The first complete mitochondrial genome of Cheyletus malaccensis (Acari: Cheyletidae): gene rearrangement

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Article

The first complete mitochondrial genome of *Cheyletus malaccensis* (Acari: Cheyletidae): gene rearrangement

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Abstract

The predatory mite *Cheyletus malaccensis* (Acari: Cheyletidae), commonly occurring in stores of various food commodities, is an important natural enemy of stored product pests. Disentangling the mt genome sequence of *C. malaccensis* at molecular level can decrease uncertainties during morphological identification and is useful in reconstructing the phylogeny of Acariformes group. In this study, the complete mitogenome of *C. malaccensis* was sequenced by the next-generation sequencing. After assembly and annotation, we found the circular 14,732 bp mitogenome of *C. malaccensis*, containing 13 protein coding genes, 2 ribosomal RNA (rRNA) genes and 22 transfer RNA (tRNA) genes. Compared with the ancestral mitogenome organization of arthropods, most of tRNA were truncated without D-arm or/and TψC-arm. Rearrangement was found in 12 mitogenome genes. Phylogenetic analyses based on the mitogenome data from other 29 mite species were inferred by Bayesian and maximum likelihood methods, which strongly supported the closer relationship between *C. malaccensis* and Tetranychidae than other mites. The obtained results represent the first complete mitochondrial genome record for Cheyletidae group. It may help improve molecular phylogenetic relationship and population genetics of the Cheyletidae.

Keywords: *Cheyletus malaccensis*, complete mitochondrial genome, molecular phylogenetics

Introduction

The predatory mite *Cheyletus* species, including *Cheyletus malaccensis* Oudemans (Acari: Cheyletidae), are currently widely distributed in food and feed commodity stores in Asia (Ardeshir 2017; Mariana *et al.* 2010), Europe (Stejskal *et al.* 2015) and North America (Sinha & Wallace1973). They feed on various pest phytophagous mites such as *Acarus siro* (Linnaeus), small insects such as book lice (e.g. *Liposcelis spp.*), and stored grain insect eggs and larvae (Cebolla *et al.* 2009; Hubert *et al.* 2006; Lukáš *et al.* 2007). *C. malaccensis* can develop through parthenogenesis or sexual reproduction and can bear a wide range of temperatures. Predatory activity of *C. malaccensis* was found to be compatible with another environmentally friendly pest control methods like diatomaceous earth (Palyvos *et al.* 2006) and antifeedants, such as amylase inhibitors (Hubert *et al.* 2007). These traits make *Cheyletus* species the promising natural enemies that can be widely employed to control stored products pests. However, there are significant differences among predatory and biological ability among various *Cheyletus* species. Therefore, a description of *Cheyletus* spp. at the molecular level is the prerequisite for their population genetic difference and understanding of their biological differences. Molecular understanding of these species may also contribute to accuracy and improvement of studies concerning higher phylogeny of mites and

arthropods. However, the currently available molecular data for *C. malaccensis* partially enables only its identification but they do not enable to compare geographical inter-population variability and comprehensive phylogeny analysis.

The mitochondrial (mt) genomes are increasingly used for animal species identification, population genetics and phylogeny inference presently (Chuan *et al.* 2012; Li *et al.* 2015; Nelson *et al.* 2012). It is proofed that the application of the mt genome to phylogenetic analysis has solved many problems ranging from species level to order level (Feng *et al.* 2019). The typical mt genome contains 13 protein-coding genes (PCGs), two ribosome RNA (rRNA) genes and 22 transger RNA (tRNA) genes (Boore 1999; Wolstenholme 1992). For *C. malaccensis*, the *cox1* and *rrnS* genes had been analyzed in 2016 (Yang *et al.* 2016), however, the mt genomes of Cheyletidae have not been sequenced. Species in Cheyletidae are difficult for identification according to morphological features. For example, *Cheyletus fortis* and *C. malaccensis* were formerly considered as two separate species when compared by morphological characteristics. However, recently these two species were confirmed to be the same species by molecular methods (Tian 2011). The species-specific primer to distinguish *C. eruditus* and *C. malaccensis* has also been designed (Wu *et al.* 2016), and has served well for accurate identification of both species in the laboratory practice.

The mt genome was suggested to constitute the base of molecular study regarding *C. malaccensis*. In this study we sequenced the mt genome of *C. malaccensis,* analyzed the data and genome organization, and constructed the phylogenetic tree with limited data. The general goal was to expand our understanding of *C. malaccensis* at the molecular level, and to promote the mitochondrial genome based phylogenetic study of predatory mites.

Materials

Sampling and DNA extraction

Samples of *C. malaccensis* were collected from Haikou, China, then cultured in Academy of National Food and Strategic Reserves Administration in China. The samples were identified based on their morphology characteristics (Shen 1997). Genomic DNA was extracted from 50 adult mites using TIANamp Micro DNA Kit following the instruction. The UV-Vis Spectrophotometer Q5000 (Q5000, Quawell Technology, Inc. USA) was used to quantify the extracted DNA (23.76ug) for library construction.

