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RESEARCH ARTICLE

REVISED Characterization of the Complete Mitochondrial Genome and Evaluation of COI Barcoding in *Philonis inermis* (Coleoptera: Curculionidae: Cryptorhynchinae) Using Genome Skimming

[version 3; peer review: 3 approved]

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Abstract

Background

Philonis inermis is a Neotropical stem-galling weevil specialized on the invasive vine *Passiflora foetida* and represents a promising candidate for biological control. However, no genomic or barcoding data have previously been available for this genus, limiting its taxonomic resolution and risk assessment potential.

Methods

We used shallow whole-genome sequencing of two individuals reared under controlled conditions to assemble, annotate, and compare the complete mitochondrial genome of *P. inermis* with other Cryptorhynchinae. BUSCO analysis was performed to recover nuclear single-copy orthologs and additional multicopy markers. *Cytochrome c* oxidase subunit I (COI) sequences from 20 Colombian specimens were analyzed together with 24 Cryptorhynchinae barcodes from GenBank to evaluate intra- and interspecific divergence.

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Results

The *P. inermis* mitogenome is 15,120 bp in length, AT-rich (77.0%), and contains 36 genes, including 13 protein-coding genes, 21 tRNAs, and two rRNAs. The tRNA-Ile was not detected, likely obscured within the variable control region, as reported for other cryptorhynchine weevils. Phylogenetic analysis based on mitogenomic sequences placed *P. inermis* as a well-supported clade closely related to *Eucryptorrhynchus.* COI barcode analysis revealed extremely low intraspecific divergence (pairwise K2P $\leq$ 0.006) and a pronounced barcode gap distinguishing *P. inermis* from other Cryptorhynchinae species. Genome-skimming assemblies yielded 196 single-copy orthologs, 28 duplicated BUSCOs, and a rich set of multicopy nuclear markers, including extensive rRNA fragments (18S, 28S, 5.8S, 16S) and core histones (H2A, H2B, H3, H4), which are provided as extended data for future phylogenomic applications.

Conclusion

This study presents the first complete mitochondrial genome for the genus *Philonis* and demonstrates the utility of COI barcoding for the current molecular identification of *P. inermis*, in a context where comparative mitogenomic data remain scarce. These genomic resources provide a foundation for future integrative taxonomic, comparative, and evolutionary studies, and support further evaluation of *P. inermis* as a potential biological control agent against *P. foetida.*

Keywords
Neotropical weevils; mitochondrial genome; COI barcode; Curculionidae; Passiflora foetida; biological control

article can be found at the end of the article.

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REVISED **Amendments from Version 2**

"Minor revisions have been made to Version 2 to address final editorial and reviewer suggestions. These changes include a grammatical correction and stylistic improvement in the Discussion section, specifically refining the paragraph describing mitochondrial genome composition, structural conservation, and the absence of the tRNA-Ile gene.
In addition, the Data Availability statement has been updated to include the Barcode of Life Data System (BOLD) BIN identifier (BIN: AHI5100), ensuring improved traceability and accessibility of the barcode dataset associated with this study. No changes were made to the title, authorship, figures, or core results. These revisions are minor and do not affect the scientific content or conclusions of the study but improve clarity, accuracy, and data accessibility in the final published version."

Any further responses from the reviewers can be found at the end of the article

1. Introduction

Within Cryptorhynchinae subfamily (Coleoptera: Curculionidae), the Neotropical genus *Philonis* represents an under-explored lineage of stem-galling weevils that are tightly associated with species of *Passiflora* (Passifloraceae). Among them, *Philonis inermis* has recently attracted attention as a potential biological control agent against *Passiflora foetida*, an invasive vine that causes significant ecological and economic damage in Australia (Clavijo-Giraldo et al., 2025. *Unpublished*). Although a considerable number of cryptorhynchine weevils are known as agricultural pests, some species are being studied for their potential as biological control agents. *P. inermis* is one such example, exhibiting high host specificity towards *P. foetida* and inducing gall formation that weakens or kills the host plant. However, the lack of molecular data for *Philonis* hampers its accurate phylogenetic placement and limits the development of molecular tools for its identification and monitoring in both native and introduced ranges.

Mitochondrial genomes or mitogenomes have become fundamental tools for understanding the evolutionary history, systematics, and ecology of insects.[1,2] In Coleoptera, the increasing availability of complete mitogenomes has facilitated robust phylogenetic analyses at various taxonomic levels, revealing patterns of diversification and adaptation in highly speciose families such as Curculionidae and other related weevil lineages.[3–5] Despite these advances, mitogenomic data remain scarce for the subfamily Cryptorhynchinae, which encompasses a highly diverse assemblage of weevils with complex host-plant interactions.

Although mitogenomes are powerful markers, their use in phylogenetic studies is not without limitations.[6,7] High substitution rates—particularly in third codon positions—can lead to substitution saturation in deep evolutionary branches, reducing the ability to accurately recover relationships among distantly related taxa. Such constraints are less problematic at shallow timescales, where mitochondrial genomes retain strong resolving power for population-level analyses and recent divergences. Because the present study focuses on intraspecific and closely related lineages, mitogenomic data remain well suited to our research objectives.[8]

Recent mitogenomic studies within Cryptorhynchinae have mainly focused on species of economic concern, particularly pests of woody plants and crops. Examples include *Eucryptorhynchus chinensis* and *E. brandti*, pests of *Ailanthus altissima* in China,[9,10] and the mango seed weevils *Sternochetus gravis*, *S. mangiferae*, and *S. olivieri.*[11] The hyperdiverse genus *Trigonopterus*, with hundreds of recently described species,[12] also provides important comparative resources. Although related genera such as *Aclees*[13] are not part of Cryptorhynchinae, they remain relevant for broader curculionid comparisons. In parallel with mitogenomic research, the use of the mitochondrial *Cytochrome c* oxidase subunit I (COI) gene as a DNA barcode has become an essential tool for species identification, biodiversity assessment, and the detection of cryptic diversity in weevils and other insects.[14,15] Despite its broad application in Curculionidae, COI barcoding data have been scarce for Neotropical Cryptorhynchinae, limiting our understanding of species boundaries and population structure in this group. Until now, no complete mitogenomes have been available for any Neotropical representative of Cryptorhynchinae, making *P. inermis* the first of its kind. The integration of mitogenomic and COI barcode data presented here provides a valuable reference for future studies on species delimitation, comparative genomics, and the development of molecular tools for monitoring and management of potential biological control agents.

In this context, the accurate delimitation of *P. inermis* is critical for any potential classical biological control strategy against *P. foetida.* Correct species identification, coupled with low intraspecific genetic variability, ensures the reliability and safety of introducing candidate agents into new environments. By combining complete mitochondrial genome sequencing with COI barcode analysis, this study not only provides the first comprehensive molecular characterization of *P. inermis*, but also demonstrates the utility of COI as a diagnostic marker for its unambiguous identification. These resources will serve as a foundation for both fundamental studies on Cryptorhynchinae evolution and applied research aimed at evaluating *P. inermis* as a safe and effective biocontrol agent.

This study aims to generate the first low-coverage genome sequencing–based mitochondrial genome of *Philonis inermis* and to integrate these data with COI barcode sequences in order to refine molecular identification and enable comparative analyses within Cryptorhynchinae. Through comparative analyses with available mitogenomes of related genera (*Eucryptorhynchus*, *Sternochetus*, and *Trigonopterus*), we explore patterns of gene arrangement, nucleotide composition, codon usage, and control region variability. These results not only fill a significant gap in the mitogenomic data of Neotropical Cryptorhynchinae but also provide essential molecular resources for evaluating *P. inermis* as a candidate biological control agent of *P. foetida*, linking fundamental evolutionary insights with applied biocontrol strategies.

2. Materials and methods

2.1 Sample collection and identification

Field surveys were conducted between 2021 and 2024 across dry forest habitats of northern Colombia (departments of Antioquia, Córdoba, and Bolívar; 0–200 m a.s.l.) to locate populations of *P. foetida* (Passifloraceae) exhibiting stem galls induced by *P. inermis*. The host plant was identified by botanist Wilder Buitrago Arbeláez (Herbarium of the Universidad de Antioquia, HUA, Medellín, Colombia) based on vegetative and floral characters following the diagnostic treatment reported elsewhere.[16] A voucher specimen of *P. foetida* was deposited at the HUA Herbarium under collection number HUA-1633.

