

Article

Phylogenomics and Floristic Origin of *Endiandra* R.Br (Lauraceae) from New Caledonia

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Abstract: New Caledonia is a biodiversity hotspot with flora closely related to that of Australia and has received considerable attention. *Endiandra* (Cryptocaryeae; Lauraceae) is distributed from tropical Asia to Oceania, including New Caledonia, with northeastern Australia and New Guinea as diversity centers, but the genus in New Caledonia remains understudied. Here, four species of *Endiandra* native to New Caledonia were sequenced, and their complete plastome sequences were analyzed. A plastome-based phylogenomic tree of Cryptocaryeae was reconstructed, and divergence times were estimated. The phylogenomic tree supports the monophyly of *Endiandra*. Interestingly, the species of *Endiandra* from New Caledonia were grouped into two separate subclades, with one subclade including three species and the other subclade containing only one species. The stem and crown ages of the first subclade were 33.18 Ma and 14.5 Ma, respectively, and the second subclade diverged by approximately 10.36 Ma. The structural characteristics of the newly sequenced plastomes were compared with those of *Beilschmiedia* species from different continents. The results indicate that the plastome sequences of the four species of *Endiandra* are longer than those of *Beilschmiedia*. Additionally, *Endiandra* has more simple sequence repeats (SSRs) than *Beilschmiedia*, though the difference is slight. The Guanine-Cytosine (GC) content of *Endiandra* was lower than that of *Beilschmiedia*. Five highly variable regions were identified, including *matK-rps16*, *ycf1*, *petA-psbJ*, *petN-psbM*, and *ndhF*. The *Endiandra* species in New Caledonia originated through long-distance dispersal followed by local divergence, rather than vicariance. Additionally, we identified at least two instances of floristic exchange between New Caledonia and Australia. Our study provides further evidence for understanding the biogeographic history between these two regions.

Keywords: New Caledonia; *Endiandra*; plastome; comparative genomics; phylogenomics



Academic Editor: Tadeusz Malewski

Received: 21 March 2025

Revised: 18 April 2025

Accepted: 19 April 2025

Published: 20 April 2025

Citation: Song, J.; Shao, C.; Yang, Z.; Yang, Y. Phylogenomics and Floristic Origin of *Endiandra* R.Br (Lauraceae) from New Caledonia. *Forests* **2025**, *16*, 705. <https://doi.org/10.3390/f16040705>

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1. Introduction

New Caledonia, an archipelago in the southwestern Pacific, harbors rich and unique flora, with its floristic origin attracting considerable interest [1–4]. Previous studies have suggested that New Caledonia was a fragment of Zealandia which separated from Australia in the late Cretaceous and drifted to its current location via tectonic rotation in the Paleocene [5]. However, the island remained submerged throughout much of the Paleocene and Eocene [6], precluding terrestrial plant colonization and prompting investigations into the origin of its biota.

The genus *Endiandra* R.Br. (Lauraceae, Cryptocaryeae) belongs to the subtribe Beilschmiedinae, which also includes *Beilschmiedia* Nees, *Hexapora* Hook.f., *Potameia* Thouars, *Sinopora* J.Li, N.H.Xia & H.W.Li, *Syndiclis* Hook.f., and *Yasunia* van der Werff.

Endiandra is phylogenetically close to *Beilschmiedia* but differs morphologically in stamen number; *Endiandra* typically has three stamens, whereas *Beilschmiedia* has nine [7]. *Endiandra* contains 131 species that are distributed from tropical Asia to Oceania, with diversity center in New Guinea and northeastern Australia. Nine species have been recorded from New Caledonia [8,9]. Given its restricted diversity in New Caledonia and close ties to Australian lineages, *Endiandra* serves as an ideal model to investigate the floristic origin of New Caledonia.

To date, no comprehensive phylogenetic study has focused exclusively on New Caledonian *Endiandra*. Munzinger and Gemmill [9] reconstructed a phylogenetic tree for New Caledonian Cryptocaryeae using nrITS sequences, revealing that *Endiandra* species were divided into two major clades. Song et al. [10] conducted a comprehensive phylogenetic and biogeographic study of Cryptocaryeae, which indicated that *Endiandra* likely originated from Australia and its neighboring islands. However, their analysis included only two species native to New Caledonia: *Endiandra lecardii* Guillaumin and *Endiandra poueboensis* Guillaumin. Song et al. [10] neither obtained complete plastome sequences nor analyzed the plastome structural features. As a result, it is necessary to conduct a comparative genomic study of the plastomes and reconstruct a phylogeny to understand the plastome characteristics of *Endiandra* in New Caledonia and the floristic relationships between Australia and New Caledonia.

In this study, we used herbariomics and sequenced four species of *Endiandra* from New Caledonia (*Endiandra baillonii* (Pancher & Sebert) Guillaumin, *Endiandra lecardii*, *Endiandra polyneura* Schitr., and *Endiandra poueboensis*). These represent four of the nine known endemic species, providing the most comprehensive genomic sampling of New Caledonian *Endiandra* to date. We analyzed the plastome structural characteristics of the four New Caledonian *Endiandra* species and compared them with the published plastomes of *Beilschmiedia* from Australia (*Beilschmiedia obtusifolia* (F.Muell. ex Meisn.) F.Muell.), America (*Beilschmiedia immersinervis* Sachiko Nishida) and Asia (*Beilschmiedia Linocieroides* H.W.Li). To clarify the systematic position of *Endiandra* within the Cryptocaryeae of Lauraceae, determine its monophyly, and estimate the divergence time, we obtained all available complete plastome data of the Cryptocaryeae and combined them with newly sequenced plastomes of the four *Endiandra* species from New Caledonia to reconstruct a comprehensive phylogenomic tree.

