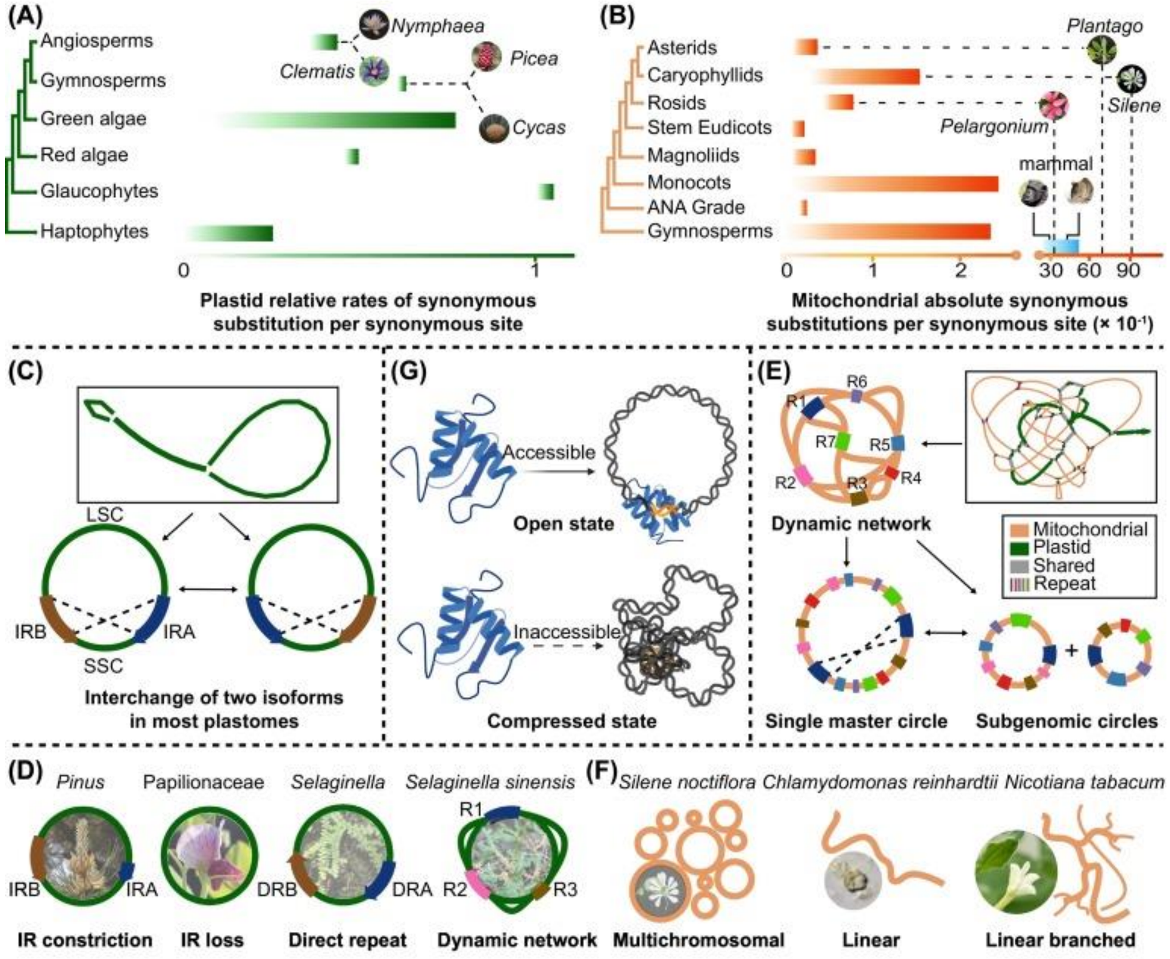
PMAT2: an efficient graphical assembly toolkit for comprehensive organellar genomes

Fuchuan Han[1,2#], Changwei Bi[1,3#*], Yicun Chen[2],
Xiaogang Dai[1], Zefu Wang[1], Huaitong Wu[1], Ning Sun[3], Yanshu Qu[1,4], Yang Yang[2],
Yangdong Wang[2*], Tongming Yin[1*]