DNA Sequencing and mt genome assembly

Total DNA of *C. malaccensis* was sent to Berry Genomics Company for library preparation, and finally sequenced on an Illumina sequencer. The insert size was 250bp with 150bp pair-end sequencing.

After getting the raw data, quality assessment was conducted using FastQCv0.11.7 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). Trimmomatic v0.36 (Lohse *et al.* 2012) was used to the remove adapter sequences. The mt genome assembly strategy followed Feng *et al.* 2018. Briely, to reconstruct the mt genome, *cox1* gene fragments were chosen as "anchors". We sequenced the *cox1* gene fragments using universal primer pairs LCO1490–HCO2198 (Folmer *et al*. 1994). We applied "map to reference" strategy and mapped all cleaned reads to the "anchor" using Geneious (Kearse *et al*. 2012). Illumina sequence-reads were assembled using the sequence *cox1* as initial references. The contigs were then extended using the assembly parameters: (1) minimum overlap 50 bp, and (2) minimum similarity 99%, until the full circular mt chromosome sequences were obtained.

The PCR amplification of *cox1* gene was in 25 ul containing 12.5ul of 2×Taq Mix (Tiangen, Beijing, China), 1 ul of each primer (10 uM), 1ul genomic DNA and 9.5ul ddH_2O. PCR cycling

conditions were: 95°for 3 min, followed by 35 cycles of 94°for 1 min, 53°for 1 min, 72°for 1 min, and finally 72°for 10 min.

Bioinformatic analyses

The protein coding genes (PCGs), ribosome RNA (rRNA) genes and transfer RNA (tRNA) genes were identified using MITOS Web Server (http://mitos.bioinf.uni-leipzig.de/index.py) (Bent *et al.*, 2013). PCGs and RNA genes were confirmed by alignment against close species while tRNA genes were confirmed by ARWEN. During tRNA search, we alternatively searched tRNA genes based on the methods by Xue *et al.* (2018). The base composition was analyzed with muscle algothrim in MEGA 7.0 (Kumar *et al.*, 2016). Nucleotide compositional skew was measured using the following formula: AT skew = A-T/A+T and GC skew = G-C/G+C.

Phylogenetic analysis

To better understand molecular phylogeny of *C. malaccensis* in Arachnida, a total of 30 Arachnida species were used in phylogenetic analysis, including 29 representative stored mite species (Table S1). All 13 PCGs were aligned in MEGA 7.0. Two rRNA genes were aligned using MAFFT v7.0 online sever (Katoh *et al.* 2019). Then ambiguous positions in the alignment of PCGs and rRNA genes were removed by using Gblocks v0.91b web server (Castresana 2000). The concatenated phylogenetic trees were reconstructed based on the two datasets: 1) dataset "PCGsrRNA", in which there are concatenated 13 protein-coding genes (*atp6*, *atp8*, *cox1*, *cox2*, *cox3*, *cob*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4l*, *nad5*, *nad6*) and two rRNA genes (*rrnL* and *rrnS*); 2) dataset "PCGs", including only 13 protein-coding genes. The Bayesian methods (BI) and maximum likehood (ML) were used to reconstruct the phylogenetic tree. The ML method was performed with PhyML (Guindon *et al.* 2010) (http:/www.atgc-montpellier.fr/phyml/) and the online Smart Model Selection for optimal model selection. General time reversible (GTR) model was finally chosen. We also applied Bayesian method using MrBayes 3.2.2 (Ronquist & Huelsenbeck 2003). The GTR+I+G model was used. The datasets were conducted with two simultaneous runs of 2 million generations, each with one cold and three heated chains. Samples were drawn every 1,000 Markov chain Monte Carlo (MCMC) steps, with the first 25% discarded as burn-in. The stationarity was considered reached and stopped run when the average standard deviation of split frequencies was below 0.01.

Results and Discussion

Mt genome organization and nucleotide composition

The length of the mt genome of *C. malaccensis* is 14,732bp (Figure 1), including 13 PCGs, two rRNAs and 22 tRNAs (Table 1). The symmetric nucleotide compositions are A:47.3%, C:14.1%, G:6.8% and T:31.8%. The content of G is small and concentrated in *cox1* (10.5%) and *cox2* (8.7%) genes, which shows that these two genes are more conservative and stable. The AT skew is 0.196, which is similar with most AT skews of the arthropod animals (Dermauw *et al.* 2009; Sun *et al.* 2014a). Four PCG genes (*nad5, nad4, nad4l, nad1*), two rRNA genes and seven tRNA genes (*trnL1, F, P, Q, L2, Y, C*) of *C. malaccensis* were encoded by the minor strand and the other were encoded by the major strand. Two tRNA genes were contained by protein coding gene, *trnH* gene located in *nad5* and *trnV* was in 16S rRNA. In addition, *trnA* was in control region. Compared with the Arthropod ancestral pattern (Palopoli *et al.* 2014), the mt genome of *C. malaccensis* has different arrangements. Rearrangement was found in 12 genes, including 11 tRNA genes (*trnE*, *S1*, *N*, *M*, *Y*, *I*, *L2*, *Q*, *R*, *V*, *L1*) and 12S rRNA gene. Except *trnR* and *trnV* were in different location, *C. malaccensis* has the similar gene rearrangement with *Demodex brevis* and *D. folliculorum* (Palopoli *et al.* 2014), belonging to Cheyletoidea. To fully understand the mitochondrial arrangement of Cheyletoidea, and analyze its characteristics, more species need to be tested.