2. Materials and Methods

2.1. Taxon Sampling, DNA Extraction, and Genomic Sequencing

Leaf samples (approximately 1 × 1 cm) were extracted from herbarium specimens collected in New Caledonia for four *Endiandra* species. Detailed sampling information is provided in Table 1. The purpose of this study was to resolve the phylogenomic relationships of species from New Caledonia, and thus we included only one sample per species. To ensure accurate identification of the four *Endiandra* species in our single-sample study, all leaf specimens were first authenticated by taxonomic experts specializing in New Caledonian Lauraceae. Additionally, we extracted nrITS sequences from these four species and aligned them with their corresponding published sequences in the NCBI (*E. baillonii*: PQ589692, *E. lecardii*: PQ589703, *E. poueboensis*: HG315592, and *E. polyneura*: PQ589705) for molecular verification. We obtained pairwise identity scores of 99.8% for *E. baillonii* and perfect 100% matches for *E. lecardii*, *E. poueboensis*, and *E. polyneura*, providing robust molecular confirmation of our taxonomic identifications. The total DNA was extracted using a modified CTAB method [11]. We conducted double extractions for each sample and combined the DNA from both processes to enhance the DNA quality. In light of the severe degradation of DNA from herbarium specimens, we did not subject the DNA

samples to supersonic fragmentation during the library construction process [12,13]. Sequencing was performed using the Illumina NovoSeq 6000 at Novogene Co., Ltd. (Beijing, China). The input amount for each DNA library was consistently 750 ng, with all libraries achieving a quality assessment grade of A. We obtained an average sequencing volume of approximately 2 GB per sample. In addition, we obtained 83 published plastomes of the Cryptocaryeae from the NCBI and the Lauraceae Chloroplast Genome Database (LCGDB), including 37 *Beilschmiedia* species, 21 *Cryptocarya* species, 13 *Endiandra* species, 1 *Eusideroxylon* species, 1 *Potameia* species, and 10 *Syndiclis* species. The distribution of sampled species of *Endiandra* was shown in Figure 1. Sequence information was provided in Supplementary Table S1, and this was used collectively for subsequent phylogenetic analysis.

Table 1. Information on voucher specimens.

Species	Collection	Locality	Herbarium
<i>Endiandra baillonii</i>	Guillaum A & Baumann-Bodenheim MG. 6659	New Caledonia	A
<i>Endiandra lecardii</i>	Lowry II & Prescott P. 6807	New Caledonia (Province du Nord)	MO
<i>Endiandra polyneura</i>	Guillaum A & Baumann-Bodenheim MG. 7213	New Caledonia	A
<i>Endiandra poueboensis</i>	McPherson G. 18988	New Caledonia (Province du Nord)	MO

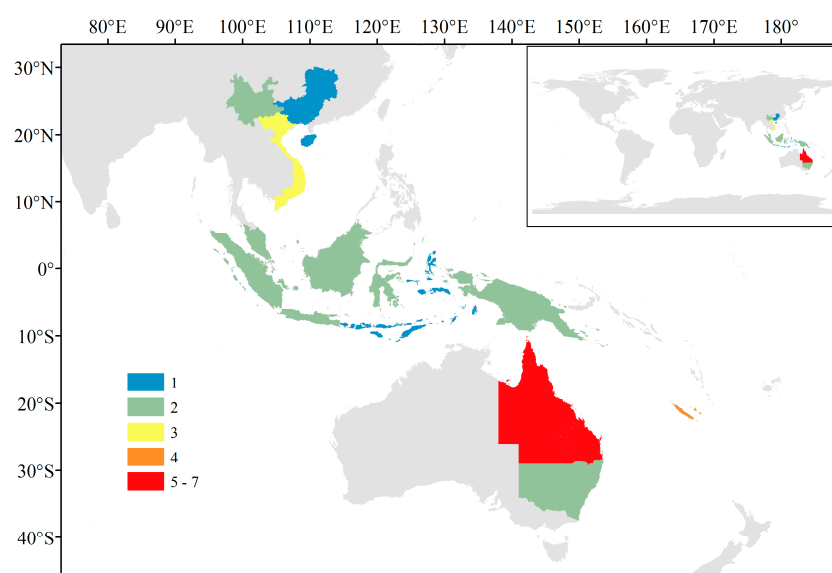


Figure 1. Distribution of sampled *Endiandra* species. Orange indicates New Caledonia (range of four newly obtained *Endiandra* species).

2.2. Genome Assembly and Annotation

We performed plastome assembly with the parameters $R = 15$, $w = 0.6$, and $k = 21, 45, 85, 115, 127$ using GetOrganelle 1.7.5.0 [14] on a Linux system. All four species were all successfully assembled into circularized plastomes with no fragment loss, demonstrating high-quality plastome sequences. For initial annotation, we utilized a published sequence (NC_051912) of *Endiandra* as a reference in Geseq (<https://chlorobox.mpimp-golm.mpg.de/geseq.html>, accessed on 24 February 2025) [15]. We manually adjusted the four sample sequences using the same sequence of *Endiandra* (NC_051912) as a reference in Geneious Prime 2023.2.1 and generated the plastome maps using OGDRAW (<https://chlorobox.mpimp-golm.mpg.de/OGDraw.html>, accessed on 26 February 2025) [16].

2.3. Phylogenomic Analyses

We established a dataset of plastomes for phylogenomic analyses using MAFFT 7.480 [17] with the “auto” alignment strategy and aligned the plastome sequences, fol-

lowed by automatic trimming with TrimAL 1.4.1 [18]. To select models, we employed ModelFinder [19]. The model selected by ModelFinder was the “best fit model”. Phylogenetic trees were reconstructed using the maximum likelihood (ML) method in IQ-TREE v2.1.2 [20].

