

Improvement of taxonomical classification of the Lauraceae family using DNA barcoding and RAD-Seq approaches

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At a glance: 85% genus identification with *matK* | 56% with *rbcL* | 39 diagnostic SNPs | 4 tribes resolved.

Why Lauraceae?

- Plant type: Mostly woody.
- Major diversity: Southeast Asia (Malesia) and the Neotropics (Fig. 1).
- Problem: Closely related species are difficult to identify due to poorly resolved taxonomy (Fig. 2).
- Need: Reliable molecular reference dataset for species identification.

Main question

Can DNA barcoding improve Lauraceae species identification and resolve problematic taxonomic relationships?

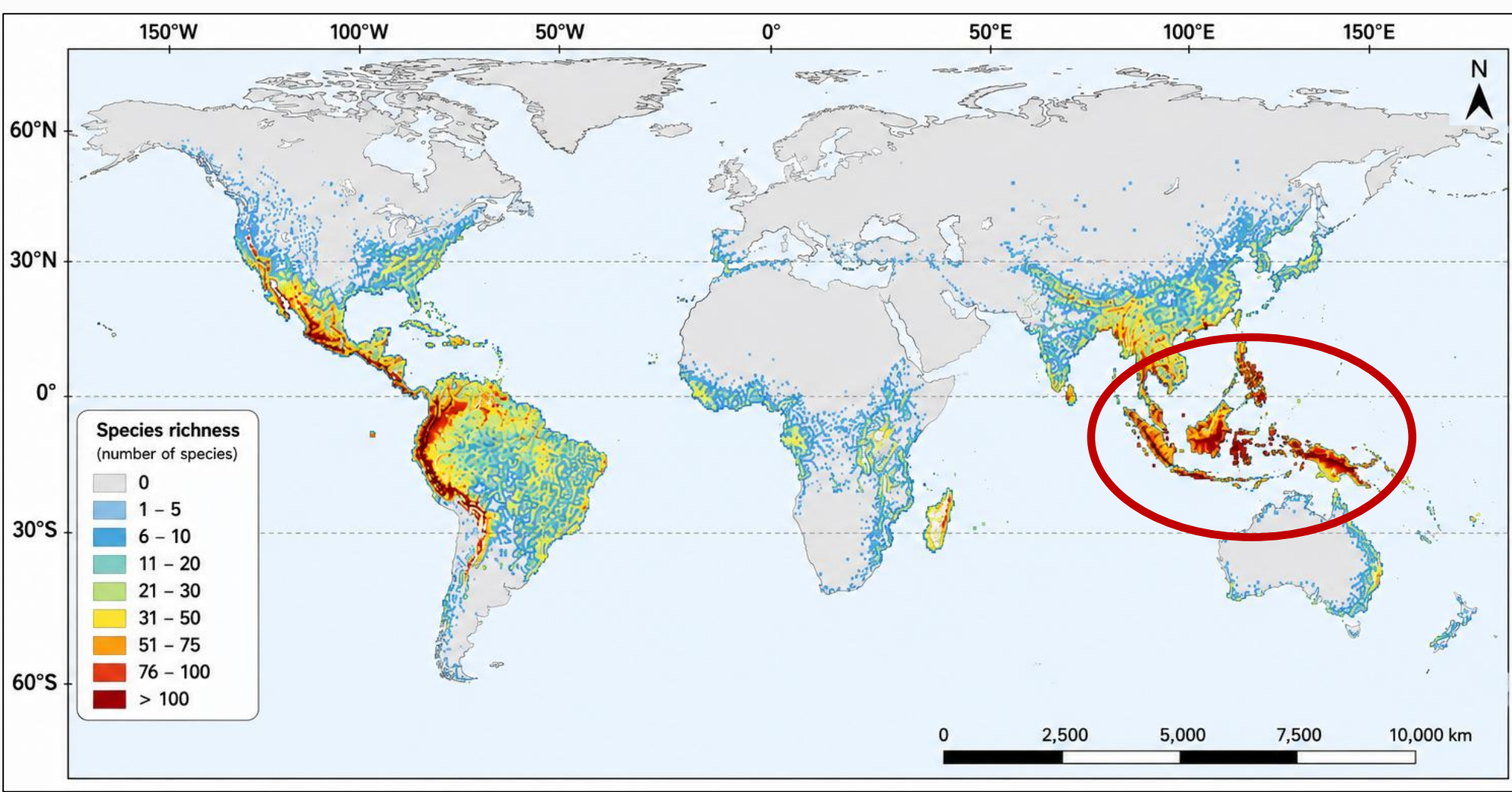
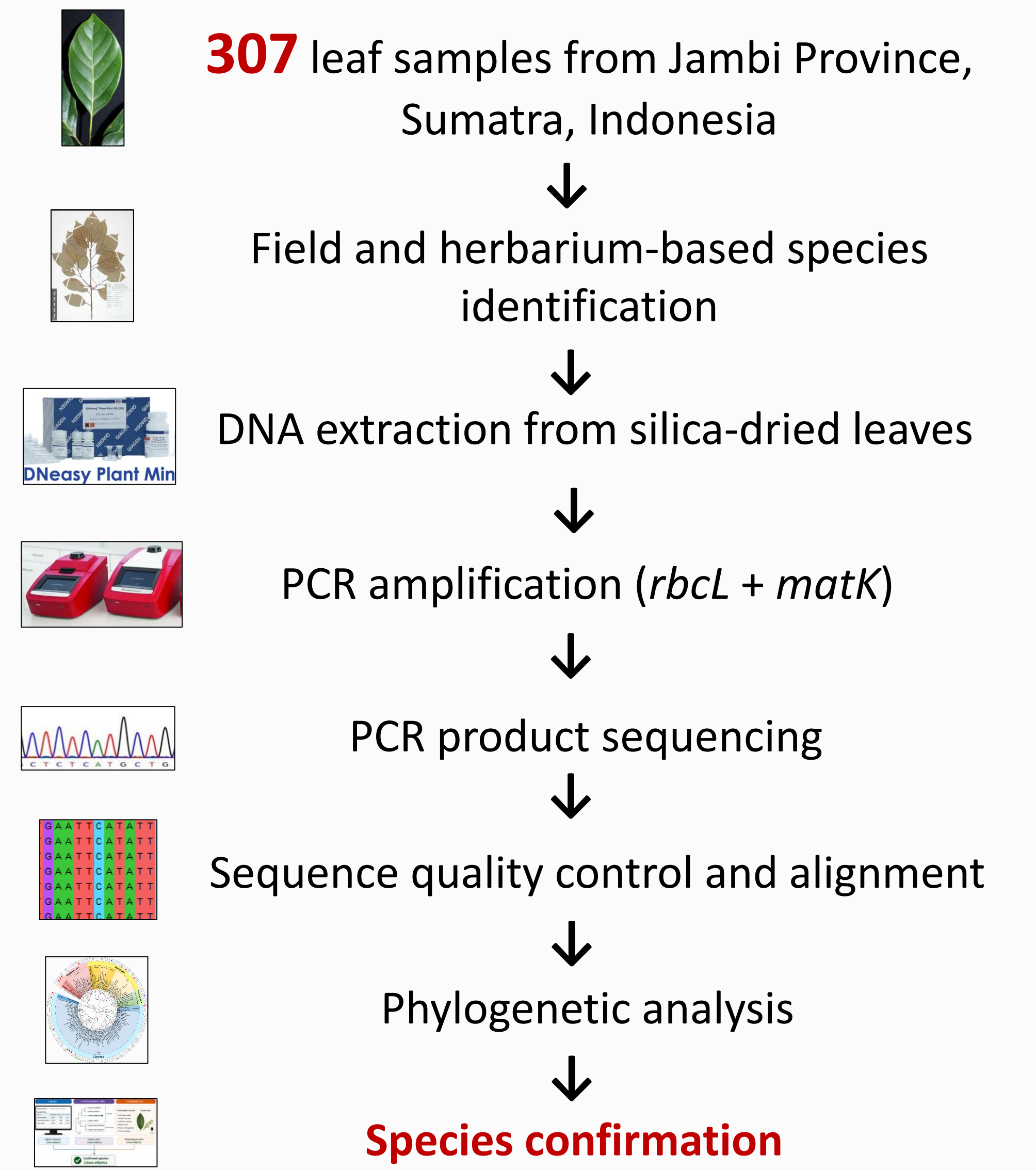


