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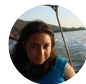

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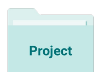

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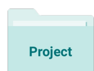

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RESEARCH ARTICLE

The mitochondrial genome of *Octostruma stenognatha* and its phylogenetic implications

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Abstract New sequencing technologies are providing a large-scale proliferation of sequence data, including complete mitochondrial genomes as a side effect of target capture methods. In this study, we use massively parallel sequencing to provide the nearly complete mitochondrial genome of the ant *Octostruma stenognatha*. The annotation of the genome revealed an interesting pattern that agrees with a recent deep reorganization in the systematics within the Formicidae family. This is the first mitogenome for the genus in a lineage, where the scarcity of mitochondrial information has restricted our understanding of its evolutionary history. This is a valuable example of the power and velocity with which products from new sequencing technologies can increase our capacity to understand evolutionary biology, especially in non-model species.

Keywords Mitogenome · Ultraconserved elements · Formicidae · Ants

Introduction

The advent of massively parallel sequencing has provided unprecedented opportunities to investigate many aspects of the tree of life (Dunn et al. 2014). Interestingly, in addition to the availability of information on nuclear genomes, the nature of many new sequencing methods has also improved our understanding of traditional sources of molecular information, such as mitogenomes (Tan et al. 2015). Mitogenomic sequences have been applied to infer relationships between organisms as soon they became most commonly available (e.g., Smith et al. 1993; Boore et al. 1998). The small size of the mitochondrial genome when compared with the nuclear allows studies involving phylogenetics, evolutionary biology, and phylogeography in a computationally feasible way (e.g., Perseke et al. 2013; Havird and Santos 2014; Shen et al. 2015). In general, modifications in mitochondrial gene order are uncommon (Boore 1999) and rarely display homoplasy (Le et al. 2000). These observations indicate the possibility of phylogenetic inferences based on gene order of the mitochondrial genome, which have been broadly applied in the field (e.g., Sankoff et al. 2000; Yuan et al. 2012; Liu et al. 2013). Mitochondrial genomes have also been shown as a powerful tool for the reconstruction of high-level phylogenetic relationship in Hymenoptera (Mao et al. 2015) and as well for basal inferences in the clade (Song et al. 2016).

The order Hymenoptera includes several clades with enormous evolutionary success, such as wasps, bees, and ants, with the latter being a dominant terrestrial taxon since Cretaceous (Dlussky et al. 2003). Despite their ecological importance (Hölldobler and Wilson 1990) and economic impacts (Way and Khoo 1992; Gutrich et al. 2007; Pérez et al. 2010), only few nuclear and mitochondrial genomes have been described for the family Formicidae to date (e.g., Gotzek et al. 2010; Hasegawa et al. 2011; de Melo Rodovalho et al. 2014; Duan et al. 2016; Liu et al. 2016). In this article, we take advantage of advances in massively parallel sequencing to provide the first mitogenome of the ant genus *Octostruma* using the strategy of assembling the genome

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from captured off-target data. This procedure is well known to provide accurate information widely in the field from humans (Picardi and Pesole 2012) to non-model amniotes (do Amaral et al. 2015). Finally, we interpret the obtained results in light of recent taxonomic changes in Myrmicinae.

Materials and methods

Total DNA was extracted from a single specimen of Octostruma stenognatha from Horto Dois Irmãos, Recife, state of Pernambuco, Brazil (08°00′32″S, 34°56′40″W). Voucher specimens from the same nest series are deposited in the myrmecological collection of the Museu de Zoologia da Universidade de São Paulo, Brazil. DNA was extracted using the kit PureLink™ Genomic DNA (Invitrogen, USA), and double strand DNA concentration was measured on a Qubit 2.0 Fluorometer (Life Technologies, Inc.) using the dsDNA High-Sensitivity Assay Kit. The initial DNA concentration for this sample was 0.56 ng/µl. Because of this low concentration, instead of running a traditional electrophoresis gel, we checked DNA integrity using a Bioanalyzer (Agilent Technologies), which showed highly fragmented DNA (possibly because of the age, size, and preservation of the specimen, which was collected almost 15 years ago). Therefore, the sample was not sheared prior to library preparation for Illumina sequencing.

