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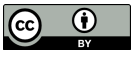
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The plastome sequence of *Laurus azorica* (Seub.) Franco, an endemic tree species of the Azores islands

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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.

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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

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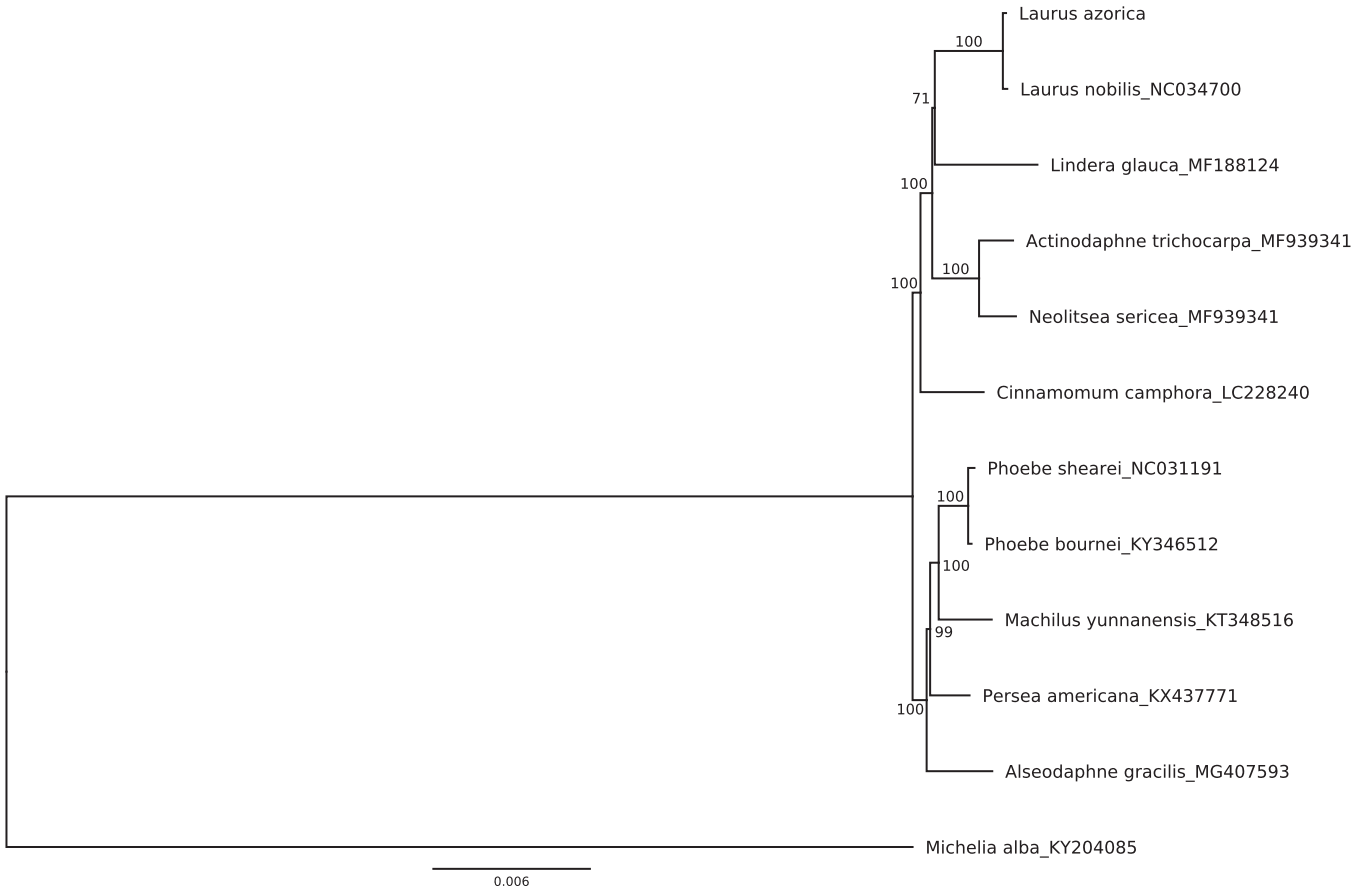


Figure 1. ML phylogenetic tree of ten selected Lauraceae plastomes sequences, plus the chloroplast sequence of *L. azorica*. The tree is rooted with *Michelia alba*. Bootstraps percentages (1000 replicates) are shown at the nodes. Scale in substitution per site.

using ORG.asm (http://phythonhosted.orgorg.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.

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