

# The complete mitochondrial genome sequence of *Kolla paulula* from Taiwan

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**ABSTRACT** The circular mitochondrial genome of *Kolla paulula*, an insect vector of *Xylella fastidiosa* causing grape Pierce's disease (PD) in Taiwan, is 14,575 bp. The genome encodes genes for 13 proteins, 2 ribosomal RNAs (rRNAs), and 22 transfer RNAs (tRNAs).

**KEYWORDS** *Kolla paulula*, mitochondrial genome, insect vector, *Xylella fastidiosa*, Taiwan

*Kolla paulula* (Hemiptera: Cicadellidae) is a sharpshooter leafhopper commonly found in Taiwan. The insect is a polyphagous, light-to-dark green species with white margins of the fore wings and, in general, not considered a crop pest in Taiwan (1). In 2013, a plant disease, Pierce's disease (PD) of grapevine, caused by *Xylella fastidiosa* was found in Taiwan (1, 2). The sharpshooter was confirmed to be a vector of *X. fastidiosa* (1, 3). *K. paulula* occurs in all vineyards and is distributed over the medium- and low-altitude areas in Taiwan (1). Current literature shows that the insect is distributed in south and east Asia (4).

Insect mitochondrial genome (mitogenome) is now the most studied genomic system in entomology (5). In GenBank, there are currently two *K. paulula* mitogenome sequences, [KY680277](#) (13,579 bp), a partial mitogenome sequence from Zhenjiang Province of China, and [MW542170](#) (14,995 bp), a complete mitogenome sequence from Guizhou Province of China. Journal publications are not yet available for both records. To facilitate the insect research, we report here a mitogenome sequence of *K. paulula* from Taiwan.

A colony of *K. paulula* was collected and maintained on *Commelina diffusa* under laboratory conditions (25°C, 60% RH [relative humidity], 13:11 L:D [light:day]) at the Taiwan Agricultural Research Institute (Longitude: 120.696404; Latitude: 24.029927). DNA was extracted from a single insect using a DNeasy blood and tissue kit (Qiagen, Valencia, CA). Whole-genomic DNA was amplified using an illustra GenomiPhi version 2 DNA amplification kit (GE Healthcare, Waukesha, WI) and sequenced using NovaSeq (2 × 150) format (Illumina, San Diego, CA) after library preparation using the Illumina TruSeq DNA PCR-free kit.

A total of 15 Giga bp data with average Q value of 36 were generated (FastQC ver. 0.12.1) (6). *De novo* assembly was performed with CLC Genomics Workbench (ver. 24.0.1) using default setting (Word-size = 45; Bubble-size = 98). A contig of 14,617 bp was identified through a BLAST+ (ver. 2.15.0) search using [MW542170](#) as query against the whole *de novo* assembly. Overlaps at the 5' and 3' ends were detected by self-BLAST of the contig and edited, resulting in a circular sequence of 14,575 bp (900 × overall coverage, GC% of 33). Sequence annotation was performed using GeSeq ver. 2.03 (7) and Proksee ver. 0.24.1 (8). Protein coding sequences were manually edited and confirmed the start and stop codons based on invertebrate mitochondrial code. The final mitogenome, KPTC1 (*K. paulula* Taichung 1), consists of genes of 13 proteins conserved to typical insect mitogenome, 22 transfer RNAs, and 2 ribosomal RNAs (Table 1).

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**TABLE 1** Selected metrics of mitochondrial genome of *Kolla paulula* KPTC1