Gall-bearing stems were excised using sterile scissors, placed in individual 50 mL sterile polypropylene tubes (Falcon, Cat. No. FALC-352070X25), and transported to the Entomology Laboratory of Universidad Nacional de Colombia (Medellín). Each gall was incubated separately under controlled environmental conditions (25 ± 2°C, 70 ± 5% relative humidity, 12:12 h light: dark cycle) until adult emergence to minimize contamination and sample mixing.

Adults were either preserved in 96% ethanol (Merck, Cat. No. 100983) for molecular work or mounted as pinned specimens for morphological examination. Species identification was confirmed through external morphological traits (rostrum length and curvature, elytral scale pattern, and sexual dimorphism) and dissection of male genitalia using a Leica EZ4 HD stereomicroscope (Leica Microsystems, Germany). Identification followed the diagnostic criteria of O'Brien[17] and comparisons with authenticated reference material. Voucher specimens were deposited in the Francisco Luis Gallego Entomological Museum (Universidad Nacional de Colombia, Medellín) under catalog numbers NC 65188–NC 65220.

2.2 DNA extraction, library preparation, and sequencing

Genomic DNA was extracted from approximately 25 mg of thoracic muscle from ethanol-preserved adults using the DNeasy Blood & Tissue Kit (Qiagen, Germany; Cat. No. 69504) according to the manufacturer's protocol. Each extraction used 180 µL Buffer ATL and 20 µL Proteinase K, with overnight digestion at 56°C, followed by standard purification and elution in 100 µL Buffer AE.

DNA concentration and purity were quantified using a NanoDrop 2000/2000c spectrophotometer (Thermo Fisher Scientific, USA; Cat. No. ND-2000) and verified by 1% agarose gel electrophoresis in 1× TAE buffer (Invitrogen, USA; Cat. No. 15558-042) with GelRed stain (Biotium, USA; Cat. No. 41003). Only samples with concentrations ≥1 ng μL^{-1} and 260/280 and 230/260 ratios between 1.8 and 2.0 were used for sequencing.

Two high-quality DNA extracts, designated Pinermis_Ant (Antioquia) and Pinermis_Cor (Córdoba), were selected for shallow whole-genome sequencing (~7× coverage). Paired-end libraries (2 × 150 bp; ~350 bp insert size) were prepared using the NEBNext Ultra II DNA Library Prep Kit for Illumina (New England Biolabs, USA; Cat. No. E7645L) following the manufacturer's protocol, including size selection with AMPure XP magnetic beads (Beckman Coulter, USA; Cat. No. A63881). Library concentrations were measured using a Qubit 4 Fluorometer (Invitrogen, USA; Cat. No. Q33226) and the Qubit dsDNA HS Assay Kit (Cat. No. Q32854). Libraries were pooled equimolarly and sequenced on an Illumina NovaSeq X platform (Illumina, USA) at Macrogen Inc. (Seoul, South Korea), generating approximately 8–10 Gb of raw paired-end sequencing data per sample, corresponding to an estimated genomic coverage of ~7×.

2.3 COI amplification and DNA barcoding

The COI barcode region (cox1) was amplified using standard insect primers LCO1490 and HCO2198.[18] PCR amplifications were carried out in 50 µL reactions containing 4 µL of genomic DNA template, 0.25 U μL^{-1} of Taq DNA Polymerase (Thermo Fisher Scientific, USA; Cat. No. EP0402), 5 µL of 10× PCR reaction buffer (supplied with the enzyme), 1 µL of 10 mM dNTP mix (Invitrogen, USA; Cat. No. 18427-013), and 1.5 µL each of forward and reverse primers (10 µM), with the remaining volume adjusted to 50 µL using nuclease-free water (Thermo Fisher Scientific, Cat. No. AM9937). Thermal cycling was performed in a T100 Bio-Rad 96-Well Thermal Cycler (Bio-Rad Laboratories, Inc., USA) under the following conditions: initial denaturation at 95°C for 5 min; 45 cycles of denaturation at 95°C for 40 s, primer annealing at 51°C for 60 s, and extension at 72°C for 45 s; followed by a final elongation step at 72°C for 10 min. PCR products were purified and sequenced by Macrogen Inc. (Seoul, Korea).

A total of 20 COI sequences from *P. inermis* were analyzed together with 24 additional COI sequences from American Cryptorhynchinae species retrieved from GenBank. Sequence alignment was conducted in MAFFT v7.525,[19] and pairwise genetic distances were calculated under the Kimura 2-Parameter (K2P) model using the ape v5.8[20] package in R. All COI sequences were additionally uploaded to the Barcode of Life Data System (BOLD), where they were linked to vouchered specimens with associated images and evaluated using BOLD workbench tools.[21] Intraspecific K2P distances were estimated only for species with more than four available COI sequences, providing an approximate measure of within-species variation in the barcode region. A Maximum likelihood (ML) phylogenetic tree based on COI sequences was conducted using the extended model selection followed by tree inference and ultra-fast non-parametric bootstrap with 1,000 replicates to evaluate node support in IQ-Tree v2.0.3.[22]

2.4 Read processing, genome assembly, and gene ortholog assessment

Raw Illumina paired-end reads were quality-filtered and trimmed using fastp,[23] and the resulting high-quality reads were assembled de novo with SPAdes.[24] Potential exogenous contamination was evaluated by classifying quality-filtered reads from both *P. inermis* libraries (Pinermis_Ant and Pinermis_Cor) with Kraken2 (v2.1.2) using the PlusPF reference database.[25] Kraken2 reports were then used to estimate the relative contribution of major taxonomic groups, including Metazoa, Bacteria, Fungi, Viruses, and unclassified reads.

We evaluated the completeness of the assembly using Benchmarking Universal Single Copy Orthologs (BUSCO v. 6.0)[26] for both sequenced individuals (Antioquia and Córdoba samples) against endopterygota_odb12 database. Complete single-copy genes were extracted from both *P. inermis* (Antioquia and Córdoba) samples and annotated by Clusters of Orthologous Genes (COG) using eggNOG-mapper (http://eggnog-mapper.embl.de/). In addition, duplicated BUSCOs and multicopy nuclear markers—including rRNA and histone loci—were recovered to provide supplementary phylogenomic resources.

2.5 Mitogenome annotation and phylogenetic tree

Assembled contigs were screened for mitochondrial sequences by BLASTN comparison to reference mitogenomes from Cryptorhynchinae (*Eucryptorhynchus brandti* - NC_025945.1; *E. chinensis* - NC_026719.1; *Trigonopterus selaruensis* - NC_050886.1; *T. tanimbarensis* - NC_050887.1; *T. jasminae* - NC_050888.1; *T. triradiatus* - NC_050889.1; *T. singkawangensis* - NC_050890.1; *T. carinirostris* - NC_050891.1; *T. kotamobagensis* - NC_050892.1; *T. porg* - NC_050893.1; *Sternochetus mangiferae* - NC_068213.1; *S. gravis* - NC_068212.1; *S. olivieri* - NC_068214.1). Mitochondrial genomes annotation was performed using GeSeq and OGDRAW webserver.[27] The mitogenome organization was compared using the GLOBAL multi-GFF3 output retrieved from the OGDRAW webserver,[27] and subsequently processed with a custom R script.

Mitogenome sequences were aligned using MAFFT v7.525[19] under the auto strategy. Poorly aligned regions were inspected and trimmed where necessary. Maximum likelihood (ML) phylogenetic inference was performed using IQ-TREE v2.0.3[22] with automatic model selection (ModelFinder) and node support assessed with 1,000 ultrafast bootstrap replicates. The resulting tree was visualized and edited in R.