TABLE 1 Annotation of the mitochondrial genome of *Cheyletus malaccensis*.

Gene	Location	Length	Strand	Start codon	Stop codon	Anticodon	Intergenic length
trnL1(cta)	1–55	55	N			CUA	0
rrnS	66–706	641	N				10
trnF(tta)	716–772	57	N			UUC	9
nad5	720–2426	1707	N	ATT	TAG		-53
trnH(cat)	1765–1815	51	J			CAT	/
nad4	2474–3742	1269	N	ATG	TAG		47
nad4l	4109–4384	276	N	ATA	TAA		366
trnT(aca)	4377–4427	51	J			ACA	-8
trnP(cca)	4429–4483	55	N			CCA	1
nad6	4487–4894	408	J	ATG	TAA		3
cob	4899–6014	1116	J	ATG	TAA		4
trnS2(tca)	5978–6024	47	J			TCA	-37
nad1	6022–6900	879	N	ATA	TAA		-3
rrnL	6907–7923	1017	N				6
trnV(gtt)	7022–7076	55	J			GUU	/
trnQ(caa)	7881–7935	55	N			CAA	-43
trnL2(tta)	7930–7983	54	N			UUA	-6
trnI(atc)	7987–8041	55	J			AUC	3
trnY(tac)	8044–8103	60	N			UUA	2
trnR(cga)	8118–8171	54	J			CGA	14
nad2	8163–9137	975	J	ATA	TAA		-9
trnW(tga)	9136–9202	67	J			UGA	-2
trnM(atg)	9202–9266	65	J			AUG	-1
trnN(aac)	9275–9335	61	J			AAC	8
trnS1(agc)	9336–9384	49	J			AGC	0
trnE(gaa)	9391–9442	52	J			GAA	6
trnC(tgc)	9470–9529	60	N			TGC	27
cox1	9547–11196	1650	J	ATT	TAA		17
cox2	11197–11841	645	J	ATG	TAA		0
trnK(ctt)	11847–11908	62	J			AAG	5
trnD(gac)	11904–11953	50	J			GAC	-5
atp8	11963–12097	135	J	ATA	TAG		9
atp6	12094–12756	663	J	ATA	TAA		-4
cox3	12768–13571	804	J	ATG	TAA		11
trnG(gga)	13550–13599	50	J			GGA	-22
nad3	13598–13933	336	J	ATA	TAA		-2
CR	13934–14732	336	J				0
trnA(gcc)	14309–14367	59	J			GCC	/

Note: N/J indicates that the gene was encoded by the minor/major strand, / indicates that tRNA gene was contained by protein coding gene or CR.

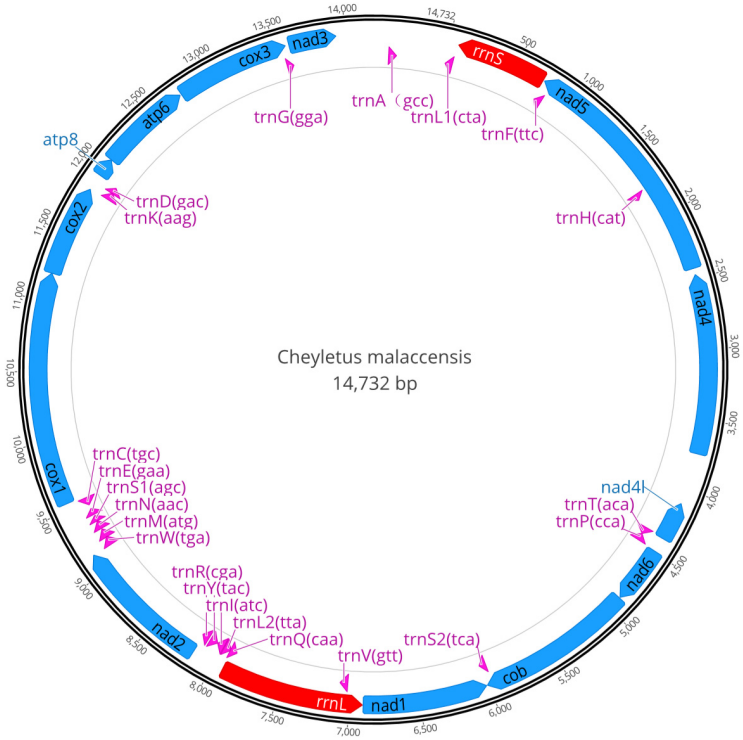

FIGURE 1. The mitochondrial genome arrangements of *Cheyletus malaccensis*.
Note: the blue is PCGs, the red is rRNA genes, the purple is tRNA genes.