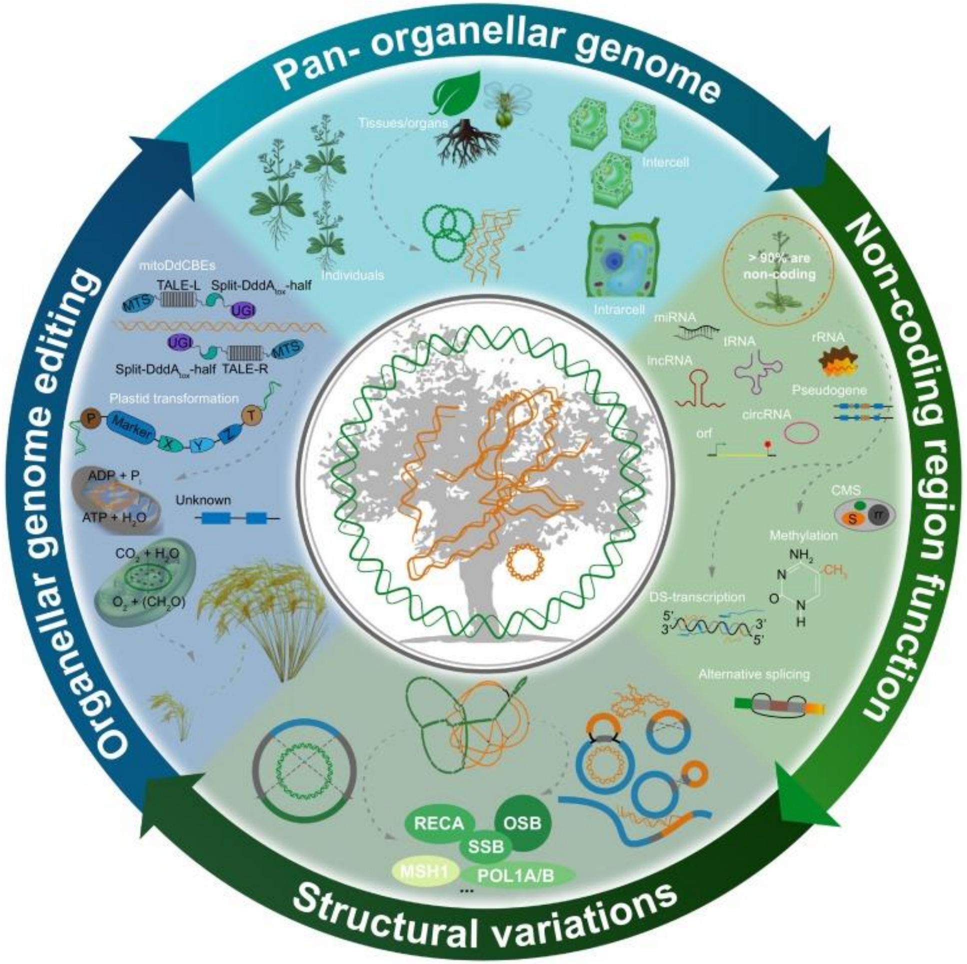
[1]State Key Laboratory of Tree Genetics and Breeding, Nanjing Forestry University, Nanjing 210037, China
[2]Research Institute of Subtropical Forestry, Chinese Academy of Forestry, Hangzhou 311400, China
[3]College of Information Science and Technology & Artificial Intelligence, Nanjing Forestry University, Nanjing 210037, China
[4]Jiangxi Provincial Key Laboratory of Oil-tea Camellia Resource Cultivation and Utilization, Jiangxi Academy of Forestry, Nanchang 330032, China

Fuchuan Han, Changwei Bi, Yicun Chen, Xiaogang Dai, Zefu Wang, Huaitong Wu, Ning Sun, et al. 2025.
PMAT2: An Efficient Graphical Assembly Toolkit for Comprehensive Organellar Genomes. ***iMeta*** 4: e70064.
https://doi.org/10.1002/imt2.70064

