



GENOME NOTE

REVISED Re-sequencing of the complete chloroplast genome of *Cinnamomum burmanni* (Nees & T.Nees) Blume (Lauraceae) from Indonesia using MinION Oxford Nanopore Technologies

[version 3; peer review: 3 approved, 2 not approved]

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V3 First published: 20 Feb 2024, 13:127
<https://doi.org/10.12688/f1000research.145790.1>

Second version: 21 May 2024, 13:127
<https://doi.org/10.12688/f1000research.145790.2>

Latest published: 16 Dec 2025, 13:127
<https://doi.org/10.12688/f1000research.145790.3>

Abstract

Cinnamomum burmanni (Nees & T.Nees) Blume (Lauraceae) belongs to the Magnoliids group and is mainly distributed in Indonesia and Southeast Asia. The complete chloroplast (cp) genome of *C. burmanni* sampled from Indonesia was assembled and annotated for the first time in this study. The length of the cp genome is 152,765 bp with a GC content of 39%, and it consists of four subregions: a large single-copy (LSC) region of 93,636 bp, a small single-copy (SSC) region of 18,893 bp and two inverted repeats (IR) regions (IRA 20,121 bp; IRB 20,115 bp). The cp genome of *C. burmanni* encodes a total of 173 unique genes, which are 96 protein-coding genes, 19 rRNA genes, and 68 tRNA genes that can be utilized for advanced genetic and genomic studies of the species.

Keywords

Conservation, complete chloroplast genome, Lauraceae, phylogenetic



This article is included in the **Genomics and Genetics** gateway.

Open Peer Review

Approval Status

	1	2	3	4	5
version 3					
(revision)	view	view	view	view	
16 Dec 2025					
version 2					
(revision)	view	view	view	view	view
21 May 2024					
version 1					
20 Feb 2024	view	view			

1. **Hoang Dang Khoa Do** , Nguyen Tat Thanh University, Ho Chi Minh City, Vietnam
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4. **Nawaz Haider Bashir**, Qujing Normal University, Qujing, China



This article is included in the **Nanopore Analysis** gateway.

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Any reports and responses or comments on the article can be found at the end of the article.

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Author roles: **Salindeho RA:** Data Curation, Formal Analysis, Investigation, Visualization, Writing – Original Draft Preparation; **Dwiyanti FG:** Project Administration, Resources, Validation, Writing – Review & Editing; **Pratama R:** Data Curation, Methodology, Validation, Writing – Review & Editing; **Matra DD:** Methodology, Validation, Writing – Review & Editing; **Majiidu M:** Data Curation, Methodology; **Siregar IZ:** Conceptualization, Funding Acquisition, Supervision, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This research was funded by the National Competitive Basic Research 2022-2023 Scheme No: 001/E5/PG.02.00PT/2022 and 001/E5/PG.02.00.PL/2023 awarded by the Ministry of Education, Culture, Research and Technology of the Republic of Indonesia entitled “Pilot Sequencing of 100 Native Forest Tree Genomes to Support Ecosystem Restoration (Rintisan Sekuensing 100 Genom Pohon Hutan Asli untuk Mendukung Restorasi Ekosistem)” granted to the corresponding author. *The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

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How to cite this article: Salindeho RA, Dwiyanti FG, Pratama R *et al.* **Re-sequencing of the complete chloroplast genome of *Cinnamomum burmanni* (Nees & T.Nees) Blume (Lauraceae) from Indonesia using MinION Oxford Nanopore Technologies [version 3; peer review: 3 approved, 2 not approved]** F1000Research 2025, 13:127 <https://doi.org/10.12688/f1000research.145790.3>

First published: 20 Feb 2024, 13:127 <https://doi.org/10.12688/f1000research.145790.1>

REVISED Amendments from Version 2

We updated the Introduction and Result sections according to reviewers suggestion.