2.4. Divergence Time Estimation

Following Yang et al. [13], we employed five fossil calibrations to date the phylogenetic tree. For narrow age-range fossils, direct bounds were applied; *Virginianthus calycanthoides* Friis et al. (C1) constrained the crown age of the Laurales to be 107.7–113 Ma [21], while *Jerseyanthus calycanthoides* Crepet et al. (C2) dated the *Calycanthus*–*Chimonanthus* split to be 85.8–86.8 Ma [21]. Similarly, *Machilus maomingensis* Jin & Tang (C5) calibrated the *Machilus* stem age to be 33.7–33.9 Ma [22], modeled as B (0.337, 0.339). For broader age estimates, we implemented lognormal distributions with offset ($p = 0.1$) and scale ($c = 0.2$) parameters. For *Neusenina tetrasporangiata* Eklund (C3), the *Neocinnamomum* stem node (72.1–86.3 Ma) [23] was calibrated to be L (0.71, 0.1, 0.2), and for *Alseodaphne changchangensis* Jin & Li (C4), the *Persea* crown group (37–48 Ma) [24] was calibrated as L (0.37, 0.1, 0.2).

Divergence time estimation was performed using MCMCtree v1.3.1 [25] under the GTR + G substitution model (model = 7) for ML-based branch length, gradient vector, and Hessian matrix estimation. We set rgene_gamma and sigma2_gamma to G (1, 27.7) and G (1, 4.5), respectively. Two independent MCMC runs were conducted (burnin = 2,000,000, sampfreq = 100, nsample = 10,000). Parameter convergence was confirmed in Tracer v1.7.2 [26], with all ESS values >200. The final tree was visualized using tvBOT [27].

2.5. Analysis of Simple Sequence Repeats and Functional Duplicated Sequences

We used MISA (<https://webblast.ipk-gatersleben.de/misa>, accessed on 27 February 2025) [28] to obtain the counts of mono-, di-, tri-, tetra-, penta-, and hexa-nucleotide repeats, with repetition thresholds set to 10, 5, 4, 3, 3, and 3, respectively. The obtained information was compiled into a table for downstream analysis. We used the REPuter tool (<https://bibiserv.cebitec.uni-bielefeld.de/reputer>, accessed on 28 February 2025) [29] to acquire repetitive sequence information, with “the maximum computed repeats” and “the minimal repeat size” set to 50 and 8, respectively. The obtained information was also tabulated. Finally, we used the “ggplot2” package [30] in R 4.4.1 [31] to visualize the information in the tables.

2.6. Analysis of IR Boundaries and Nucleotide Polymorphism

We utilized CPJSDraw v1.0.0 [32] to conduct the analysis of IR boundaries, employing sequences in the gb format for this purpose. For the nucleotide polymorphism analysis, we employed DnaSP v5 [33] software prior to the analysis. The sequences were aligned using MAFFT 7.480 [17], and subsequent analysis was performed using the fasta format with specified parameters (window length = 600, step size = 200).

2.7. Codon Usage Bias Analysis

Because codon usage bias analysis required protein-coding sequences (CDS), we extracted the 79 CDS from the plastomes in Geneious Prime 2023.2.1, exported them as a csv file, and then converted the csv file to fasta format using a Perl script [34]. Subsequently, we removed sequences that did not meet the analysis requirements. After screening, we used MEGA to calculate the relative synonymous codon usage (RSCU) values for each sequence. During this process, the RSCU values of codons encoding Met (M) (ATG/AUG), Trp (W) (TGG/UGG), and the three stop codons (TAG, TGA, and TAA) were excluded. Finally, we summarized the RSCU values across all sequences and generated a visualization using the “ggplot2” package [30] in R 4.4.1 [31].

Divergence time estimation revealed that the stem age of *Endiandra* was 37.58 Ma (95% HPD: 26.46~61.54 Ma), and the crown age was 33.18 Ma (95% HPD: 23.3~53.01 Ma). The four New Caledonian *Endiandra* were grouped into two separate subclades; the first subclade comprised three species (*E. baillonii*, *E. poueboensis*, and *E. lecardii*), while the second subclade contained only one species (*E. polyneura*). For the first subclade, the stem

and crown ages were 33.18 Ma and 14.5 Ma (95% HPD: 3.13~30.73 Ma), respectively. The second subclade containing only *E. polyneura* diverged from its sister *E. xanthocarpa* at 10.36 Ma (95% HPD: 2.27~22.16 Ma) (Figure 3).