Introduction



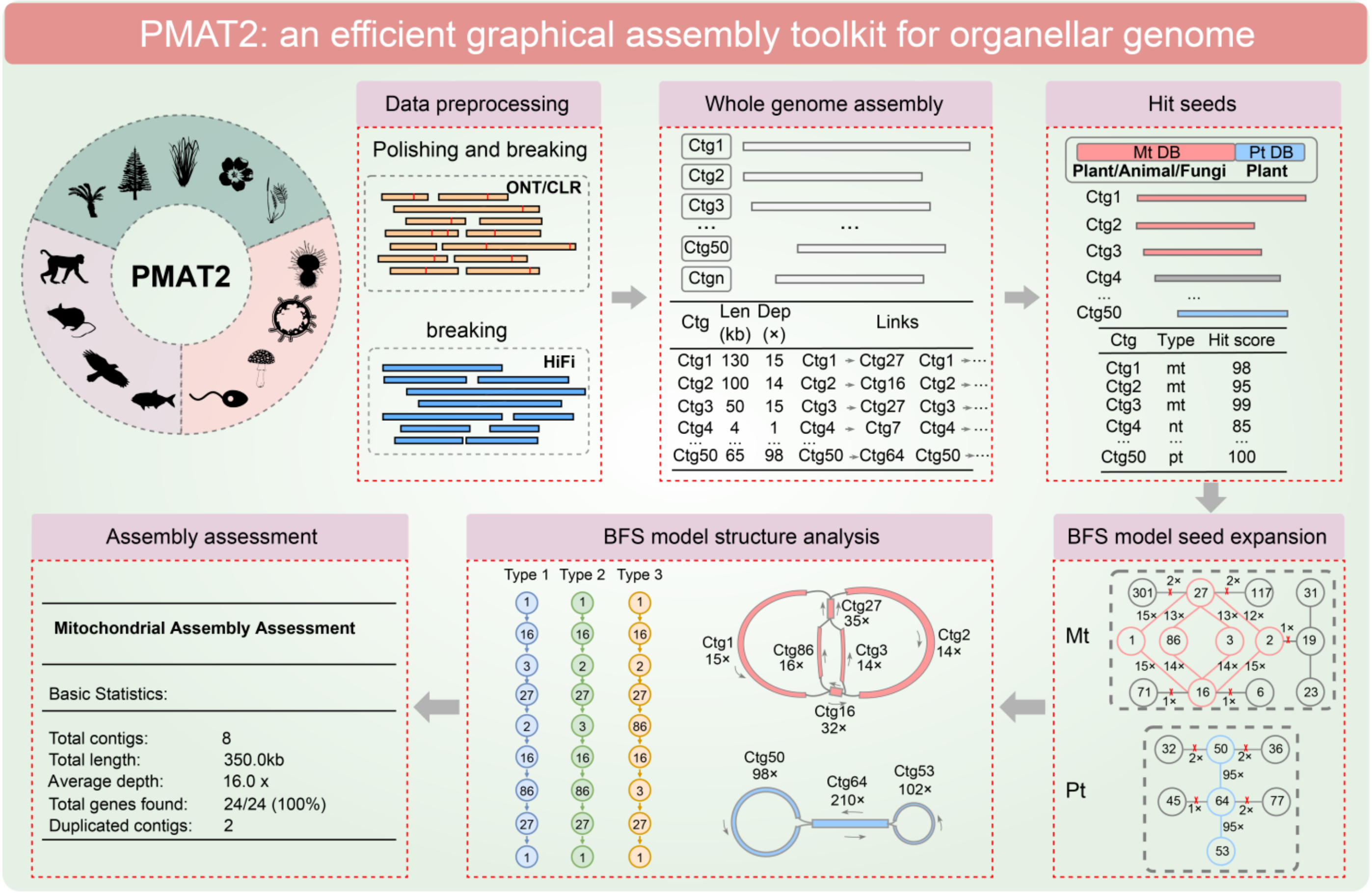
Trends in Plant Science



Trends in Plant Science

Wang Jie, et al., 2024, *Trends in Plant Science*

Highlights



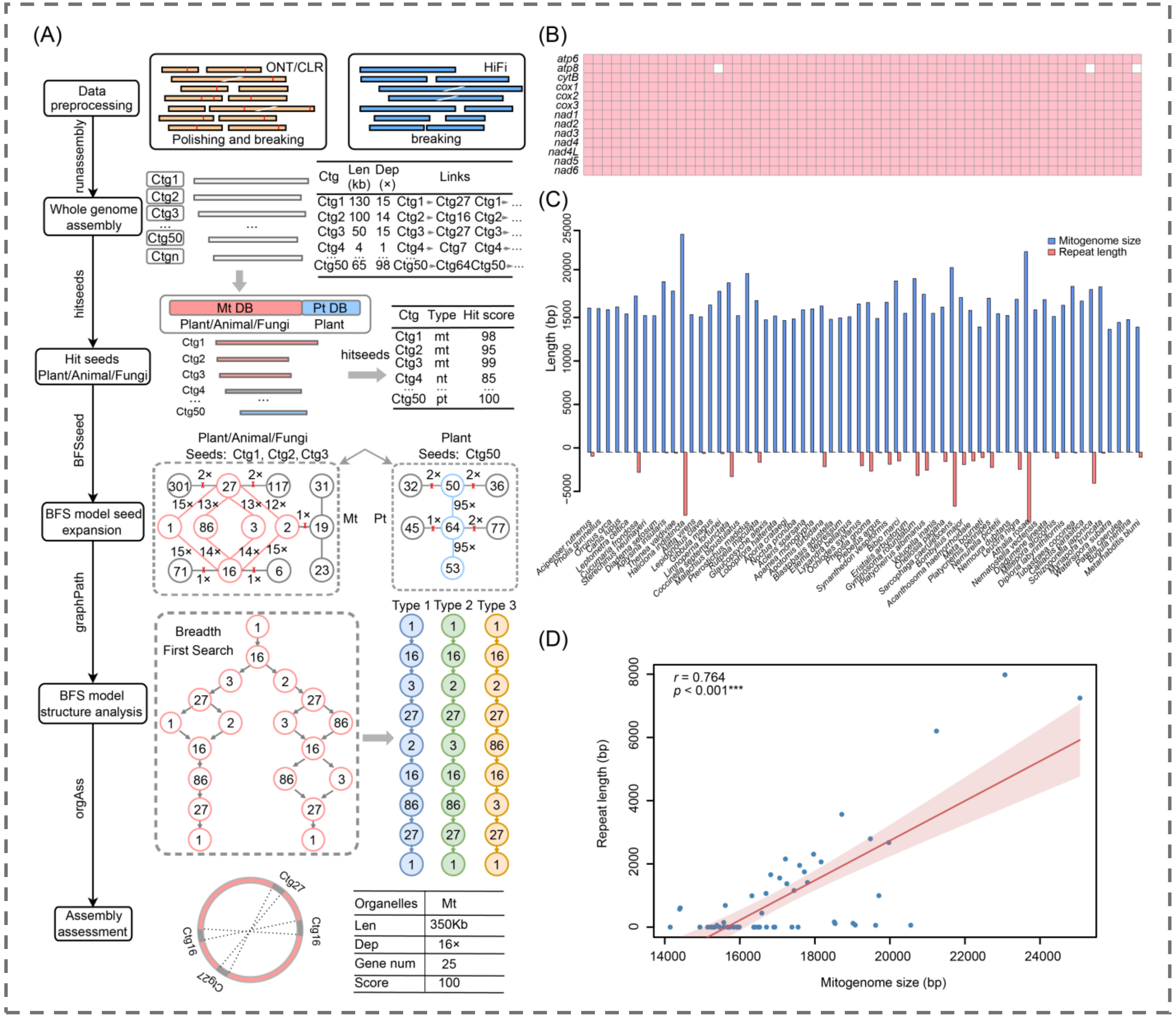
- PMAT2 is developed in C language, supporting the assembly of mitochondrial genomes from animals, plants, and fungi, as well as chloroplast genomes from plants, providing comprehensive optimization strategies across diverse taxonomic groups.