The total length of intergenic sequences in *C. malaccensis* was 548 bp, including two intergenic sequences longer than 30 bp, 366 bp (between *nad4* gene and *nad4l* gene) and 47 bp (between *nad4* gene and *nad5* gene). The total length of *C. malaccensis* overlapping regions was 195 bp with three overlapping regions longer than 30 bp: 53 bp (between *trnF* gene and *nad5* gene), 43 bp (between *trnQ* gene and *trnV* gene) and 37 bp (between *trnS2* gene and *cob* gene), respectively.

Protein coding genes

The mt genome of *C. malaccensis* has three kinds of start codon (ATT, ATA, ATG) and two kinds of stop codon (TAA, TAG). ATT is the start codon of *cox1* and *nad5*, ATA is the start codon of *atp8, atp6, nad3, nad4l, nad1* and *nad2*. ATG is the start codon for other genes. TAG is the stop codon of *atp8, nad5* and *nad4*, while the other genes end with TAA.

The tRNA and rRNA genes

Twenty-two tRNA genes were found in the mt genome of *C. malaccensis*. All present tRNA genes were extremely truncated, ranging in size from 47 bp to 67 bp. Four tRNA (*trnM*, *W*, *N* and *K*) have complete cloverleaf secondary structures, most of predicted tRNA genes are folded into the atypical cloverleaf secondary structures with the absence of either D-arm or TψC-arm (Figure 2). As reported in some species in Arachnida, which also found the tRNA lost one arm either the D-arm or TψC-arm such as *Panonychus citri* (Yuan *et al.* 2010), *D. brevis* and *D. folliculorum* (Palopoli *et al.* 2014), *Caloglyphus berlesei* (Sun *et al*. 2014b) and *Tyrophagus longior* (Yang & Li 2015). It seems that lose arms is a normal situation in Arachnida and it does not affect mitochondrial protein synthesis.