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

Introduction

Cinnamomum burmanni (or cinnamon) is an endemic woody shrub belonging to the Lauraceae family, which is widely distributed in Indonesia, covering West Sumatra, North Sumatra, Jambi, Bengkulu, Java Island, and Maluku Islands (Suwanto *et al.*, 2014). The species grows in altitudes between 0 and 2000 m above sea level. The tree can grow up to 15 m tall, and the wood is grey with a very distinctive aroma and sweet taste, so its wood is widely used for spices, cosmetics, and herbs. The active compounds contained in cinnamon wood are cinnamaldehyde, flavonoids, alkaloids, tannins, saponins, coumarins, steroids, eugenol, and phenols, which act as anti-bacterial, anti-tumor, antioxidant, anti-inflammatory, anti-cancer, and anti-diabetic agents (Indarto *et al.*, 2022).

The chloroplast (cp) genome sequence of *C. burmanni* from China was previously elucidated by Yang *et al.* (2019) utilizing 11 universal primer pairs for long-range PCR in next-generation sequencing. However, their study provided only a phylogenetic tree, and the corresponding sequence data and cp genome map are not readily accessible (<https://lcgdb.wordpress.com>). In the present study, we present genomic resources for *C. burmanni* from Indonesia, generated through the long-read sequencing method utilizing MinION technology from Oxford Nanopore Technologies. This study includes a comprehensive list of genes within the chloroplast genome of *C. burmanni*, which was not included in the previous study. Such information is of considerable significance as a foundation for further genetic investigations. Additionally, the study of the cp genome *C. burmanni* from Indonesia using PCR-free library preparation method and long-read sequencing generated by MinION Oxford Nanopore Technologies (ONT) has not been carried out, whereas this information is needed to improve correct species identification and to optimize the sustainable use of genetic resources for this species. MinION is a third-generation sequencing technology with nanopore technology (Oxford Nanopore Technologies (ONT), 2017). Furthermore, the present study aimed to re-sequence and assemble the complete cp genome *C. burmanni* from Indonesia using MinION Oxford Nanopore Technologies (ONT).

Methods

Fresh leaf samples were collected from one individual *C. burmanni* tree in Lembang Subdistrict, West Bandung Regency, West Java Province, Indonesia. The collected leaf sample was subsequently used for DNA extraction and sequencing in the field. The data analysis of the chloroplast genome was performed at the Laboratory of Forest Genetics and Molecular Forestry, Department of Silviculture, Faculty of Forestry and Environment, IPB University.

C. burmanni genomic DNA was extracted using the Qiagen DNeasy Plant Mini Kit (cat. nos. 69104 and 69106) following the manufacturer's protocol with slight modifications. Extraction was first done by grinding fresh leaf samples to which 400 µl of Buffer AP1 and 1 µl of mercaptoethanol had been added using a mortar and pestle. The disrupted sample was placed into a 1.5 ml microcentrifuge tube. The mixture was then incubated for 10 min at 65°C using Mini Heating Dry Bath Incubator MD-MINI (Major Science Co., Ltd). Afterward, 130 µl Buffer P3 was added into the microtube and then vortexed using Biosan V-32 Multi-Vortex and incubated for 5 min on ice. The mixture was centrifuged for 2 min at 8000 × g using a portable microcentrifuge on the Bento Lab device (Bento Bioworks Ltd). The lysate was pipetted into a QIAshredder spin column placed in a 2 ml collection tube. The lysate was centrifuged for 2 min at 8000 × g using a portable microcentrifuge on the Bento Lab device (Bento Bioworks Ltd). The flow-through was transferred into a new tube without disturbing the DNA pellet. 1.5 volumes of Buffer AW1 were then added and mixed by pipetting. 650 µl of the mixture was transferred into a DNeasy Mini spin column placed in a 2 ml collection tube and subsequently centrifuged for 1 min at 6000 × g. The flow-through was discarded, and the spin column was placed into a new 2 ml collection tube. 500 µl Buffer AW2 was added to the spin column and centrifuged for 1 min at 6000 × g. The flow-through was then discarded and the spin column was transferred to a new 1.5 ml microcentrifuge tube. 50 µl Buffer AE was added for elution and subsequently incubated for 5 min at room temperature (15–25°C) before centrifuging for 1 min at 6000 × g. The quantity of genomic DNA was measured by the Invitrogen Qubit 1.0 fluorometer with the Qubit dsDNA BR assay kit.