- PMAT2 improves the structural resolution of graph-based organelle genome assemblies and integrates enhanced computational capabilities to efficiently handle complex genomic structures.

- PMAT2 introduces a new function for assessing assembly completeness, offering a reliable standard for evaluating the completeness of assembled organelle genomes.

Results

- PMAT2 workflow and mitochondrial genome assembly results in animals.



Ctg	Len (kb)	Dep (×)	Links
Ctg1	130	15	Ctg1 ▸ Ctg27 Ctg1 ▸ ...
Ctg2	100	14	Ctg2 ▸ Ctg16 Ctg2 ▸ ...
Ctg3	50	15	Ctg3 ▸ Ctg27 Ctg3 ▸ ...
Ctg4	4	1	Ctg4 ▸ Ctg7 Ctg4 ▸ ...
...	...	...	...
Ctg50	65	98	Ctg50 ▸ Ctg64 Ctg50 ▸ ...

Ctg	Type	Hit score
Ctg1	mt	98
Ctg2	mt	95
Ctg3	mt	99
Ctg4	nt	85
...	...	...
Ctg50	pt	100

Organelles	Mt
Len	350Kb
Dep	16×
Gene num	25
Score	100

PMAT2 consists of six modules:

Step 1: Data preprocessing

Step 2: Whole-genome assembly

Step 3: Find candidate contigs

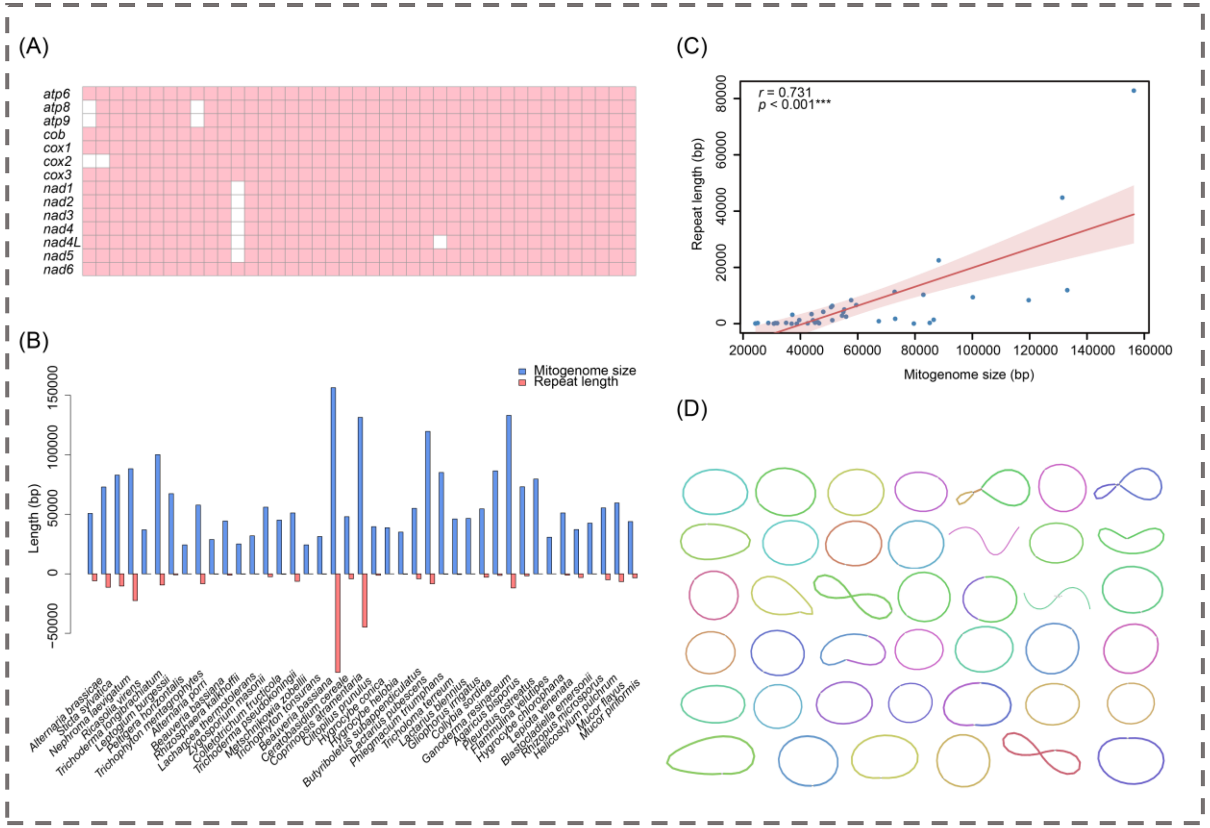
Step 4: BFS model seed expansion

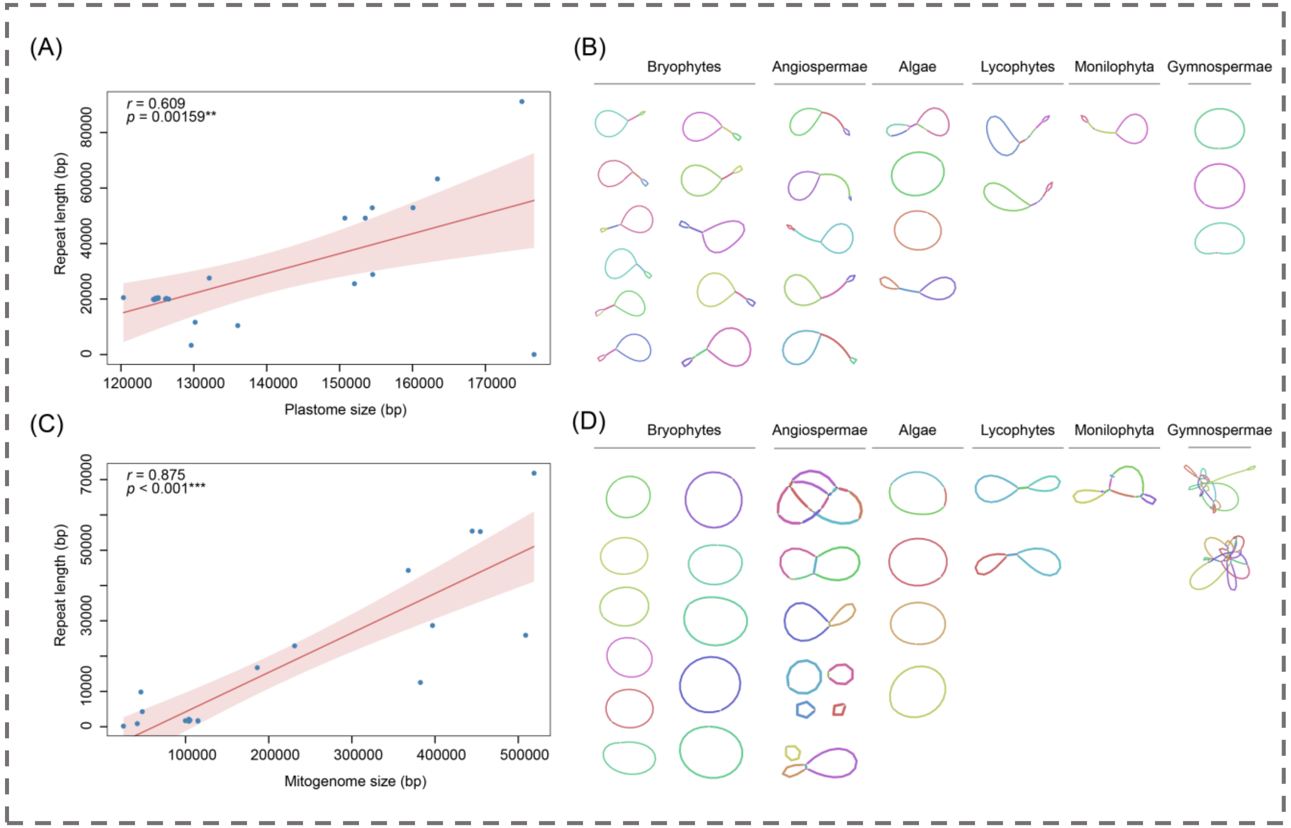
Step 5: BFS model structure analysis

Step 6: Assembly assessment

Results

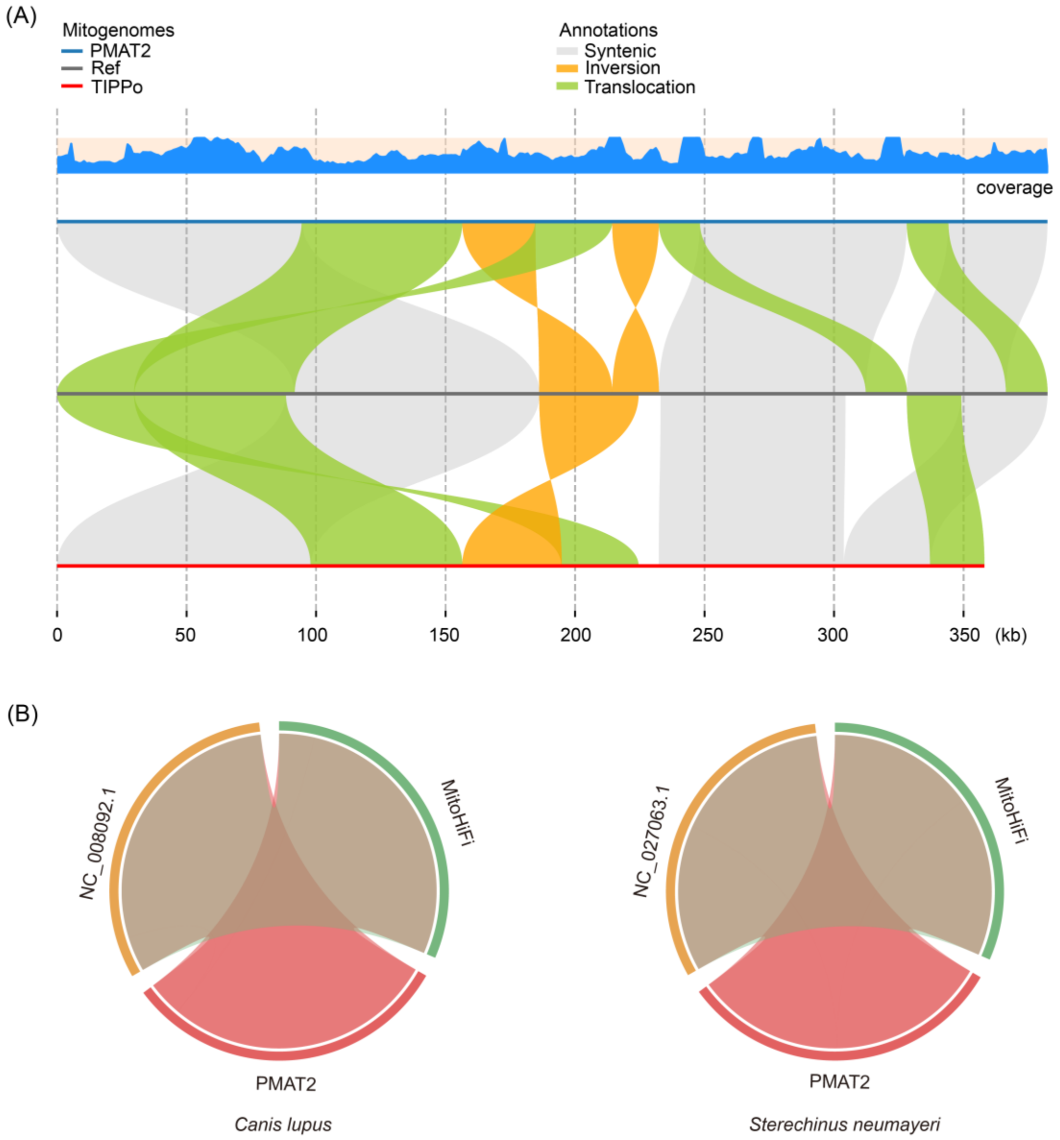
- Assembly results of fungal mitochondrial genomes
- Assembly results of plant organelle genomes





