



## Complete chloroplast genome sequences of *Poikilospermum lanceolatum* (Urticeae)

Xianhan Huang, Tao Deng, Nan Lin, Zhenyu Lv, Xu Zhang, Zhuo Zhou, Yuehua Wang & Hang Sun

To cite this article: Xianhan Huang, Tao Deng, Nan Lin, Zhenyu Lv, Xu Zhang, Zhuo Zhou, Yuehua Wang & Hang Sun (2019) Complete chloroplast genome sequences of *Poikilospermum lanceolatum* (Urticeae), *Mitochondrial DNA Part B*, 4:2, 2131-2132, DOI: [10.1080/23802359.2019.1623117](https://doi.org/10.1080/23802359.2019.1623117)

To link to this article: <https://doi.org/10.1080/23802359.2019.1623117>



© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 11 Jul 2019.



Submit your article to this journal [↗](#)



Article views: 270




View related articles [↗](#)



View Crossmark data [↗](#)

## Complete chloroplast genome sequences of *Poikilospermum lanceolatum* (Urticeae)

Xianhan Huang<sup>a,b,c</sup> , Tao Deng<sup>b</sup>, Nan Lin<sup>b,c,d</sup>, Zhenyu Lv<sup>e</sup>, Xu Zhang<sup>b,c,d</sup>, Zhuo Zhou<sup>b</sup>, Yuehua Wang<sup>a</sup> and Hang Sun<sup>b</sup>

<sup>a</sup>School of Life Sciences, Yunnan University, Kunming, China; <sup>b</sup>Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China; <sup>c</sup>University of Chinese Academy of Sciences, Beijing, China; <sup>d</sup>Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, China; <sup>e</sup>School of Life Sciences, Yunnan Normal University, Kunming, China

### ABSTRACT

The complete chloroplast genome of *Poikilospermum lanceolatum* was sequenced using HiSeq4000 of Illumina. The length of this genome was 153,454 bp, including a large single copy (LSC) region (84,202 bp), a small single copy (SSC) region (18,172 bp), and two inverted repeat (IR) regions (25,540 bp). The overall GC content of the genome of *P. lanceolatum* was 36.9%. The genome included 111 unique genes (78 protein-coding genes, 29 tRNA genes, and four rRNA genes). Phylogenetic analysis based on 67 protein-coding genes showed that Boehmerieae was sister to *P. lanceolatum*, with 100% bootstrap values.

### ARTICLE HISTORY

Received 3 May 2019  
Accepted 17 May 2019

### KEYWORDS

Chloroplast genome;  
*Poikilospermum lanceolatum*;  
phylogenetic analysis

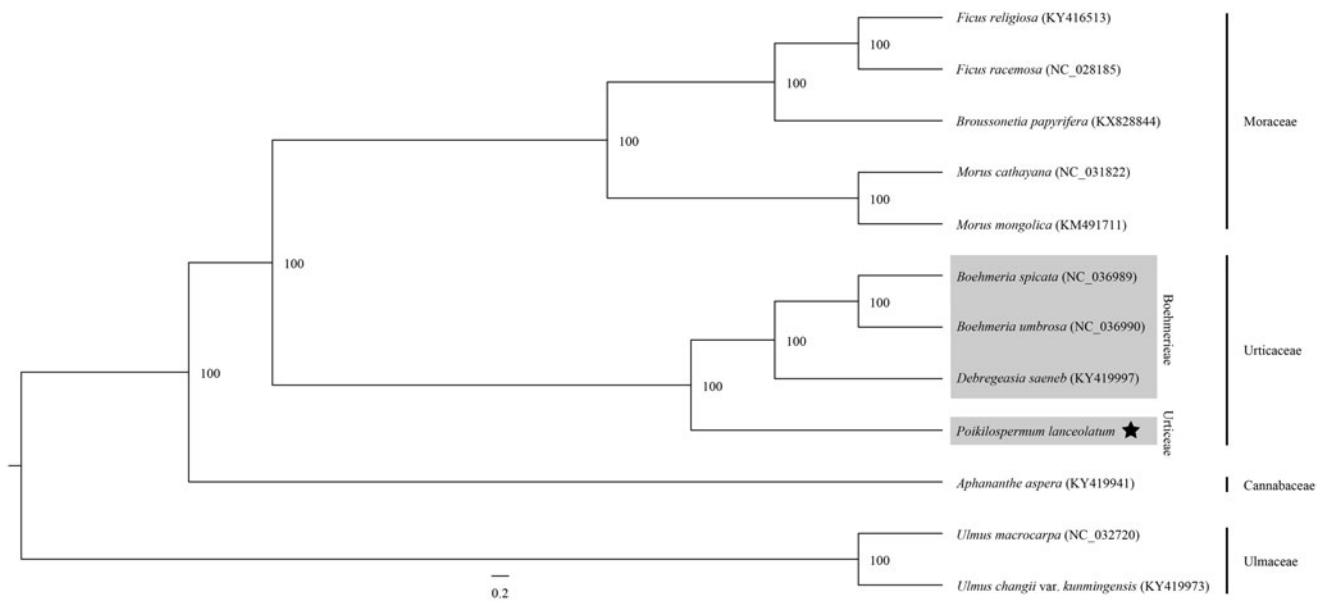
*Poikilospermum* Zippelius ex Miquel (Urticeae) consists of approximately 27 species and is distributed from Sino-Himalayan region through Malaysia to the Bismarck Archipelago (Chew 1963; Chen et al. 2003). This genera was published by Miquel in 1864 (Miquel 1864); however, its systematic position has been controversial since then (Berg 1978; Chen et al. 2003). Up to now, there is no any species of *Poikilospermum*, even Urticeae with reported complete plastid genome. Therefore, we aim to establish and characterize the complete chloroplast genome of *Poikilospermum lanceolatum* and ascertain its phylogenetic position in this study.