The high molecular weight of 400 ng evaluated DNA proceeded to PCR-free library preparation, which followed the Nanopore protocol for Rapid sequencing gDNA – Field Sequencing Kit (SQK-LRK 001) version FSK_9049_v1_revR_14Aug2019. The prepared DNA library was sequenced using the MinION R9.4.1 flow cell (FLO-MIN106D) on a MinION Mk1B sequencer (Oxford Nanopore Technologies). The runs were visualized by MinKnow v3.6.5 software (<http://community.nanoporetech.com> Oxford Nanopore Technologies).

Basecalling with super accuracy mode (SUP) to translate Fast5 raw data into Fastq (DNA-Seq of *Cinnamomum burmanni*. NCBI Accession number SRX22198906) data was performed using the Guppy program (RRID: SCR_023196) v4.2.3+8aca2af8 (Wick *et al.*, 2019). Quality control was done using NanoStat v1.5.0 and NanoPlot (RRID:SCR_024128) v1.28.2 (De Coster *et al.*, 2018). Chloroplast genome assembly was performed using Galaxy Server (RRID:SCR_006281) version 23.1.1.dev0 (Sloggett *et al.*, 2013). The assembly includes a filtering step to filter reads quality ($Q > 7$) and length minimum of reads (> 500 bp), using the Flye program (RRID:SCR_017016) v2.9 (Kolmogorov *et al.*, 2020) and polishing the assembly results using the MEDAKA consensus program (RRID: SCR_005857) v1.4.4 (Oosterbroek *et al.*, 2021). The cpDNA data was then annotated using the GeSeq (RRID: SCR_017336) on the CHLOROBOX platform (Tillich *et al.*, 2017) to assign functions to the predicted genes and generate a map representation of the chloroplast genome.

Results

The sequencing resulted in a total of 59,589 reads, total bases of 140,909,220 bp, and read length N50 4,377 bp. The assembly resulted in 288 contigs, contig_246 annotated as cp genome with coverage of 37x. The cp genome showed a typical quadripartite structure (Figure 1) with a length of 152,765 bp, consisting of small single copy (SSC 18,893 bp) and