3. Results

3.1 Genome skimming of *P. inermis*

We obtained a total of 23.5 and 15.6 million reads for the *P. inermis* individuals from Antioquia and Córdoba, respectively (Table 1). The assemblies yielded N50 values of 21 and 50, with approximately 213,000 and 233,000 contigs for the Antioquia and Córdoba individuals, respectively (Table 1). Taxonomic profiling of unmapped reads using Kraken2 (confidence = 0.5) indicated low levels of microbial contamination in both libraries. Bacterial reads accounted

Table 1. Genome sequencing, assembly, and completeness statistics for two individuals of *Philonis inermis*.

Parameter	Pinermis_Ant	Pinermis_Cor
High-quality reads	23 495 598	15 632 458
Assembled genome size (Mbp)	263.1	139.3
Contigs N50 (Kbp)	21	50
Contigs number	213 631	233 401
Complete BUSCOs	1954	201
Complete and single-copy BUSCOs	1930	196
Complete and duplicated BUSCOs	24	5

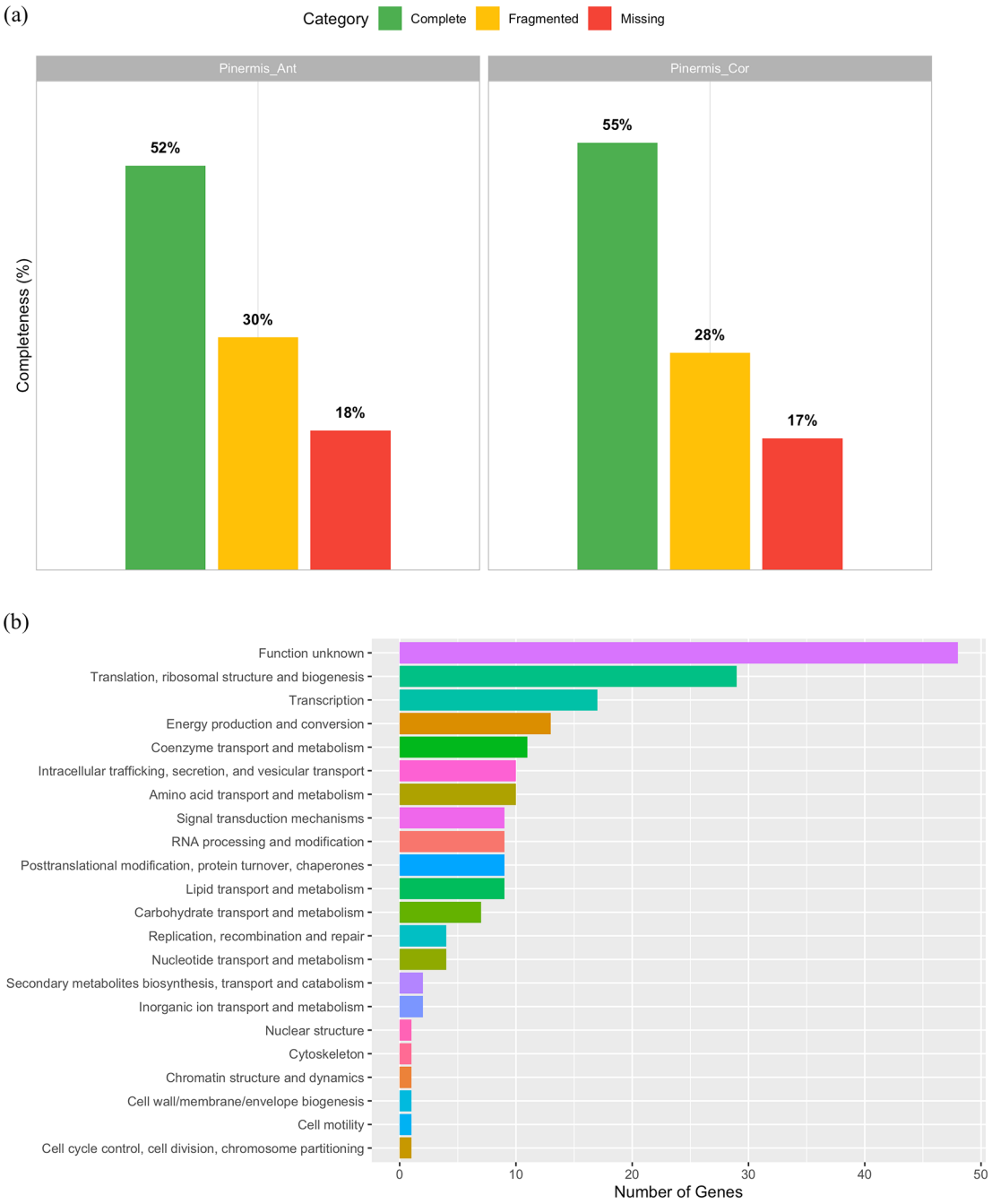


Figure 1. Genome-skimming assessment for *Philonis inermis*. (a) BUSCO completeness profiles for two genome assemblies (Endopterygota_odb12; 3,754 genes): Pinermis_Ant (52% complete, 30% fragmented) and Pinermis_Cor (55% complete, 28% fragmented). (b) Distribution of COG functional categories for the 196 single-copy BUSCO orthologs recovered in both assemblies.

for ~8% of unmapped reads in both samples, while fungal and viral reads were negligible (<0.3% and <0.01%, respectively). A proportion of unmapped reads (11.0% in *Pinermis_Ant* and 17.8% in *Pinermis_Cor*) was assigned to *Homo sapiens*; however, these reads did not assemble into contigs and were excluded from downstream analyses. Overall, contamination was minor and did not impact assembly quality or mitogenome reconstruction.

BUSCO analysis of the shallow-genome assemblies recovered, out of 3,754 expected Endopterygota genes, 52% complete and 30% fragmented in Pinermis_Ant, and 55% complete and 28% fragmented in Pinermis_Cor (Figure 1a), yielding >45% non-complete (fragmented + missing) loci in both assemblies, consistent with notable fragmentation. Despite this, we identified 196 single-copy orthologs having non-stop codons shared by both samples that were assigned to 22 COG functional categories (Supplementary S1). The distribution was dominated by Function unknown (24.1%),

followed by Translation, ribosomal structure and biogenesis (14.6%) and Transcription (8.5%) (Figure 1b). Core cellular and metabolic processes were moderately represented, including Energy production and conversion (6.5%), Coenzyme transport and metabolism (5.5%), Amino acid transport and metabolism (5.0%), Intracellular trafficking, secretion, and vesicular transport (5.0%), and RNA processing; lipid metabolism; post-translational modification/chaperones; signal transduction each at ~4.5%. Carbohydrate metabolism reached 3.5%, whereas nucleotide metabolism and replication/repair were ~2.0% (Figure 1b). Overall, even with fragmented assemblies, conserved informational functions are well captured, while a substantial fraction of single-copy orthologs remains uncharacterized. In addition to these single-copy loci, we also recovered 28 duplicated BUSCOs spanning diverse nuclear functions (including amino-acid and carbohydrate metabolism, redox processes, transport, and chromatin modification), as well as a broad set of multicopy rRNA genes (18S, 28S, 16S) and more than 150 histone-related loci (canonical H2A/H2B/H3/H4, histone variants, and associated chromatin-modifying proteins) from both assemblies (Supplementary Tables S2–S3). These multicopy nuclear markers provide an additional reservoir of phylogenetically informative sequences for future comparative studies.

3.2 Mitogenome characterization of *Philonis inermis*

The representative mitochondrial genome of *P. inermis* was 15,120 bp in length and contained 36 features typically found in insect mitogenomes: 13 protein-coding genes (PCGs), two ribosomal RNAs (rRNAs), and 21 transfer RNAs (tRNAs). The only gene not identified was tRNA-Ile (trnI) (Figure 2a). The overall nucleotide composition was strongly biased toward adenine and thymine (A+T = 77.02%), a pattern widely reported in mitochondrial genomes of weevils and other insect and arthropod taxa (Figure 2b).

