

Evolution of nickel hyperaccumulation by *Stackhousia tryonii* (Celastraceae), a serpentinite-endemic plant from Queensland, Australia

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Abstract. To elucidate the evolutionary origin of nickel (Ni) hyperaccumulation by the Australian serpentinite-endemic plant *Stackhousia tryonii* Bailey, phylogenetic analyses of chloroplast and nuclear DNA for *Stackhousia* and its close relatives were combined with assays of plant-tissue Ni concentrations. Thirty-five plants from 20 taxa were analysed by sequencing nuclear rDNA (ITS) and the plastid *trnL*–*F* region. Phylogenetic analysis of sequence data was conducted under maximum parsimony and Bayesian search criteria. In all, 100 plants from 39 taxa, including all 33 *Stackhousia* species, were analysed for Ni concentration by radial inductively coupled plasma atomic-emission spectrometry (ICP–AES). In phylogenetic analyses, *S. tryonii* was monophyletic, nested within a monophyletic *Stackhousia*. Only *S. tryonii* contained concentrations of Ni above the hyperaccumulation threshold (0.1%; 1000 ppm), containing between 0.25% (2500 ppm) and 4.1% (41 000 ppm) Ni by dry weight. Nickel-hyperaccumulation ability appears to have been acquired once during diversification of *Stackhousia*, by *S. tryonii*.

Introduction

Plant adaptation to extreme edaphic conditions has long been of interest to botanists (Mason 1946; Minguzzi and Vergnano 1948; Kruckeberg 1951, 1986; Bradshaw 1952). World-wide, ~368 species of vascular plants, representing 44 families, are known to accumulate Ni in their above-ground tissues, up to concentrations exceeding 0.1% (1000 ppm) by dry weight (Reeves and Baker 2000; Table 1), a phenomenon known as Ni hyperaccumulation (Brooks *et al.* 1977a; Reeves 1992). Nickel-hyperaccumulating plants are restricted to Ni-rich soils, particularly those derived from serpentinite rock (Reeves and Baker 2000; Reeves 2003). Serpentinite is formed in the Earth's mantle by metamorphosis of igneous rocks (Brooks 1987). Exposures of serpentinite rock occur world-wide but are most common near tectonic plate boundaries (Brooks 1987). In addition to high concentrations of Mg and Fe, the minerals composing serpentinite also contain high concentrations of heavy metals such as Cr, Co and Ni. When serpentinite is weathered, the resulting soils tend to contain excessive amounts of the elements listed above, especially Ni (Brooks 1987). Hereafter, we refer to these soils as 'serpentinite-derived soils' rather than 'serpentine' (e.g. Brooks 1987), so as to avoid confusion between the rocks themselves and the soils derived from them. It is also important to note that high concentrations of Ni are found in rock types other than serpentinite, some of which may weather to form Ni-rich soils that support Ni hyperaccumulators (Reeves and Baker 2000). Nickel-hyperaccumulating plants are known from Ni-rich soils

in Australasia, South-east Asia, Africa, Europe and North America (Reeves and Baker 2000; Table 1), with the greatest diversity occurring in Cuba and New Caledonia (Jaffré 1992; Reeves *et al.* 1996; Reeves 2003). Recently, Ni-hyperaccumulating plants have become the subject of intensive systematic (reviewed in Reeves and Baker 2000), ecological (reviewed in Boyd 2004), physiological (reviewed in Salt and Krämer 2000) and genetic (reviewed in Pollard *et al.* 2002) study. Research is motivated by interest in understanding the Ni-hyperaccumulation trait, as well as potential use of these plants for both detoxification (phytoremediation) of Ni-contaminated soils (reviewed in Baker *et al.* 2000) and phytomining (reviewed in Brooks *et al.* 1998).

Most Ni-hyperaccumulating species are members of families that do not otherwise display a propensity for this trait (Reeves and Baker 2000; Table 1). This observation, combined with the wide phylogenetic spread of the Ni-hyperaccumulating phenotype, encompassing ferns (1 sp.), monocots (4 genera, 4 spp.), and eudicots (97 genera, 363 spp.; Table 1), has led to the idea that Ni hyperaccumulation has evolved independently in multiple plant groups (Reeves and Baker 2000). Recent research points to several potential advantages of Ni hyperaccumulation that may have led to the independent evolution of this trait in multiple plant groups, including resistance to drought, competitive advantage via allelopathy and chemical defence (reviewed in Boyd 2004). Nevertheless, some plant families display a clear propensity for the production

Table 1. Plant groups containing Ni-hyperaccumulating species

Major group and family are based on Mabberley (2008). The total number of Ni-hyperaccumulating species known for family and the number of genera in a family with Ni-hyperaccumulating species are given; circumscriptions are based on Mabberley (2008). Primary literature or review papers are listed in the References^A; see also Brooks (1987, 1995, 1998), Baker and Brooks (1989), Reeves (1992, 2006), Baker *et al.* (2000) and Reeves and Baker (2000) for other lists. Species not identified to genus in the primary literature (total of ~4; Reeves *et al.* 2007) are not included in the table. Complete list is available from the corresponding author on request

Major group and family	No. of species	No. of genera	References ^A
Ferns			
Pteridaceae	1	1	13, 46
Monocots			
Commelinaceae	1	1	36
Iridaceae	1	1	46
Juncaceae	1	1	16, 52, 54
Poaceae	1	1	16
Eudicots & magnoliids			
Acanthaceae	8	5	9, 13–14, 36, 45–46
Amaranthaceae	1	1	46
Anacardiaceae	1	1	9
Argophyllaceae	2	1	18
Asteraceae	46	12	9, 13–14, 16, 30–31, 37–38, 45–47, 52, 55–56
Boraginaceae	1	1	14, 46
Brassicaceae	87	8	1, 7, 12, 15–16, 27–29, 35, 38–43, 51–54
Buxaceae	17	1	44
Campanulaceae	1	1	16
Caryophyllaceae	6	2	16, 25, 47, 52
Celastraceae	1	1	5, present study
Clusiaceae	4	1	45
Convolvulaceae	4	3	9, 34, 46
Cunoniaceae	8	2	18, 21
Dichapetalaceae	1	1	4, 17
Dipterocarpaceae	1	1	32
Euphorbiaceae	83	12	4, 6, 14, 18, 24, 36, 44, 46, 48
Fabaceae	5	5	9, 16, 34, 46, 52, 56
Lamiaceae	1	1	26
Lythraceae	1	1	46
Malvaceae	7	3	45–46, 57
Meliaceae	1	1	2, 4
Myristicaceae	1	1	57
Myrtaceae	6	2	45
Ochnaceae	3	2	2, 4, 36, 45
Oleaceae	1	1	45
Oncothecaceae	1	1	18
Orobanchaceae	1	1	14, 46
Passifloraceae	6	2	14, 46
Plantaginaceae	1	1	16, 52, 54
Ranunculaceae	1	1	16
Rubiaceae	16	6	3, 14, 19, 36, 45–46
Salicaceae	19	4	22
Sapotaceae	2	2	20, 57
Saxifragaceae	3	1	16, 52
Thymelaeaceae	1	1	36
Velloziaceae	1	1	13, 46
Verbenaceae	5	1	14, 46
Violaceae	8	3	8, 10–11, 18–19, 23, 33–34, 36, 49–50

