



HAL
open science

The plastome sequence of *Laurus azorica* (Seub.) Franco, an endemic tree species of the Azores islands

Xi-Jian Liang, D. D. Hinsinger, Rui Bento Elias, Joeri Sergej Strijk

► To cite this version:

Xi-Jian Liang, D. D. Hinsinger, Rui Bento Elias, Joeri Sergej Strijk. The plastome sequence of *Laurus azorica* (Seub.) Franco, an endemic tree species of the Azores islands. *Mitochondrial DNA Part B Resources*, 2019, 4 (1), pp.363-365. 10.1080/23802359.2018.1545536 . hal-03370647

HAL Id: hal-03370647

<https://hal.inrae.fr/hal-03370647>

Submitted on 4 Apr 2023


HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

The plastome sequence of *Laurus azorica* (Seub.) Franco, an endemic tree species of the Azores islands

Xi-Jian Liang^a, Damien Daniel Hinsinger^b, Rui Bento Elias^{b,c} and Joeri Sergej Strijk^{a,d} 

^aBiodiversity Genomics Team, Plant Ecophysiology & Evolution Group, Guangxi Key Laboratory of Forest Ecology and Conservation, College of Forestry, Nanning, Guangxi, PR China; ^bAlliance for Conservation Tree Genomics, Pha Tad Ke Botanical Garden, Luang Prabang, Lao PDR; ^cState Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, College of Forestry, Guangxi University, Nanning, Guangxi, PR China; ^dCE3C – Centre for Ecology, Evolution and Environmental Changes/Azorean Biodiversity Group and Universidade dos Açores - Faculdade de Ciências Agrárias e do Ambiente, Angra do Heroísmo, Açores, Portugal

ABSTRACT

Laurus azorica is an endemic tree species from Azores archipelago. In this study, we generated the plastome sequence as a first step in a global assessment of island endemic Lauraceae. The total chloroplast genome was 153,061 bp in length, with a large single copy (LSC) region of 87,226 bp and a small single copy (SSC) region of 18,033 bp, separated by two inverted repeats (IRs) regions of 23,901 bp. The overall GC content was 37.3%, and 43.1%, 35.4%, and 31.1% in the IRs, LSC, and SSC regions, respectively. It contained 106 genes, including 79 coding genes, 24 tRNA genes, and four rRNA genes. A phylogenetic analysis confirmed that *L. azorica* was clustered with *L. nobilis* within the family Lauraceae.

ARTICLE HISTORY

Received 14 October 2018
Accepted 2 November 2018

KEYWORDS

Lauraceae; complete chloroplast genome; *Laurus azorica*; islands endemic trees

Lauraceae are an ancient family of woody plants found in tropical and subtropical regions, with centers of diversity in South America and Southeast Asia (Chanderbali et al, 2001). They comprise more than 3000 species in ~50 genera worldwide. In addition to high commercial value for edible fruits (e.g. avocado – *Persea americana*) and spices (e.g. cinnamon – *Cinnamomum verum*), Lauraceae are also an important structural and evolutionary component of wet tropical forests (Christenhusz and Byng 2016).

However, despite their abundance and widespread occurrence, Lauraceae remain poorly known and difficult to identify, primarily due to the absence of clear morphological and molecular diagnostic characters (Werff and Geography 2001, Little et al, 2009). Plastome sequencing can therefore increase the identification success by providing a comprehensive set of data (Hinsinger and Strijk 2017).

Laurus L. is the type genus of the Lauraceae family and holds three species, *L. nobilis* L. (the true laurel) being used as culinary herb, and two other species, *L. azorica* and *L. novocanariensis*, endemic from Azores and Canary Islands, respectively (Córdoba and Medina 1976; Barbero et al. 1980). Here we report the complete chloroplast sequence of *L. azorica* to provide resources for delineation of the taxonomical status of this species and improve its *in situ* conservation.

Laurus azorica is a dioecious tree, endemic to the Azores, present in all islands of the archipelago. It is one of the most frequent species in montane cloud forests of the Azores (Elias et al. 2011) but in the past it was probably much more

abundant because it was one of the typical laurel forest species (especially in the submontane belt), that dominated the landscape of the archipelago before human settlement (Elias et al. 2016). Presently, *L. azorica* may be found mostly between 100 and 1000 m a.s.l., but it is more abundant between 300 and 600 m a.s.l., and frequent up to 900 m. In the past *L. azorica* berries were used to produce oil for medicinal purposes and lighting (Dias 1946). Although this was not the preferred tree for the purpose, the wood of this species was also used to produce coal (Costa 1950). Nevertheless, the main cause for the decline of the species was the replacement of Laurel forests by pastures and plantation forests, and invasion by exotic trees. As *L. azorica* occurs on the nine islands of the Azores archipelago, we expect its plastome sequence will provide valuable data to further study the population structure among and between islands, and will improve our understanding of the systematics and the evolutionary history of the Lauraceae.