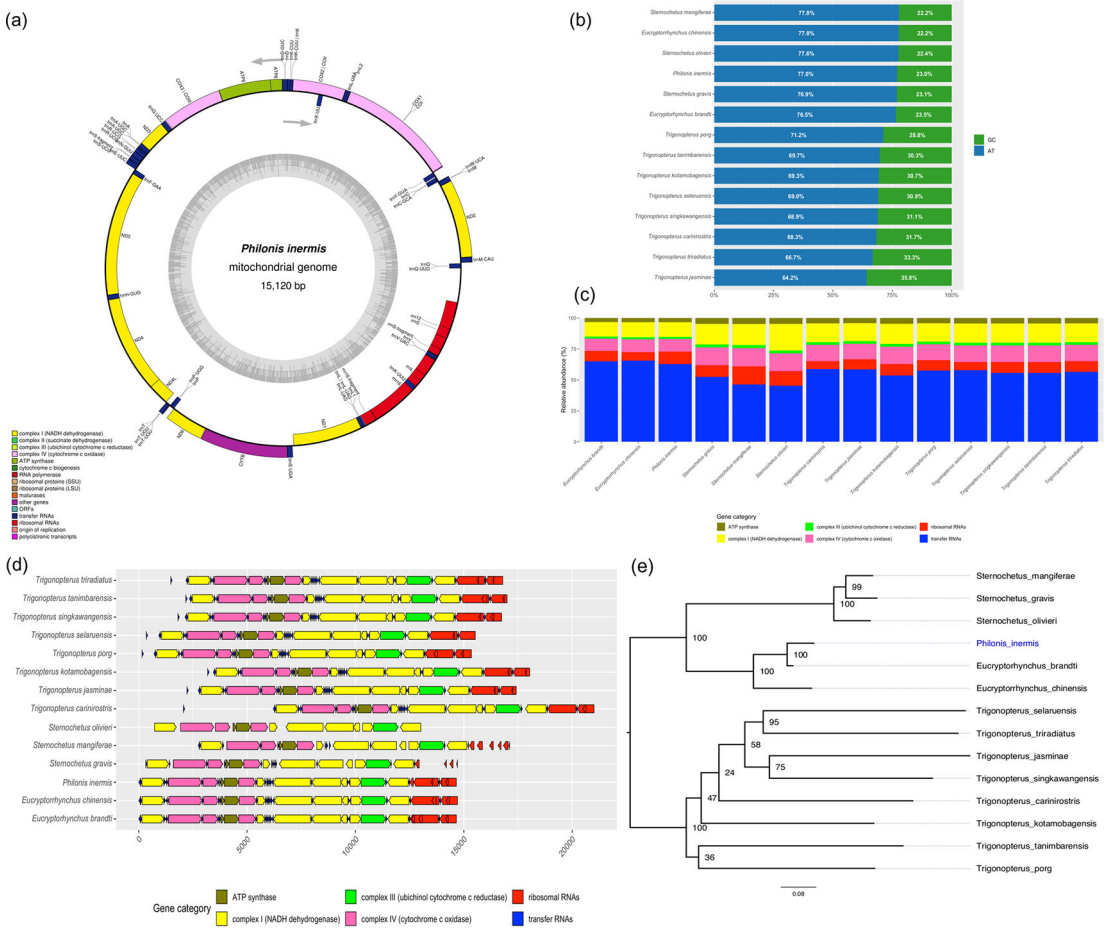


Figure 2. Mitogenome characterization of *Philonis inermis*. (a) Circular map of the complete mitochondrial genome of *P. inermis* showing gene annotation and organization. (b) Comparative nucleotide composition (AT vs. GC content) of *P. inermis* and other Cryptorhynchinae mitogenomes. (c) Relative abundance of annotated gene categories across *P. inermis* and related Cryptorhynchinae species. (d) Synteny and structural arrangement of annotated genes in *P. inermis* compared with related Cryptorhynchinae mitogenomes. (e) Maximum likelihood phylogenetic tree inferred from complete mitogenome sequences of *P. inermis* and representative Cryptorhynchinae species. GenBank accession numbers for all included sequences are provided in the Methods section. Bootstrap support values (1,000 replicates) are shown at nodes.

Comparative analyses revealed that *Eucryptorhynchus* spp. and *P. inermis* possess the highest total gene counts among the examined Cryptorhynchinae, primarily due to an increased number of tRNAs (Figure 2c). In contrast, *Sternochetus* spp. exhibit a lower overall gene count, reflecting a reduction in tRNA genes. The numbers of protein-coding genes, rRNAs, and other categories remain largely conserved across genera, with only minor differences observed (Figure 2c). Furthermore the mitochondrial genome structure of *P. inermis* was highly conserved and syntenic with other Cryptorhynchinae species, without major rearrangements, despite minor variations in gene spacing and orientation (Figure 2d). These patterns indicate strong conservation of mitochondrial gene content and organization within Cryptorhynchinae, with variation mainly associated with tRNA gene numbers. The preliminary phylogenetic reconstruction based on complete mitochondrial genome sequences placed *P. inermis* as sister to the *Eucryptorrhynchus* clade with strong support (BS = 100), while *Sternochetus* species clustered into a distinct lineage within Cryptorhynchinae. In contrast, relationships among *Trigonopterus* species were less resolved, with several nodes showing low support (Figure 2e). These results should be considered preliminary, as the current topology is influenced by the limited and uneven mitogenomic representation available in public databases.

3.3 DNA barcoding and intraspecific variation of COI gene in *P. inermis*

The COI barcode sequences of *P. inermis* from multiple Colombian populations exhibited extremely low intraspecific divergence, with pairwise Kimura 2-Parameter (K2P) distances ranging from 0 to 0.006 (Figure 3a), consistent across external and BOLD-based analyses. This low genetic variability, evident from both the distance matrix and density distributions, supports the genetic homogeneity of *P. inermis* across sampled localities, especially when compared with other Cryptorhynchinae species (Figure 3b). Comparison with additional Cryptorhynchinae COI sequences from