^AReferences: Adigüzel and Reeves (2002) (1); Baker and Proctor (1988) (2); Baker *et al.* (1985) (3); Baker *et al.* (1992) (4); Batianoff *et al.* (1990) (5); Berazaín Iturralde (1981) (6); Brooks and Radford (1978) (7); Brooks and Wither (1977) (8); Brooks and Yang (1984) (9); Brooks *et al.* (1977a) (10); Brooks *et al.* (1977b) (11); Brooks *et al.* (1979) (12); Brooks *et al.* (1990) (13); Brooks *et al.* (1992) (14); Doksoopulo (1961) (15); Gabbrielli *et al.* (1987) (16); Homer *et al.* (1991) (17); Jaffré (1980) (18); Jaffré and Schmid (1974) (19); Jaffré *et al.* (1976) (20); Jaffré *et al.* (1979a) (21); Jaffré *et al.* (1979b) (22); Kelly *et al.* (1975) (23); Kersten *et al.* (1979) (24); Kruckeberg *et al.* (1993) (25); Lisanti (1952) (26); Menezes de Sequeira (1969) (27); Mengoni *et al.* (2003) (28); Minguzzi and Vergnano (1948) (29); Morrey *et al.* (1989) (30); Morrey *et al.* (1992) (31); Proctor *et al.* (1989) (32); Proctor *et al.* (1994) (33); Rajakaruna and Bohm (2002) (34); Reeves (1988) (35); Reeves (2003) (36); Reeves and Adigüzel (2004) (37); Reeves and Adigüzel (2008) (38); Reeves and Brooks (1983) (39); Reeves *et al.* (1980) (40); Reeves *et al.* (1981) (41); Reeves *et al.* (1983a) (42); Reeves *et al.* (1983b) (43); Reeves *et al.* (1996) (44); Reeves *et al.* (1999) (45); Reeves *et al.* (2007) (46); Roberts (1992) (47); Schmid (1991) (48); Severne (1974) (49); Severne and Brooks (1972) (50); Vergnano Gambi and Gabbrielli (1979) (51); Vergnano Gambi and Gabbrielli (1981) (52); Vergnano Gambi *et al.* (1979) (53); Vergnano Gambi *et al.* (1982) (54); Wild (1970) (55); Wild (1974) (56); Wither and Brooks (1977) (57).

of Ni-hyperaccumulating species (Table 1), and recent research indicates that differences in tissue Ni concentration among groups of angiosperms may be attributed, at least in part, to ancient evolutionary processes (Broadley *et al.* 2001). Little is known, however, about species-level relationships within angiosperm taxa that contain Ni hyperaccumulators, preventing inference of general patterns in evolution of Ni hyperaccumulation, including the relative contribution of recent versus ancient processes to the evolution of this trait.

The Australasian genus *Stackhousia* contains ~33 species of herbaceous annuals or perennials (Barker *in press*), 31 of which are endemic to Australia (Barker *in press*; Fig. 1, Table 2). *Stackhousia* is a member of the Stackhousioideae subfamily of Celastraceae, which also contains the Australia-endemic genera *Tripterococcus* (3 spp.) and *Macgregoria* (1 sp.; Barker 1984; Fig. 1, Table 2). Most species of *Stackhousia* are adapted to seasonally dry habitats, and occupy soils derived from a variety of rock types (Table 2). Although at least two species of

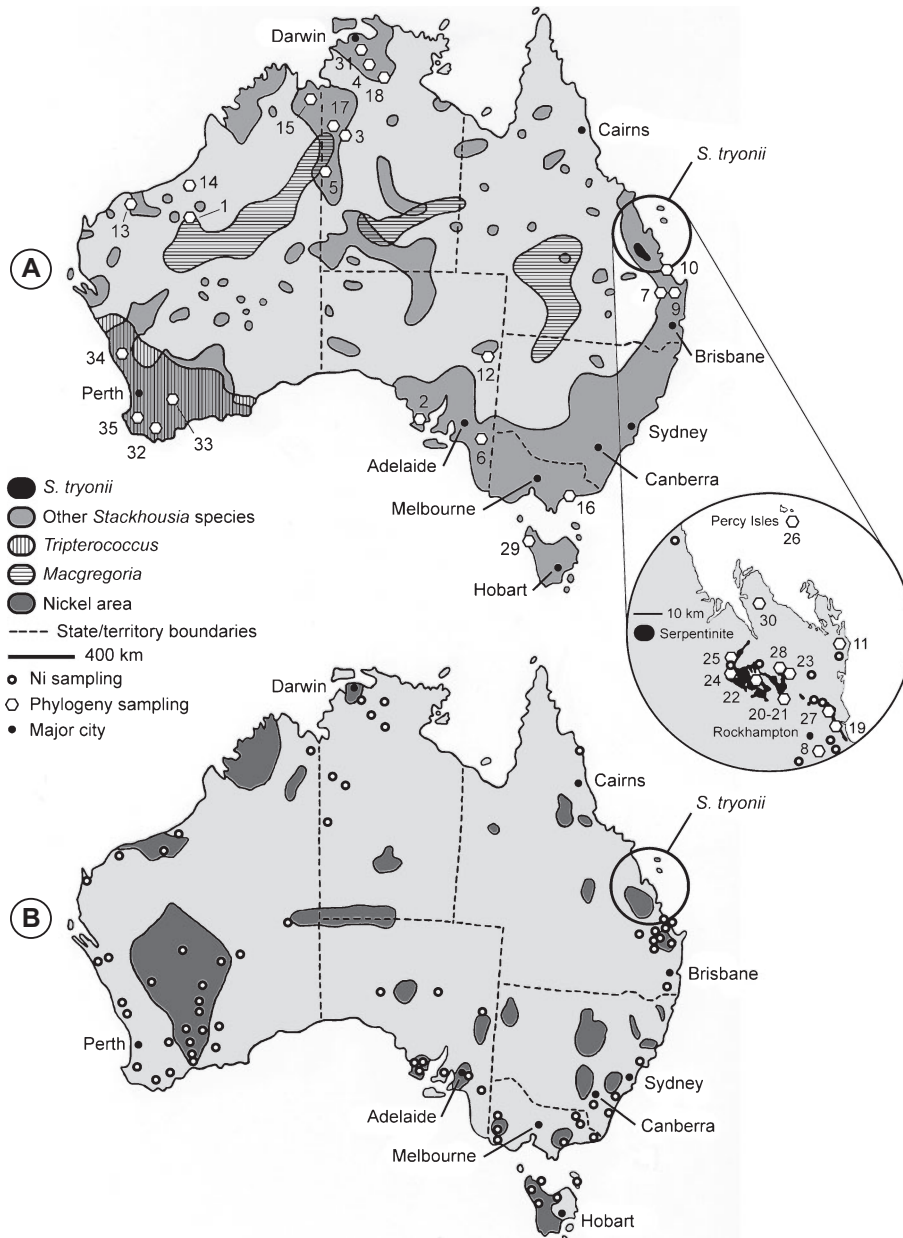


Fig. 1. Distribution of Stackhousioideae in Australia, Ni areas of Australia, and Ni and DNA sampling for the present study. (A) Distribution of Stackhousioideae in Australia; samples used for DNA sequencing and phylogenetic analysis are indicated with open, numbered hexagons (Tables 2, 3). (B) Ni areas of Australia (Ratajkoski *et al.* 2005); sampling for Ni analysis is indicated with open circles. Inset: extent of serpentinite rock outcrop in Port Curtis region of Queensland (Batianoff *et al.* 1990) and sampling of *Stackhousia* for Ni analysis and DNA sequencing.