The KAPA Hyper prep kit (Kapa Biosystems) and protocol was chosen to process the Illumina libraries. A bead technique (Fisher et al. 2011) was used with an alternative for SPRI beads (Rohland and Reich 2012) in the library preparation. We used approximately 30 ng of total starting DNA and all reactions, except PCR, were carried out using ¼ of volume indicated by the manufacturer (M. Branstetter pers. com.). The sample was individually labeled using the iTru dual-indexing adapter system (B. Faircloth and T. Glenn, pers. com.), which are similar to the TruSeq layout barcodes (Faircloth and Glenn 2012), and we obtained 4.96 ng/µl of adapter ligated DNA from 16 PCR cycles. A target enrichment system (Gnirke et al. 2009) was performed to obtain ultraconserved elements (UCEs) specifically designed for Hymenoptera (Faircloth et al. 2014) using a modified protocol from Faircloth et al. (2012). We pooled our sample with seven other samples as part of another study for target enrichment (Ströher et al. unpublished results). The pool was concentrated to 147 ng/µl in a vacuum centrifuge and later enriched for 1510 UCEs using manufactured RNA capture probes (MyBaits, Mycroarray, Inc.) and followed the manufacturer's indications except for the on-bead (biotinized) PCR. Two washes were performed to remove off-target sequences; however, this is not totally efficient, leaving copies of mitochondrial DNA in the library. Bioanalyzer (Agilent Technologies) was also used to measure the size of the enriched material, followed by a real-time PCR to access the library concentration adopting the Kapa Library Quantification kit (Kapa Biosystems, Inc.). The pool was combined with five other pools at equimolar ratios and sequenced on Illumina HiSeq 2000 sequencer, using 100-bp paired-end reads at the University of California Santa Cruz, Genome Technology Center.

After sequencing, we used the Illumina bcl2fastq Conversion Software v1.8.4 to convert BCL files into FASTQ and to separate multiplexed samples. Sequence quality control was evaluated using FastQC 0.11.3 (Andrews 2010). This sample produced a total of 2,823,754 sequences. The Trimmomatic tool (Lohse et al. 2012), implemented through Illumiprocessor (Faircloth 2013), was used to remove low-quality regions, barcodes, and adapters. Phyluce (Faircloth 2016) was used to perform the assembly using the default Trinity tool (Grabherr et al. 2011) generating 25,820 contigs with mean length of 358 bp. The resulted contigs were processed with the phyluce workflow for UCEs analysis using a minimum of 80X coverage and 80% identity. A total of 651 unique UCEs were recovered for this sample. As predicted in this kind of large-scale sequencing (Hung et al. 2013), off-target regions are also captured and sequenced in a sufficient way to produce the mitochondrial genome in one contig, usually identified as the longest one. With this result, we performed the mtDNA genome annotation using MITOS (Bernt et al. 2013) with the Invertebrate genetic code, and the base composition was calculated using Geneious 8.1.5 (Kearse et al. 2012). The DNA sequence is available in GenBank with the accession number KX758608.

Results and discussion

The mitogenome of *Octostruma stenognatha* presented here for the first time is composed of 37 genes (22 tRNAs, 2 rRNAs, and 13 protein-coding genes), for a total of 14,183 bp without the control region (Fig. 1a). As observed in other hymenopterans (Wei et al. 2010; Xiao et al. 2011), the base composition in the mtDNA genome of *O. stenognatha* is highly A + T-rich, with only 19.4% being G + C. This is very similar to the base pair composition found in another member of Attini tribe, *Atta laevigata,* where base composition is 80.8% A + T (de Melo Rodovalho et al. 2014). In *Octostruma stenognatha*, 14 genes are encoded by the minus strand and 23 by the plus strand. Regarding the absence of the control region, the challenges in sequencing and assembling this particular part of the mitogenome in insects are recognized for a long time and appear to be related with the high A + T composition allied with repeats sections (Saito et al. 2005; Cameron et al. 2008). Therefore, our result is not unpredicted, since other studies were