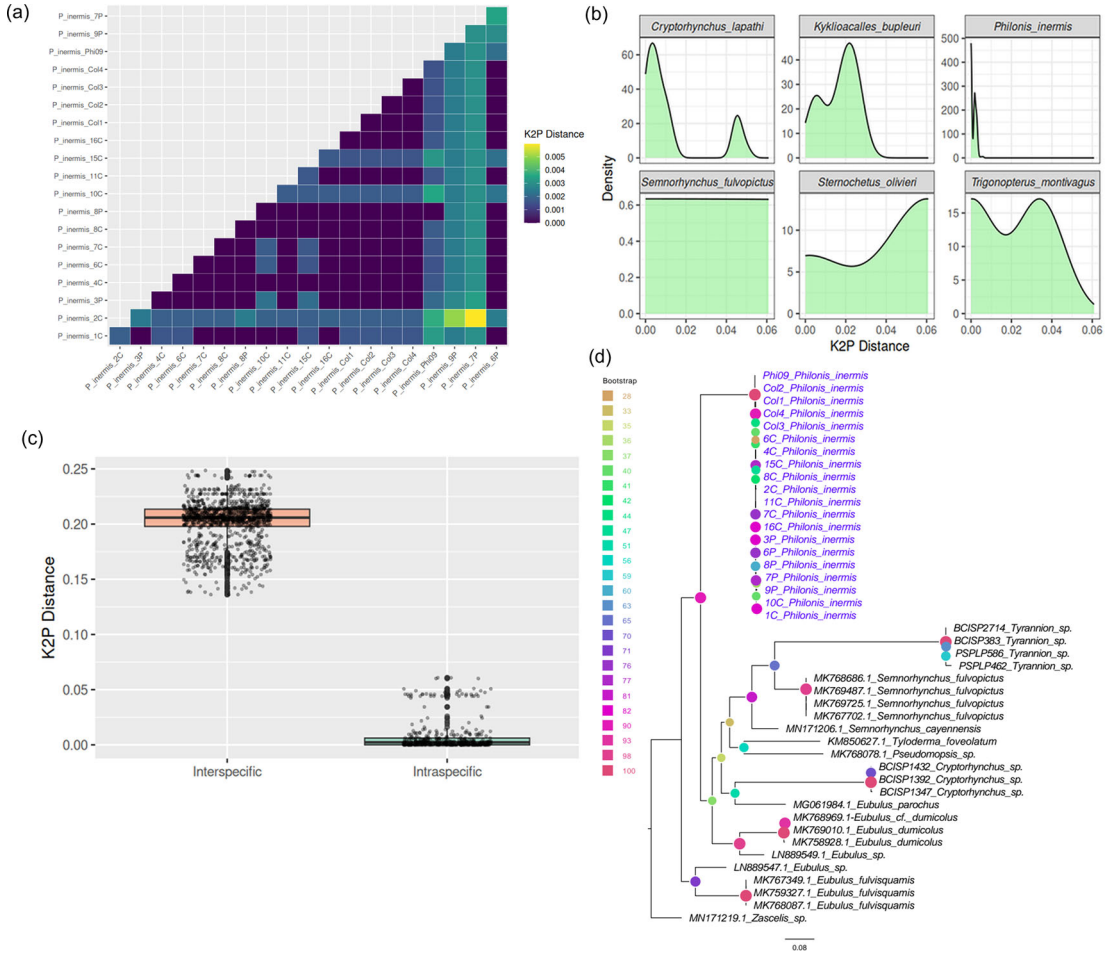


Figure 3. COI barcode variation and phylogenetic placement of *Philonis inermis*. (a) Pairwise Kimura 2-Parameter (K2P) distances among Colombian *P. inermis* specimens. (b) Density plots of K2P distances in *P. inermis* compared with selected Cryptorhynchinae species. (c) Comparison of intra- and interspecific K2P distances across Cryptorhynchinae, illustrating a clear barcode gap. (d) Maximum likelihood tree based on COI sequences showing *P. inermis* as a distinct, well-supported clade among Neotropical Cryptorhynchinae.

GenBank revealed a clear barcode gap: intraspecific K2P distances in *P. inermis* were substantially lower than interspecific distances across Cryptorhynchinae, which were typically greater than 0.15 (Figure 3c). This distinct separation highlights the effectiveness of COI barcoding for reliably identifying *P. inermis* and distinguishing it from related taxa. A maximum likelihood tree constructed from COI sequences (Figure 3d) clustered all *P. inermis* specimens together with strong bootstrap support, forming a well-defined lineage among Neotropical Cryptorhynchinae and further validating its molecular distinctiveness.

4. Discussion

Despite family Curculionoidae is rendering as one of the most diverse groups of Coleoptera, encompasses approximately 62,000 species distributed among 5,800 described genera,[28] many attributes about genome structure, diversity, and ecological role of Neotropical species belonging to Crypthorynchinae subfamily such *P. inermis* is poorly unknowledge so far.

The weevils of the Neotropical genus *Philonis* (Curculionidae: Cryptorhynchinae) represent a largely unexplored lineage within the diverse assemblage of gall-inducing insects. Here, we present the first genomic resources for this genus based on low-coverage genome sequencing, including the complete mitochondrial genome and an assessment of COI DNA barcode accuracy. These data provide a foundation for future studies of genetic diversity, population structure, and evolutionary history, and may also inform applied research in biological control of the invasive vine *Passiflora foetida* L.

The relatively fragmented assemblies reflect the shallow genome-skimming strategy adopted in this study, which was specifically designed to recover the complete mitochondrial genome and representative nuclear markers rather than to generate a high-contiguity nuclear assembly. Our primary objective was to establish genomic resources for taxonomic validation and phylogenetic inference, for which modest sequencing depth is sufficient. Although increased coverage and the incorporation of long-read technologies would substantially improve assembly contiguity, such approaches were beyond the scope of the present study.

Consistent with the limited coverage, BUSCO profiles indicate that neither assembly captures the complete nuclear gene space; nonetheless, we recovered 196 shared single-copy orthologs, 191 of which contain intact open reading frames and were assigned to 22 COG functional categories. These loci encompass core informational and metabolic functions and collectively constitute a robust marker panel for future comparative and phylogenomic analyses in *Philonis inermis* and related Neotropical Cryptorhynchinae. The substantial proportion of unclassified COGs further highlights the limited genomic characterization of this lineage and underscores the potential for discovery as additional genomic data become available. In parallel, the recovery of duplicated BUSCOs and extensive rRNA and histone gene clusters provides complementary multicopy markers that may prove useful for resolving deeper or more complex evolutionary relationships. Future work integrating long-read sequencing and Hi-C scaffolding will be essential to resolve repetitive regions, reduce fragmentation, and ultimately achieve chromosome-scale assemblies for this ecologically important genus.

The mitochondrial genome of *P. inermis* exhibits a nucleotide composition biased toward (A+T), as well as gene order and orientation that are highly conserved, and consistent with the ancestral insect mitogenome architecture. Comparative analyses with complete mitogenomes from other Cryptorhynchinae genera revealed strong structural and syntenic conservation across the group.[9,10,12,29] As reported for other species such as *Eucryptorrhynchus chinensis* and *E. brandti* the mitogenome of *P. inermis* lacks an identifiable deficiency of tRNA-Ile gene.[10] The trnI gene is likely located within the highly variable control region, where high elevated divergence hampers automated annotation and precise boundary delimitation, making its detection a common challenge.[30]

Mitogenome-based tree place *Philonis* close to *Eucryptorrhynchus*, but we treat this as preliminary, given the limited and uneven mitogenomic sampling across Cryptorhynchinae. Broad, multi-gene frameworks show that relationships above the genus level can be difficult to stabilize in this subfamily, and that extensive sampling across loci is required to resolve deeper nodes.[31,32] In particular, Riedel et al.[32] recovered a large-scale molecular phylogeny that points to an American origin for Cryptorhynchinae and highlights the value of integrating mitochondrial and nuclear markers for robust placement. Our results align with this perspective: the topology we report is a useful working hypothesis that should be tested with expanded taxon and locus coverage.

If proximity to *Eucryptorrhynchus* is confirmed, the comparison is ecologically instructive. *Ailanthus altissima* (Simaroubaceae), the tree-of-heaven, is a fast-growing invasive tree native to China that readily colonizes disturbed habitats and can displace native vegetation. Within this host context, *E. scrobiculatus* and *E. brandti* are highly specialized on *A. altissima.* In parts of their native range, they are considered pests; however, they have also been evaluated as potential biological control agents where *A. altissima* is invasive, and climate-suitability assessments

suggest differential responses of the two congeners to future climates.[10,33] This dual "pest vs. biocontrol" context underscores why clear systematics and robust diagnostics matter when considering host-specific herbivores for applied programs.

Interestingly, all other cryptorhynchine weevils with complete mitochondrial genomes currently reported are documented agricultural pests of economic importance in Asia or Oceania, highlighting a significant gap for Neotropical species. In contrast, *P. inermis* is a stem-galling specialist with a narrow host range restricted to *P. foetida*, an invasive vine in Australia.[34]

At a broader scale, historical biogeography indicates a complex macroevolutionary backdrop for Cryptorhynchinae, with major diversity centers in the Neotropics and Australasia and signals consistent with an American origin.[3,32,35] Comparative insights from flightless *Trigonopterus* show repeated crossings of major biogeographic barriers (e.g., Wallace's Line), rapid radiations and finely structured endemism, and these features complicate deep-time reconstructions when sampling is sparse.[36] These patterns provide a cautionary frame for interpreting single-marker or low-taxon trees and reinforce the need for expanded, balanced sampling when refining the placement of *Philonis.*

Assessment for COI gene DNA barcoding regions indicates high accuracy on molecular identification of *P. inermis*, with minimal genetic divergence among Colombian individuals from three populations (K2P distances ≤ 0.006). This low intraspecific variability underscores the genetic coherence of the species and confirms that the sampled populations across Colombia belong to the same taxonomic unit. Despite the limited flight ability of *P. inermis*, this genetic homogeneity may be influenced by passive dispersal associated with its host (*P. foetida*), a hypothesis that warrants further investigation. Furthermore, both inter – and intraspecific genetic distance gaps support the COI barcode as a suitable tool for species identification in Neotropical cryptorhynchine weevils, exceeding values reported for related species from Asia, Europe, and Oceania.[36,37] Under this scenario, our COI results supports unambiguous diagnosis of *P. inermis.* This pattern aligns with the central rationale for DNA barcoding as a standardized, taxonomically integrative tool.[15,38] The maximum likelihood tree constructed from COI sequences clustered all *P. inermis* specimens together with strong statistical support, further confirming its genetic uniformity and separation from other Neotropical taxa. Collectively, these barcode results provide a robust molecular baseline for species identification and support the consideration of *P. inermis* as a promising candidate for biological control programs targeting *P. foetida.*

