



Corrigendum: Species Identification of *Dracaena* Using the Complete Chloroplast Genome as a Super-Barcode

Zhonglian Zhang^{1,2}, Yue Zhang², Meifang Song², Yanhong Guan² and Xiaojun Ma^{1*}

¹ Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China, ² Yunnan Branch of Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences & Peking Union Medical College, Jinghong, China

OPEN ACCESS

Edited and reviewed by:

Hugo J. De Boer,
University of Oslo, Norway

*Correspondence:

Xiaojun Ma
mayixuan10@163.com

Specialty section:

This article was submitted to
Ethnopharmacology,
a section of the journal
Frontiers in Pharmacology

Received: 17 December 2019

Accepted: 15 January 2020

Published: 13 February 2020

Citation:

Zhang Z, Zhang Y, Song M, Guan Y
and Ma X (2020) Corrigendum:
Species Identification of *Dracaena*
Using the Complete Chloroplast
Genome as a Super-Barcode.
Front. Pharmacol. 11:51.
doi: 10.3389/fphar.2020.00051

Keywords: *Dracaena* Vand. ex L., chloroplast genome, identification, super-barcode, Liliaceae

A Corrigendum on

Species Identification of *Dracaena* Using the Complete Chloroplast Genome as a Super-Barcode by Zhang Z, Zhang Y, Song M, Guan Y and Ma X (2019). *Front. Pharmacol.* 10:1441. doi: 10.3389/fphar.2019.01441

In the original article, the figure legends were associated with the wrong figures. **Figure 4** should be **Figure 2**, **Figure 2** should be **Figure 3**, and **Figure 3** should be **Figure 4**. The legends remain the same. The figures and their correct legends appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Copyright © 2020 Zhang, Zhang, Song, Guan and Ma. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

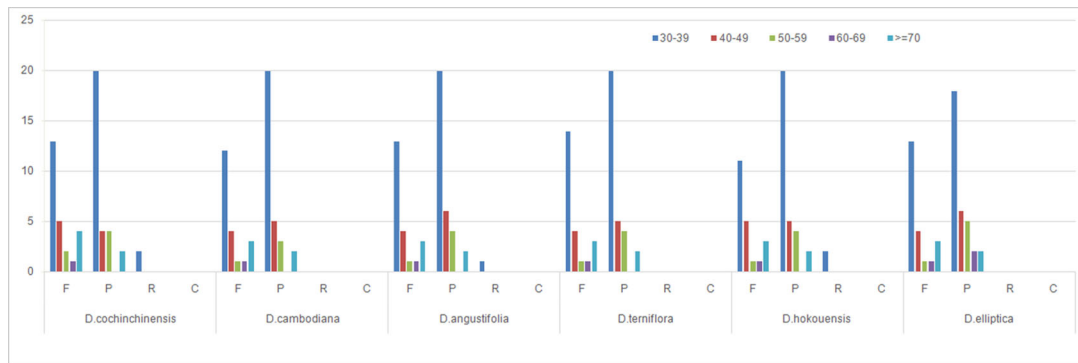


FIGURE 2 | Repeat analysis in six *Dracaena* CP genomes. REPuter was used to identify repeat sequences with length ≥ 30 bp and sequence identified $\geq 90\%$ in the CP genomes. F, P, R, and C indicate the repeat types F (forward), P (palindrome), R (reverse), and C (complement), respectively. Repeats with different lengths are indicated in different colors.

