook 2005). The *trn* genes are indicated by single-letter amino acid codes L_1, L_2, S_1, and S_2, and denote $trnL^{CUN}$, $trnL^{UUR}$, $trnS^{AGN}$, and $trnS^{UCN}$, respectively. Genes are transcribed from left to right except those indicated by underlining. Gene movements, relative to the ancestral organization, are indicated with arrows.



four chains (three heated and one cold) ran simultaneously. For each analysis, we conducted four independent runs for 1 000 000 generations, with trees being sampled every 100 generations. Burn-in was discarded according to the plot of generation against the likelihood scores and the sump command in MrBayes. The percentage of trees recovering a particular clade was used as a measure of that clade's posterior probability (Huelsenbeck and Ronquist 2001).

Results and discussion

Genome size and gene content

The almost complete mt genome sequence of *T. basalis* is 15 768 bp (Fig. 1). We were not able to obtain the sequence of part of the noncoding region. Although the sequencing strategy should have sequenced the noncoding region just as frequently as the coding regions, the inability to identify fragments that could be added to our mt contigs is possibly due to the presence of repeats. We did attempt to amplify the noncoding region by conventional PCR, but we were unable to obtain amplicons, as has been reported for a number of hymenopteran mt genomes (Castro and Dowton 2005; Castro et al. 2006; Oliveira et al. 2008). We were able to identify 36 of the 37 genes usually found in animal mt genomes (Table 2); 13 protein-coding genes, 21 of the 22 *trn* genes, 2 *rrn* genes, and part of the AT-rich region. Several short noncoding regions were identified. The longest of these is 60 bp long, and it is located between the $trnS_1$ and *nd5* genes.

Table 2. Locations and nucleotide sequence lengths of genes in the *Trissolcus basalis* mt genome, the lengths of predicted amino acid sequences of protein-coding genes, and their initiation and termination codons.

		Size		Codon	
Gene/region	Nucleotide position	No. of nucleotides	No. of amino acids	Initiation	Termination
trnC	2–62	61			
trnY	82–147	66			
trnQ	178–249	73			
trnI	253–318	66			
trnA	322–387	66			
nd2	447–1425	979	327	ATA	T
trnW	1426–1489	64			
cox1	1490–3025	1536	512	ATA	TAA
trnaL$_2$	3040–3109	70			
cox2	3110–3787	678	226	ATT	TAA
trnD	3790–3858	69			
trnK	3856–3927	72			
a8	3928–4095	168	56	ATT	TAA
a6	4079–4737	659	220	ATG	TA
cox3	4738–5530	793	265	ATG	T
trnG	5531–5598	68			
nd3	5605–5949	345	115	ATA	TAA
trnN	5952–6019	68			
trnE	6017–6080	64			
trnF	6084–6150	67			
trnS$_1$	6154–6212	59			
nd5	6275–7984	1710	570	ATT	TAA
trnH	7985–8049	65			
nd4	8080–9429	1350	450	ATG	TAA
nd4L	9423–9695	273	91	ATA	TAG
trnT	9709–9774	66			
trnP	9774–9837	64			
nd6	9839–10428	590	197	ATA	TA
cob	10429–11565	1137	379	ATG	TAA
trnS$_2$	11581–11650	70			
nd1	11655–12566	912	304	ATA	TAA
trnL$_1$	12573–12638	66			
rrnL	12639–13908	1270			
rrnS	13909–14660	752			
trnM	14661–14727	67			
trnV	14729–14793	65			

There are five genes that overlap: two between protein-coding genes (*a8* and *a6*, and *nd4* and *nd4L*) and three between *trn* genes (*trnD* and *trnK*, *trnN* and *trnE*, and *trnT* and *trnP*).

Nucleotide content

As has been widely published in other insect mt genomes (Simon et al. 1994), the nucleotide content of *T. basalis* is heavily biased towards adenine and thymine (Table 3). The entire sequence has 43.7% A, 9.8% C, 40.5% T, and 6.0% G. The total A+T content is 84.2%, which is typical of other hymenopteran mt genomes. For example, it is almost as high as that of *Apis mellifera* (84.9%: Crozier and Crozier 1993) but higher than that of *Perga condei* (78%: Castro and Dowton 2005) and *Vanhornia eucnemidarum* (80.1%: Castro et al. 2006).