From an applied perspective, the combination the mitogenome and COI barcoding supports accurate recognition across Colombian populations, which is a prerequisite for any subsequent risk assessment. Furthermore, this approach strengthens integrative taxonomy, biosecurity, and classical weed biocontrol workflows. Barcodes offer interoperable, scalable diagnostics for look-alike taxa and immature stages, facilitate data sharing across laboratories and jurisdictions, and support post-release monitoring, both of which are key steps to minimize non-target risk.[15,38,39] The global invasive potential documented for *S. mangiferae* under climate change further illustrates why strong diagnostics and early detection pipelines are increasingly critical for curculionid lineages with agricultural relevance.[40]

Limitations and next steps follow directly from our results. First, phylogenetic inferences from current mitogenome sampling should be treated as provisional. Resolving deeper nodes will require denser Neotropical sampling, including close relatives of *Philonis*, and multi-locus or genomic matrices that integrate nuclear markers. Second, expanding the geographic and host-associated sampling for COI (and additional markers) will help quantify population structure and confirm the breadth of the barcode gap. Third, low-coverage, short-read genome skimming inherently underrepresents repetitive and GC-extreme regions and can collapse recent paralogs, yielding fragmented assemblies and biasing functional annotations toward conserved single-copy genes; increasing sequencing depth and integrating long reads and Hi-C will mitigate these biases. Together, these steps will strengthen both the systematic placement of *Philonis* and the applied utility of its genetic resources for monitoring and potential biocontrol assessment.

5. Conclusions

We provide the first mitogenomic reference for *P. inermis* (15,120 bp; ~77% A+T), with conserved gene order and deficiency of tRNA-Ile likely obscured within the variable control region. Maximum-likelihood analyses recover *P. inermis* as a well-supported clade and tentatively near *Eucryptorrhynchus*, a hypothesis that awaits denser taxon and locus sampling. COI barcodes from 20 Colombian individuals show extremely low intraspecific divergence (K2P ≤ 0.006) and a pronounced barcode gap from other American cryptorhynchine weevils, enabling reliable, field-ready diagnostics. Low-coverage genome sequencing recovered 196 single-copy orthologs along with a complementary set of duplicated BUSCOs and multicopy rRNA and histone genes, furnishing anchors for future genome-scale phylogenetics and comparative genomics. Together, these resources demonstrate the utility of COI barcoding for the current molecular identification of *P. inermis*, establish a molecular foundation for systematics and population-level studies, and inform the risk-aware evaluation of *P. inermis* as a host-specific candidate for classical biological control of

P. foetida. Priority next steps include long-read and Hi-C genome assemblies and expanded geographic and taxonomic sampling—including nuclear markers—to resolve deeper relationships and better quantify population structure.

Data availability statement

Underlying data

The raw sequencing datasets generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA1322535. The complete mitochondrial genome and COI partial sequences of *Philonis inermis* are available in GenBank under accession numbers PX645216, and PX353910–PX353929. The corresponding barcode dataset, including voucher information and specimen images, is available in the Barcode of Life Data System (BOLD) under PINEBIN: AHI5100.

Extended data

Figshare/Zenodo Repository

"*Supplementary Tables S1–S3 – Characterization of the Complete Mitochondrial Genome and Evaluation of COI Barcoding in Philonis inermis (Coleoptera: Curculionidae: Cryptorhynchinae) Using Genome Skimming*." https://doi.org/10.5281/zenodo.17793370.

This project contains the following extended data:

- **Supplementary Table S1.** Single-copy BUSCO orthologs recovered from *Philonis inermis* genome skimming assemblies, including locus identifiers, functional annotations, and sequence lengths.
- **Supplementary Table S2.** List of duplicated (multicopy) BUSCO genes detected in the *endopterygota_odb12* run, together with annotations for each multicopy ortholog. These loci represent additional nuclear genes of potential interest for phylogenomic studies.
- **Supplementary Table S3.** Extracted multicopy nuclear markers—including complete or partial **rRNA clusters** and **core histone genes** recovered directly from the *P. inermis* assemblies. Only loci ≥1 kb were retained. For each locus, we provide coordinates, strand orientation, percent identity, alignment length, and extracted sequence.
- All extended data files are publicly available at Zenodo (DOI: 10.5281/zenodo.17793370).

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

Acknowledgments

The authors express their sincere gratitude to Wilder Buitrago Arbeláez (Herbarium of the Universidad de Antioquia, HUA, Medellín, Colombia) for the identification of the host plant *Passiflora foetida* and for providing herbarium reference material. The authors also acknowledge the assistance of ChatGPT, a language model developed by OpenAI, for providing valuable insights and stylistic suggestions that improved the clarity and readability of this manuscript.

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Current Peer Review Status: ✔ ✔ ✔

Version 2

Reviewer Report 08 April 2026

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✔ **Renee Ali**
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The authors have considered recommendations and made appropriate changes which has improved the manuscript making it suitable for indexing.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: mosquito population genomics, entomology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 08 April 2026

https://doi.org/10.5256/f1000research.197074.r470431

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✔ **Arun Arumugaperumal**
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The article reports the mitogenome sequence of *Philonis inermis*, a stem-galling weevil. The authors could have separated the mitochondria and could have done a mitogenome sequencing. Instead, they have sequenced the genomic DNA at low coverage and assembled the mitochondrial DNA. Then they have compared it with related insects and arrived at a phylogenetic tree. The

absence of mitochondrial sequences from other members of the genus is a limitation. Given that, this sequence reported here will be of value to anybody working with the insect.

The authors can deposit the R-script used for analyses in a repository. The paragraph in discussion section starting with "The mitochondrial genome of *P. inermis* exhibits nucleotide a composition.." needs to be carefully checked. I think it is not conveying the intended meaning.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics; Bioinformatics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 19 March 2026

https://doi.org/10.5256/f1000research.197074.r468385

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It is great to see that the authors have addressed all the suggestions and answered all the questions. From my perspective, therefore, I have no further objections to the publication of the

manuscript.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: DNA barcoding, molecular phylogenetics, mitochondrial genomics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 22 November 2025

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The manuscript “Characterization of the complete mitochondrial genome and evaluation of COI barcoding in Philonis inermis (Coleoptera: Curculionidae: Cryptorhynchinae) using genome skimming” by Clavijo-Giraldo and co-authors presents the complete mitochondrial genome of Philonis inermis, a Neotropical stem-galling weevil that is specialized on the invasive vine Passiflora foetida. Beside the characterization of the mitochondrial genome, the authors provide new DNA barcode data of 20 specimens from Colombia, analyzing the intra- and interspecific genetic divergence of this marker by combining the new data with already published sequences from GenBank/NCBI. In my eyes, the topic of this manuscript is interesting and for suitable for a publication in “F1000Reserach”. However, there are some points that should be added or discussed in a broader context (see below).

Without doubt, mitogenomes represent powerful phylogenetic markers. Drawbacks of using mitochondrial genomes in phylogenetic studies, however, include high substitution rates, leading to substitution saturation especially in deep evolutionary branches. In addition to the extracted BUSCO genes, it is quite easily to extract other useful multicopy nuclear genes as the rRNA and/or histone clusters from the given raw data as well. Whereas these genes are no focus-genes of the given study, they can become useful in further ongoing studies. Therefore, the authors should think about providing these popular phylogenetic marker genes as additional supplement, too.

No contamination check has been done so far. I think that the amount of sequences of bacteria, fungi etc. will be very low, but nonetheless it should checked (e.g., using Kraken).