Table 2. Taxa comprising subfamily Stackhousioideae (Celastraceae)

Taxon and section are as recognised by Barker (in press; unpubl. data). Ni, the number of populations assayed for nickel concentration in the present study (Appendix 1). DNA, the number of populations for which ITS and *trnL*-F were both sequenced in the present study (Table 3, Appendix 1). Substrate, soil type or geologic parent material on which the taxon is typically found. Taxa with standardised informal names (Barker 2005, in press): *Stackhousia* sp. 1, *S. sp. Colliculate cocci* (W.R. Barker 6025) W.R.Barker; *S. sp. 2, S. sp. McIvor River* (J.R. Clarkson 5201) Queensland Herbarium; *S. sp. 3, S. sp. Puberulent* (N.G. Walsh 4835) W.R.Barker; *S. sp. 4, S. sp. Sharply tuberculate cocci* (P.K. Latz 8376) W.R.Barker; *S. sp. 5, S. sp. West Kimberly* (W.R. Barker 6856) W.R.Barker

Taxon	Section	Ni	DNA	Distribution	Substrate
<i>Macgregoria racemigera</i>	n.a.	2	1	Central Australia	Sand
<i>Stackhousia annua</i>	<i>Racemosae</i>	1	0	S Australia	Limestone
<i>S. aspericocca</i> subsp. <i>aspericocca</i> ^B	<i>Racemosae</i>	2	1	SE Australia	Various
<i>S. aspericocca</i> subsp. <i>muelleri</i> ^B	<i>Racemosae</i>	3	0	SE Australia	Various
<i>S. cartilaginea</i> ^B	<i>Stackhousia</i>	1	0	Central Australia	Sand
<i>S. clementii</i>	<i>Stackhousia</i>	2	1	Australia	Limestone
<i>S. dielsii</i>	<i>Racemosae</i>	1	0	SW Australia	Sand
<i>S. georgei</i>	<i>Racemosae</i>	6	0	SW Australia	Various
<i>S. huegelii</i>	<i>Racemosae</i>	1	0	SW Australia	Various
<i>S. intermedia</i>	<i>Stackhousia</i>	1	1	Australasia	Various
<i>S. lasiocarpa</i> ^B	<i>Racemosae</i>	2	0	W Australia	Granite
<i>S. latzii</i> ^B	<i>Carinato-alatae</i>	1	1	Central Australia	Gypseous
<i>S. linariifolia</i>	<i>Racemosae</i>	2	1	SE Australia	Various
<i>S. macrantha</i> ^B	<i>Racemosae</i>	16	5	E Australia	Various
<i>S. megaloptera</i>	<i>Carinato-alatae</i>	3	0	Central Australia	Sand
<i>S. minima</i>	<i>Sclerococca</i>	1	0	New Zealand	Various
<i>S. monogyna</i> subsp. <i>maidenii</i> ^B	<i>Racemosae</i>	1	0	SE Australia	Various
<i>S. monogyna</i> subsp. <i>monogyna</i> ^A	<i>Racemosae</i>	4	0	SE Australia	Various
<i>S. muricata</i>	<i>Stackhousia</i>	1	1	S Australia	Various
<i>S. nematomera</i> ^B	<i>Stackhousia</i>	1	0	SW Australia	Various
<i>S. nuda</i>	<i>Stackhousia</i>	2	0	SE Australia	Various
<i>S. occidentalis</i>	<i>Stackhousia</i>	2	1	W Australia	Various
<i>S. oedipoda</i> ^B	<i>Stackhousia</i>	1	1	N Australia	Various
<i>S. pubescens</i>	<i>Racemosae</i>	2	0	SW Australia	Various
<i>S. pulvinaris</i>	<i>Sclerococca</i>	1	0	SE Australia	Various
<i>S. scoparia</i>	<i>Stackhousia</i>	2	0	SW Australia	Various
<i>Stackhousia</i> sp. 1	<i>Stackhousia</i>	1	1	W Australia	Sand
<i>Stackhousia</i> sp. 2	<i>Stackhousia</i>	1	0	E Australia	Sand
<i>Stackhousia</i> sp. 3	<i>Racemosae</i>	1	1	E Australia	Sand
<i>Stackhousia</i> sp. 4	<i>Stackhousia</i>	1	1	N Australia	Various
<i>Stackhousia</i> sp. 5	<i>Stackhousia</i>	1	1	E Australia	Various
<i>S. spatulata</i>	<i>Carinato-alatae</i>	2	0	SE Australia	Various
<i>S. tryonii</i>	<i>Racemosae</i>	15	10	E Australia	Serpentinite
<i>S. umbellata</i>	<i>Stackhousia</i>	1	0	W Australia	Limestone
<i>S. viminea</i> ^A	<i>Stackhousia</i>	8	2	SE Australia	Various
<i>S. virgata</i>	<i>Stackhousia</i>	2	1	E Australia	Various
<i>Tripterococcus brachylobus</i> ^B	n.a.	1	1	SW Australia	Various
<i>T. brunonis</i>	n.a.	3	2	SW Australia	Various
<i>T. paniculatus</i> ^B	n.a.	1	1	SW Australia	Various

^ATaxa known to occur both on and off serpentinite-derived soils. ^BNew names being formally published by Barker (in press).

Stackhousia are known to occur on serpentinite-derived soils (Batianoff *et al.* 1990; Bidwell 2000), only one, *Stackhousia tryonii*, is serpentinite-endemic. *S. tryonii* is found only on the serpentinite-derived soils of Queensland's Port Curtis District (Batianoff *et al.* 1990; Fig. 1). Previous research (Batianoff *et al.* 1990) demonstrated that *S. tryonii* is a hyperaccumulator of Ni, sequestering up to 4.1% of this element in its leaves, the third-highest concentration known for a plant (Reeves 2003). *S. tryonii* is the only member of *Stackhousia*, or the Celastraceae, known to hyperaccumulate Ni (Table 1). At least two other species of *Stackhousia* are known to occur on Ni-rich soils; however, they do not hyperaccumulate Ni (Batianoff *et al.* 1990; Bidwell 2000).

The position of *S. tryonii* as the only known Ni-hyperaccumulating member of its genus indicates that this plant represents an independent origin of the Ni-hyperaccumulation trait, making *Stackhousia* a good candidate for study of the evolution of Ni hyperaccumulation. Although past studies have dealt with the physiology of Ni hyperaccumulation in *S. tryonii* (Bhatia *et al.* 2003, 2004, 2005a, 2005b), the broader evolution of this trait in *Stackhousia* has not been considered in detail. Our study combines phylogenetic analysis of DNA sequence data with information on tissue Ni concentration in a broad sampling of Stackhousioideae to answer the following three related questions concerning the evolution Ni hyperaccumulation in this genus:

(1) do unusual concentrations of Ni accumulation occur in members of Stackhousioideae other than *S. tryonii*; (2) how many times has Ni accumulation evolved in Stackhousioideae; and (3) how does evolution of the Ni hyperaccumulating trait in *Stackhousia* compare with that in other groups of plants?

Materials and methods

Taxonomic and population sampling

DNA and Ni analysis vouchers were selected from existing herbarium collections or from plants collected for this project. Specimens were identified according to Barker (1984, *in press*).

Several taxon names used in the present paper represent new names for new taxa, or new combinations (Tables 1, 2), that are in the process of being formally described and named in a taxonomic revision of Stackhousioideae (Barker *in press*). These new names and new combinations are to be treated as manuscript names by the second author if the present work predates publication of the taxonomic paper. Five specimens included in the analysis represent further undescribed species (W. R. Barker, unpubl. data); these are treated using standardised informal names (Barker 2005; Tables 2, 3, Appendix 1). DNA from 35 plants was studied, representing 20 taxa (Tables 2, 3, Appendix 1). An additional 65 specimens, representing all 39 currently recognised Stackhousioideae (Barker *in press*; W. R. Barker, unpubl. data), were analysed for Ni concentration (Table 2, Appendix 1). To increase the probability of sampling previously unknown Ni hyperaccumulators, an effort was made to select specimens from regions thought to contain Ni-rich soils and/or outcrops of Ni-rich rock. This was accomplished by choosing specimens collected from serpentinite-derived soils (Murray 1969; Batianoff *et al.* 1990; Bidwell 2000) or from areas where Ni-rich rocks are known or likely to occur (Jaireth *et al.* 2005; Ratajkoski *et al.* 2005; Hendrickx 2009; Fig. 1).