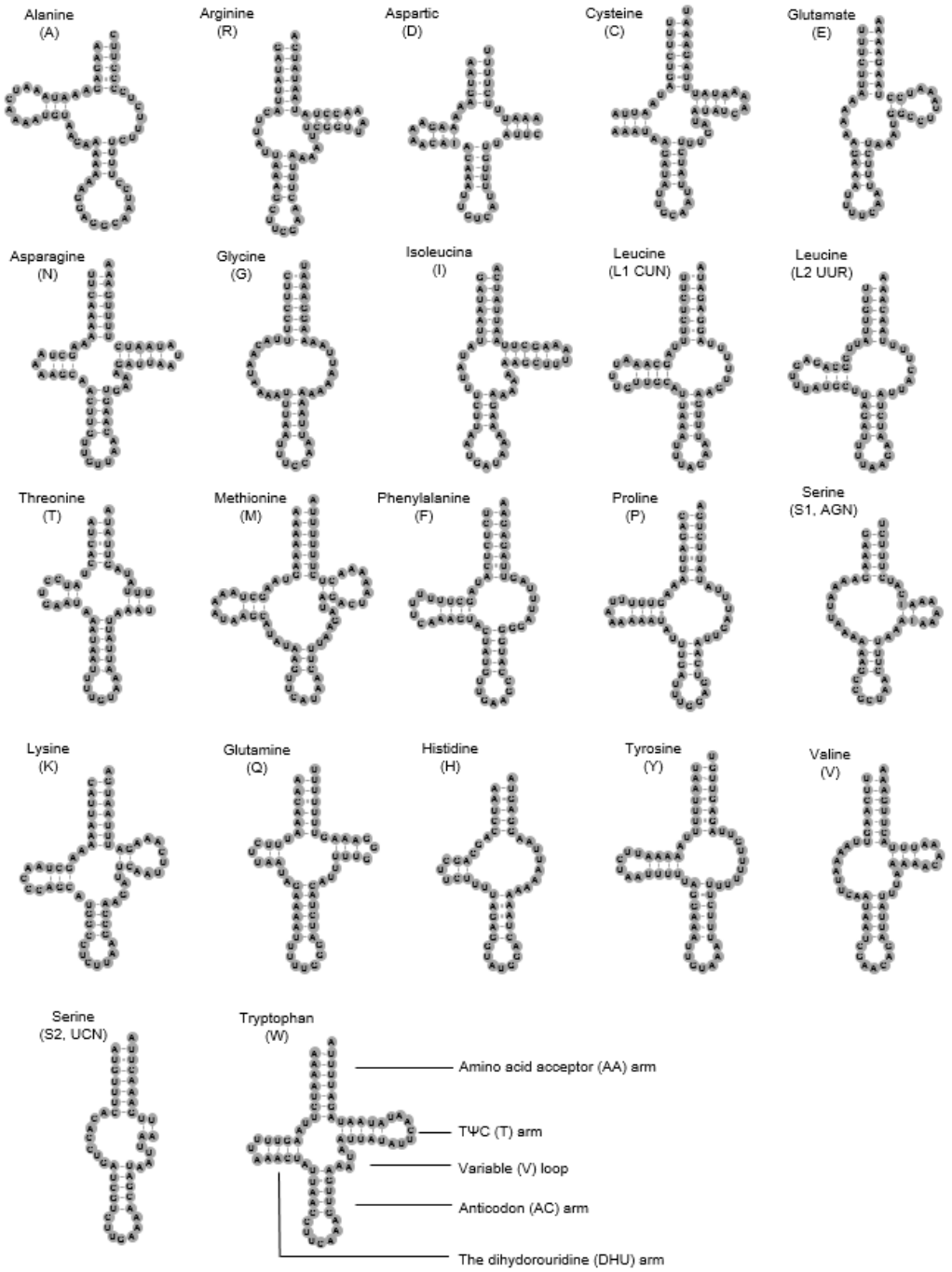

FIGURE 2. The 22 tRNAs of *Cheyletus malaccensis*

For *C. malaccensis*, rearrangements of tRNA genes occur much more than other genes. The truncated tRNA genes observed in *C. malaccensis* would seem to require the evolution of extensive tRNA editing capabilities. The molecular machinery necessary for these unusual tRNAs to function might provide an explanation for *C. malaccensis* adaptability and becoming the dominant predator mite in grain depot.

Phylogeny

Leveraging two datasets (PCG123rRNA and PCG) as well as two methods (BI and ML), we reconstructed the phylogeny of Acariformes which had been reported on NCBI (Figure 3). We uncovered for the first time the mt genome belonging to Cheyletidae, which provided a good opportunity to resolve its phylogenetic position. Cheyletidae had the closest relationship to Tetranychidae (PCGsrRNA Bayesian posterior probability / PCGs Bayesian posterior probability / PCGsrRNA ML bootstrap value/ PCGs ML bootstrap value = 1/1/89/87) and they formed a clade with sister relationship with Demodicidae (support values = 1/1/96/94). The phylogenetic relationship among the three families would be clear with the implement of our mt genome data. Phylogenetic relationships among these families could be more clear when supplementing enough molecular information of Acariformes.