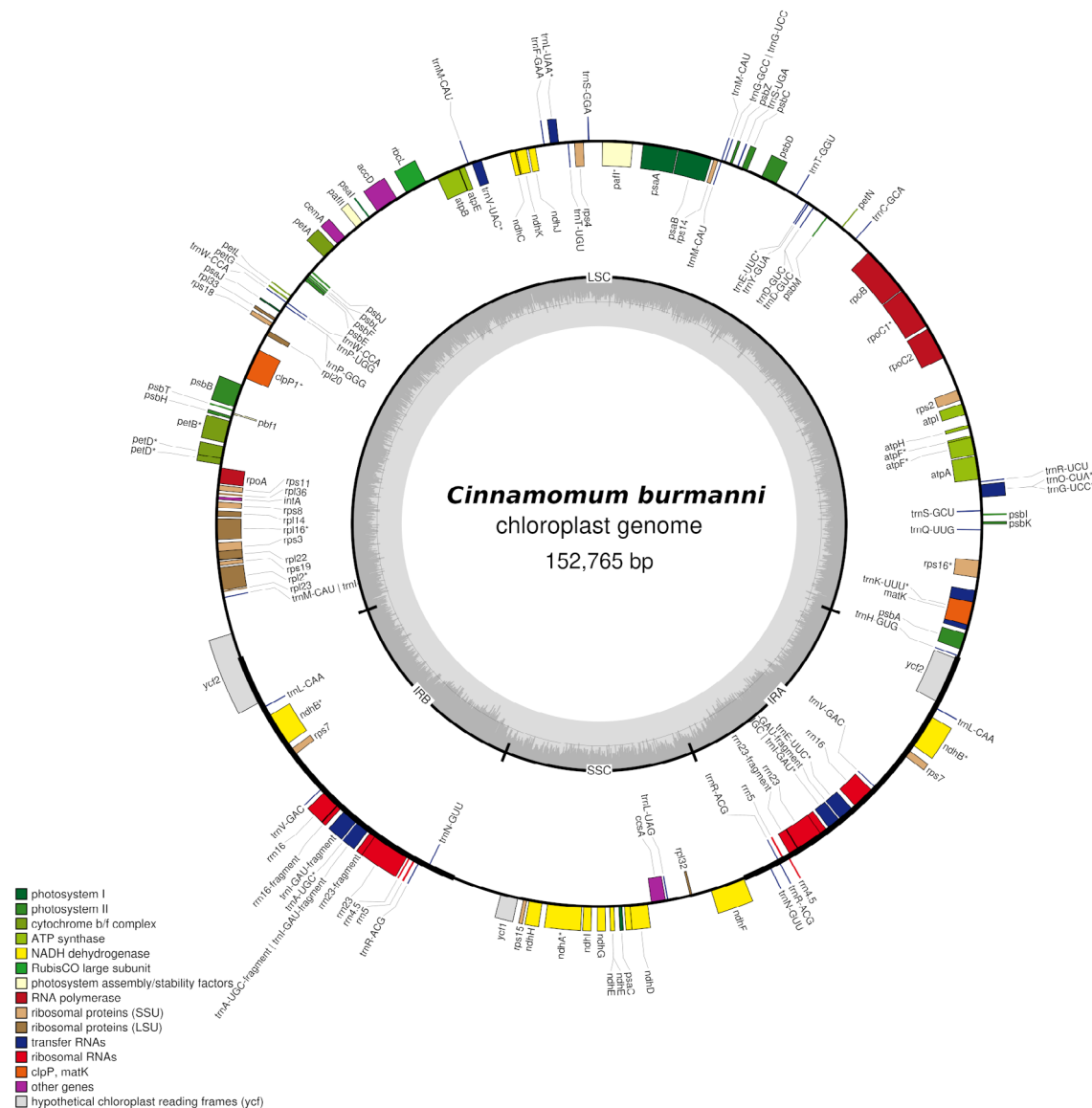


Figure 1. The complete chloroplast genome of *Cinnamomum burmanni*. Genes shown inside and outside the circle are transcribed clockwise and counterclockwise, respectively. Annotated genes are colored according to the functional categories.

Table 1. List of genes in the chloroplast genome of *Cinnamomum burmanni*.