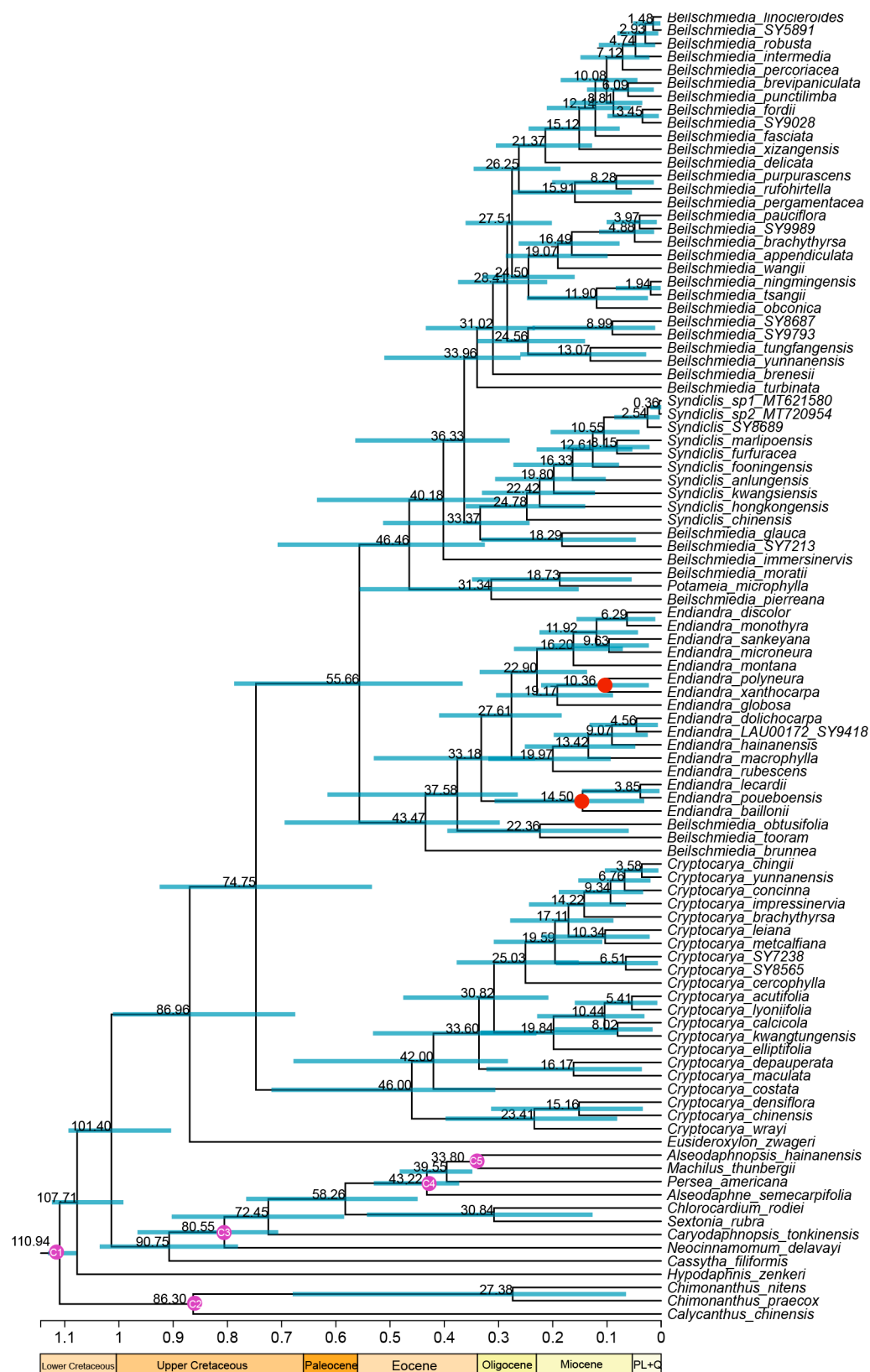


Figure 3. Time tree. The numbers at the nodes represent the mean divergence times, with blue bars indicating 95% HPD. Purple circles mark five fossil calibration points. Red circles highlight the divergence node of *Endiandra* from New Caledonia.

3.2. Characteristics of the New Caledonian *Endiandra*

The complete plastome sequences of four *Endiandra* species exhibited the typical Lauraceae structure, consisting of a pair of inverted repeats (IRs), a large single-copy (LSC) region, and a small single-copy (SSC) region (Figure 4). However, the length of each region varied among the species. The sequence of *E. polyneura*, at 158,339 bp was the longest among the four species. Its LSC region measured 89,044 bp, the SSC region was 18,259 bp long, and each of the two IRs was 25,518 bp in length. The plastome sequence of *E. baillonii* was 158,313 bp long, with the LSC region being 89,094 bp long, the SSC region being 18,213 bp long, and both of the IRs being 25,503 bp long. The plastome sequence of *E. lecardii* was 158,261 bp long, with the LSC region being 89,062 bp long, the SSC region being 18,203 bp long, and both of the IRs being 25,498 bp long. The plastome sequence of *E. poueboensis*, which was 158,259 bp long and the shortest among the four species, had an LSC region 89,060 bp in length, an SSC region 18,199 bp long, and IRs which were each 25,500 bp long. The plastome sequences of the four *Endiandra* species were longer than those of the *Beilschmiedia* species. The GC content of the four *Endiandra* species was 39.0%, lower than that of the three *Beilschmiedia* species (Table 2). All four plastomes of the New Caledonian *Endiandra* contained 131 genes in total, with the CDS, rRNA, and tRNA being 86, 8, and 37, respectively (Table 2).