Molecular methods

Total genomic DNA was extracted from fresh or herbarium tissue by using the DNeasy Plant Mini Kit (Qiagen, Germantown, MD, USA) according to manufacturer instructions. For a majority of herbarium specimens, DNA was extracted using embryos excised from intact seeds. We took this approach following initial herbarium work in which it was discovered that seeds from Stackhousioideae herbarium sheets yield much higher quality total DNA than the vegetative parts of the same specimens, allowing for more rapid and reliable collection of DNA-sequence data. For extractions of seed DNA, up to 10 seeds from a single plant were pooled before preparation. Polymerase chain reactions (PCR) were performed on GeneAmp (Perkin-Elmer Bioscience, Waltham, MA, USA) or Gradient Palm-Cycler (Corbett Research, Mortlake, NSW, Australia) thermocyclers. Excess primer and dNTP were removed using the enzymes exonuclease I (New England Biolabs, Ipswich, MA, USA; 0.2 units μL^{-1} PCR product) and antarctic phosphatase (New England Biolabs, 1 unit μL^{-1} PCR product), incubated for 15 min at 37°C, followed by 15 min at 80°C. PCR reactions were performed using either Qiagen *Taq* DNA polymerase or AmpliTaq Gold DNA polymerase (Perkin-Elmer Bioscience, Waltham, MA, USA). Primers ITS4 (White *et al.* 1990) and ITS5 (Blattner 1999) were used to amplify the ITS1–5.8S-ITS2

region of the nuclear rDNA. Primers 'c' and 'f' (Taberlet *et al.* 1991) were used to amplify the *trnL*-F chloroplast region, comprising the *trnL* intron and the *trnL*-F intergenic spacer. For AmpliTaq Gold, amplification was performed using an initial incubation at 95°C for 10 min and 30 cycles of three-step PCR (10 s at 95°C, 30 s at 45°C and 2 min at 72°C), followed by final extension at 72°C for 7 min. For Qiagen *Taq* DNA polymerase, both initial incubation and the first step of PCR took place at 94°C, with the former lasting 1 min. DNA sequences were determined bi-directionally on ABI PRISM 3100 Genetic Analyzers (Applied Biosystems, Foster City, CA, USA) at the Duke University Institute for Genome Science and Policy Sequencing and Genetic Analysis Facility.

Outgroup selection

Previous phylogenetic analyses (Simmons *et al.* 2001, 2008; Zhang and Simmons 2006) revealed a close relationship between Stackhousioideae and a group of Austral–Pacific Celastraceae genera. However, none of these studies unequivocally identified the sister-group to Stackhousioideae and we therefore selected outgroups from the Celastraceae genera identified as most closely related to Stackhousioideae by Simmons *et al.* (2008). Previously published sequences (Simmons *et al.* 2008) from each of the following species were used to root individual gene trees and the combined analysis: *Apatophyllum flavovirens*, *Denhamia oleaster*, *Dicarpellum pancheri*, *Hypsophila dielsiana*, *Menepetalum schlechteri* and *Psammomoya choretroides* (Table 3).

Phylogenetic analysis

DNA sequences were assembled and edited using Sequencher 4.1 (Gene Codes Corporation, Ann Arbor, MI, USA). Edited sequences were deposited in GenBank (Table 3). As noted by Simmons *et al.* (2008), the internal transcribed spacer regions (ITS1, ITS2) are very highly divergent between the members of the Stackhousioideae and their putative close relatives among the Celastraceae. To avoid problems of ambiguity inherent in aligning such highly divergent DNA sequences, we recoded ITS1 and ITS2 as missing data for the six outgroup taxa (Table 3) but retained these regions for all members of Stackhousioideae. Sequences were aligned using CLUSTAL W (Larkin *et al.* 2007) under default settings. Ambiguously aligned regions of ITS and *trnL*-F were identified and excluded from subsequent analysis (Fig. A1, available as an Accessory Publication on the *Australian Systematic Botany* website).

Maximum parsimony (MP) phylogenetic analyses were conducted using PAUP* 4.0b10 (Swofford 2000), with all characters equally weighted and unordered. Indels were treated as missing data. Heuristic searches were performed using 1000 random sequence addition replicates and tree bisection–reconnection (TBR) branch swapping. Branches were collapsed if their minimum lengths were zero ('amb-'). Non-parametric bootstrap analyses (Felsenstein 1985) were conducted using 1000 pseudoreplicates and full heuristic tree search settings, with 1000 random sequence addition replicates and TBR branch swapping.

Phylogenetic analyses under the Bayesian criterion were conducted by using the best-fit models of evolution from the

Table 3. Samples examined for genetic analysis

The numbers in the Map column correspond to numbering in Fig. 1; –, indicates an outgroup (not mapped). Taxon or population: for species represented by more than one population, populations are individually numbered for reference to molecular phylogenetic trees; see Appendix 1, for complete specimen data. GenBank accession numbers: both ITS and *trnL*-F accession numbers, respectively, are given, separated by semicolon; for outgroups, two separate *trnL*-F accession numbers are given, separated by a comma (see Materials and methods). Collection [herbarium]; state: NSW, New South Wales; NT, Northern Territory; QLD, Queensland; SA, South Australia; Tas., Tasmania; Vic., Victoria; WA, Western Australia; SN, no collection number given. Substrate, rock or soil type on which the plant was found growing; –, indicates that rock or soil type was not mentioned on the specimen, or that accession represents an outgroup. Ni, the actual or maximum (see Table 2; Appendix 1) tissue Ni concentration for the plant specimen; –, Ni concentration not analysed (outgroups)