Results

- Assembly and collinearity analysis of multichromosomal mitochondrial genomes



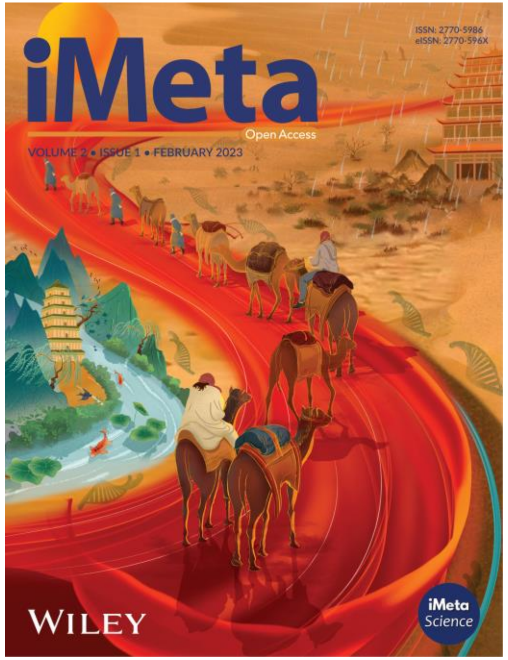
Summary

- In this study, we present PMAT2, a high-efficiency tool for organelle genome assembly.
- PMAT2 exhibits broad applicability, enabling accurate and efficient assembly of mitochondrial genomes in animals, fungi, and plants, as well as chloroplast genomes in plants.
- PMAT2 provides an efficient solution to key technical challenges in organelle genome assembly, offering high accuracy, completeness, and robustness across diverse taxa.
- Website: https://github.com/aiPGAB/PMAT2

Fuchuan Han, Changwei Bi, Yicun Chen, Xiaogang Dai, Zefu Wang, Huaitong Wu, Ning Sun, et al. 2025. PMAT2: An Efficient Graphical Assembly Toolkit for Comprehensive Organellar Genomes. ***iMeta*** 4: e70064. https://doi.org/10.1002/imt2.70064

***iMeta*:** Integrated metaomics to understand the biology, med and environment

WILEY



"***iMeta***" launched in 2022 by iMeta Science Society, impact factor (IF) **33.2**, ranking top 65/22249 in world and 2/161 in the microbiology. It aims to publish innovative and high-quality papers with broad and diverse audiences. **Its scope is similar to *Cell*,** *Nature Biotechnology/Methods/Microbiology/Medicine/Food*. Its unique features include video abstract, bilingual publication, and social media with 600,000 followers. Indexed by **SCIE/ESI**, **PubMed**, **Google Scholar** etc.

"***iMetaOmics***" launched in 2024, with a **target IF>10, and its scope is similar to *Nature Communications***, ***Cell Reports***, *Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics,* etc.

"***iMetaMed***" launched in 2025, with a **target IF>15, similar to *Med, Cell Reports Medicine***, *eBioMedicine, eClinicalMedicine* etc.

Society: http://www.imeta.science
Publisher: https://wileyonlinelibrary.com/journal/imeta
iMeta: https://wiley.atyponrex.com/journal/IMT2
Submission: iMetaOmics: https://wiley.atyponrex.com/journal/IMO2
iMetaMed: https://wiley.atyponrex.com/journal/IMM3

iMetaScience

iMetaScience

office@imeta.science
imetaomics@imeta.science

Promotion Video

Update
2025/6/18