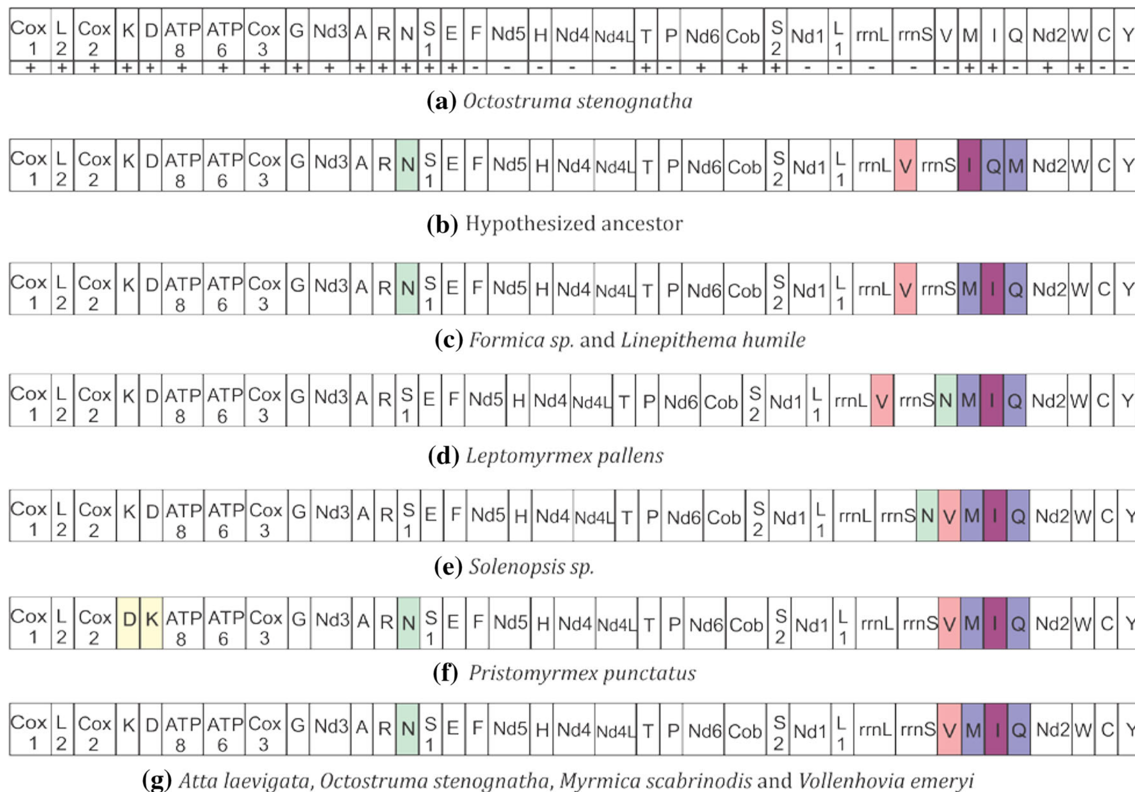

Fig. 1 **a** Mitogenome gene order of *Octostruma stenognatha* and corresponding strand. **b** Hypothetical ancestor (Boore et al. 1998). **c**–**f** *Colored boxes* indicate differences in gene order in relation to the hypothetical ancestor in the indicated species. *Single letters* refer to tRNAs

specific designed for the sequencing of insects, and mitogenomes also had no success in recovering the control region (Mao et al. 2012; Ramakodi et al. 2015).

Although some mitochondrial gene order rearrangement, especially in tRNAs, can be observed in Hymenoptera (Dowton and Austin 1999), only a few changes could be observed in *Octostruma stenognatha* when compared with the hypothetical pancrustacean ancestral (Boore et al. 1998) (Fig. 1b). That is not true in other hymenopterans, such as wasps, in which the gene order rearrangement is widespread, not only for tRNAs, but also for protein-coding genes (Xiao et al. 2011). Several models have been suggested to explain how mitochondrial genes are rearranged, but this issue is still poorly understood (Cameron 2014). Therefore, when comparing the available ants mitogenomes with other hymenopterans, the gene arrangement is relatively stable (e.g., Gotzek et al. 2010; Hasegawa et al. 2011; Berman et al. 2014; de Melo Rodovalho et al. 2014; Yang et al. 2016) indicating that this can be a characteristic in the Formicidae family. The position of the trnV gene, after and not between the ribosomal genes, is unusual when compared with other ants (Berman et al. 2014; Yang et al. 2016) and the hypothetical ancestral gene order (Gotzek et al. 2010), although this feature can be found in some Myrmicine ants (e.g., Hasegawa et al. 2011; Babbucci et al. 2014) and is not exclusive to Hymenoptera (Mao et al. 2015). The higher mobility of tRNAs in relation to other genes is expected, given that shifts in gene order are not equally frequent across mitogenomes (Moritz 1987). Although phylogenetic inference using gene order can be problematic when homoplasy can occur in the group, this feature can still be accounted for (Babbucci et al. 2014). An example in Hymenoptera is the paraphyly and basal position of Symphyta that was recently supported by the use of new mitochondrial genomes (Song et al. 2016).