Map	Taxon or population	GenBank accession numbers	Collection [herbarium]; state	Substrate	Ni (ppm)
1	<i>Macgregoria racemigera</i>	GU169119; GU169154	<i>RJ Chinnock 9683</i> [AD]; WA	Sand	<9
2	<i>Stackhousia aspericocca</i> subsp. <i>asp.</i> ^C	GU169099; GU169134	<i>D Hopton 235</i> [AD]; SA	–	<4
3	<i>S. clementii</i>	GU169128; GU169163	<i>WR Barker 2829</i> [AD]; NT	Limestone	<3
4	<i>S. intermedia</i>	GU169120; GU169155	<i>RM Barker 367</i> [AD]; NT	–	<6
5	<i>S. latzii</i> ^C	GU169115; GU169150	<i>PK Latz 12870</i> [AD]; NT	Gypseous	<2
6	<i>S. linariifolia</i>	GU169108; GU169143	<i>ENS Jackson 2317</i> [AD]; SA	–	<3
7	<i>S. macrantha</i> (1) ^C	GU169097; GU169132	<i>AR Bean 11956</i> [BRI]; QLD	Ironstone	<5
8	<i>S. macrantha</i> (2) ^C	GU169100; GU169135	<i>D Halford Q8806</i> [BRI]; QLD	Clay	<7
9	<i>S. macrantha</i> (3) ^C	GU169114; GU169149	<i>PI Forster 31822</i> [BRI]; QLD	–	<8
10	<i>S. macrantha</i> (4) ^C	GU169117; GU169152	<i>PR Sharpe 5346</i> [BRI]; QLD	Peat	<9
11	<i>S. macrantha</i> (5) ^C	GU169124; GU169159	<i>T Ritchie SN</i> [BRI]; QLD	Granite	<20
12	<i>S. muricata</i>	GU169123; GU169158	<i>T Hall 400</i> [AD]; SA	–	<5
13	<i>S. occidentalis</i>	GU169126; GU169161	<i>WR Barker 2118</i> [AD]; WA	Sand	<8
14	<i>S. oedipoda</i> ^C	GU169125; GU169160	<i>WR Barker 2042</i> [AD]; WA	Sand	<2
15	<i>Stackhousia</i> sp. 1 ^A	GU169129; GU169164	<i>WR Barker 6825</i> [AD]; WA	–	<5
16	<i>Stackhousia</i> sp. 3 ^A	GU169113; GU169148	<i>NG Walsh 4835</i> [AD]; VIC	Sand	<7
17	<i>Stackhousia</i> sp. 4 ^A	GU169116; GU169151	<i>PK Latz 8376</i> [AD]; NT	Sand	<5
18	<i>Stackhousia</i> sp. 5 ^A	GU169130; GU169165	<i>WR Barker 6856</i> [AD]; NT	–	<4
19	<i>S. tryonii</i> (1) ^B	GU169103; GU169138	<i>DO Burge 1014b</i> [AD]; QLD	Serpentinite	41 000
20	<i>S. tryonii</i> (2) ^B	GU169102; GU169137	<i>DO Burge 1013c</i> [AD]; QLD	Serpentinite	16 400
21	<i>S. tryonii</i> (3) ^B	GU169101; GU169136	<i>DO Burge 1013a</i> [AD]; QLD	Serpentinite	19 400
22	<i>S. tryonii</i> (4) ^B	GU169104; GU169139	<i>DO Burge 1017a</i> [AD]; QLD	Serpentinite	30 000
23	<i>S. tryonii</i> (5) ^B	GU169105; GU169140	<i>DO Burge 1018a</i> [AD]; QLD	Serpentinite	14 100
24	<i>S. tryonii</i> (6) ^B	GU169106; GU169141	<i>DO Burge 1019b</i> [AD]; QLD	Serpentinite	20 000
25	<i>S. tryonii</i> (7) ^B	GU169107; GU169142	<i>DO Burge 1020a</i> [AD]; QLD	Serpentinite	15 800
26	<i>S. tryonii</i> (8)	GU169109; GU169144	<i>GN Batianoff 11405</i> [BRI]; QLD	Serpentinite	20 000
27	<i>S. tryonii</i> (9)	GU169110; GU169145	<i>GN Batianoff 98121</i> [BRI]; QLD	Serpentinite	10 500
28	<i>S. tryonii</i> (10)	GU169112; GU169147	<i>J Elsol SN</i> [BRI]; QLD	Serpentinite	8200
29	<i>S. viminea</i> (1)	GU169096; GU169131	<i>GS Hope SN</i> [CANB]; TAS	Peat	<20
30	<i>S. viminea</i> (2)	GU169111; GU169146	<i>J Brushe 1332</i> [BRI]; QLD	–	<10
31	<i>S. virgata</i>	GU169121; GU169156	<i>RM Barker 398</i> [AD]; NT	–	<4
32	<i>Tripterococcus brachylobus</i> ^C	GU169098; GU169133	<i>AS George 15067</i> [AD]; WA	Sand	<6
33	<i>T. brunonis</i> (1)	GU169118; GU169153	<i>R Bates 4282</i> [AD]; WA	–	<3
34	<i>T. brunonis</i> (2)	GU169127; GU169162	<i>WR Barker 2256</i> [AD]; WA	Sand	<2
35	<i>T. paniculatus</i> ^C	GU169122; GU169157	<i>s.d. Hopper 4736</i> [AD]; WA	Sand	<4
–	<i>Apatophyllum flavovirens</i>	EU328714; EU328849, EU328919	See Simmons <i>et al.</i> (2008)	–	–
–	<i>Denhamia oleaster</i>	EU328724; EU328840, EU328910	See Simmons <i>et al.</i> (2008)	–	–
–	<i>Dicarpellum pancheri</i>	EU328703; AY935756, AY935756	See Simmons <i>et al.</i> (2008)	–	–
–	<i>Hypsophila dielsiana</i>	EU328704; EU328846, EU328916	See Simmons <i>et al.</i> (2008)	–	–
–	<i>Menepetalum schlechteri</i>	EU328710; EU328853, EU328923	See Simmons <i>et al.</i> (2008)	–	–
–	<i>Psammomoya choretroides</i>	EU328712; EU328852, EU328922	See Simmons <i>et al.</i> (2008)	–	–

^ATaxa with standardised informal names (Barker 2005, unpubl. data; see Table 2, Appendix 1).

^BPlants for which Ni concentration was determined by using freshly collected silica-dried material rather than tissue obtained from herbarium specimens.

^CNew names being formally published by Barker (*in press*).

AIC output of the program MrModelltest (Nylander 2004), selecting separate models for the two data partitions. Sampling of trees was performed using the program MrBayes 3 (Ronquist and Huelsenbeck 2003). Three runs of 1 000 000 MCMC generations were performed using one heated and three cold chains, sampling every 1000 generations. Independent chains were then checked for convergence (standard deviation of split frequencies nearing 0.001). Following visual inspection of

likelihood-score plots, the initial 100 000 generations of sampling (100 trees) were discarded as burnin and phylogenetic trees were reconstructed from the remaining data. Each of the three independent runs was used for tree building to verify the similarity of the results.

ITS and *trnL*-F provided nearly identical tree topologies under both Bayesian and MP criteria (for ITS, see Figs A2 and A3, and for *trnL*-F, see Figs A4 and A5, all available as

Accessory Publications on the Australian Systematic Botany website). Furthermore, the incongruence length-difference test (Farris *et al.* 1994) did not indicate a significant disagreement between the datasets ($P=0.18$). Thus, ITS and *trnL*-F data were combined for subsequent analyses. Preliminary analyses of combined data showed that *S. tryonii* and *S. macrantha* were reciprocally monophyletic, with low divergence among sampled populations within each species. To reduce computation time, only two exemplars for each of these species were included in subsequent analyses.

Methods of Ni analysis

Samples (0.03–0.4 g) of leaves, flowers, stems or fruits from herbarium specimens or silica-dried material collected in the field (Tables 2, 3) were assayed for Ni concentration. Preliminary analysis of Ni for freshly collected silica-dried tissue versus herbarium material representing the same population of *S. tryonii* (data not shown) indicated that these two methods of preservation did not strongly influence the Ni concentration. Material for analysis was selected according to availability on each specimen and sometimes consisted of more than one tissue type. This approach was chosen on the basis of previous research (Batianoff *et al.* 1990; Bhatia *et al.* 2003), which showed that all parts of the Ni-hyperaccumulator *S. tryonii* accumulate Ni at comparable concentrations. Analyses were performed by Waite Analytical Services, Adelaide University, Australia (WAS). Samples were oven-dried overnight at 80°C and digested in borosilicate tubes by using a combination of nitric acid and hydrochloric acid, with 5–6 h of heating at up to 140°C (WAS Digestion Code: HA). Concentrations of Ni, as well as 19 other elements known to occur in plant tissues, were determined by radial ICP–AES on a Ciro Vision (SPECTRO Analytical Instruments, Kleve, Germany) spectrometer. For Ni-hyperaccumulating plants, dilutions of digestion products were performed before analysis. For certain low-mass samples, Ni concentration was below the Ni detection threshold of the spectrometer. For these samples, Ni concentration is reported as a maximum based on the predicted detection threshold (reporting limit) for a sample of that mass (Table 3). Some samples contained elevated concentrations of titanium, indicating contamination by soil or processing equipment. Titanium concentration was not significantly correlated with that of any other element (two-tailed *t*-test of Pearson's product–moment correlation, $P>0.05$), indicating that soil contamination did not contribute significantly to other reported elemental concentrations.

Results

DNA sequences

The nuclear ribosomal ITS region, comprising ITS1, the 5.8S gene and ITS2, but not including bases from the 26S and 18S genes, varied in length from 593 bp (*S. sp. Sharply tuberculata coccii* (P.K. Latz 8376) W.R. Barker, Rabbit Flat Roadhouse, Northern Territory; Table 3, *S. sp.* 4) to 625 bp (*S. latzii*, Lake Mackay, Northern Territory; Table 3). The ITS alignment contained 659 characters (Fig. A1), 114 of which were excluded from analysis (see above). Of the included

characters, 223 were constant, 85 were variable but not parsimony-informative, and 237 were parsimony-informative. The chloroplast *trnL*-F region varied in length from 949 bp (*S. viminea*, Shoalwater Bay, Queensland; Table 3, *S. viminea* 2) to 989 bp (*S. aspericocca* subsp. *aspericocca*, Eyre Peninsula, South Australia; Table 3). The alignment of *trnL*-F contained 1170 characters (Fig. A1), 421 of which were excluded from analysis. Of the included characters, 555 were constant, 79 were variable but not parsimony-informative, and 115 were parsimony-informative.