For the mt protein-coding genes of *T. basalis*, the A+T content is a little lower than that of the entire mt genome sequence. However, the first and second codon positions have a lower A+T content (78.9% and 75.4%, respectively), while the third codon position shows a much higher A+T content (92.3%). Conversely, both the *rrn* and *trn* genes have a higher A+T content (87.9% and 88.7%, respectively) when compared with the average for the genome. The nucleotide content bias is inferred to result from mutational pressure (Asakawa et al. 1991; Foster et al. 1997).

Codon usage and amino acid composition

The codon usage in the *T. basalis* mt genome is highly skewed towards codons that are high in A+T content (Table 4). Codons such as CTG (Leu) and CGC (Arg), encoded

Table 3. Nucleotide composition (%) of the *Trissolcus basalis* mt genome.

	Length (bp)	A	C	T	G	A+T
Entire sequence	15 768	43.7	9.8	40.5	6.0	84.2
Protein-coding sequence	11 130	36.5	9.1	45.7	8.6	82.2
J-strand	6885	38.5	11.4	42.8	7.4	81.3
N-strand	4245	33.4	5.5	50.5	10.6	83.9
Codon position						
1st	3710	40.9	8.7	38.0	12.4	78.9
2nd	3710	23.6	14.0	51.8	10.6	75.4
3rd	3710	45.0	4.8	47.3	2.9	92.3
Ribosomal RNA gene sequences	2022	42.7	4.0	45.1	8.1	87.9
Transfer RNA gene sequences	1396	46.4	4.7	42.3	6.5	88.7
J-strand	1002	46.6	5.3	42.1	5.9	88.7
N-strand	394	45.9	3.3	42.6	7.9	88.5
AT-rich region	974	42.8	5.1	47.0	5.0	89.8

by both C- and G-rich codons, are rarely used. Conversely, the AT-rich codons ATT (Ile), TTA (Leu), TTT (Phe), and ATA (Met) are the four most frequently used codons (465, 460, 407, and 341 times, respectively). Within a particular synonymous codon family, AT-rich codons are predominantly used. For example, leucine can be coded by six alternative codons, but TTA is used much more frequently than any other. The relative synonymous codon usage (RSCU: Nei and Kumar 2000) for TTA is 5.23. The RSCU measures the relative proportion that a codon is used within a particular synonymous codon family—the maximum RSCU value for the leucine codon family is 6. For each codon family, the sum of the A- and T-rich codons is close to the maximum possible RSCU value. Similar codon usage bias has been observed in other hymenopteran mt genomes (Castro et al. 2006; Cha et al. 2007; Wei et al. 2009).

Translation initiation and termination codons

Thirteen protein-coding genes were identified using an ORF finder. Table 2 shows the position of these genes in the mt genome of *T. basalis*, their lengths, and translation initiation and termination codons. Conventional ATA, ATT, or ATG initiation codons are assigned to all of the 13 protein-coding genes. Nine genes (*a8*, *cob*, *cox1*, *cox2*, *nd1*, *nd3*, *nd4*, *nd4L*, and *nd5*) are predicted to use the complete termination codons TAA or TAG. Four other genes have incomplete termination codons: TA for *a6* and *nd6*, and T for *nd2* and *cox3*. Incomplete termination codons have been commonly reported for other insect species (Clary and Wolstenholme 1985; Crozier and Crozier 1993). It has been proposed that the complete termination codon (TAA) is created by polyadenylation after transcription (Ojala et al. 1981).

Transfer RNA genes

Twenty-one *trn* genes (59–73 bp) were identified in the *T. basalis* mt genome. Fourteen *trn* genes are encoded on the J-strand (the strand encoding the majority of genes, as defined by Simon et al. 1994), with seven encoded on the N-strand (the minority strand). Their predicted secondary structures are typical cloverleaf structures, except for $trnS_1$ (see Supplementary data,[1] Fig. S1). The D-stem in the dihydrouridine (DHU) arm is absent in the $trnS_1$ gene, which has been reported in other hymenopteran species (Castro et al. 2006; Wei et al. 2010*b*). In addition, mismatched base pairs appear in the DHU stem and acceptor stem, which is common in the insect *trn* genes (Shao and Barker 2003; Zhou et al. 2009). The anticodons are identical to their counterparts in most other published hymenopteran mt genomes.