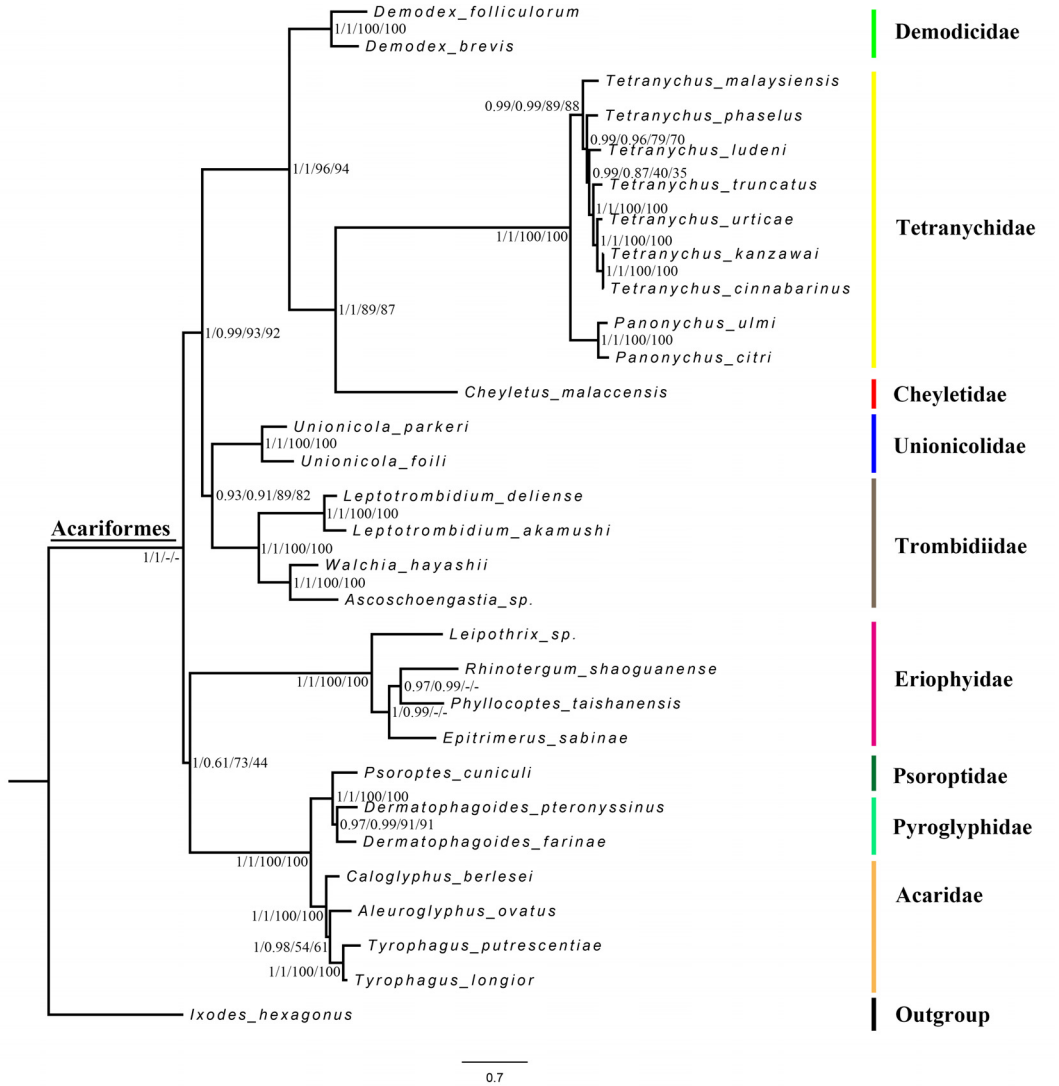

FIGURE 3. Phylogenetic tree of 30 species from Acariformes.
Note: The values in each node represented posterior probabilities of Bayesian methods and bootstrap value from maximum likehood method: PCGsrRNA Bayesian/ PCGs Bayesian/ PCGsrRNA ML/ PCGs ML.

Summary

This study reported the complete mitochondrial genome of *C. malaccensis*, presenting its structure and sequence. According to our knowledge, it is the first description of the complete mitochondrial genome recorded for Cheyletidae. The size of *C. malaccensis* mitogenome is 14,732 bp. Most of tRNA were truncated without D-arm or/and TψC-arm. Rearrangement was found in 12 mitogenome genes. Furthermore, the phylogeny of Acariformes inferred with all 29 reported mt genomes, prove that *C. malaccensis* is more close to Tetranychidae than other mites. This study enriched the database of mt genome of Acariformes. We hope that the obtained results and the discovered unresolved questions will stimulate further studies regarding molecular phylogenetic relationship and population genetics using mitochondrial gene fragments.

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Author contributions statement

YW, YC and ZHL conceived the ideas for the study; YW collected the samples; YML performed the experiments; SQF, LYX and YML analyzed the data; YML, SQF, YC, ZHL, VS, RA and YW composed the manuscript. All authors have read and approved the final manuscript.

Additional information

Accession code: The sequencing data have been deposited in the NCBI with the accession code MT273119

Competing financial interests: The authors declare no competing financial interests.

References

Ardeshir, F. (2017) Cheyletid mites (Acari: Trombidiformes) in stored grains in Iran. *Persian Journal of Acarology*, 6, 11–24.

Bent, M., Dnonath, A. & Jühling, F. (2013) MITOS: Improved de novo metazoan mitochondrial genome annotation. *Molecular Phylogenetics and Evolution*, 69, 313–319. https://doi.org/10.1016/j.ympev.2012.08.023

Boore, J.L. (1999) Animal mitochondrial genomes. *Nucleic Acids Research*, 27, 1767–1780. https://doi.org/10.1093/nar/27.8.1767

Castresana, J. (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular Phylogenetics and Evolution*, 17, 540–552. https://doi.org/10.1093/oxfordjournals.molbev.a026334

Cebolla, R., Stano, P. & Hubert, J. (2009) Prey range of the predatory mite *Cheyletus malaccensis* (Acari: Cheyletidae) and its efficacy in the control of seven stored-product pests. *Biological Control,* 50, 1–6. https://doi.org/10.1016/j.biocontrol.2009.03.008

Chuan, M.A., Yang, P., Jiang, F., Chapuis, M.P., Shali, Y., Sword, G.A. & Kang, L.A. (2012) Mitochondrial genomes reveal the global phylogeography and dispersal routes of the migratory locust. *Molecular Ecology*, 21, 4344–4358. https://doi.org/10.1111/j.1365-294X.2012.05684.x

Dermauw, W., Leeuwen, T.V., Vanholme, B. & Tirry, L. (2009) The complete mitochondrial genome of the house dust mite *Dermatophagoides pteronyssinus* (Trouessart): a novel gene arrangement among

arthropods. *BMC Genomics,* 10, 107.
https://doi.org/10.1186/1471-2164-10-107

Feng, S., Li, H., Song, F., Wang, Y., Stejskal, V., Cai, W. & Li, Z. (2019) A novel mitochondrial genome fragmentation pattern in *Liposcelis brunnea*, the type species of the genus *liposcelis* (Psocodea: Liposcelididae). *International Journal of Biological Macromolecules*, 132, 1296–1303.
https://doi.org/10.1016/j.ijbiomac.2019.04.034

Feng, S., Yang, Q., Li, H., Song, F., Stejskal, V., Opit, G.P., Cai, W., Li, Z. & Shao, R. (2018) The highly divergent mitochondrial genomes indicate that the booklouse, *Liposcelis bostrychophila* (Psocoptera: Liposcelididae) is a cryptic species. *G3- Genes Genomes Genetics,* 8, 1039–1047.
https://doi.org/10.1534/g3.117.300410

Folmer, O. (1994) DNA primers for amplification of mitochondrial cytochrome coxidase subumit I from metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, 3, 294–299.