| Gene (anti-codon) | Type   | Location     | Size (bp) | Strand | Start codon    | Stop codon       |
|-------------------|--------|--------------|-----------|--------|----------------|------------------|
| trnI(gat)         | tRNA   | 193..258     | 66        | +      | — <sup>a</sup> | —                |
| trnQ(ttg)         | tRNA   | 256..323     | 68        | —      | —              | —                |
| trnM(cat)         | tRNA   | 324..393     | 70        | +      | —              | —                |
| nad2              | CDS    | 394..1362    | 969       | +      | ata            | taa              |
| trnW(tca)         | tRNA   | 1360..1428   | 69        | +      | —              | —                |
| trnC(gca)         | tRNA   | 1419..1479   | 61        | —      | —              | —                |
| trnY(gta)         | tRNA   | 1481..1545   | 65        | —      | —              | —                |
| cox1              | CDS    | 1550..3085   | 1536      | +      | atg            | tag              |
| trnL2(taa)        | tRNA   | 3086..3149   | 64        | +      | —              | —                |
| cox2              | CDS    | 3150..3826   | 677       | +      | att            | ta— <sup>b</sup> |
| trnK(ctt)         | tRNA   | 3829..3898   | 70        | +      | —              | —                |
| trnD(gtc)         | tRNA   | 3898..3961   | 64        | +      | —              | —                |
| atp8              | CDS    | 3970..4113   | 144       | +      | ata            | taa              |
| atp6              | CDS    | 4110..4757   | 648       | +      | ata            | taa              |
| cox3              | CDS    | 4758..5537   | 780       | +      | atg            | taa              |
| trnG(tcc)         | tRNA   | 5537..5598   | 62        | +      | —              | —                |
| nad3              | CDS    | 5599..5952   | 354       | +      | atc            | tag              |
| trnA(tgc)         | tRNA   | 5951..6012   | 62        | +      | —              | —                |
| trnR(tcg)         | tRNA   | 6011..6074   | 64        | +      | —              | —                |
| trnN(gtt)         | tRNA   | 6072..6140   | 69        | +      | —              | —                |
| trnS1(gct)        | tRNA   | 6142..6205   | 64        | +      | —              | —                |
| trnE(ttc)         | tRNA   | 6207..6270   | 64        | +      | —              | —                |
| trnF(gaa)         | tRNA   | 6270..6332   | 63        | —      | —              | —                |
| nad5              | CDS    | 6334..8007   | 1674      | —      | ttg            | taa              |
| trnH(gtg)         | tRNA   | 8008..8069   | 62        | —      | —              | —                |
| nad4              | CDS    | 8070..9360   | 1291      | —      | atg            | t— <sup>b</sup>  |
| nad4l             | CDS    | 9384..9665   | 282       | —      | atg            | taa              |
| trnT(tgt)         | tRNA   | 9668..9731   | 64        | +      | —              | —                |
| trnP(tgg)         | tRNA   | 9732..9796   | 65        | —      | —              | —                |
| nad6              | CDS    | 9799..10287  | 489       | +      | att            | taa              |
| cob               | CDS    | 10280..11416 | 1137      | +      | atg            | taa              |
| trnS2(tga)        | tRNA   | 11416..11479 | 64        | +      | —              | —                |
| nad1              | CDS    | 11479..12411 | 933       | —      | att            | taa              |
| trnL1(tag)        | tRNA   | 12411..12475 | 65        | —      | —              | —                |
| rrnL              | rRNA   | 12455..13486 | 1032      | —      | —              | —                |
| —                 | Repeat | 13141..13293 | 153       | +      | —              | —                |
|                   | Region |              |           |        |                |                  |
| trnV(tac)         | tRNA   | 13645..13711 | 67        | —      | —              | —                |
| rrnS              | rRNA   | 13713..14485 | 773       | —      | —              | —                |

<sup>a</sup>—, not applicable.<sup>b</sup>Incomplete termination/stop codon.

A BLASTn search using the KPTC1 as a query against the National Center for Biotechnology Information (NCBI) core\_nr database (update date:2025/09/25) identified [MW542170.1](#) as the top hit (Query Coverage = 98%, Percent Identity = 90.25%). However, [KY680277](#), the other Chinese *K. paulula* mitogenome, was distantly related (Query Coverage = 79%, Percent Identity = 73.80%). Meanwhile, over 40 leafhopper mitogenomes from multiple species showed Query Coverage = 98% but Percent Identity ≤80%, for example, *Nanatka castenea* ([NC\\_070000.1](#), journal citation not available) with Percent Identity of 80.24%.

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## DATA AVAILABILITY

This complete mitogenome sequence of KPTC1 has been deposited in DDBJ/EMBL/GenBank under the accession number [PX130412](#). The Illumina read data for the mitogenome are available under BioProject accession number [PRJNA1334032](#) and SRA number [SRS26688334](#). The version described in this paper is the first version, [PX130412.1](#).

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