Ribosomal RNA genes

The small and large ribosomal RNA genes (*rrnS* and *rrnL*) are located on the N-strand. Unlike other hymenopteran mt genomes, they are directly adjacent to each other, without the *trnV* gene between them. The *rrnS* gene is 752 bp with an A+T content of 86.2%. The *rrnL* gene is 1270 bp with an A+T content of 88.8%. These sizes are similar when compared with other Hymenoptera. Based on the range of hymenopteran taxa included in Table 1, *rrnS* ranges from 600 to 811 nucleotides, while *rrnL* ranges from 868 to 1541 nucleotides. The A+T content of *rrnS* is similar when compared with other hymnopteran taxa (Table 1), in which the A+T content ranges from 74.1% to 91.2%. The A+T content of *rrnL* is at the higher end of the range; it is only lower than that of *Cotesia* (89.72%) and *Macrocentrus* (89.55%).

Noncoding regions

The longest noncoding region (partial AT-rich region) of *T. basalis* is 974 bp, which is located between the *rrnS* and *trnC* genes (Fig. 1). The A+T content is 89.8%, which is not markedly higher compared with the remainder of the genome. There are several other short noncoding regions ranging from 2 to 60 bp, which are located throughout the genome. Interestingly, the 60 bp noncoding region has the anticodon of *trnR* (the *trn* gene that could not be found) and the length is similar to the *trn* genes, but it could not be folded into a cloverleaf structure unless overlapping more than 30 bp with *nd5*. If this section is ascribed to the *trnR* gene, the slightly shorter *nd5* gene lacks a stop codon (either complete or incomplete). Recently, some truncated *trn* genes were reported in the mt genomes of velvet worms, with *trn* editing converting the primary transcripts to conventional *trn* structures (Segovia et al. 2011). It is conceivable that the missing *trnR* gene is present in this noncoding region, and it is completed by a similar mechanism. We also investigated

[1]Supplementary data are available with the article through the journal Web site (http://nrcresearchpress.com/doi/suppl/10.1139/g2012-005).

Table 4. Codon usage for protein-coding genes of the *Trissolcus basalis* mt genome.

Codon	Amino acid	No. of codons	RSCU
TTT	Phe	407	1.92
TTC	Phe	18	0.08
TTA	Leu	460	5.23
TTG	Leu	15	0.17
CTT	Leu	28	0.32
CTC	Leu	1	0.01
CTA	Leu	23	0.26
CTG	Leu	1	0.01
ATT	Ile	465	1.88
ATC	Ile	30	0.12
ATA	Met	341	1.92
ATG	Met	15	0.08
GTT	Val	55	1.93
GTC	Val	4	0.14
GTA	Val	48	1.68
GTG	Val	7	0.25
TCT	Ser	92	2.45
TCC	Ser	9	0.24
TCA	Ser	102	2.71
TCG	Ser	4	0.11
CCT	Pro	41	1.45
CCC	Pro	17	0.6
CCA	Pro	55	1.95
CCG	Pro	0	0.0
ACT	Thr	48	1.52
ACC	Thr	11	0.35
ACA	Thr	66	2.1
ACG	Thr	1	0.03
GCT	Ala	34	1.92
GCC	Ala	7	0.39
GCA	Ala	27	1.52
GCG	Ala	3	0.17
TAT	Tyr	161	1.69
TAC	Tyr	30	0.31
TAA	*	12	1.85
TAG	*	1	0.15
CAT	His	50	1.64
CAC	His	11	0.36
CAA	Gln	54	1.93
CAG	Gln	2	0.07
AAT	Asn	252	1.82
AAC	Asn	25	0.18
AAA	Lys	155	1.9
AAG	Lys	8	0.1
GAT	Asp	46	1.74
GAC	Asp	7	0.26
GAA	Glu	61	1.74
GAG	Glu	9	0.26
TGT	Cys	25	1.85
TGC	Cys	2	0.15
TGA	Trp	79	1.93
TGG	Trp	3	0.07
CGT	Arg	8	0.84
CGC	Arg	1	0.11
CGA	Arg	26	2.74
CGG	Arg	3	0.32
AGT	Ser	20	0.53
AGC	Ser	0	0.0
AGA	Ser	70	1.86
AGG	Ser	4	0.11
GGT	Gly	17	0.45
GGC	Gly	4	0.11
GGA	Gly	99	2.61
GGG	Gly	32	0.84

Note: RSCU, relative synonymous codon usage; *, stop codon.