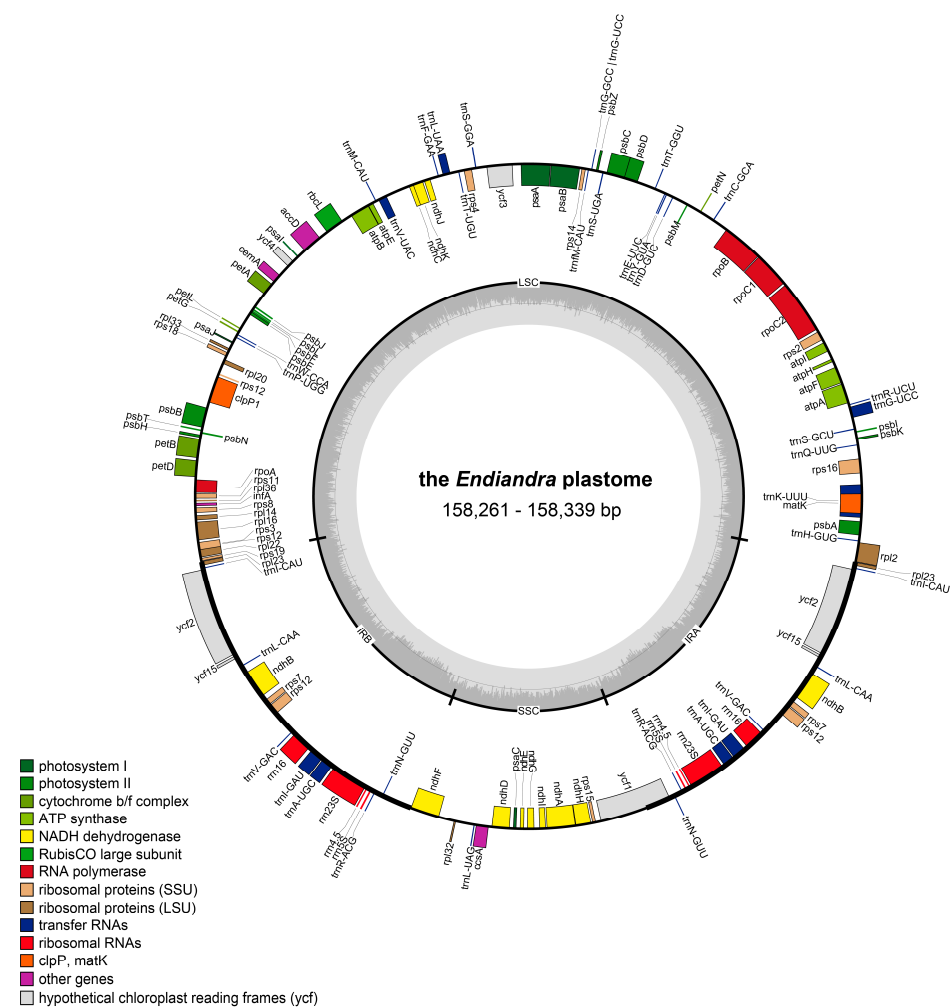
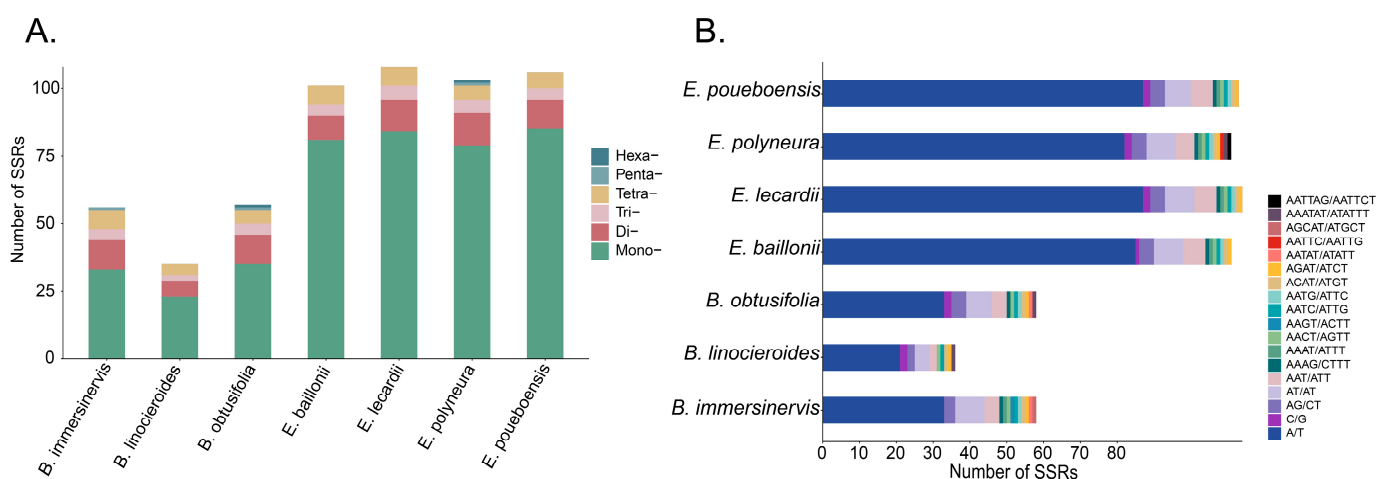


Table 2. Summary of a comparison of sequences of species of *Beilschmiedia* and *Endiandra*.

	<i>E. baillonii</i>	<i>E. lecardii</i>	<i>E. polyneura</i>	<i>E. poueboensis</i>	<i>B. immersinervis</i>	<i>B. linocieroides</i>	<i>B. obtusifolia</i>
Size (bp)	158,313	158,261	158,339	158,259	157,497	157,311	157,254
GC (%)	39.0	39.0	39.0	39.0	39.2	39.2	39.3
Lsc size in bp	89,094	89,062	89,044	89,060	88,561	88,506	88,313
Ssc size in bp	18,213	18,203	18,213	18,199	18,026	17,964	17,998
IRs size in bp	25,498	25,498	25,518	25,500	25,459	25,424	25,475
Number of coding sequences	86	86	86	86	84	84	84
Number of rRNA	8	8	8	8	8	8	8
Number of tRNA	37	37	37	37	37	37	37

3.3. Analysis of Repeated Sequences

An analysis of simple sequence repeats (SSRs) revealed that the selected species of *Beilschmiedia* and *Endiandra* all contained six types of SSRs (i.e., mononucleotide repeats, dinucleotide repeats, tetranucleotide repeats, trinucleotide repeats, pentanucleotide repeats, and hexanucleotide repeats) (Figure 5A), but significant variation was found in the numbers. The total SSRs of *B. immersinervis*, *B. linocieroides*, and *B. obtusifolia* were 56, 35, and 57, respectively, while the total SSRs of *E. baillonii*, *E. lecardii*, *E. polyneura*, and *E. poueboensis* were 101, 108, 103, and 106, respectively. As depicted in Figure 5A, the primary difference in total SSRs between the two genera lay in the quantity of mononucleotide repeats (*B. immersinervis* (33), *B. linocieroides* (23), *B. obtusifolia* (35), *E. baillonii* (81), *E. lecardii* (84), *E. polyneura* (79), and *E. poueboensis* (85)).

**Figure 5.** Number of simple sequence repeats (SSRs). (A) Variation in six types of SSRs across the seven species compared. (B) Variation in different repeat unit types across the seven species compared.