Functional category	Group of genes	Name of genes
Self-replication	Large subunit ribosomal proteins	<i>rpl32, rpl33, rpl20, rpl36, rpl14, rpl16*(×2), rpl22, rpl2*(×2), rpl23</i>
	DNA dependent RNA polymerase	<i>rpoC2, rpoC1*(×2), rpoB, rpoA</i>
	Small subunit ribosomal proteins	<i>rps7, rps12**(×2), rps15, rps7, rps16*(×2), rps2, rps14, rps4, rps18, rps11, rps8, rps3, rps19, rps12-fragment*</i>
	rRNAs	<i>rrn16, rrn23, rrn5, rrn4.5</i>
	tRNAs	<i>trnL-CAA, trnV-GAC, trnE-UUC, trnA-UGC*(×2), trnN-GUU, trnL-UAG, trnN-GUU, trnR-ACG, trnR-ACG, trnI-GAU*(×2), trnV-GAC, trnL-CAA, trnH-GUG, trnK-UUU*(×2), trnQ-UUG, trnG-UCC*(×2), trnR-UCU, trnC-GCA, trnD-GUC, trnY-GUA, trnT-GGU, trnS-UGA, trnG-GCC, trnM-CAU, trnJm-CAU, trnS-GGA, trnT-UGU, trnL-UAA*(×2), trnF-GAA, trnV-UAC*(×2), trnW-CCA, trnP-UGG, trnI-CAU, trnS-GCU</i>
	Subunit of ATP synthase	<i>atpA, atpF*(×2), atpH, atpI, atpE, atpB</i>
	Subunit of NADH-dehydrogenase	<i>ndhB*(×2), ndhH, ndhA*(×2), ndhI, ndhG, ndhE, ndhD, ndhF, ndhJ, ndhK, ndhC</i>
Photosynthesis	Subunits of cytochrome b/f complex	<i>petN, petA, petL, petG, petB*(×2), petD*(×2)</i>
	Subunits of photosystem I	<i>psaC, psaB, psaA, psaI, psaJ</i>
	Subunits of photosystem II	<i>psbK, psbI, psbM, psbD, psbC, psbZ, psbJ, psbL, psbF, psbE, psbB, psbT, psbH, psbA</i>
	Subunit rubisco	<i>rbcl</i>
	Photosystem assembly factors	<i>pafI**(×2), pafII</i>
	Photosystem biogenesis factor	<i>Pbf1</i>
	Subunit of acetyl-CoA-carboxylase	<i>accD</i>
	C-type cytochrome synthesis gene	<i>ccsA</i>
Other functions	Envelope membrane protein	<i>cemA</i>
	ATP-dependent protease subunit P	<i>clpP1**(×2)</i>
	Maturase	<i>matK</i>
	Conserved open reading frames	<i>ycf1 (×2), ycf2 (×2)</i>
	Transitional initiation factor	<i>infA</i>

*Gene containing single intron.

**Gene containing two introns.

Genes located in the IR regions are indicated by the (×2) symbol.

large single copy (LSC 93,636 bp) regions separated by a pair of inverted repeat A (IRA 20,121 bp) and inverted repeat B (IRB 20,115 bp) regions (Figure 1). The *C. burmanni* chloroplast genome contained 173 unique genes, including 96 coding sequences, 68 transfer RNA (tRNA), and 19 ribosomal RNA (rRNA) genes (Table 1). The *C. burmanni* sequence had a GC content of 39% (LSC 38%; SSC 34%; IR 44%) and a coverage depth 37x. The results of the typical quadripartite structure were similar to the *C. burmanni* reported by Yang *et al.* (2019). The chloroplast genome assembly of *C. burmanni* has 10 bp less (152,765 bp) than previously reported by Yang *et al.* (2019) (152,775 bp). However, the general GC ratio of each region is comparable at 38% (LSC), 34% (SSC), and 44% (IR).

Data availability

Underlying data

NCBI's Short Read Archive (SRA): DNA-Seq of *Cinnamomum burmanni*. Accession number SRX22198906; <https://www.ncbi.nlm.nih.gov/sra/SRX22198906> (IPB University, 2023).

Acknowledgements

The authors thank Mrs. Siska Nurfajri and Ms. Nabila Salsabila Salmah, the alumni of the Department of Silviculture, Faculty of Forestry and Environment, IPB University, for their valuable assistance in DNA extraction.

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Open Peer Review

Current Peer Review Status:     

Version 3

Reviewer Report 12 January 2026

<https://doi.org/10.5256/f1000research.193459.r441776>

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Minh Trong Quang 

University of Medicine and Pharmacy, Ho Chi Minh City, Vietnam

I have carefully reviewed the revised version of the manuscript as well as the authors' responses to previous reviewer comments. The authors have addressed the major technical and presentation-related concerns raised during earlier review rounds, including improvements to the Introduction, clarification of the sequencing and assembly workflow, correction of inconsistencies between Figure 1 and Table 1, and clearer reporting of chloroplast genome structure and gene content. The methodological description is now more focused, and the Results section more clearly reports key assembly statistics and genome features.

While some limitations inherent to a Genome Note remain (e.g., limited comparative and evolutionary interpretation), these are now appropriately aligned with the scope and aims of the article.