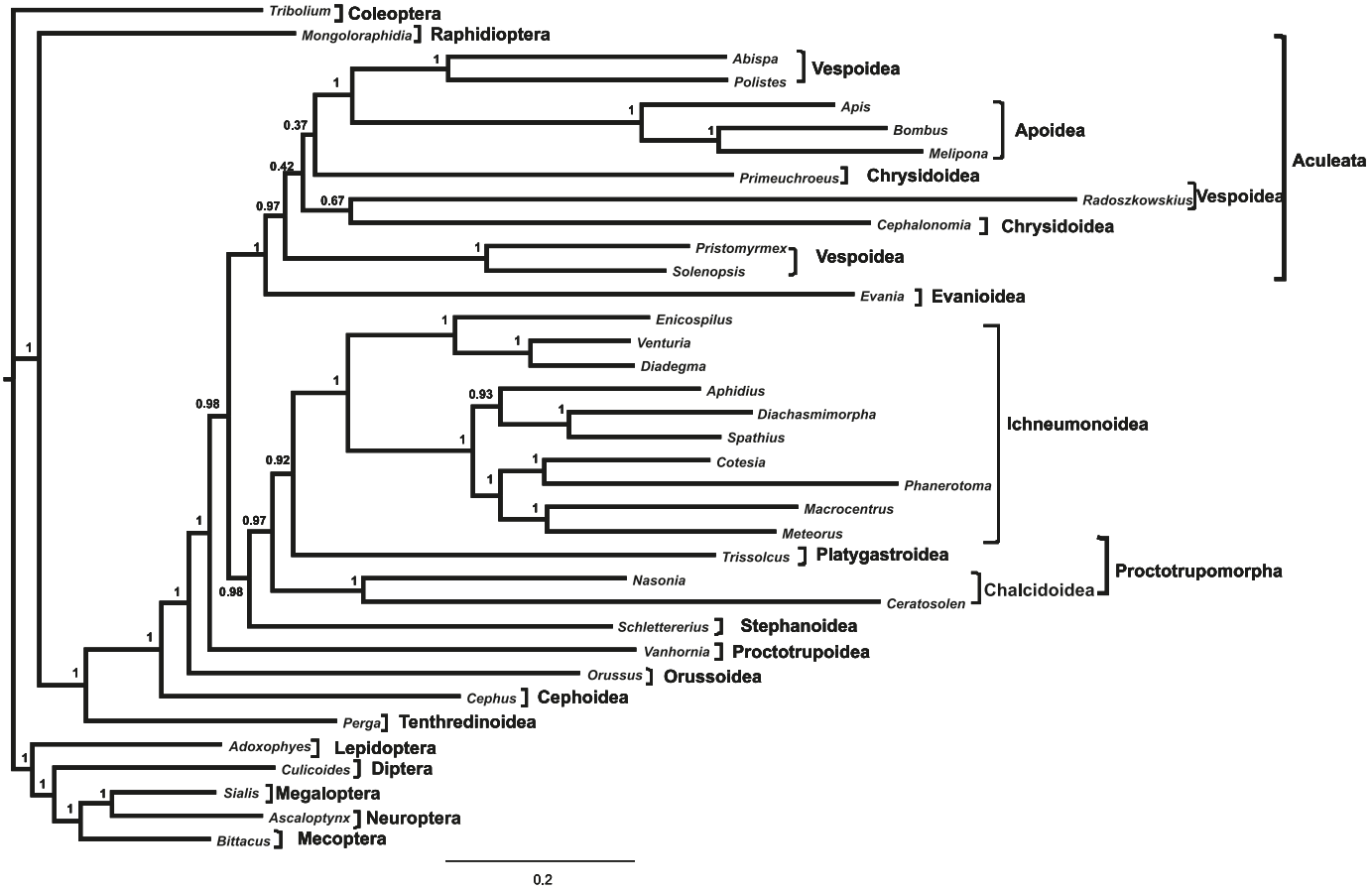
whether *trnR* was present in other noncoding regions, including the *trnA-nd2* junction, but we could find no regions that could be folded into a *trnR* gene.

