

Provided for non-commercial research and education use.  
Not for reproduction, distribution or commercial use.



This article appeared in a journal published by Elsevier. The attached copy is furnished to the author for internal non-commercial research and education use, including for instruction at the authors institution and sharing with colleagues.

Other uses, including reproduction and distribution, or selling or licensing copies, or posting to personal, institutional or third party websites are prohibited.

In most cases authors are permitted to post their version of the article (e.g. in Word or Tex form) to their personal website or institutional repository. Authors requiring further information regarding Elsevier's archiving and manuscript policies are encouraged to visit:

<http://www.elsevier.com/copyright>

Contents lists available at [SciVerse ScienceDirect](http://SciVerse.ScienceDirect.com)

## Molecular Phylogenetics and Evolution

journal homepage: [www.elsevier.com/locate/ympev](http://www.elsevier.com/locate/ympev)

## Application of the phylogenetic informativeness method to chloroplast markers: A test case of closely related species in tribe Hydrangeeae (Hydrangeaceae)

Carolina Granados Mendoza<sup>a,\*</sup>, Stefan Wanke<sup>b</sup>, Karsten Salomo<sup>b</sup>, Paul Goetghebeur<sup>a</sup>, Marie-Stéphanie Samain<sup>a</sup>

<sup>a</sup> Ghent University, Department of Biology, Research Group Spermatophytes, K.L. Ledeganckstraat 35, 9000 Gent, Belgium

<sup>b</sup> Technische Universität Dresden, Institut für Botanik, Zellescher Weg 20b, 01062 Dresden, Germany

## ARTICLE INFO

## Article history:

Received 4 May 2012

Revised 19 September 2012

Accepted 24 September 2012

Available online 12 October 2012

## Keywords:

Accuracy

Coded indels

Hydrangea

Nodal support

Phylogenetic signal

Resolution

## ABSTRACT

In evolutionary biology appropriate marker selection for the reconstruction of solid phylogenetic hypotheses is fundamental. One of the most challenging tasks addresses the appropriate choice of genomic regions in studies of closely related species. Robust phylogenetic frameworks are central to studies dealing with questions ranging from evolutionary and conservation biology, biogeography to plant breeding. Phylogenetic informativeness profiles provide a quantitative measure of the phylogenetic signal in markers and therefore a method for locus prioritization. The present work profiles phylogenetic informativeness of mostly non-coding chloroplast regions in an angiosperm lineage of closely related species: the popular ornamental tribe Hydrangeeae (Hydrangeaceae, Cornales, Asterids). A recent phylogenetic study denoted a case of resolution contrast between the two strongly supported clades within tribe Hydrangeeae. We evaluate the phylogenetic signal of 13 highly variable plastid markers for estimating relationships within and among the currently recognized monophyletic groups of this tribe. A selection of combined loci based on their phylogenetic informativeness retrieved more robust phylogenetic hypotheses than simply combining individual markers performing best with respect to resolution, nodal support and accuracy or those presenting the highest number of parsimony informative characters. We propose the *rpl32-ndhF* intergenic spacer (IGS), *trnV-ndhC* IGS, *trnL-rpl32* IGS, *psbT-petB* region and *ndhA* intron as the best candidates for future phylogenetic studies in Hydrangeeae and potentially in other Asterids. We also contrasted the phylogenetic informativeness of coded indels against substitutions concluding that, despite their low phylogenetic informativeness, coded indels provide additional phylogenetic signal that is nearly free of noise. Phylogenetic relationships obtained from our total combined analyses showed improved resolution and nodal support with respect to recently published results.

© 2012 Elsevier Inc. All rights reserved.

## 1. Introduction

Variability is an indispensable requirement for phylogenetic signal. Molecular markers have been examined for phylogenetic utility by purely quantifying their amount of variability (e.g. number of potentially or parsimony informative characters; Kårehed et al., 2008; Mort et al., 2007; Shaw et al., 2005; Shaw et al., 2007) and/or by inspecting distribution of variability across a tree (Borsch et al., 2009; Kårehed et al., 2008; Mort et al., 2007; Müller et al., 2006; Townsend, 2007). Within the second approach two strategies can be distinguished.

The first of them searches for those markers providing the highest support for the largest number of possible clades, being the degree of resolution, nodal support and, in some instances, accuracy considered as ultimate indicators of the phylogenetic signal (e.g. Ekrem et al., 2010; Kårehed et al., 2008; Mort et al., 2007). Colless (1980) proposed the Consensus Fork Index (CFI) for the estimation of phylogenetic resolution by measuring the divergence of a consensus tree from a complete polytomy. Methods for assessing nodal support are in concordance with employed phylogenetic inference approaches, for instance posterior probabilities (PP) in Bayesian Inference (BI; Makowsky et al., 2010). Measures of accuracy of tree topologies generally evaluate the ability of markers to recover “true” nodes present in a second reliable reference tree (see Kårehed et al. (2008) for a summary of these strategies). Resolution, nodal support and accuracy values are often considered as the basis to estimate the strength or acceptability of phylogenetic hypotheses. However, their values have been considered as uncertain indicators of the phylogenetic signal since they are known to

\* Corresponding author. Fax: +32 (0)9 264 53 34.

E-mail addresses: [Carolina.GranadosMendoza@UGent.be](mailto:Carolina.GranadosMendoza@UGent.be) (C. Granados Mendoza), [Stefan.Wanke@TU-Dresden.de](mailto:Stefan.Wanke@TU-Dresden.de) (S. Wanke), [Karsten.Salomo@TU-Dresden.de](mailto:Karsten.Salomo@TU-Dresden.de) (K. Salomo), [Paul.Goetghebeur@UGent.be](mailto:Paul.Goetghebeur@UGent.be) (P. Goetghebeur), [MarieStephanie.Samain@UGent.be](mailto:MarieStephanie.Samain@UGent.be) (M.S. Samain).