Among the 18 repeat units (Figure 5B), there was also a significant difference in the total number between *Beilschmiedia* and *Endiandra*. The mononucleotide repeat unit A/T accounted for this large difference in the total numbers. The number of A/T repeat units in *B. immersinervis*, *B. linocieroides*, and *B. obtusifolia* was 33, 21, and 33, respectively, while the number of A/T repeat units in *E. baillonii*, *E. lecardii*, *E. polyneura*, and *E. poueboensis* was 85, 87, 82, and 87, respectively.

The selected species of *Beilschmiedia* and *Endiandra* contained four types of repetitive sequences (Figure 6A): palindromic repeats (P), forward repeats (F), reverse repeats (R), and

complementary repeats (C). In general, the total number of repetitive sequence types did not vary significantly among the species. However, notable differences were found when examining the individual types. All species of *Beilschmiedia* possessed a higher number of palindromic repeats (P) (*B. immersinervis* (23), *B. linocieroides* (23), and *B. obtusifolia* (27)) when compared with the species of *Endiandra* (*E. baillonii* (19), *E. lecardii* (20), *E. polyneura* (19), and *E. poueboensis* (19)). *B. linocieroides* (15) possessed the highest number of forward repeats (F), while *E. baillonii* (9) had the lowest number. *E. baillonii* (15) had the highest number of reverse repeats (R), whereas *B. linocieroides* (7) and *B. obtusifolia* (7) had the lowest number. In terms of complementary repeats (C), *E. baillonii* (7) had the highest number, while *B. immersinervis* (3), *B. linocieroides* (3), and *E. polyneura* (3) had the lowest number.

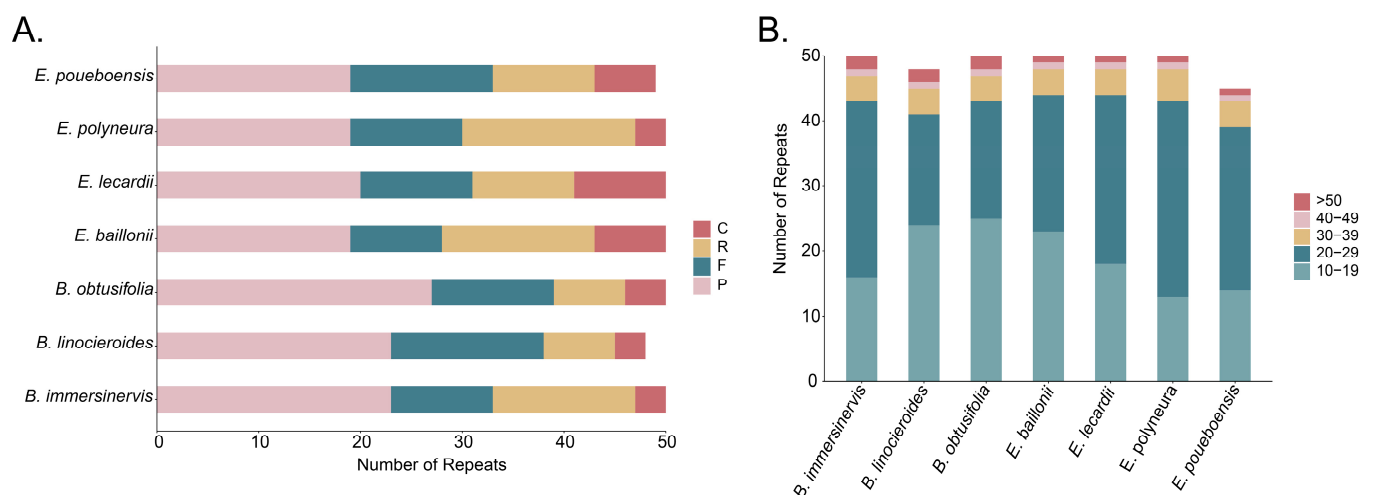


Figure 6. Characteristics of repetitive sequences. (A) Variation in the four types of repetitive sequences across the seven species compared. P = palindromic repeats; F = forward repeats; R = reverse repeats; C = complement repeats. (B) Variation in repetitive sequences of different lengths across the seven species compared.

According to an analysis of the lengths, the seven species displayed similar total numbers across the five length categories (Figure 6B). However, when examining the specific length ranges, differences emerged. *B. obtusifolia* had the greatest number of sequences (25) in the 10–19 bp range, *E. polyneura* had the greatest number (30) in the 20–29 bp range, and *E. polyneura* also had the greatest number (5) in the 30–39 bp range. The remaining species had four sequences in this range. In the 40–49 bp range, all species had one sequence, and in the >50 bp range, the species of *Beilschmiedia* possessed two sequences each, while the species of *Endiandra* had one sequence each.

3.4. Analysis of IR Boundaries

We conducted a comparative analysis of the boundaries of the four IR junctions: JLB (LSC/IRb), JSB (SSC/IRb), JSA (SSC/IRa), and JLA (LSC/IRa) (Figure 7). The boundaries of LSC/IRb, SSC/IRa, and LSC/IRa were consistent across the seven species compared. The LSC/IRb boundary was located within the *rpl23* gene. In *Beilschmiedia*, the interval length between the LSC/IRb boundary and *rps19* was consistently 13 bp, whereas in *Endiandra*, this interval exhibited significantly greater variation, spanning from 63 to 76 bp. The SSC/IRa boundary was located within the *ycf1* gene. In *Beilschmiedia*, the interval between the SSC/IRa boundary and *trnN* ranged from 2251 to 2259 bp, while in *Endiandra*, this interval was consistently 2276 bp across all species. The LSC/IRa boundary was located within the intergenic region between *rpl23* and *rpl2*. In *Beilschmiedia*, the interval between the LSC/IRa boundary and *rpl2* ranged from 11 to 12 bp, whereas in *Endiandra* this interval

B. immersinervis
157,497 bp

B. linocieroides
157,311 bp

B. obtusifolia
157,254 bp

E. baillonii
158,313 bp

E. lecardii
158,261 bp

E. polyneura
158,339 bp

E. poueboensis
158,259 bp

3.5. Nucleotide Polymorphism and Codon Usage Bias Analysis

Our analysis of the codon usage bias (Figure 9) indicated that the RSCU values of all codons calculated for the seven species did not display significant differences among them. However, from a codon perspective, codons ending with C or G had lower RSCU values (<1.0), while those ending with A or U had higher RSCU values (>1.0).