Genomic DNA was extracted from silica-dried leaves of *L. azorica* collected on the Terceira island (38°45'00.3" N 27°19'57.4"W), using a modified SDS protocol (Healey et al. 2014). Library construction and sequencing were performed by Novogene (Beijing, PR China) on an Illumina HiSeq2500 system, following manufacturer instructions. Vouchers were deposited in the herbarium of the Azores University (AZU), with DNA material stored in the laboratory of the Biodiversity Genomics Team (Guangxi University, Nanning, PR China), under accession BGT3615. We performed a *de novo* assembly

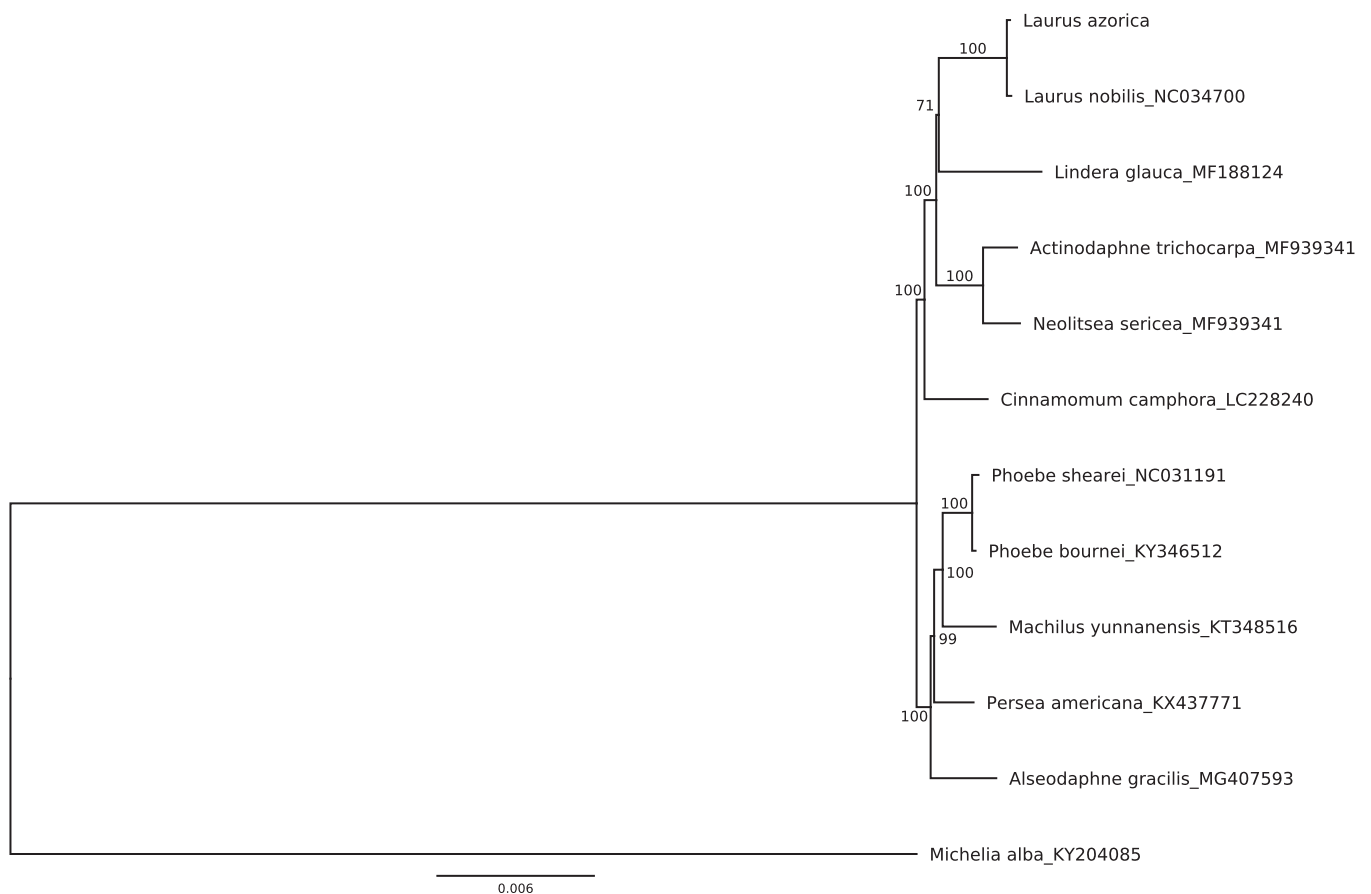


Figure 1. ML phylogenetic tree of ten selected Lauraceae plastomes sequences, plus the chloroplast sequence of *L. azorica*. The tree is rooted with *Michelia alba*. Bootstraps percentages (1000 replicates) are shown at the nodes. Scale in substitution per site.

using ORG.asm (<http://phythonhosted.org/asm/>), and annotated the assembled plastome using cpGAVAS (Schenk et al. 2012), followed by manual adjustments in Geneious (R9, Biomatters, www.geneious.com).