Fresh leaves of *P. lanceolatum* were collected from Bulangxiang town of Menghai county in Yunnan Province (21°34'43.914" N, 100°19'59.4624" E). The voucher specimens were deposited in the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN, ZH026). *P. lanceolatum* was sequenced using HiSeq4000 of Illumina at the Beijing Novogene Bioinformatics Technology Co., Ltd (Nanjing, China). NOVOPlasty 2.7.2 (Dierckxsens et al. 2017), a seed-extend based assembler, was used to assemble the plastome and *Boehmeria spicata* (NC\_036989) was used as the seed sequence. The plastome of *P. lanceolatum* was annotated using Geneious 9.0.2 (Kearse et al. 2012) against the plastome of *B. spicata* and *Morus mongolica* (KM491711). The

DOGMA was used to correct the annotation (Wyman et al. 2004).

The complete chloroplast genome of *P. lanceolatum* (MK778867) was 153,454 bp in size. This genome was with a typical quadripartite structure, containing SSC with the length of 18,172 bp, LSC with the length of 84,202 bp and two IR regions with the length of 25,540 bp. The GC content of this genome was 36.9%. There were 130 predicted functional genes in the genome, including 111 different genes (78 protein-coding genes, 29 tRNA genes, and four rRNA genes) and 19 duplicated genes. In the 111 genes, 19 included one intron, and only three included two introns (*clpP*, *rps12*, and *ycf3*).

Phylogenetic position of *P. lanceolatum* was analysed based on the 67 shared protein-coding gene sequences of this species and other 11 species, belonging to Boehmerieae of Urticaceae, Cannabaceae, Rosaceae, and Ulmaceae. The sequences were aligned in MAFFT (Kato et al. 2002). The maximum-likelihood phylogenetic tree was reconstructed using RaxML (Stamatakis 2014). The ML analysis showed that *P. lanceolatum* was sister to Boehmerieae with 100% bootstrap values, which was congruent with the precious studies (Kim et al. 2015; Wu et al. 2013) (Figure 1). Our results here could be further applied for



**Figure 1.** Phylogeny of *Poikilospermum lanceolatum* and other 11 species of Rosales based on the 67 common protein-coding gene sequences using maximum-likelihood method. The numbers at the nodes indicate bootstrap support values.

evolutionary and phylogenetic studies of *Poikilospermum*, Urticeae, even Urticaceae.

## Disclosure statement

No potential conflict of interest was reported by the authors.

## Acknowledgements

We thank Drs. M.S. Song, C. Davidson, D.E. Boufford and S. Christoph for assisting with collection of plant materials.

## Funding

This study was supported by grants-in-aid from the Major Program of the National Natural Science Foundation of China [31590823], the National Key R&D Program of China [2017YFC0505200], and the Strategic Priority Research Program of Chinese Academy of Sciences [XDA20050203] to H. Sun, and the National Natural Science Foundation of China [NSFC, 31700165] and the West Light Foundation of the Chinese Academy of Sciences to T. Deng.

## ORCID

Xianhan Huang  <http://orcid.org/0000-0003-2009-7025>

## References

- Berg CC. 1978. Cecropiaceae a new family of the Urticales. *Taxon*. 27: 39–44.
- Chen CJ, Friis I, Wilmot-Deer CM. 2003. *Poikilospermum*. In: Wu ZY, Raven PH, editors. *Flora of China*. Beijing: Science Press & Beijing & Missouri Botanical Garden Press; p. 180–181.
- Chew WL. 1963. A revision of the genus *Poikilospermum* (Urticaceae). *Gardens' Bull Singapore*. 20:1–103.
- Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res*. 45:e18
- Katoh K, Misawa K, Kuma K, Miyata T. 2002. Mafft: a novel method for rapid multiple sequence alignment based on fast fourier transform. *Nucleic Acids Res*. 30:3059–3066.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28: 1647–1649.
- Kim C, Deng T, Chase MW, Zhang DG, Nie ZL, Sun H. 2015. Generic phylogeny and character evolution in Urticeae (Urticaceae) inferred from nuclear and plastid DNA regions. *Taxon*. 64:65–78.
- Miquel F. 1864. *Poikilospermum* Zippel., genus novum Urticacearum. *Ann Musei Bot Lugduno-Batavi*. 1:203.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30:1312–1313.
- Wu ZY, Monro AK, Milne RI, Wang H, Yi TS, Liu J, Li DZ. 2013. Molecular phylogeny of the nettle family (Urticaceae) inferred from multiple loci of three genomes and extensive generic sampling. *Mol Phylogenet Evol*. 69:814–827.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20:3252–3255.