A recently proposed new hypothesis for the phylogenetic relationships within the ant group Myrmicinae (Ward et al. 2014) has challenged some earlier ideas about the evolutionary relationships within the subfamily—the largest among ants. Based on 11 nuclear genes, Ward et al. (2014) reduced drastically the number of tribes from 25 to 6. In one of the most noteworthy changes, the tribe Attini is not restricted to fungus-growing species, but rather includes other genera, such as *Octostruma*. This genus has a long history of instability in its taxonomy, with its systematic position being first described as a subgenus of *Rhopalothrix* (Forel 1917). Only 30 years later, *Octostruma* was elevated to genus (Brown 1948), being subsequently allocated into the tribe Basicerotini (Brown 1949). The genus remained stable in that position for more than 50 years, until being

transferred to the tribe Dacetini (Baroni Urbani and De Andrade 1994). However, Bolton (1994) almost immediately restored the position of *Octostruma* within Basicerotini. In 2007, Baroni Urbani and De Andrade not only returned *Octostruma* to Dacetini, but also considered this genus a junior synonym of *Basiceros*. This classification was not adopted by most of the subsequent authors, so that *Octostruma* appears as a valid genus in the paper by Ward et al. (2014), as it was finally transferred to the tribe Attini. The fact that *Octostruma stenognatha* has an identical mitochondrial gene order as *Atta laevigata* (de Melo Rodovalho et al. 2014) corroborates the recent change of the genus inside the Attini tribe (Ward et al. 2014). In addition, as a final corroboration that the annotation of the mitogenome was correct, we recovered the place of the trnN gene as the same as the ancestral, position that is being claimed to be the "authentic" one for ants with mitogenomes already sequenced (Babbucci et al. 2014), as opposed to other findings (Gotzek et al. 2010; Berman et al. 2014). The *Octostruma* mitogenome has also high similarity with another member of the tribe Attini: *Wasmannia auropunctata* (Duan et al. 2016), the only possible divergence it is an inversion between the control region and the trnV gene that cannot be verified in this study.

Conclusions

The recent technological advances are accelerating the number of mitogenomes available. Using massively parallel sequencing, we provide here the first mitochondrial genome for the *Octostruma* genus. The characteristics of this mitogenome are very similar to other hymenopterans and comparing this genome with those of other ants is consistent with recent taxonomic changes in the Myrmicinae clade. We expect that soon we will be able to compare genomes widely in Formicidae, making possible a better understanding of the evolutionary history in this family.

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References

Andrews S. (2010). FastQC: a quality control tool for high throughput sequence data. Available online at: http://www.bioinformatics.babraham.ac.uk/projects/fastqc.

Babbucci M, Basso A, Scupola A, Patarnello T, Negrisolo E (2014) Is it an ant or a butterfly? Convergent evolution in the Mitochondrial Gene Order of Hymenoptera and Lepidoptera. Genome Biol Evol 6:3326–3343. doi:10.1093/gbe/evu265

Baroni Urbani C, de Andrade ML (1994) First description of fossil Dacetini ants with a critical analysis of the current classification of the tribe (amber collection Stuttgart: Hymenoptera, Formicidae. VI: Dacetini). Stuttgarter Beiträge zur Naturkunde Serie B 198:1–65

Berman M, Austin CM, Miller AD (2014) Characterisation of the complete mitochondrial genome and 13 microsatellite loci through next-generation sequencing for the new Caledonian spider-ant Leptomyrmex pallens. Mol Biol Rep 41:1179–1187. doi:10.1007/s11033-013-2657-5

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF (2013) MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol 69:313–319. doi:10.1016/j.ympev.2012.08.023