The plastome of *L. azorica* was 153,011 bp in length. It contains a large single-copy (LSC) region (93,511 bp), a small single-copy (SSC) region (18,492 bp), and two inverted repeats (IRs) (41,008 bp). 179 genes, with 80 coding regions, 28 ribosomal RNA genes and 95 tRNA genes were annotated. The overall GC content of the cp genome was 39.1%, and 44.1%, 37.9%, 33.9% in the IRs, LSC and SSC regions, respectively. The plastome sequence was deposited in Genbank (MK041220).

Ten other Lauraceae plastomes were retrieved from GenBank, and used to reconstruct a phylogenetic tree using PhyML (ref). The ML tree highlighted both the close relationship of *L. azorica* with *L. nobilis* and of the *Laurus* spp. with *Lindera glauca* (Figure 1). Our results also confirmed the split of the family in two main groups. The length of the branch leading to the genus *Laurus* indicates either an old divergence from the rest of the family, or a possible increase in the plastome substitution rate as *Laurus* adapted to the Mediterranean climate.

Acknowledgements

We would like to acknowledge Fernando Pereira for sampling the material of *Laurus azorica*.

Funding

This work was supported by grants from Guangxi University (Nanning), the State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources (GXU) and the provincial government of Guangxi Province ("100 Talents" Program; recruitment of overseas talents for colleges and universities in Guangxi) to J.S.S., and grants from China Postdoctoral Science Foundation [Nos. 2015M582481 and 2016T90822] to D.D.H and Natural Science Foundation of Guangxi Province

ORCID

Joeri Sergej Strijk  <http://orcid.org/0000-0003-1109-7015>

References

- Barbero M, Benabid A, Peyre C, Quézel PJADJBDM. 1980. Sur la présence au Maroc de "*Laurus azorica*" (Seub.). Franco. 37: 467–472.
- Chanderbali AS, Werff HVD, Renner SS. 2001. Phylogeny and historical biogeography of Lauraceae: evidence from the chloroplast and nuclear genomes. Ann Missouri Bot Gard. 88:104–134.
- Christenhusz MJM, Byng JW. 2016. The number of known plants species in the world and its annual increase. Phytotaxa. 261:201–217.
- Córdoba LCYFD, Medina FO. 1976. Estudio sobre la vegetación y flora forestal de las Canarias occidentales.(1): p1-6. Excmo, Cabildo Insular.
- Costa C. 1950. Arvoredos dos Açores: algumas achegas para a sua história. Comissão Reguladora Dos Cereais Do Arquipélago Dos Açores. 11: 45–60.
- Dias UM. 1946. Ponta Delgada: descrição de quando foi lugar e vila e de cidade: escorço histórico. Tipografia A Crença. Ponta Delgada, Açores.

- Elias RB, Dias E, Pereira F. 2011. Disturbance, regeneration and the spatial pattern of tree species in Azorean mountain forests. *Commun Ecol.* 12:23–30.
- Elias RB, Gil A, Silva L, Fernandez-Palacios JM, Azevedo EB, Reis F. 2016. Natural zonal vegetation of the Azores Islands: characterization and potential distribution. *Phytocoenologia.* 46:107–123.
- Healey A, Furtado A, Cooper T, Henry RJPM. 2014. Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. *Plant Methods.* 10:1–8.
- Hinsinger DD, Strijk JSJ. 2017. Toward phylogenomics of Lauraceae: the complete chloroplast genome sequence of *Litsea glutinosa* (Lauraceae), an invasive tree species on Indian and Pacific Ocean islands. *Plant Gene.* 9:71–79.
- Little SA, Stockey RA, Penner B. 2009. Anatomy and development of fruits of Lauraceae from the Middle Eocene Princeton Chert. *Am J Bot.* 96:637–651.
- Schenk L, Schnitzer S, Adolph H, Holzhausen J, Matheis E, Kuhlmeijer AJBG. 2012. CpGAVAS, an integrated web server for the annotation, visualization, analysis, and GenBank submission of completely sequenced chloroplast genome sequences. *BMC Genomics.* 13:715–715.
- Van Der Werff HJ. 2001. An annotated key to the genera of Lauraceae in the flora Malesiana region. *Blumea* 46:125–140.