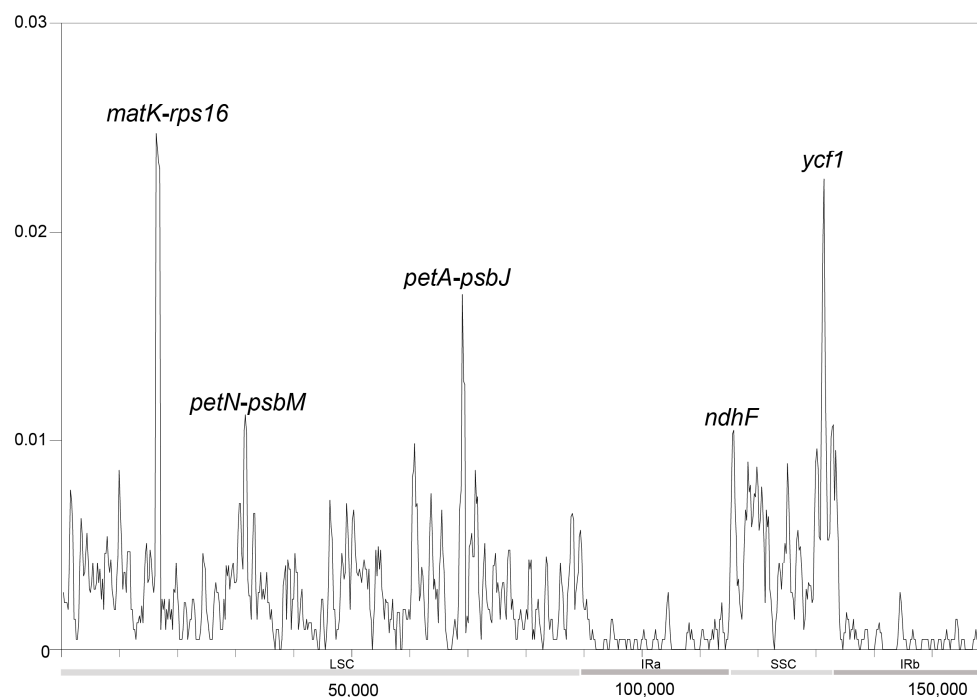


Figure 8. Variation in nucleotide polymorphism (Pi).

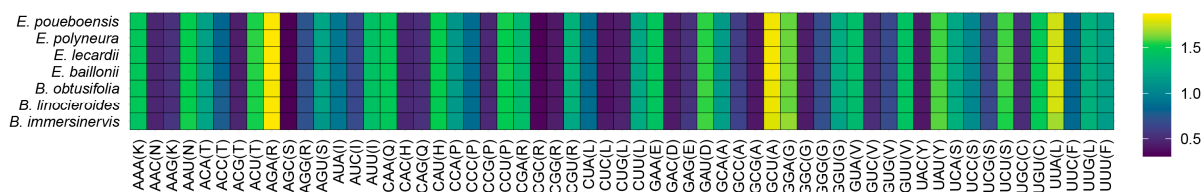


Figure 9. Heatmap of codon distribution for all shared protein-coding genes in the plastomes of the seven species. Lighter colors indicate higher RSCU values.

4. Discussion

4.1. Phylogenomics of the Cryptocaryae and the New Caledonian Species of *Endiandra*

We conducted a phylogenomic study on the Cryptocaryae based on complete plastome sequences and obtained a well-resolved phylogenomic tree. The findings are consistent with those of Li et al. [35], confirming that *Beilschmiedia* is not monophyletic. The American species of *Beilschmiedia* and the Asian species of *Beilschmiedia* formed a clade, and the African species of *Beilschmiedia* and *Potameia* constituted a separate clade. *Syndiclis*, together with two sympatric *Beilschmiedia* species, formed a clade. We also corroborated the monophyly of *Endiandra*, though its monophyletic status requires further validation through more extensive sampling. Our phylogenomic tree demonstrates that *Endiandra* and the Australian *Beilschmiedia* formed a larger clade. However, given the likely polyphyletic nature of *Beilschmiedia* itself, our results can only suggest a closer phylogenetic affinity between *Endiandra* and the Australian *Beilschmiedia*. We acknowledge that the exact evolutionary relationship between *Endiandra* and Australian *Beilschmiedia* remains to be elucidated through further investigation.

Our new phylogenomic tree suggests that the four newly sequenced species of *Endiandra* from New Caledonia do not form a monophyletic group. *Endiandra lecardii*, *E. poueboensis*, and *E. baillonii* constitute a small subclade, which diverged early in *Endiandra*. *Endiandra polyneura* alone is sister to the Australian species *E. xanthocarpa*. The phylogenetic relationship of *E. polyneura* is also supported by the nrITS-based phylogenetic tree [9]. The identification of the four New Caledonian *Endiandra* samples we collected was verified by

experts and nrITS sequence alignment. However, we are aware that the limited sample size imposes constraints on fully resolving phylogenetic relationships within the genus. Therefore, we are committed to expanding the species sampling across all *Endiandra* species in future research efforts. This will enable us to refine and enhance the understanding of the phylogeny, thereby providing a more comprehensive view of the evolutionary relationships within *Endiandra*.