Fig. 1. Species richness in Lauraceae (Li et al. 2025).



Fig. 2. Morphologically closely related Lauraceae species.

Materials and methods



Key findings

- DNA barcoding improved Lauraceae identification and phylogenetic resolution (Table 1).
- 85% *matK*** **56% *rbcL*** — Genus-level identification
- 39 diagnostic SNPs** — 12 tribe-specific + 27 genus-specific.
- Combined *rbcL* + *matK* improved resolution of four major tribes and the *Phoebe* genus (Fig. 3).
- Morphological misidentifications: 26/307** samples corrected using morphology, BLAST and phylogeny (Fig. 4-5).

Table 1: *matK* and *rbcL* efficiency in genus identification.

Primer	No. of fasta sequence	No. of Lauraceae samples	Genus level identification % (based on NCBI & BOLD BLAST)
<i>matK</i>	163*	123	85% (105/123)
<i>rbcL</i>	228	177	56% (100/177)

*307 samples → 276 DNA extracts → 205 *matK* + 259 *rbcL* PCR products.



bc_2198_DMFO220_Litsea elliptica
Correctly identified field samples



KR4556_Cryptocarya densiflora.
Misidentified. Corrected as Litsea elliptica.

Fig. 4. DNA barcoding corrected morphological misidentifications.



Fig. 5. Seedling morphology can lead misidentification.