Guindon, S., Dufayard, J.F. & Lefortb, V. (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Systematic Biology*, 59, 307–321.
https://doi.org/10.1093/sysbio/syq010

Hubert, J., Hýblová, J., Műnzbergová, Z., Pekár, S., Křížkova-Kudlíková, I. Dolečková-Marešová, L., Stejskal, V. & Mareš, M. (2007) Combined effect of an antifeedant alpha-amylase inhibitor anda predator *Cheyletus malaccensis* in controlling the stored-product mite *Acarus siro*. *Physiological Entomology*, 32, 41–49.
https://doi.org/10.1111/j.1365-3032.2006.00539.x

Hubert, J., Műnzbergová, Z., Kučerová, Z. & Stejskal, V. (2006) Comparison of communities of stored product mites in grain mass and grain residues in the Czech Republic. *Experimental and Applied Acarology*, 39, 149.
https://doi.org/10.1007/s10493-006-0026-y

Katoh, K., Rozewicki, J. & Yamada, K.D. (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics*, 20, 1160–1166.
https://doi.org/10.1093/bib/bbx108

Kearse, M., Moir, R., Wilson, A., Stone-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.
https://doi.org/10.1093/bioinformatics/bts199

Kumar, S., Stecher, G. & Tamura, K. (2016) MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*, 33, 1870–1874.
https://doi.org/10.1093/molbev/msw054

Li, H., Shao, R., Song, N., Song, F., Jiang, P., Li, Z. & Cai, W. (2015) Higher-level phylogeny of paraneopteran insects inferred from mitochondrial genome sequences. *Scientific Reports*, 5, 1–10.
https://doi.org/10.1038/srep08527

Lohse, M., Bolger, A.M., Nagel, A., Fernie, A.R., Lunn, J.E., Stitt, M. & Usadel, B. (2012) RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. *Nucleic Acids Research,* 40, W622–W627.
https://doi.org/10.1093/nar/gks540

Lukáš, J., Stejskal, V., Jarošík, V., Hubert, J. & Žd'árková, E. (2007) Differential natural performance of four *Cheyletus* predatory mite species in Czech grain stores. *Journal of Stored Products Research*, 43, 97–102.
https://doi.org/10.1016/j.jspr.2005.12.002

Mariana, A., Heah, S.K., Wong, A.L. & Ho, T.M. (2010) The occurrence of arthropods in processed rice products in Malaysia. *Asian Pacific Journal of Tropical Medicin*e, 3, 552–554.
https://doi.org/10.1016/S1995-7645(10)60133-2

Nelson, L.A., Lambkin, C.L., Batterham, P., Wallman, J.F., Dowton, M., Whiting, M.F., Yeates, D.K. & Cameron, S.L. (2012) Beyond barcoding: a mitochondrial genomics approach to molecular phylogenetics and diagnostics of blowflies (Diptera: Calliphoridae). *Gene*, 511, 131–134.
https://doi.org/10.1016/j.gene.2012.09.103

Palopoli, M.F., Minot, S., Pei, D., Satterly, A. & Endrizzi, J. (2014) Complete mitochondrial genomes of the human follicle mites *Demodex brevis* and *D. folliculorum*: novel gene arrangement, truncated tRNA genes, and ancient divergence between species. *BMC Genomics*, 15, 1124.
https://doi.org/10.1186/1471-2164-15-1124

Palyvos, N.E., Athanassiou, C.G. & Kavallieratos, N.G. (2006) Acaricidal effect of a diatomaceous earth for-

mulation against *Tyrophagus putrescentiae* (Astigmata: *Acaridae*) and its predator *Cheyletus malaccensis* (Prostigmata: *Cheyletidae*) in four grain commodities. *Journal of Economic Entomology*, 99, 229–236. https://doi.org/10.1603/0022-0493(2006)099[0229:AEOADE]2.0.CO;2

Rogalski, M., Karcher, D. & Bock, R. (2008) Superwobbling facilitates translation with reduced tRNA sets. *Nature Structural & Molecular Biology*, 15, 192–198. https://doi.org/10.1038/nsmb.1370

Ronquist, F. & Huelsenbeck, J.P. (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19, 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Sun, E., Li, C., Li, S., Gu, S. & Nie, L. (2014b) Complete mitochondrial genome of *Caloglyphus berlesei* (Acaridae: Astigmata): the first representative of the genus *Caloglyphus*. *Journal of Stored Products Research*, 59, 282–284. https://doi.org/10.1016/j.jspr.2014.06.010

Sun, E., Li, C., Nie, L. & Jiang, Y. (2014a) The complete mitochondrial genome of the brown leg mite, *Aleuroglyphus ovatus* (Acari: Sarcoptiformes): evaluation of largest non-coding region and unique tRNAs. *Experimental and Applied Acarology*, 64, 141–157. https://doi.org/10.1007/s10493-014-9816-9

Shen, Z.P. (1997) The biology of stored mites—*Cheyletus malaccensis*. *Grain Storage*, 5, 50–51.