Genome organization

The mitochondrial genome organization of *T. basalis* is shown in Fig. 1. All of the protein-coding and *rrn* genes have identical positions and transcriptional directions when compared with the organization of the ancestral pancrustacean (Crease 1999; Cook 2005) (Fig. 1), which (as far as is known) is the same organization as the ancestral hymenopteran (Dowton et al. 2009*b*). However, the positions of a number of *trn* genes differ from the ancestral organization. For example, the ancestral positions of *trnC*, *trnY*, and *trnW* are between the *nd2* and *cox1* genes, while in *T. basalis*, *trnC* and *trnY* are between *nd2* and the nonsequenced region (presumably the noncoding region). Similarly, *trnA*, *trnD*, *trnI*, *trnM*, *trnQ*, *trnR*, and $trnS_1$ are not in the ancestral positions.

We then compared the organization of the *T. basalis* mt genome with three other hymenopteran taxa (all from the Proctotrupomorpha), to investigate whether any of the *trn* gene rearrangements were shared with close allies. The Proctotrupomorpha have been consistently recovered as a monophyletic group in molecular phylogenetic studies (Dowton and Austin 2001; Castro and Dowton 2006; Heraty et al. 2011). Shared gene rearrangements are considered reliable indicators of shared ancestry (Boore et al. 1995), and they have been used to infer phylogeny in the Hymenoptera (Dowton 1999), although examples of homoplastic gene rearrangements have been reported (Flook et al. 1995; Dowton and Austin 1999). The mt genome organizations of these three additional taxa from the Proctotrupomorpha are shown in Fig. 1 to facilitate comparisons. All of the protein-coding and *rrn* genes are positioned identically in *T. basalis* and *Vanhornia*. In the available mitogenomic sequences of *Ceratosolen* and *Nasonia*, *Ceratosolen* has an inversion of at least five protein-coding genes (Xiao et al. 2011), while *Nasonia* has an inversion of six protein-coding genes and a translocation of one protein-coding gene (Oliveira et al. 2008). With respect to the position of the larger protein-coding and *rrn* genes, there are three blocks of genes that are present in all four taxa: *cox1-cox2-a8-a6-cox3*, *nd4-nd4L-nd6-cob*, and *nd1-rrnL-rrnS*. However, despite the conservation of the organization of the larger genes in these blocks, the *trn* genes are not conserved, with only three *trn* genes remaining in their ancestral locations in all four taxa (*trnH*, *trnT*, and *trnP*). The $trnS_2$ gene is present in its ancestral location in

Fig. 2. Bayesian analysis of mitogenomic sequences based on the Muscle alignment dataset, including first and second codon positions from protein-coding genes, and the two *rrn* genes. *Tribolium* (Coleoptera) was specified as the outgroup. Posterior probabilities are shown at each node.



three Proctotrupomorpha taxa, with its position unknown in *Nasonia*. All remaining *trn* genes have rearranged in one or more taxa. Interestingly, the *trnA* gene is in the same derived position (next to the *rrnS* gene) in both *Ceratosolen* and *Nasonia*. These are the only two included representatives from the Chalcidoidea—this gene rearrangement may thus be a synapomorphy for a subset of the Chalcidoidea.

Phylogenetic analysis and considerations

Phylogenetic analyses were performed using 36 complete or partial mt genomes, with 29 of these taxa from the Hymenoptera. This is more than double the number of hymenopteran taxa compared with previous studies (14 taxa: Dowton et al. 2009*a*). The most comprehensive analyses of holometabolan relationships place the Hymenoptera at the base of the Holometabola (Savard et al. 2006; Wiegmann et al. 2009), which make it difficult to choose an outgroup. For this reason, we included a range of homometabolous taxa in the analysis. MrBayes allows only a single taxon to be the outgroup, so we chose *Tribolium* (Coleoptera) as the outgroup, but any of the other holometabolous insects would have been appropriate. Two Bayesian analyses (all codon positions included or the third codon positions excluded) were performed for each of the alignment datasets (Clustal W and Muscle).

The intraordinal relationships within the Hymenoptera were broadly congruent across the four analyses, although there were some differences in the topologies. The major difference occurred between analyses that included all codon positons and those that excluded the third codon positions.

In the 29 hymenopteran taxa, there are 10 taxa from the Aculeata, which contains the superfamilies Apoidea, Chrysidoidea, and Vespoidea. The analyses with the third codon positions excluded recovered the Aculeata as a monophyletic group, while the analyses with all codon positions recovered a controversial clade, with *Evania* (a member of Evaniomorpha) disrupting the Aculeata. This contrasts with previous studies (Dowton et al. 2009*a*), in which the Aculeata were recovered as a clade in both analyses (i.e., including or excluding third codon positions). This suggests that the exclusion of third codon positions improves phylogenetic accuracy when analyzing hymenopteran relationships using the whole mt genome, which is consistent with previous analyses (Castro and Dowton 2007; Dowton et al. 2009*a*; Cameron et al. 2009). By contrast, exclusion of third codon positons has not had a positive effect on phylogenetic reconstruction in some insect orders (Diptera: Cameron et al. 2007; Orthoptera: Fenn et al. 2008).