Conclusion

- Morphology + DNA barcoding** → Improve species identification & resolve taxonomic relationships.
- Additional nuclear + plastid markers → will distinguish closely related species.

rbcL + *matK*:

Phylogenetic resolution improves with combined markers.

bootstrap

- 0.5
- 0.63
- 0.75
- 0.88
- 1

External symbols

- Genus misidentified

Tribe level colored ranges

- Outgroup
- Cryptocaryeae
- Perseeae
- Cinnamomeae
- Laureae

Genus level colored ranges

- Outgroup
- Endiandra
- Beilschmiedia
- Cryptocarya
- Alseodaphne
- Dehaasia
- Nothaphoebe
- Phoebe
- Cinnamomum
- Camphora
- Lindera
- Actinodaphne
- Litsea

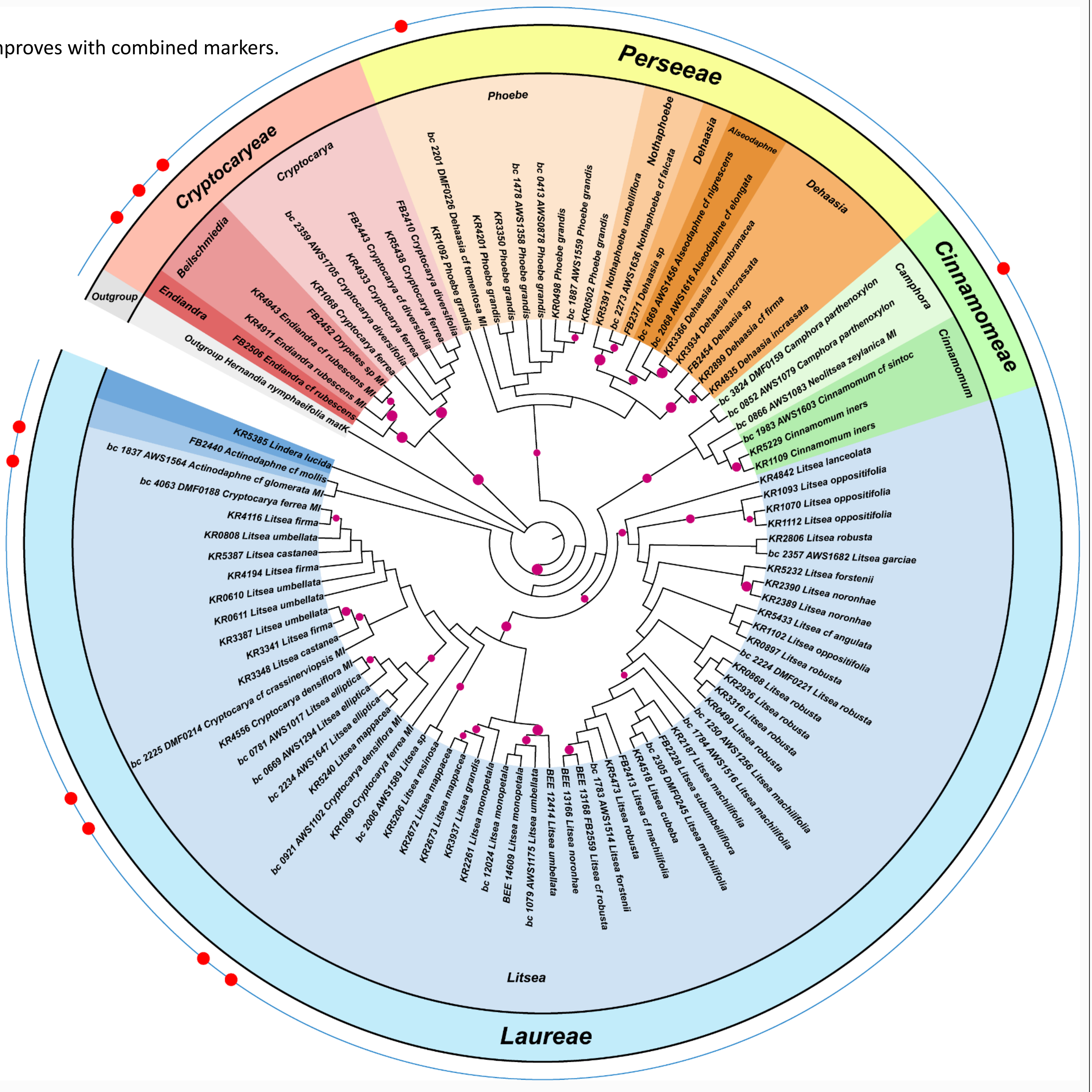


Fig. 3. Concatenated *rbcL* + *matK* data improve phylogenetic resolution compared with individual markers.

Future work

- RAD-Seq:** Genome-wide SNP discovery; Species-diagnostic markers; Without reference genome.
- Additional markers:** *trnH-psbA*, *rpb2* and ITS; Initial species identification.

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References

Li L, Liu B, Song Y, et al. (2025). Global advances in phylogeny, taxonomy and biogeography of Lauraceae. Plant Diversity. 47: 341-364.