Introduction

*Lannea coromandelica* (Houtt.) Merr. is a deciduous tree, which can grow up to 5–10 m tall, with gray-white bark, thick, branchlets densely covered with rust-colored stellate hairs. Leaves are odd-pinnate often clustered at branchlets, 10–33 cm long, with (5-)7-9(-11) pairs of leaflets, 2 or 5 pairs of rachis and cylindrical petioles, sparsely covered with rust-colored stellate hairs. The flowers are small, yellow or purplish, arranged in terminal branched or unbranched racemes. Drupes are ovate, slightly compressed, purplish-red when ripe, 6–10 mm long, ca. 0.5 mm wide, glabrous. Tannin extracts can be extracted from the bark of *L. coromandelica*, and fishnets can be stained with extracts. The stem bark fiber can be woven into coarse cloth. Seeds can be pressed into oil. Bark can be used as medicine, with free radical scavenging, anti-tumor, inhibition of cancer cells and other effects. Therefore, we reported the complete plastome of *L. coromandelica* (Houtt.) Merr. in this study, which is expected to improve the quality of the relevant collection, medical application and phylogenetic investigation of Anacardiaceae.

In this study, a fruiting cultivar of *L. coromandelica* (Houtt.) Merr. was sampled from Qionghai city in Hainan (109.24'E, 18.55'N). A voucher specimen (voucher code: X F Zhang, A245, HUTB) and its DNA were deposited in the Herbarium of Hainan University, Hainan province, China (code of herbarium: HUTB).

The experiment was carried out as reported in Zhu et al. (2018). Clean data were assembled using the plastid of *Rhus typhina* NC 046837.1 as a reference with MITOBim v1.8 (Hahn et al. 2013). The plastome was annotated against the plastome of *Rhus typhina* NC 046837.1 by using Geneious R8.0.2 (Biomatters Ltd, Auckland, New Zealand) with subsequent correction of the annotation conducted with DOGMA (Wyman et al. 2004).

Our results show that the plastome of *L. coromandelica*, has a typical quadripartite structure of angiosperms and a full length of 162,460 bp, consisting of 26,877 base pairs for two Inverted Repeats (IRs), 89,599 base pairs for the Large Single Copy (LSC) region and 19,107 base pairs for the Small Single-Copy (SSC) region. The plastome consists of 130 genes, consisting of 85 protein-coding genes (six of which are duplicated in the IR) and 37 tRNA genes (eight of which are duplicated in the IR) and 8 rRNA genes (5s rRNA, 4.5s rRNA, 23s rRNA and 16s rRNA) (four of which are duplicated in the IR). The total G/C content of the plastome of *L. coromandelica* was 37.7%, and the G/C content of the LSC, SSC, and IR regions were 35.8, 32.2, and 42.8%, respectively.

We constructed a maximum likelihood (ML) phylogeny of 13 published complete plastomes of Anacardiaceae using the online CIPRES portal (http://www.phylo.org/portal2/logininput.action) with 1,000 bootstraps (Stamatakis 2006). *Acer velutinum* NC 056236.1, *Aesculus assamica* NC 056237.1 and *Commiphora foliacea* NC 041103.1 were used as outgroups. By inferring the phylogenetic relationship based on the existing data and related taxa, we find that *Lannea coromandelica* is closer to *Sclerocarya birea* than other species in this study (Figure 1).

The current data and investigation show that most nodes of the plastome ML trees are fully supported. At present, the plastid sequence of common Anacardiaceae plants has gradually increased. This is of great significance for promoting the
related protection and phylogenetic research of Anacardiaceae plants, and for deepening the understanding of these plants.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The genome sequence data supporting the results of this study are publicly available in NCBI GenBank (https://www.ncbi.nlm.nih.gov/) with registration number MZ929419. The associated BioProject, SRA, and BioSample numbers are PRJNA748537, SRR15651128 and SAMN20858431, respectively.

References

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. Nucleic Acids Res. 41(13): e129.

Stamatakis A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics. 22(21):2688–2690.

Wyman SK, Jansen RK, Boone JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.

Zhu ZX, Mu WX, Wang JH, Zhang JR, Zhao KK, Friedman CR, Wang HF. 2018. Complete plastome sequence of Dracaena cambodiana (Asparagaceae): a species considered “vulnerable” in Southeast Asia. Mitochondrial DNA B Resour. 3(2):620–621.