Dataset alignment strategies may also affect the recovered topology (Cameron et al. 2004, 2009). Comparison of the topologies recovered from the datasets aligned by Clustal W and Muscle (both with third codon positions excluded) indi-

cated that the topology produced from the Muscle alignment was more congruent with expected relationships than the Clustal W alignment. Analysis of both datasets recovered a range of monophyletic superfamilies, such as Apoidea, Chalcidoidea, and Ichneumonoidea, but the relationships within the superfamilies varied between the two strategies. For example, within the Braconidae, the Muscle analysis recovered relationships entirely congruent with the most recent analysis of Sharanowski et al. (2011); the monophyly of the noncyclostomes (*Cotesia* + *Phanerotoma* + *Macrocentrus* + *Meteorus*), the monophyly of the cyclostomes (*Spathius* + *Diachasmimorpha*), the monophyly of the microgastroids (*Cotesia* + *Phanerotoma*), and a sister relationship between the cyclostomes and the Aphidiinae (*Aphidius*). By contrast, the Clustal W topology failed to support these expected relationships. This suggests that the phylogenetic relationships at lower taxonomic levels are more sensitive to the alignment strategy.

For the reasons outlined above, we present the tree of the dataset aligned by Muscle, excluding the third codon positons (Fig. 2). Relationships among the Symphyta are recovered as expected—there are only three symphytans included, and they form a paraphyletic grade at the base of the Hymenoptera; Tenthredinoidea + (Cephoidea + (Orussoidea + Apocrita)). As expected, a monophyletic Aculeata is recovered, as is a monophyletic Apoidea. *Evania* + Aculeata form a clade, consistent with the resolution of the Aculeata inside the Evaniomorpha in more taxon-rich analyses (Castro and Dowton 2006; Heraty et al. 2011; Sharkey et al. 2011). However, support for a range of relationships within the Aculeata is low, with posterior probabilities below 0.95. Terminal branch lengths are very long compared with internode lengths. Further, compared with previous analyses, internal relationships within the Aculeata are less congruent with expectation, despite the increase in taxonomic sampling. For example, the Chrysidoidea are not recovered as monophyletic; although Heraty et al. (2011) also failed to recover a monophyletic Chrysidoidea. Similarly, the Vespoidea are polyphyletic, but this is in agreement with recent, broader analyses of hymenopteran relationships (Heraty et al. 2011; Sharkey et al. 2011). Alternatively, Pilgrim et al. (2008) recovered a paraphyletic Vespoidea. Together, these observations suggest that the uncontroversial relationships recovered by Dowton et al. (2009*a*) may have been due to the narrow taxon sampling—for example, the two vespoids are closely related (both from the Vespidae), biasing the analysis toward a finding of monophyly. It suggests that a higher taxonomic sampling is necessary to reliably recover relationships within the aculeates.

With respect to the Proctotrupomorpha, four taxa from three superfamilies (Proctotrupoidea, Platygastroidea, and Chalcidoidea) are included in our analysis. The four taxa failed to form a clade as *Vanhornia* (Proctotrupoidea) was misplaced, while the Chalcidoidea and Platygastroidea were recovered as a grade above the Ichneumonoidea. Within the Ichneumonoidea, the well-established sister group relationship between the Ichneumonidae and Braconidae are well supported (Rasnitsyn 1988; Dowton et al. 1997). In addition, the two groups (cyclostomes and noncyclostomes) of Braconidae were well recovered.

Conclusions

We obtained the nearly complete mt genome of *T. basalis*, which is the first record of a mt genome of the superfamily Platygastroidea. Comparison of the genome organization of *T. basalis* with other Proctotrupomorpha taxa identifies a number of gene rearrangements, which might provide informative characters for the resolution of relationships among the Proctotrupomorpha. Phylogenetic analyses using the entire mt genome sequences indicate that, despite the large number of characters provided by the mt genome, increased taxonomic sampling is likely necessary to reliably recover evolutionary relationships at the family and superfamily levels in the Hymenoptera.

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