The only use of mitogenomes in phylogenetic studies can have some serious limitations that should be mentioned/discussed (see above).

In terms of the DNA barcode analysis, I recommend the creation of a project on the Barcode of Life Data System (BOLD; https://boldsystems.org/), the most popular workbench/sequence library for DNA barcode analysis, to (re)analyze the CO1 data set using the software tools offered there. This is especially true for the BIN approach (BOLD; Ratnasingham and Hebert (2013): PLOS ONE 8: e66213). Please check for already published sequences of closely related species on BOLD that should be included in such analysis. I feel that the assignment of a BIN will be very useful.

Is this beetle able to fly? This can have a strong effect on its dispersal and therefore genetic structure as well.

Other minor suggestions:

It would be nice to present a photo of the weevil species if available (e.g., check iNaturalist).

Where has the analyzed DNA been stored?

Change "Cytochrome c oxidase subunit I" to "Cytochrome c (in italics) oxidase subunit I"

A high AT-ratio is not only found in weevils but insects and arthropods in general.

What is a "shadow genome"?

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: DNA barcoding, molecular phylogenetics, mitochondrial genomics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 23 Feb 2026

Andrés Gómez-Palacio

Dr. Michael J Raupach

We thank the reviewer for their positive evaluation and for recognizing the relevance of our study. We have carefully addressed all points raised and revised the manuscript accordingly. Detailed responses are provided below.

Without doubt, mitogenomes represent powerful phylogenetic markers. Drawbacks of using mitochondrial genomes in phylogenetic studies, however, include high substitution rates, leading to substitution saturation especially in deep evolutionary branches.

Response:
We thank the reviewer for highlighting an important limitation of mitochondrial genomes in phylogenetic inference. We agree that despite their utility, high substitution rates can cause substitution saturation, particularly at deeper evolutionary timescales.

To address this, we have expanded the Introduction to explicitly acknowledge these constraints and to clarify that our study focuses on intraspecific and shallow-level phylogenetic resolution, where mitochondrial genomes and COI remain informative and widely used.

We have added the following text to the manuscript:
"Although mitogenomes are powerful markers, their use in phylogenetic studies is not without limitations. High substitution rates—particularly in third codon positions—can lead to substitution saturation in deep evolutionary branches, reducing the ability to accurately recover relationships among distantly related taxa. Such constraints are less problematic at shallow timescales, where mitochondrial genomes retain strong resolving power for population-level analyses and recent divergences. Because the present study focuses on intraspecific and closely related lineages, mitogenomic data remain well suited to our research objectives"

In addition to the extracted BUSCO genes, it is quite easily to extract other useful multicopy nuclear genes as the rRNA and/or histone clusters from the given raw data as well. Whereas these genes are no focus-genes of the given study, they can become useful in further ongoing studies. Therefore, the authors should think about providing these popular phylogenetic marker genes as additional supplement, too.

Response*:*
We thank the reviewer for this insightful suggestion. In addition to the 196 single-copy BUSCO orthologs already reported, we re-examined the BUSCO output (endopterygota_odb12) and identified 28 duplicated BUSCOs representing multicopy nuclear loci (now provided in Table S2). Furthermore, we extracted additional multicopy marker genes, including rRNA and histone clusters,

directly from the assemblies (Table S3). These sequences have been deposited alongside the single-copy BUSCO set and are now explicitly referenced in the manuscript.

Although the present study focuses on the mitogenome and COI, we fully agree that these multicopy nuclear markers constitute a valuable resource for future phylogenomic or comparative genomic analyses. Accordingly, we have added a brief summary of these data in the Results section and clarified their potential utility in the Discussion.

No contamination check has been done so far. I think that the amount of sequences of bacteria, fungi etc. will be very low, but nonetheless it should checked (e.g., using Kraken).

***Response**:*
We thank the reviewer for this suggestion. We have now performed a dedicated contamination assessment using Kraken2 (v2.1.2) with the PlusPF reference database. To specifically enrich for non-target sequences, quality-filtered reads were first mapped to the de novo assemblies, and unmapped read pairs were subsequently classified taxonomically. The analysis confirmed that bacterial, fungal, and viral sequences represent only a minor fraction of the reads in both libraries. Details of this analysis have been added to the Methods section, and the results are summarized in the revised manuscript.

The only use of mitogenomes in phylogenetic studies can have some serious limitations that should be mentioned/discussed (see above).

***Response**:*
We appreciate the reviewer's continued emphasis on this issue and fully agree that mitochondrial genomes alone have important limitations for phylogenetic inference, particularly due to substitution saturation at deeper evolutionary levels. We have revised the manuscript to explicitly state that mitogenomic data should not be interpreted as providing robust resolution of deep phylogenetic relationships. Instead, we clarify that their use in this study is restricted to intraspecific comparisons and shallow divergences, for which mitochondrial markers remain informative and widely applied. We also note that resolving deeper evolutionary relationships will require complementary nuclear genomic data, which is beyond the scope of the present study.

In terms of the DNA barcode analysis, I recommend the creation of a project on the Barcode of Life Data System (BOLD; https://boldsystems.org/), the most popular workbench/sequence library for DNA barcode analysis, to (re)analyze the CO1 data set using the software tools offered there. This is especially true for the BIN approach (BOLD; Ratnasingham and Hebert (2013): PLOS ONE 8: e66213). Please check for already published sequences of closely related species on BOLD that should be included in such analysis. I feel that the assignment of a BIN will be very useful.

***Response**:*
We thank the reviewer for this valuable suggestion. Following this recommendation, we created a dedicated project in the Barcode of Life Data System (BOLD; project code PINE) and re-analyzed the complete COI dataset using the analytical tools available in the BOLD workbench. All COI sequences were uploaded and linked to vouchered specimens, including associated specimen images, and sequence validation was performed within BOLD.

Kimura 2-parameter (K2P) distance analyses and neighbor-joining clustering were conducted using BOLD's distance summary and tree-building tools. These analyses confirmed extremely low intraspecific divergence among Philonis inermis sequences, consistent with our previous results based on pairwise K2P distances (0–0.006), and showed that all sequences form a single cohesive cluster.

We additionally surveyed BOLD for publicly available COI sequences of Philonis and closely related taxa within Cryptorhynchinae. No public barcode records for Philonis inermis or closely related congeners were found, indicating that the dataset generated here represents the first BOLD reference for this species. Consequently, no Barcode Index Number (BIN) was assigned by BOLD, which is expected for single-species datasets lacking comparable reference sequences and does not reflect a lack of genetic coherence. This behavior is consistent with the algorithmic nature of BIN assignment as described by Ratnasingham and Hebert (2013).

All barcode data and associated voucher information are available in BOLD under project code PINE, providing a baseline reference for future comparative and taxonomic studies of this genus.

Is this beetle able to fly? This can have a strong effect on its dispersal and therefore genetic structure as well.

***Response**:*
We thank the reviewer for this observation. Philonis inermis is a poor flyer, and therefore active dispersal is expected to be limited. However, this species is a parasite associated with P. foetida, and its dispersal may occur passively via host movement, potentially facilitating connectivity among geographically separated populations. Consistent with this hypothesis, COI sequences from individuals collected across multiple Colombian localities (e.g., Antioquia and Córdoba) exhibited extremely low intraspecific divergence (minimal K2P distances), suggesting a genetically homogeneous population at the spatial scale examined. Nevertheless, the role of host-mediated dispersal remains hypothetical and should be further investigated using broader geographic sampling and additional nuclear markers. A brief sentence discussing this hypothesis and emphasizing that it requires further investigation has now been included in the Discussion section.

Other minor suggestions:

It would be nice to present a photo of the weevil species if available (e.g., check iNaturalist).

***Response**:*
We note that voucher-linked photographs of Philonis inermis are already available in the associated BOLD Systems project and correspond directly to some of the specimens analyzed in this study. Therefore, additional images from external sources (e.g., iNaturalist) were not included.

Where has the analyzed DNA been stored?