Phylogeny

Bayesian and MP analyses of the combined data provided similar topologies (Figs 2, 3). Maximum parsimony analysis of the combined data resulted in four equally parsimonious trees (length = 1138, CI = 0.66, RI = 0.75). In Bayesian and MP consensus trees, *Stackhousia* and *Tripterococcus* were recovered as monophyletic, with the monotypic *Macgregoria* sister to *Stackhousia* (Figs 2, 3). Within *Stackhousia*, *S. tryonii* was recovered as monophyletic, closely related to an accession of *S. viminea* from Sundown Point, Tasmania (Fig. 1: #29; Table 3, Appendix 1) and to the Queensland-endemic *S. macrantha* (Figs 2, 3, Clade B). A second group of *Stackhousia* (Figs 2, 3, Clade A), comprising eight accessions, was also strongly supported. For the single population of *S. tryonii* for which more than one plant was included in the molecular phylogenetic analyses (Canoona Creek, Queensland; Fig. 1, #20, #21; Table 3, Appendix 1), plants grouped strongly with each other in preliminary analyses (97% bootstrap support; results not shown). These plants represent alternate colours in an apparent corolla-colour dimorphism within *S. tryonii*, with some plants blue to purple (Table 3, *S. tryonii* 3) and others white (Table 3, *S. tryonii* 2).

Nickel analyses

For most samples, tissue Ni concentration did not exceed the detection threshold (reporting limit) of the spectrometer (see Materials and methods). Within this group ($n=76$), Ni concentration did not exceed 30 ppm (Table 3, Fig. 4, Appendix 1). For samples that exceeded the detection threshold of the spectrometer, Ni concentrations for specimens of Stackhousioideae other than *S. tryonii* varied from 0.0001% (1 ppm) to 0.017% (171 ppm) Ni, with an average of 24 ppm ($n=9$; Table 3, Fig. 4, Appendix 1). Among samples of the known Ni hyperaccumulator *S. tryonii*, Ni concentrations varied from 0.25% (2500 ppm) for a plant from the Limestone Creek watershed near Mount Wheeler, Queensland (Appendix 1, D. O. Burge 1016a) to 4.1% (41 000 ppm) for a plant from Koppel Sands Road, Queensland (Fig. 1: #19, Table 3, Appendix 1). For one population of *S. tryonii* from the Canoona Creek watershed, Queensland (Fig. 1: #20 and #21, Table 3, Appendix 1), two adjacent plants were assayed for their Ni concentration. The first plant contained 16 400 ppm Ni (Table 3, *S. tryonii* 2), whereas the second contained 19 400 ppm (Table 3, *S. tryonii* 3). As described above, these plants represent alternate colours in an apparent corolla-colour dimorphism within *S. tryonii*, blue to purple (Table 3, *S. tryonii* 3) and white (Table 3, *S. tryonii* 2).

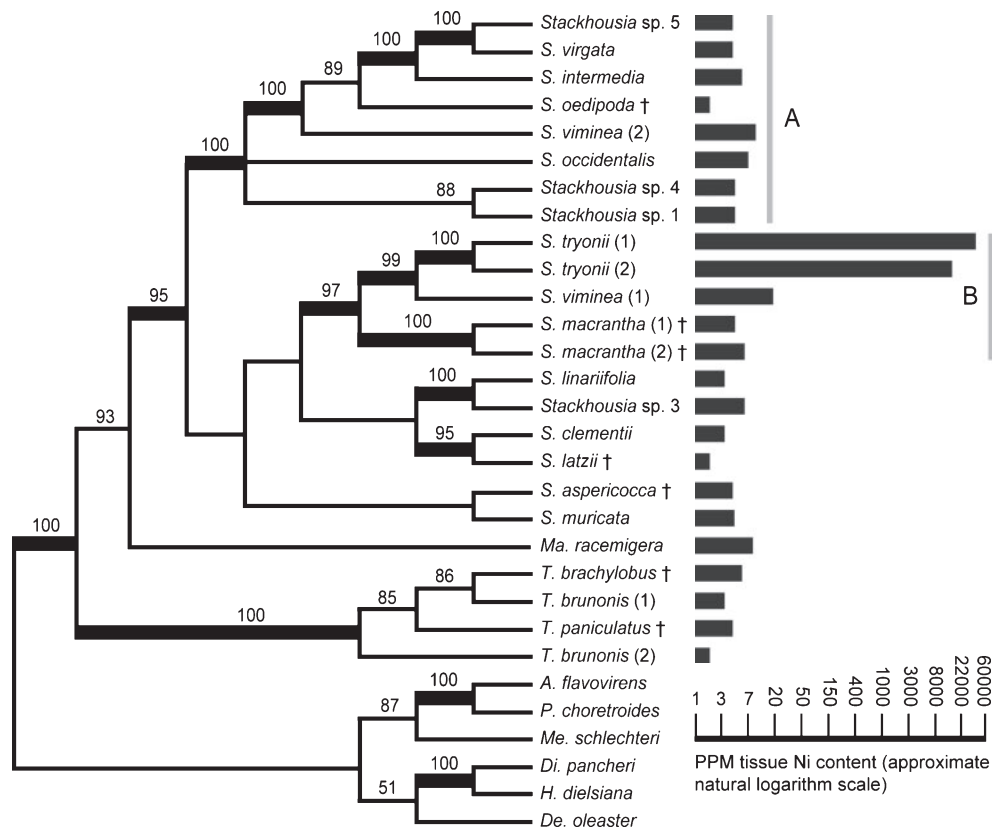


Fig. 2. Maximum parsimony consensus tree from analysis of combined ITS and *trnL*-F data, with Ni concentrations for individual plants mapped using shaded bars. Bootstrap support (BS) values for 1000 replicates of bootstrap resampling, given above branches. Heavy branches indicate BS support values >95%. Ni concentrations are mapped as natural logarithm of ppm Ni (Table 3; Appendix 1), and these are derived from the same specimens as those in DNA sequencing (Table 3). *S. aspericocca* = *S. aspericocca* subsp. *aspericocca* (Table 3). A, B: clades discussed in text. See Table 3 and Appendix 1 for data on individual populations. †, new names being formally published by Barker (*in press*).

Discussion

Phylogenetic relationships

Our results support recognition of the three genera comprising Stackhousioideae, including the monotypic genus *Macgregoria*, which is the sister taxon to *Stackhousia* (Figs 2, 3). Relationships among *Stackhousia*, *Macgregoria* and *Tripterococcus* recovered in the present study agree with previous work on molecular systematics of Celastraceae (Simmons *et al.* 2008). Although our sampling within *Stackhousia* is not exhaustive (20 of 35 taxa; Table 2), available data have revealed two major well supported clades within *Stackhousia*. The first (Figs 2, 3, Clade A) corresponds to *Stackhousia* section *Stackhousia* (Barker *in press*; Table 2). The second (Figs 2, 3, Clade B) contains *S. tryonii* and *S. macrantha*, both members of the *Racemosae* section of *Stackhousia* (Barker *in press*), and one accession of *S. viminea* (section *Stackhousia*) from western Tasmania (Fig. 1: #29, Figs 2, 3, *S. viminea* 1; Table 3). The Queensland-endemic *S. macrantha* is closely related to the widespread *S. monogyna* (Barker *in press*). *S. tryonii* and *S. monogyna* have long been considered closely related (Batianoff *et al.* 1990), if not synonymous (Barker 1984), which is consistent with the phylogenetic proximity of *S. tryonii* and *S. macrantha* seen in

the present study. However, the relationship of a single accession of *S. viminea* (section *Stackhousia*) from Tasmania (Fig. 1: #29) to this group is perplexing, because it violates morphology-based sectional limits (Barker *in press*) and represents a wide disjunction for a member of a well supported clade otherwise limited to central and southern Queensland. Both ITS and *trnL*-F were sequenced twice using the same DNA extraction obtained from this plant, to test for PCR contamination or sequence-curation mistakes. Although identical sequences were obtained during both attempts, it is possible that the unusual placement of this plant is an artefact of contamination at the level of herbarium sheet or DNA extraction. In contrast, a second accession of *S. viminea*, from the Shoalwater Bay area of Queensland, ~50 km north-east of the northernmost *S. tryonii* population (Fig. 1: #30), is nested within the clade corresponding to section *Stackhousia* (Figs 2, 3, *S. viminea* 2; Table 3), in agreement with morphology-based sectional limits (Barker *in press*).

