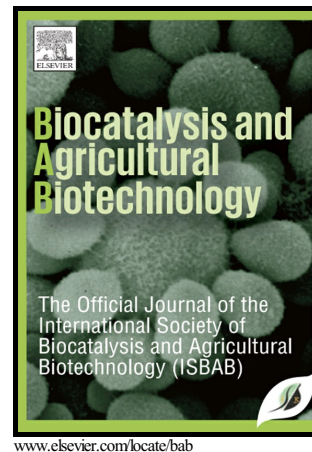


Author's Accepted Manuscript

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PII: S1878-8181(18)30429-8
DOI: <https://doi.org/10.1016/j.bcab.2018.09.019>
Reference: BCAB876

To appear in: *Biocatalysis and Agricultural Biotechnology*

Received date: 22 June 2018
Revised date: 20 August 2018
Accepted date: 20 September 2018

Cite this article as: Katharine R. Hind, Ayelign M. Adal, Tim M. Upton and Soheil S. Mahmoud, An assessment of plant DNA barcodes for the identification of cultivated *Lavandula* (Lamiaceae) taxa, *Biocatalysis and Agricultural Biotechnology*, <https://doi.org/10.1016/j.bcab.2018.09.019>

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An assessment of plant DNA barcodes for the identification of cultivated *Lavandula* (Lamiaceae) taxaKatharine R. Hind^{a*,1}, Ayelign M. Adal^a, Tim M. Upson^{b1}, Soheil S. Mahmoud^{a*}^aDepartment of Biology, University of British Columbia, Kelowna, BC, Canada^bCambridge University Botanic Garden, 1 Brookside, Cambridge, UK

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Abstract

Historically, species identification in plants has relied upon detailed comparisons of morphological and anatomical features. Among *Lavandula*, morphological assessments are often paired with essential oil biochemistry to identify species, and the use of molecular taxonomic approaches has been limited mostly to wild species. We tested a molecular approach to identify three related, commercially important lavender taxa, two of which (*L. angustifolia* and *L. x intermedia*) are widely cultivated in British Columbia, Canada for commercial essential oil production. We tested the plant DNA barcode markers *matK* and *rbcL* as well as the plastid *trnH-psbA* spacer and the nuclear internal transcribed spacer (ITS), which have been used for species discrimination in other closely related plant species. Among tested markers, the selected primers were unable to amplify the *matK* region, a finding that has been reported for several genera in the Lamiaceae. Based on sequence comparison and tree analysis, the plastid markers, *rbcL* and *trnH-psbA* alone did not discriminate between *L. angustifolia*, *L. latifolia* and *L. x intermedia*, perhaps due to hybridization and/or introgression that occurs naturally between these two taxa. The ITS delineated the three species with few exceptions between *L. angustifolia* and *L. x intermedia*. The ITS concatenated with *rbcL*, *trnH-psbA* and *rbcL+ trnH-psbA* were able to discriminate the cultivated *L. latifolia* from that of *L. angustifolia* and *L. x intermedia*.

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