Sinha, R.N. & Wallace, H.A.H. (1973) Population dynamics of stored-product mites. *Oecologia*. 12, 315–327. https://doi.org/10.1007/BF00345046

Stejskal, V., Hubert, J., Aulicky, R. & Kucerova, Z. (2015) Overview of present and past and pest-associated risks in stored food and feed products: European perspective. *Journal of Stored Products Research*, 64, 122–132. https://doi.org/10.1016/j.jspr.2014.12.006

Tian, Y. (2011) Systems analysis of common Cheyletids (Acari: Cheyletidae) based on mitochondrial CO I and 12S rRNA gene. Master's Thesis, Nan-chang University. (in Chinese)

Wolstenholme, D.R. (1992) Animal mitochondrial DNA: structure and evolution. *International Review of Cytology*, 141, 173–216. https://doi.org/10.1016/S0074-7696(08)62066-5

Wu, Y., Li, F., Li, Z., Stejskal, V., Aulicky, R., Kučerová, Z., Zhang, T., He, P. & Cao, Y. (2016) Rapid diagnosis of two common stored-product predatory mite species based on species-specific PCR. *Journal of Stored Products Research*, 69, 213–216. https://doi.org/10.1016/j.jspr.2016.08.006

Xue, X., Deng, W., Qu, S., Hong, X. & Shao, R. (2018) The mitochondrial genomes of sarcoptiform mites: are any transfer RNA genes really lost? *BMC Genomics*, 19, 466. https://doi.org/10.1186/s12864-018-4868-6

Yang, B. & Li, C. (2015) The complete mitochondrial genome of *Tyrophagus longior* (Acari: Acaridae): gene rearrangement and loss of tRNAs. *Journal of Stored Products Research,* 64, 109–112. https://doi.org/10.1016/j.jspr.2015.10.001

Yang, X., Ye, Q., Xin, T., Zou, Z. & Xia, B. (2016) Population genetic structure of *Cheyletus malaccensis* (Acari: Cheyletidae) in China based on mitochondrial CO I and 12S rRNA gene. *Experimental and Applied Acarology*, 69, 117–128. https://doi.org/10.1007/s10493-016-0028-3

Yuan, M., Wei, D., Wang, B., Dou, W. & Wang, J. (2010) The complete mitochondrial genome of the citrus red mite *Panonychus citri* (Acari:Tetranychidae): high genome rearrangement and extremely truncated tRNAs. *BMC Genomics*, 11, 597–613. https://doi.org/10.1186/1471-2164-11-597

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TABLE S1. Mitochondrial genomes of mites (from NCBI) used in the phylogenetic tree

GenBank accession code	Species	Length
NC034150	*Rhinotergum shaoguanense*	13646
NC029209	*Phyllocoptes taishanensis*	13475
NC028725	*Tyrophagus longior*	13271
NC026102	*Demodex folliculorum*	14150
NC026101	*Demodex brevis*	14211
NC026079	*Tyrophagus putrescentiae*	13288
NC024679	*Tetranychus phaselus*	13084
NC024678	*Tetranychus malaysiensis*	13049
NC024637	*Caloglyphus berlesei*	14273
NC012571	*Panonychus ulmi*	13115
NC007600	*Leptotrombidium deliense*	13731
KX027362	*Leipothrix sp.*	14216
KR604966	*Epitrimerus sabinae*	13531
KM111296	*Tetranychus truncatus*	13089
KJ957822	*Psoroptes cuniculi*	14247
KJ729018	*Tetranychus ludeni*	13064
KJ729017	*Tetranychus kanzawai*	13091
KJ571488	*Aleuroglyphus ovatus*	14305
HQ386015	*Unionicola parkeri*	14734
HM753535	*Tetranychus cinnabarinus*	13092
HM189212	*Panonychus citri*	13077
GQ465336	*Dermatophagoides farinae*	14266
EU884425	*Dermatophagoides pteronyssinus*	14203
EU856396	*Unionicola foili*	14738
EU345430	*Tetranychus urticae*	13103
AB300501	*Ascoschoengastia sp.*	16067
AB300500	*Walchia hayashii*	14857
AB194045	*Leptotrombidium akamushi*	13698
KR259803	*Hypsosinga pygmaea*	14193