***Response**:*
The total genomic DNA analyzed in this study is deposited in the entomological biobank of the Grupo de Investigación en Sistemática Molecular (GSM), Universidad Nacional de

Colombia, Medellín, Colombia.

Change "Cytochrome c oxidase subunit I" to "Cytochrome c (in italics) oxidase subunit I"

Response:
The term "Cytochrome c oxidase subunit I" has been corrected to "Cytochrome c oxidase subunit I" throughout the manuscript.

A high AT-ratio is not only found in weevils but insects and arthropods in general.

Response:
We have revised the text to clarify that the high A+T bias observed is a common feature of mitochondrial genomes not only in weevils but also across insects and arthropods in general.

What is a "shadow genome"?

Response:
The term "shadow genome" has been corrected to low-coverage genome sequencing (genome skimming) throughout the manuscript.

Competing Interests: No competing interests were disclosed.

Reviewer Report 22 November 2025

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Renee Ali
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Even though this manuscript offers useful genetic information about *Philonis inermis*, a number of sections need to be significantly revised before it can be accepted. The manuscript as it is currently worded suggests that the BUSCO was utilized to support the mitogenome's completeness; nevertheless, it should be made explicit that it was used to access the nuclear portion of the shallow sequence assemblies. Additionally, even though the study demonstrated that nuclear single copy orthologs can be accessed from low coverage sequences, this was given more attention than the mitochondrial genome, which is meant to be the primary emphasis as stated in the title. Additionally, the assemblies appear to be rather fragmented; the reasons why greater coverage was not attempted should be addressed. *Additionally, there are inconsistencies between the methods and results; for example no mention was made how phylogenetic analysis was done*

for complete mitogenomes only for the COI genes yet there is a tree represented in Figure 2 e which also lacks accession numbers
"This study presents the first complete mitochondrial genome for the genus *Philonis* and confirms the reliability of COI barcoding for its accurate identification. These genomic resources lay the foundation for integrative taxonomic, comparative, and evolutionary studies, and support the evaluation of *P. inermis* as a potential biological control agent against *P. foetida."* - I suggest editing statement , since there was no comparison or analysis of the other protein coding genes in the mitochondrial genomes present to compare you cannot confirm reliability of COI for accurate ID, instead is useful for current status due to lack of other available information.

Minor suggestions
1.Use "shallow genome skimming" in place of "shadow-genome."
2. Substitute "absence of a detectable trnI gene" for "deficiency of tRNA-Ile."
3. When clarification is required, substitute "cryptorhynchine weevils" for "cryptorhynchine."

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
No

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
No

Are the conclusions drawn adequately supported by the results?
No

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: mosquito population genomics, entomology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 23 Feb 2026

Andrés Gómez-Palacio

Dr. Renee Ali

We appreciate this observation and agree that the mitochondrial genome constitutes the primary focus of the study, as reflected in the title. In the revised manuscript, we have restructured the Results and Discussion sections to place clearer emphasis on mitogenome characterization, organization, nucleotide composition, and phylogenetic placement.

The analysis of nuclear single-copy orthologs is now explicitly framed as a complementary outcome of the shallow genome-skimming approach rather than a central objective. While these nuclear markers provide valuable additional genomic resources, they are presented as secondary to the mitogenome assembly and COI barcoding analyses, which remain the core contributions of this work. We believe these revisions better align the manuscript structure with its stated primary emphasis.

Additionally, the assemblies appear to be rather fragmented; the reasons why greater coverage was not attempted should be addressed.

***Response*:**
We thank the reviewer for this important observation. The assemblies presented in this study were generated using a shallow genome-skimming strategy intentionally designed to recover the complete mitochondrial genome and representative nuclear markers (e.g., BUSCO orthologs), rather than to produce a high-contiguity nuclear genome assembly. Our primary objective was to establish foundational genomic resources for taxonomic validation and phylogenetic inference, for which moderate sequencing depth is sufficient.

As expected under this design, BUSCO analysis indicates partial recovery of the nuclear gene space, reflecting the limited coverage typical of genome-skimming approaches. Nevertheless, we successfully recovered 196 shared single-copy orthologs (191 with intact ORFs), as well as duplicated BUSCOs and multicopy rRNA and histone clusters, demonstrating that the data are sufficient for marker-based comparative and phylogenomic applications.

We agree that increased sequencing depth and incorporation of long-read technologies would substantially improve assembly contiguity and completeness. Such efforts are planned for future work but were beyond the scope of the present study. We have now clarified this rationale in the Discussion section to avoid ambiguity regarding the study design and objectives.

Additionally, there are inconsistencies between the methods and results; for example, no mention was made how phylogenetic analysis was done for complete mitogenomes only for the COI genes yet there is a tree represented in Figure 2 e which also lacks accession numbers

***Response**:*
We thank the reviewer for identifying this inconsistency. The original submission did not explicitly describe the phylogenetic analysis performed using complete mitochondrial genome sequences, although it was presented in Figure 2e. We have now added a dedicated subsection in the Methods detailing the alignment procedure (MAFFT v7.525), model selection and maximum likelihood inference in IQ-TREE v2.0.3, and the use of 1,000 ultrafast bootstrap replicates. Additionally, GenBank accession numbers for all mitogenome sequences included in the analysis have been incorporated into the Methods section. These

revisions resolve the methodological inconsistency and improve reproducibility.

"This study presents the first complete mitochondrial genome for the genus *Philonis* and confirms the reliability of COI barcoding for its accurate identification. These genomic resources lay the foundation for integrative taxonomic, comparative, and evolutionary studies, and support the evaluation of *P. inermis* as a potential biological control agent against *P. foetida."* - I suggest editing statement, since there was no comparison or analysis of the other protein coding genes in the mitochondrial genomes present to compare you cannot confirm reliability of COI for accurate ID, instead is useful for current status due to lack of other available information.

Response:
We thank the reviewer for this clarification. We agree that, given the absence of comparative analyses of other mitochondrial protein-coding genes, our data do not allow us to confirm the overall reliability of COI barcoding in a broader comparative framework. Accordingly, we have revised the statement to moderate the claim and to indicate that COI barcoding is useful for the current molecular identification of Philonis inermis under the limited availability of comparative genomic data.

Minor suggestions

1. Use "shallow genome skimming" in place of "shadow-genome."

Response:
Following the reviewer's suggestion and previous comments from Dr. Michael J. Raupach, the term "shadow genome" has been replaced throughout the manuscript with "low-coverage genome sequencing" which more accurately reflects the sequencing approach used.

1. Substitute "absence of a detectable trnI gene" for "deficiency of tRNA-Ile."

Response:
The phrase "deficiency of tRNA-Ile" has been revised to "absence of a detectable trnI gene" throughout the manuscript.

1. When clarification is required, substitute "cryptorhynchine weevils" for "cryptorhynchine."

Response:
We thank the reviewer for this clarification. Throughout the manuscript, instances of the term "cryptorhynchine" have been revised to "cryptorhynchine weevils" where additional clarity was required,

Competing Interests: No competing interests were disclosed.

Comments on this article

Version 1

Author Response 23 Feb 2026

Andrés Gómez-Palacio

We sincerely thank the reviewer for the careful evaluation of our manuscript and for the constructive comments and suggestions provided. We apologize for the delay in submitting our revised response, which was due to a combination of scheduled academic commitments, holiday periods, and the time required to properly implement several substantive revisions requested by the reviewers. These included updates to the associated BOLD Systems project, the incorporation of additional multicopy genes analyses (e.g., BUSCO), and the implementation of a dedicated contamination assessment using Kraken2, among others.

All reviewer comments have now been thoroughly addressed, and the manuscript has been revised accordingly. In particular, we have (i) performed and documented a contamination analysis based on taxonomic classification of unmapped reads, (ii) expanded the Discussion to better contextualize the use and limitations of mitochondrial genomes in phylogenetic inference, (iii) clarified methodological terminology and analytical scope, and (iv) refined several sections to improve clarity and consistency. We believe these revisions have strengthened the methodological rigor and interpretative framework of the study, and we are grateful to the reviewer for their insightful suggestions, which substantially improved the quality of the manuscript.

Competing Interests: No competing interests were disclosed.

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