Boore JL (1999) Animal mitochondrial genomes. Nucleic Acids Res 27:1767–1780. doi:10.1093/nar/27.8.1767

Boore JL, Lavrov DV, Brown WM (1998) Gene translocation links insects and crustaceans. Nature 392:667–668. doi:10.1038/33577

Brown WL Jr (1948) A preliminary generic revision of the higher Dacetini (Hymenoptera: Formicidae). Trans Am Entomol Soc 74:101–129

Brown WLJ (1949) Revision of the ant tribe Dacetini. I. Fauna of Japan, China and Taiwan. Muschi 20:1:25

Cameron SL (2014) Insect mitochondrial genomics: implications for evolution and Phylogeny. Annu Rev Entomol 59:95–117. doi:10.1146/annurev-ento-011613-162007

Cameron SL, Dowton M, Castro LR, Ruberu K, Whiting MF, Austin AD, Diement K, Stevens J (2008) Mitochondrial genome organization and phylogeny of two vespid wasps. Genome 51:800–808. doi:10.1139/g08-066

de Melo Rodovalho C, Lyra ML, Ferro M, Bacci Jr M (2014) The Mitochondrial genome of the leaf-cutter ant *Atta laevigata*: a Mitogenome with a large number of Intergenic spacers. PLoS One 9(5):e97117. doi:10.1371/journal.pone.0097117

Dlussky GM, Brothers DJ, Rasnitsyn AP (2003) The first late Cretaceous ants (Hymenoptera: Formicidae) from southern Africa, with comments on the origin of the Myrmicinae. Insect Syst Evol 35:1–13. doi:10.1163/187631204788964727

do Amaral RF, Neves LG, Resende MFR, Mobili F, Miyaki CY, Pellegrino KCM, Biondo C (2015) Ultraconserved elements Sequencing as a low-cost source of complete Mitochondrial Genomes and Microsatellite markers in non-model Amniotes. PLoS One 10:e0138446. doi:10.1371/journal.pone.0138446

Dowton M, Austin AD (1999) Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the Hymenoptera. Mol Biol Evol 16:298–309. doi:10.1093/oxfordjournals.molbev.a026111

Duan X-Y, Peng X-Y, Qian Z-Q (2016) The complete mitochondrial genomes of two globally invasive ants, the Argentine ant *Linepithema humile* and the little fire ant *Wasmannia auropunctata*. Conserv Genet Resour. doi:10.1007/s12686-016-0555-6

Dunn CW, Giribet G, Edgecombe GD, Hejnol A (2014) Animal Phylogeny and its evolutionary Implications. Annu Rev Ecol Evol Syst 45:371–395. doi:10.1146/annurev-ecolsys-120213-091627

Faircloth BC (2013) Illumiprocessor: a Trimmomatic wrapper for parallel adapter and quality trimming. http://dx.doi.org/10.6079/J9ILL

Faircloth BC (2016) PHYLUCE is a software package for the analysis of conserved genomic loci. Bioinformatics 32:786–788. doi:10.1093/bioinformatics/btv646

Faircloth BC, Glenn TC (2012) Not all sequence tags are created equal: designing and validating sequence identification tags robust to Indels. PLoS One 7:e42543. doi:10.1371/journal.pone.0042543

Faircloth BC, McCormack JE, Crawford NG, Harvey MG, Brumfield RT, Glenn TC (2012) Ultraconserved elements anchor Thousands of genetic markers spanning multiple evolutionary Timescales. Syst Biol 61:717–726. doi:10.1093/sysbio/sys004

Faircloth BC, Branstetter MG, White ND, Brady SG (2014) Target enrichment of ultraconserved elements from arthropods provides a genomic perspective on relationships among Hymenoptera. Mol Ecol Resour 15:489–501. doi:10.1111/1755-0998.12328

Fisher S, Barry A, Abreu J, Minie B, Nolan J, Delorey TM, Young G, Fennell TJ, Allen A, Ambrogio L, Berlin AM, Blumenstiel B, Cibulskis K, Friedrich D, Johnson R, Juhn F, Reilly B, Shammas R, Stalker J, Sykes SM, Thompson J, Walsh J, Zimmer A, Zwirko Z, Gabriel S, Nicol R, Nusbaum C (2011) A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. Genome Biol 12:R1. doi:10.1186/gb-2011-12-1-r1