The remaining molecular phylogenetic relationships within *Stackhousia* do not tend to agree with the morphology-based sectional limits (Barker *in press*). However, this conflict is not strongly supported because of an overall lack of phylogenetic resolution at the base of the *Stackhousia* tree (Figs 2, 3). It is

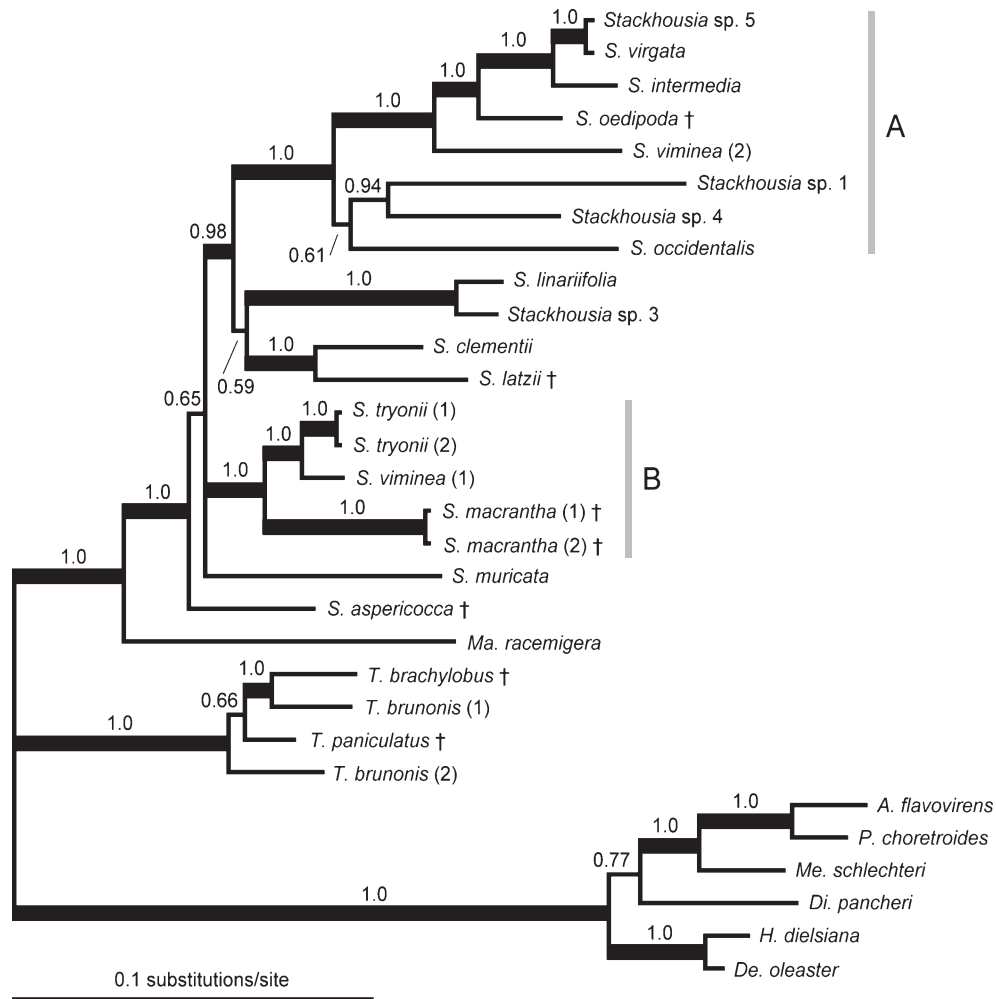


Fig. 3. Bayesian consensus phylogram from analysis of combined ITS and *trnL*-F data. Posterior probabilities (PP) are given above branches. Heavy branches indicate PP of >0.95. *S. aspericocca* = *S. aspericocca* subsp. *aspericocca* (Table 3). Clades A and B are discussed in the text. See Table 3 for data on individual populations. †, new names being formally published by Barker ([in press](#)).

interesting to note, however, that *S. clementii* (section *Stackhousia*) and *S. latzii* (section *Carinato-alatae*) are resolved as sister taxa in both MP and Bayesian analyses (Figs 2, 3). The relationship of *S. latzii* to *S. clementii* may indicate a close relationship of the small *Carinato-alatae* section (3 species; Table 2) to the much larger *Stackhousia* section. Overall, however, exhaustive comparison of molecular phylogenetic relationships with relationships implied by morphology (Barker [in press](#)) will have to await expanded sampling of DNA sequence data from additional taxa and populations.

Evolution of Ni hyperaccumulation

Our study indicates that the Ni-hyperaccumulation trait was acquired once during diversification of the Stackhousioideae, namely by *S. tryonii*. The relationship of *S. tryonii* to *S. viminea* also bears on the question of how Ni hyperaccumulation

evolved in *S. tryonii*. A specimen of *S. viminea* collected from serpentinite-derived soils near the town of Gympie in south-eastern Queensland (Appendix 1, R. L. Specht 810) contained 0.017% (171 ppm) Ni, well in excess of concentrations found in normal (non-Ni-accumulating) plants growing on soils containing ordinary amounts of Ni (Fig. 4; Batianoff *et al.* 1990). Because DNA sequence data are not yet available for this marginally Ni-accumulating plant, it is not possible, at this time, to determine whether it is related to the Ni hyperaccumulator *S. tryonii*. However, as mentioned above, one population of *S. viminea* from Sundown Point, Tasmania (Fig. 1: #29, Table 3, Appendix 1) is closely related to *S. tryonii* (Figs 2, 3, *S. viminea* 1), raising the question of whether the existence of marginal Ni accumulation in *S. viminea* may bear on the evolution of Ni hyperaccumulation by *S. tryonii*. Expanded sampling of *S. viminea* from Tasmania and eastern Australia, particularly in regions of serpentinite or other Ni-rich rock outcrop, might reveal the existence of other Ni-tolerant or Ni-accumulating plants with