4.2. Plastome Characteristics of the New Caledonian Species of *Endiandra*

The newly obtained plastomes in our study of *Endiandra* are similar to those previously reported in the *Beilschmiedia* group in terms of size, structure, and other aspects [35]. Li et al. [35] analyzed the genome of the species of *Endiandra* from Australia and compared it with other members of the *Beilschmiedia* group. They found no significant differences between *Endiandra* and *Beilschmiedia* in the number or type of simple sequence repeats (SSRs). In this study, however, we found noticeable differences in the SSRs between *Beilschmiedia* and the New Caledonian *Endiandra*. In addition, we also identified differences between the two genera in the position of the SSC/IRb boundary regions and the IR region. The New Caledonian species displayed significant expansion, indicating that the species of *Endiandra* from New Caledonia have evolved distinct characteristics, which is probably related to the local environment [36].

Our comparative genomic analysis of the four New Caledonian *Endiandra* species revealed distinct characteristics in *E. polyneura*, including the unique presence of hexanucleotide SSRs absent in congeners, exclusive possession of three specific mononucleotide repeat types (AATTG/AATTC, AAATAT/ATATTT, and AATTAG/AATTCT), and markedly different functional repeat profiles, exhibiting the highest reverse repeats (R) and lowest complement repeats (C) among the studied species. These structural divergences in repeat elements may explain the phylogenetic distinctness of *E. polyneura*, which failed to cluster with its congeneric species in our analysis.

The plastomes of *Beilschmiedia* and *Endiandra* exhibited overall structural similarities. This is primarily attributable to their close phylogenetic relationship [10,35,37] and the relatively slow evolutionary rate of plastomes [38,39]. Our analysis of nucleotide polymorphism suggests that the IR regions in the plastome are rather conserved, which is consistent with the findings of other plastome analyses [40,41]. The substitution rate in the IR regions is significantly lower than that in the SC region [40,42–44], a feature likely related to the maintenance of plastid structural stability [45]. Furthermore, we identified five hypervariable regions, namely *matK-rps16*, *petN-psbM*, *petA-psbJ*, *ndhF*, and *ycf1*. These hypervariable regions can serve as valuable references for taxonomic studies on species of *Endiandra* [46].

4.3. The Floristic Origin of *Endiandra* in New Caledonia

Previous studies have proposed two hypotheses regarding the biogeographic origins of New Caledonian flora. The first is the Gondwanan vicariance hypothesis, suggesting that species of *Endiandra* were already present in New Caledonia when it separated from Gondwana and subsequently underwent in situ survival and gradual diversification. The second is the long-distance dispersal hypothesis, arguing that the species colonized the island via oceanic currents or bird-mediated dispersal [47–49]. According to Song et al. [10], *Endiandra* originated from Australia and subsequently dispersed to New Caledonia. Our divergence time estimates indicate that the earliest divergence of the *E. lecardii*-*E. poueboensis*-*E. bailonii* subclade from the remaining *Endiandra* species was at 33.18 Ma, much later than the formation of the island. These findings lead us to favor the long-distance dispersal hypothesis for the arrival of *Endiandra* in New Caledonia.

Our findings also corroborated the study by Munzinger and Gemmill [9], who said that the *Endiandra* species of New Caledonia are the result of at least two separate dispersal events followed by diversification. The findings imply that floristic exchanges between New Caledonia and Australia occurred multiple times. Our findings provide new clues for elucidating the biogeographic history of New Caledonia and the adjacent Australia. However, since both our study and that of Song et al. [10] included only a limited number of *Endiandra* species (without all New Caledonian representatives being sampled), our current understanding on the origin of the genus on this island remains preliminary. Further studies will be required to reach more definitive conclusions.

5. Conclusions

We used *Endiandra* from New Caledonia as a case to test the vicariance and dispersal hypothesis on the floristic origin and conducted a comparative genomic and phylogenomic study of the genus and its closely related genera. Our phylogenomic study indicates that the four sampled *Endiandra* species native to New Caledonia were grouped into two separate subclades, with three of them forming a subclade and *E. polyneura* and two Australian species of *Endiandra* constituting a separate subclade. The divergence time estimation indicates that the earliest divergence of the New Caledonian *Endiandra* occurred at 33.18 Ma, which is later than the geological formation of the island, suggesting that the New Caledonian *Endiandra* originated from dispersal rather than vicariance. In addition, the genus *Endiandra* colonized New Caledonia via at least two independent dispersal events, with the neighboring Australia representing the most probable source, given the strong biogeographic connectivity between these two regions. Our study provides a new case to elucidate the floristic origins of New Caledonia. In future studies, we aim to refine the phylogenomic and biogeographic understanding of *Endiandra* by incorporating a broader sampling of species within this genus.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/f16040705/s1>. Table S1: Sequence information of the Cryptocaryae from the NCBI and LGADB.

Author Contributions: Conceptualization, Y.Y.; methodology, J.S. and C.S.; software, J.S. and C.S.; validation, Y.Y.; formal analysis, J.S.; investigation, J.S.; resources, Y.Y.; data curation, J.S.; writing—original draft preparation, J.S.; writing—review and editing, J.S. and Y.Y.; visualization, Y.Y.; supervision, Y.Y. and Z.Y.; project administration, Y.Y.; funding acquisition, Y.Y. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the National Natural Science Foundation of China (Nos. 32270217).

Data Availability Statement: The complete plastome sequence data of *Endiandra baillonii*, *E. lecardii*, *E. polyneura*, and *E. poueboensis* will be submitted to the NCBI (<https://www.ncbi.nlm.nih.gov>, accessed on 24 March 2025) during the revision process.

Acknowledgments: We thank David Boufford of Harvard University Herbaria for his help with the English.

Conflicts of Interest: The authors declare no conflicts of interest.

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