Overall, the revised manuscript represents a technically sound and useful genomic resource that adds geographic representation for *Cinnamomum burmanni* plastomes and should be of value to researchers working in plant genomics and chloroplast genome studies.

I therefore have **no further major comments** to make on this revised version.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Bioinformatics, Genetics, Biotechnology

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 10 January 2026

<https://doi.org/10.5256/f1000research.193459.r441775>

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Jakub Sawicki 

Department of Botany and Nature Protection, University of Warmia and Mazury in Olsztyn, Olsztyn, Poland

The authors resolved all raised issues. I recommend acceptance.

Competing Interests: No competing interests were disclosed.

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 31 December 2025

<https://doi.org/10.5256/f1000research.193459.r441778>

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Nawaz Haider Bashir

Qujing Normal University, Qujing, Yunnan, China

The authors have incorporated the necessary changes in the revised version.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Entomologist, Evolutionary Biology

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 16 December 2025

<https://doi.org/10.5256/f1000research.193459.r441779>

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Hoang Dang Khoa Do 

Nguyen Tat Thanh University, Ho Chi Minh City, Ho Chi Minh, Vietnam

Dear Authors,

Thank you very much for revising the manuscript.

However, many issues were not addressed, and the text was the same as previous version without clear explanation.

Therefore, I am not confident for further reviewing this manuscript.

Best regards.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics, Chloroplast genome evolution, Phylogeny

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Version 2

Reviewer Report 20 November 2025

<https://doi.org/10.5256/f1000research.166509.r424130>

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Zinian WU

Chinese Academy of Agricultural Sciences, Beijing, Beijing, China

1. The description of sequencing in the Methods section is excessively detailed, and most content pertains to routine operations performed by the sequencing company. It is recommended to condense this part: briefly state the sequencing method, data volume, and other core information in one sentence, and focus on the analysis and discussion of the results.

2. The chloroplast genome typically has a quadripartite structure, consisting of four regions (LSC, SSC, IRa, and IRb), where IRa and IRb are equal in length and inverted in direction. However, the lengths of the two IR regions assembled by the authors are 20,121 bp and 20,115 bp, respectively, which is obviously incorrect. Consequently, the annotation results are inevitably inaccurate, and the authors are advised to further verify and correct them.

In summary, it is recommended to reject the manuscript and invite resubmission after revisions.

Are the rationale for sequencing the genome and the species significance clearly described?

No

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of the sequencing and extraction, software used, and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a usable and accessible format, and the assembly and annotation available in an appropriate subject-specific repository?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: genome

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Reviewer Report 12 November 2025

<https://doi.org/10.5256/f1000research.166509.r421284>

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Nawaz Haider Bashir

Qujing Normal University, Qujing, Yunnan, China

This Genome Note describes the re-sequencing and assembly of the chloroplast genome of *Cinnamomum burmanni* from Indonesia. The topic has significant relevance and potential value, particularly since it adds geographic representation to existing plastome data. The authors have already revised and improved the manuscript in accordance with the reviewers' comments. However, the manuscript still requires substantial improvements, such as:

In the introduction, it is not clear why resequencing the plastome is necessary since there is already a complete *C. burmanni* plastome (China accession).

Remove repeated sentences in the introduction, like "MinION, one of the ONT devices."

Differences between Indonesian and Chinese accessions and their biological significance need to be explained.

Figure 1: ycf1 appears in Figure 1 but is missing in Table 1.

Results of sequencing can be made clear with total reads, average read length, longest read,

percentage of reads used for cp assembly, and chloroplast vs. nuclear read percentages.

Are the rationale for sequencing the genome and the species significance clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of the sequencing and extraction, software used, and materials provided to allow replication by others?

Partly

Are the datasets clearly presented in a usable and accessible format, and the assembly and annotation available in an appropriate subject-specific repository?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Entomologist, Evolutionary Biology

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.

