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

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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 cladograms, 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