Forel A (1917) Cadre synoptique actuel de la faune universelle des fourmis. Bulletin de la Société Vaudoise des Sciences Naturelles 51:229–253

Gnirke A, Melnikov A, Maguire J, Rogov P, LeProust EM, Brockman W, Fennell T, Giannoukos G, Fisher S, Russ C, Gabriel S, Jaffe DB, Lander ES, Nusbaum C (2009) Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. Nat Biotechnol 27:182–189. doi:10.1038/nbt.1523

Gotzek D, Clarke J, Shoemaker D (2010) Mitochondrial genome evolution in fire ants (Hymenoptera: Formicidae). BMC Evol Biol 10:300. doi:10.1186/1471-2148-10-300

Grabherr MG, Haas BJ, Yassour M, Levin JZ, Thompson DA, Amit I, Adiconis X, Fan L, Raychowdhury R, Zeng Q, Chen Z, Mauceli E, Hacohen N, Gnirke A, Rhind N, di Palma F, Birren BW, Nusbaum C, Lindblad-Toh K, Friedman N, Regev A (2011) Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nat Biotechnol 29:644–652. doi:10.1038/nbt.1883

Gutrich JJ, VanGelder E, Loope L (2007) Potential economic impact of introduction and spread of the red imported fire ant, *Solenopsis invicta*, in Hawaii. Environ Sci Policy 10:685–696. doi:10.1016/j.envsci.2007.03.007

Hasegawa E, Kobayashi K, Yagi N, Tsuji K (2011) Complete mitochondrial genomes of normal and cheater morphs in the parthenogenetic ant Pristomyrmex punctatus (Hymenoptera: Formicidae). Myrmecol News 15(85):90

Havird JC, Santos SR (2014) Performance of single and Concatenated sets of Mitochondrial genes at Inferring Metazoan relationships relative to full Mitogenome data. PLoS One 9:e84080. doi:10.1371/journal.pone.0084080

Hölldobler B, Wilson EO (1990) The ants. Belknap Press of Harvard University Press, Cambridge

Hung C-M, Lin R-C, Chu J-H, Yeh C-F, Yao C-J, Li S-H (2013) The de novo assembly of Mitochondrial Genomes of the extinct passenger pigeon (Ectopistes migratorius) with next generation sequencing. PLoS One 8:e56301. doi:10.1371/journal.pone.0056301

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A (2012) Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649. doi:10.1093/bioinformatics/bts199

Le TH, Blair D, Agatsuma T, Humair P-F, Campbell NJH, Iwagami M, Littlewood DTJ, Peacock B, Johnston DA, Bartley J, Rollinson D, Herniou EA, Zarlenga DS, McManus DP (2000) Phylogenies inferred from Mitochondrial gene orders–a cautionary tale from the parasitic Flatworms. Mol Biol Evol 17:1123–1125. doi:10.1093/oxfordjournals.molbev.a026393

Liu G-H, Shao R, Li J-Y, Zhou D-H, Li H, Zhu X-Q (2013) The complete mitochondrial genomes of three parasitic nematodes of birds: a unique gene order and insights into nematode phylogeny. BMC Genom 14:414. doi:10.1186/1471-2164-14-414

Liu N, Duan X-Y, Qian Z-Q, Wang X-Y, Li X-L, Ding M-Y (2016) Characterization of the complete mitochondrial genome of the Myrmicine ant *Vollenhovia emeryi* (Insecta: Hymenoptera: Formicidae). Conserv Genet Resour. doi:10.1007/s12686-016-0535-x

Lohse M, Bolger AM, Nagel A, Fernie AR, Lunn JE, Stitt M, Usadel B (2012) RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. Nucl Acids Res 40:W622–W627. doi:10.1093/nar/gks540

Mao M, Valerio A, Austin AD, Dowton M, Johnson NF (2012) The first mitochondrial genome for the wasp superfamily Platygastroidea: the egg parasitoid Trissolcus basalis. Genome 55:194–204. doi:10.1139/g2012-005

Mao M, Gibson T, Dowton M (2015) Higher-level phylogeny of the Hymenoptera inferred from mitochondrial genomes. Mol Phylogenet Evol 84:34–43. doi:10.1016/j.ympev.2014.12.009