Reviewer Report 11 October 2025

<https://doi.org/10.5256/f1000research.166509.r417958>

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Minh Trong Quang 

University of Medicine and Pharmacy, Ho Chi Minh City, Vietnam

Your Genome Note is a useful contribution that documents a MinION-based chloroplast assembly for Indonesian *Cinnamomum burmanni*, but to make it scientifically sound and maximally reusable, please

- (i) strengthen the rationale by stating explicitly what ONT long reads add beyond the existing Chinese plastome (e.g., resolving repeats, verifying IR junctions, detecting structural/indel differences) and include a concise, tabulated comparison (genome size, GC%, LSC/SSC/IR lengths, IR junction coordinates, gene content);
- (ii) deposit the assembled plastome (FASTA) and its annotation (GenBank flatfile and/or GFF3) in a subject-specific repository (GenBank/ENA/DDBJ) and cite the accession(s) in the Data Availability section, alongside a clear list of all deposited file types (FASTQ and, if possible, FAST5/POD5);

assembly FASTA; GFF3/GBK; circular genome map) with checksums/DOIs; (iii) resolve the IR asymmetry (IRa vs IRb lengths) by validating junctions with read-depth plots and alignment/dot-plots—either justify true asymmetry or correct the assembly—and report the outcome briefly in Results/Discussion; (iv) improve reproducibility by providing key commands/parameters for each step (Guppy model and thresholds; read filtering; Flye options including genome size/plasmid mode; number of polishing iterations and Medaka model; circularization/rotation procedure; GeSeq reference sets and identity thresholds; any manual curation of starts/stops and introns), plus a simple pipeline schematic; (v) add minimal HMW DNA QC evidence (method and metrics, image or table) to support the reported read N50 and correct the MinKNOW wording to reflect its role during acquisition rather than post-run visualization; (vi) ensure internal consistency between Figure 1 and Table 1 (e.g., presence of *ycf1*; remove “fragment” labels), standardize numerical formatting (e.g., 152,765 bp), and trim repeated sentences in the Introduction; and (vii) enrich the Results with mapping proportion to chloroplast, percent reads retained after filtering, basic assembly stats, and a coverage-depth plot across the plastome. These revisions will clarify the manuscript’s added value, secure data accessibility, and substantially improve technical rigor and reproducibility.

Are the rationale for sequencing the genome and the species significance clearly described?

Partly

Are the protocols appropriate and is the work technically sound?

Partly

Are sufficient details of the sequencing and extraction, software used, and materials provided to allow replication by others?

Partly

Are the datasets clearly presented in a usable and accessible format, and the assembly and annotation available in an appropriate subject-specific repository?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Bioinformatics, Genetics, Biotechnology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Reviewer Report 11 June 2024

<https://doi.org/10.5256/f1000research.166509.r280927>

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Hoang Dang Khoa Do

Nguyen Tat Thanh University, Ho Chi Minh City, Ho Chi Minh, Vietnam

Dear Authors,

Thank you very much for your revised manuscript.

The manuscript was revised based on the reviewer's comments.

However, some issues have not been resolved.

1) The d 152.775 bp in the text. unequal length of IR regions was not discussed with the reason.

2) Comparison between the China and Indonesia *Cinnamomum burmanni* is too simple. Please add more details.

3) Figure 1 was not revised (please delete "fragment" in the gene names).

Other comments for minor issues.

1) ycf1 gene was shown in Figure 1, but it is absent in Table 1.

2) Please use the format of 152,765 bp and 152,775 bp for 152.765 bp and

Thank you.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics, Chloroplast genome evolution, Phylogeny

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.

Reviewer Report 11 June 2024

<https://doi.org/10.5256/f1000research.166509.r280926>

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Jakub Sawicki

Department of Botany and Nature Protection, University of Warmia and Mazury in Olsztyn, Olsztyn, Poland

The revised version has improved, but it still requires some corrections.

Introduction: The last two sentences should be removed because they repeat previous statements.

Methods Section:

1. MinKnow is not intended for post-run visualization.
2. The authors did not assess HMW DNA fragment distribution, which raises questions about how they determined the N50 value and whether their results accurately reflect this metric.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Chloroplast genomics, nanopore sequencing

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.

