



Revised circumscription of *Nothofagus* and recognition of the segregate genera *Fuscospora*, *Lophozonia*, and *Trisyngyne* (Nothofagaceae)

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Abstract

The generic taxonomy of the Nothofagaceae is revised. We present a new phylogenetic analysis of morphological characters and map these characters onto a recently published phylogenetic tree obtained from DNA sequence data. Results of these and previous analyses strongly support the monophyly of four clades of Nothofagaceae that are currently treated as subgenera of *Nothofagus*. The four clades of Nothofagaceae are robust and well-supported, with deep stem divergences, have evolutionary equivalence with other genera of Fagales, and can be circumscribed with morphological characters. We argue that these morphological and molecular differences are sufficient for the four clades of Nothofagaceae to be recognised at the primary rank of genus, and that this classification will be more informative and efficient than the currently circumscribed *Nothofagus* with four subgenera.

Nothofagus is recircumscribed to include five species from southern South America, *Lophozonia* and *Trisyngyne* are reinstated, and the new genus *Fuscospora* is described. *Fuscospora* and *Lophozonia*, with six and seven species respectively, occur in New Zealand, southern South America and Australia. *Trisyngyne* comprises 25 species from New Caledonia, Papua New Guinea and Indonesia. New combinations are provided where necessary in each of these genera.

Key words: DNA sequence data, Fagales, generic names, genus concept, new combinations

Table of contents

Introduction	1
Criteria for recognising genera	3
Materials and methods	4
Results	5
Discussion	9
Taxonomy	11
Acknowledgements	21
References	21
Appendix 1	27
Appendix 2	29
Appendix 3	30

Introduction

The genus *Nothofagus* Blume (1851: 307) as it is currently circumscribed comprises 42 species of deciduous and evergreen forest trees that have a disjunct Southern Hemisphere distribution. Species occur in South America (south-western Argentina and Chile), Australia (south-eastern Australia and Tasmania), New Zealand, New Guinea (Papua New Guinea, Indonesia, and also New Britain and the D'Entrecasteaux

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