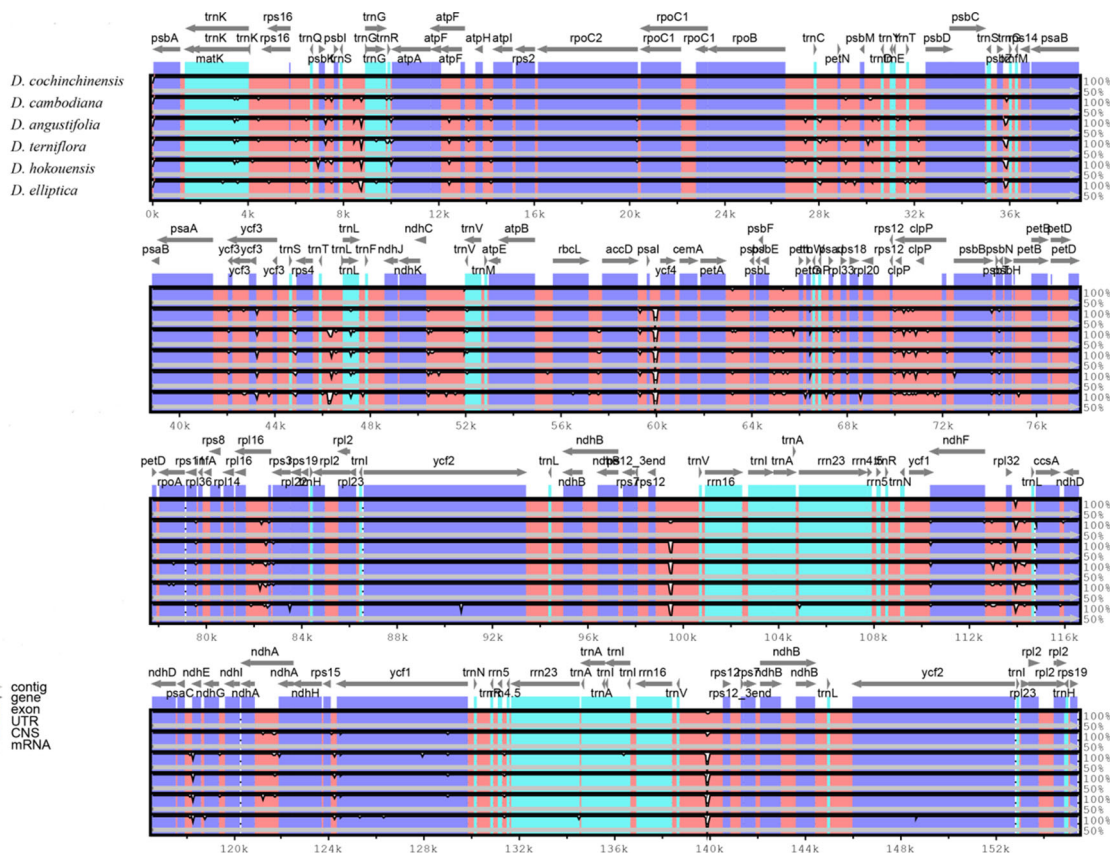


FIGURE 3 | Structure comparison of the six *Dracaena* CP genomes by using the mVISTA program. Gray arrows and thick black lines above the alignment indicate genes with their orientation and the position of the IRs, respectively. A cut-off value of 70% identity was used for the plots, and the Y-scale represents the percent identity between 50% and 100%.

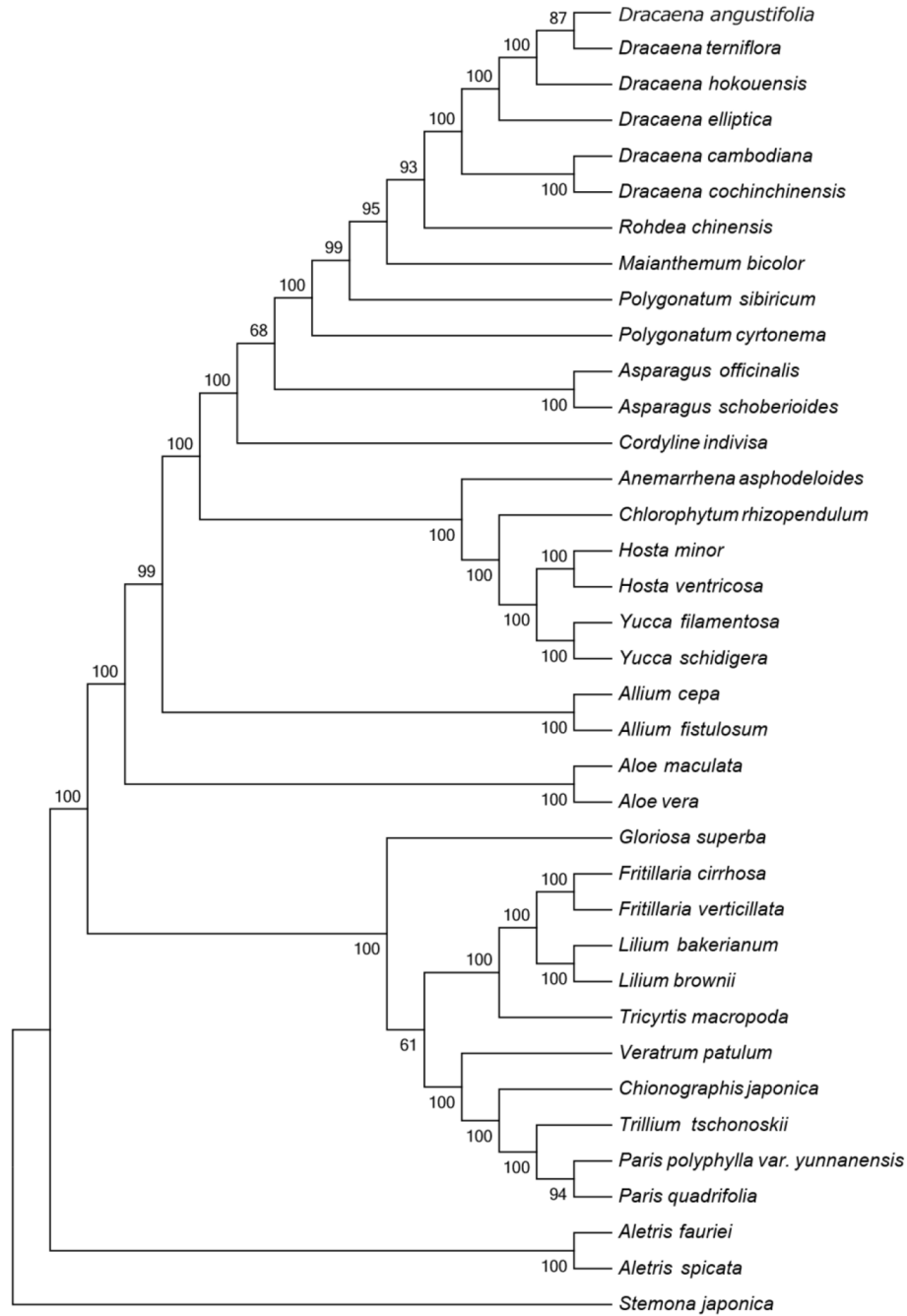


FIGURE 4 | Phylogenetic tree constructed using MP based on complete CP genomes of six *Dracaena* and other 31 species. Numbers above the branches are the bootstrap support values.