Moritz C (1987) Evolution of animal Mitochondrial Dna: relevance for population biology and systematics. Annu Rev Ecol Syst 18:269–292. doi:10.1146/annurev.ecolsys.18.1.269

Pérez SP, Corley JC, Farji-Brener AG (2010) Potential impact of the leaf-cutting ant *Acromyrmex lobicornis* on conifer plantations in northern Patagonia, Argentina. Agric For Entomol 13:191–196. doi:10.1111/j.1461-9563.2010.00515.x

Perseke M, Golombek A, Schlegel M, Struck TH (2013) The impact of mitochondrial genome analyses on the understanding of deuterostome phylogeny. Mol Phylogenet Evol 66:898–905. doi:10.1016/j.ympev.2012.11.019

Picardi E, Pesole G (2012) Mitochondrial genomes gleaned from human whole-exome sequencing. Nat Methods 9:523–524. doi:10.1038/nmeth.2029

Ramakodi MP, Singh B, Wells JD, Guerrero F, Ray DA (2015) A 454 sequencing approach to dipteran mitochondrial genome research. Genomics 105:53–60. doi:10.1016/j.ygeno.2014.10.014

Rohland N, Reich D (2012) Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. Genome Res 22:939–946. doi:10.1101/gr.128124.111

Saito S, Tamura K, Aotsuka T (2005) Replication origin of mitochondrial DNA in insects. Genetics 171:1695–1705

Sankoff D, Bryant D, Deneault M, Lang BF, Burger G (2000) Early Eukaryote evolution based on Mitochondrial Gene Order Breakpoints. J Comput Biol 7:521–535. doi:10.1089/10665270075005092

Shen H, Braband A, Scholtz G (2015) The complete mitogenomes of lobsters and crayfish (Crustacea: Decapoda: Astacidea) reveal surprising differences in closely related taxa and convergences to Priapulida. J Zool Syst Evol Res 53:273–281. doi:10.1111/jzs.12106

Smith MJ, Arndt A, Gorski S, Fajber E (1993) The phylogeny of echinoderm classes based on mitochondrial gene arrangements. J Mol Evol 36:545–554. doi:10.1007/bf00556359

Song S-N, Tang P, Wei S-J, Chen X-X (2016) Comparative and phylogenetic analysis of the mitochondrial genomes in basal hymenopterans. Sci Rep 6:20972. doi:10.1038/srep20972

Tan MH, Gan HM, Schultz MB, Austin CM (2015) Corrigendum to 'MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes' [Mol. Phylogenet. Evol. 85 (2015) 180–188]. Mol Phylogenet Evol 87:118. doi: 10.1016/j.ympev.2015.03.017

Ward PS, Brady SG, Fisher BL, Schultz TR (2014) The evolution of Myrmicine ants: phylogeny and biogeography of a hyperdiverse ant clade (Hymenoptera: Formicidae). Syst Entomol 40:61–81. doi:10.1111/syen.12090

Way M (1992) Role of ants in pest-management. Annu Rev Entomol 37:479–503. doi:10.1146/annurev.ento.37.1.479

Wei S, Shi M, Sharkey MJ, van Achterberg C, Chen X (2010) Comparative mitogenomics of Braconidae (Insecta: Hymenoptera) and the phylogenetic utility of mitochondrial genomes with special reference to Holometabolous insects. BMC Genom 11:371. doi:10.1186/1471-2164-11-371

Xiao J-H, Jia J-G, Murphy RW, Huang D-W (2011) Rapid evolution of the Mitochondrial genome in Chalcidoid Wasps (Hymenoptera: Chalcidoidea) driven by parasitic lifestyles. PLoS One 6:e26645. doi:10.1371/journal.pone.0026645

Yang S, Li X, Cai L-G, Qian Z-Q (2016) Characterization of the complete mitochondrial genome of *Formica selysi* (Insecta: Hymenoptera: Formicidae: Formicinae). Mitochondrial DNA 27(5):3378–3380

Yuan Y, Li Q, Yu H, Kong L (2012) The complete Mitochondrial Genomes of Six Heterodont Bivalves (Tellinoidea and Solenoidea): variable gene arrangements and phylogenetic implications. PLoS ONE 7:e32353. doi:10.1371/journal.pone.0032353

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