Version 1

Reviewer Report 25 April 2024

<https://doi.org/10.5256/f1000research.159786.r262304>

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Jakub Sawicki 

Department of Botany and Nature Protection, University of Warmia and Mazury in Olsztyn, Olsztyn, Poland

This paper presents a clear and well-structured investigation into the chloroplast genome of Indonesian *Cinnamomum burmanni*. The authors effectively introduce the plant's significance and the rationale for studying its genome, highlighting the knowledge gap regarding this specific Indonesian variety. Authors propose the use of MinION Oxford Nanopore Technologies for sequencing and provide a detailed, step-by-step methodological outline. This includes sample collection, DNA extraction techniques, sequencing hardware, and a comprehensive list of software used for analysis. While a bit more context on chloroplast genome research and the reasoning behind specific methodological choices would be beneficial, the paper overall offers a solid foundation for understanding their research aims and procedures.

However the reviewed Genome Note has some issues that should be solved before acceptance:

1. The justification of study is unclear since the reference genome was previously sequenced. Why the ONT sequencing was used and what are possible pros of using this approach
2. Meanwhile the second genome is reported, the paper lacks of any comparison between Chinese and Indonesian accessions.
3. The described DNA extraction protocol is not suitable for HMW DNA. There's no size distribution or validation at this point.
4. The results section lack of any details on sequencing results including total output, percentage of read used for assembly, N50 reads and assembly coverage.

5. How the authors handle heteroplasmy?
6. At the least but not last, the SRA accession data do not contain fastq/fast5/pod5/ reads.

Are the rationale for sequencing the genome and the species significance clearly described?

Partly

Are the protocols appropriate and is the work technically sound?

Partly

Are sufficient details of the sequencing and extraction, software used, and materials provided to allow replication by others?

Partly

Are the datasets clearly presented in a usable and accessible format, and the assembly and annotation available in an appropriate subject-specific repository?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Chloroplast genomics, nanopore sequencing

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Author Response 13 May 2024

Richard Salindeho

Dear Editor and Reviewer,

Thank you for your comment and suggestion.

We have responded to all reviewer's comments as you may find in the following link

[Response to Reviewer's comments](#)

Sincerely yours,
Corresponding author

Competing Interests: No competing interests were disclosed.

Reviewer Report 18 March 2024

<https://doi.org/10.5256/f1000research.159786.r255270>

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Hoang Dang Khoa Do

Nguyen Tat Thanh University, Ho Chi Minh City, Ho Chi Minh, Vietnam

1/ "MinION is a third-generation sequencing technology with nanopore technology (Oxford Nanopore Technologies (ONT), 2017)". MinION is one of the devices of ONT for performing sequencing. Therefore, please revise the sentence.

2/ Please revise the Figure 1. There are several errors in gene names such as three ndhK, rrn16 fragment, rps12 absence, etc...

3/ Also, please revise the Figure 1 legend with more detail about Figure 1.

4/ The protocol for DNA extraction can be found in the kit. Therefore, mentioning it again in the method part is unnecessary. The authors should add more details about the results and comparison between the new and old chloroplast genomes of *Cinnamomum burmanni*.

5/ Please add the coverage depth of the new chloroplast genome.

6/ The IR regions do not have the same length. Please add the reason for this uncommon in chloroplast genome.

Are the rationale for sequencing the genome and the species significance clearly described?

Partly

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of the sequencing and extraction, software used, and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a usable and accessible format, and the assembly and annotation available in an appropriate subject-specific repository?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics, Chloroplast genome evolution, Phylogeny

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 07 Apr 2024

Richard Salindeho

Dear Reviewer,

Thank you for the constructive inputs to our manuscript.
We have responded to all reviewer's comment's as you may find in the following link

[Response to Reviewer's comments](#)

Please note that the revised Figure 1 is presented in this [link](#)

Best Regards.
Richard Andreas Salindeho

Competing Interests: No competing interests were disclosed.

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