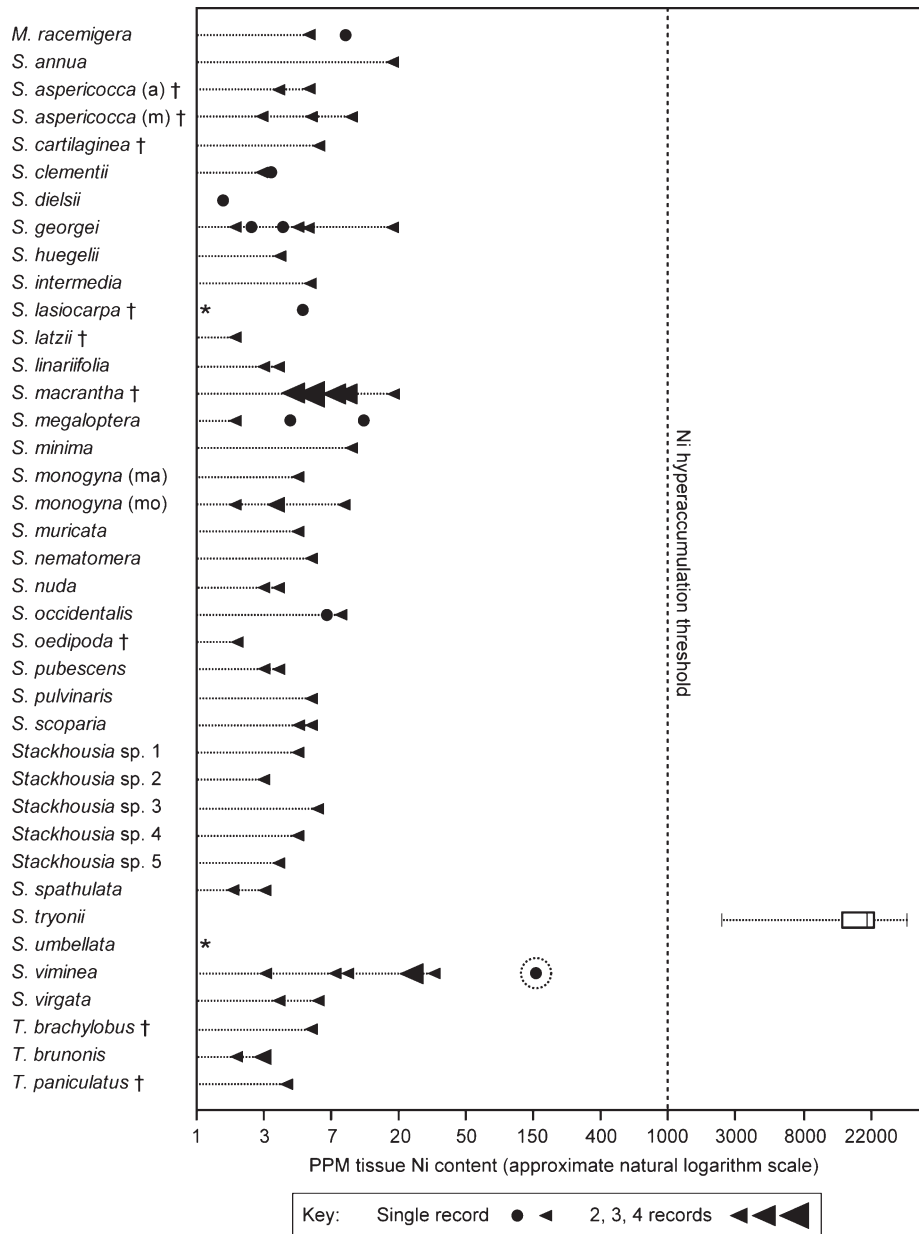


Fig. 4. Results of Ni concentration analysis for all Stackhousioideae taxa. For assays below detection threshold (reporting limit) of ICP instrument (see Materials and methods), maximum values are indicated with solid triangles at the end of dashed lines. Assays within reporting limit are indicated with dark circles or box plot. Asterisk indicates estimated Ni concentration of <1 ppm. *S. aspericocca* (a): *S. aspericocca* subsp. *aspericocca*. *S. aspericocca* (m): *S. aspericocca* subsp. *muelleri*. *S. monogyna* (ma): *S. monogyna* subsp. *madenii*. *S. monogyna* (mo): *S. monogyna* subsp. *monogyna*. †, new names being formally published by Barker (in press). Only the samples of *S. tryonii*, and a single sample of *S. viminea* (R.L. Specht 810, indicated by a dotted circle), are from known serpentinite-derived soils.

close genetic affinities to *S. tryonii*. As noted above, however, the close relationship between *S. tryonii* and *S. viminea* implied by the phylogenetic results may be an artefact of contamination, and should be interpreted with caution.

Our study is the third to report on molecular phylogenetic relationships within a group of plants containing Ni hyperaccumulators. Mengoni *et al.* (2003) reported that Ni-

hyperaccumulating members of *Alyssum* section *Odontarrhena* (Brassicaceae) were polyphyletic with respect to non-hyperaccumulating species in ITS-based gene trees, suggesting that Ni hyperaccumulation evolved early during diversification of *Alyssum* section *Odontarrhena*, with subsequent loss in several lineages. Alternatively, it is possible that the trait evolved multiple times in that group. However, the presence

of Ni hyperaccumulators in other Brassicaceae genera (Table 1; Reeves 1988; Reeves and Baker 2000) indicates that the trait may have a more ancient evolutionary origin in the Brassicaceae. In fact, in an expanded molecular phylogenetic study on European members of the Alysseae tribe of Brassicaceae, two independent origins of Ni hyperaccumulation were inferred, one in a group composed of the genera *Leptoplax* (formerly *Peltaria*; Table 1) and *Bornmuellera*, and one in *Alyssum* section *Odontarrhena* (Cecchi *et al.* 2010), in agreement with the findings of Mengoni *et al.* (2003).

Alyssum and *Stackhousia* may represent opposite extremes on a continuum regarding the evolution of Ni hyperaccumulation. In this case, *Stackhousia* would represent an early stage, with a single, isolated, presumably young Ni-hyperaccumulating species. *Alyssum* would represent an advanced condition, comprising a geographically widespread diversification of Ni-hyperaccumulating plants. Alternatively, the difference between *Alyssum* and *Stackhousia* may reflect a difference in ecological opportunity. Specifically, the Ni-hyperaccumulating trait may have developed as early in *Stackhousia* as in *Alyssum*, but resulted in far less diversification of the Ni-hyperaccumulation trait in *Stackhousia* because of the rarity of serpentinite outcrops in Australia (Murray 1969; Jaireth *et al.* 2005; Ratajkoski *et al.* 2005; Hendrickx 2009), compared with the areas of Mediterranean Europe and Turkey where Ni-hyperaccumulating *Alyssum* appear to have evolved (Brooks and Radford 1978; Brooks *et al.* 1979; Reeves *et al.* 1983a; Mengoni *et al.* 2003).

Comparison of *Alyssum* and *Stackhousia* with other angiosperm taxa containing Ni hyperaccumulators (Table 1) suggests that the evolutionary dynamics of Ni hyperaccumulation inferred for these two groups may reflect major patterns in nature. Most Ni hyperaccumulators belong to families that contain other Ni hyperaccumulators (Table 1), such as the Brassicaceae (24% of known Ni hyperaccumulators) or Euphorbiaceae (23% of known Ni hyperaccumulators). Although some genera within these families have given rise to a large number of Ni hyperaccumulators, as in *Alyssum*, the overall pattern appears to be one of polyphyly, the Ni-hyperaccumulating trait arising in multiple genera within a family. Apparent multiple origins of Ni hyperaccumulation within families, and within genera that are members of those families (Mengoni *et al.* 2003), suggests the influence of ancient evolutionary events on the present distribution of the trait, as has been suggested by Broadley *et al.* (2001). Specifically, it may be that pre-disposition for Ni hyperaccumulation evolved early during the diversification of these families, or within the diversification of vascular plants as a whole (Broadley *et al.* 2001), and that extant Ni hyperaccumulators have evolved through selection on this underlying genetic architecture, much as has been hypothesised for symbiotic nitrogen fixation in angiosperms (Soltis *et al.* 1995).

In contrast, 23 Ni-hyperaccumulating species belong to families that do not contain additional cases of the trait (Table 1), including *S. tryonii*, the only known Ni-hyperaccumulating member of the entire order Celastrales. Strong phylogenetic isolation of these Ni hyperaccumulators, which represent nearly half of the vascular plant families known to contain Ni-hyperaccumulating species, suggests that the trait

may have evolved independently in each of them. The Celastrales, for example, last shared a common ancestor with another lineage containing Ni-hyperaccumulating plants (the Malpighiales) at least 71.6 million years ago (Magallón and Castillo 2009).

The present study relied on tissue from herbarium specimens to determine whether plants were hyperaccumulating Ni. Although most of Ni-hyperaccumulating species are strictly endemic to Ni-rich soils, such as those derived from serpentinite (Brooks 1987), there are examples of hyperaccumulating species that grow both on and off Ni-rich soils (Boyd and Martens 1998). In these species, the trait is usually found to be constitutive, although populations growing off Ni-rich soils do not express the trait because of a lack of available Ni (Boyd and Martens 1998). Because some plants have the ability to hyperaccumulate Ni but not express the trait under low-Ni soil conditions, Ni measurements from field-collected plant tissues should be paired with soil-chemistry data and experimental data, or both, so as to reliably determine the Ni-hyperaccumulating ability of a plant. The results of the present study, as well as other studies based on Ni assays from field-collected tissue, should be interpreted in light of this idea. Overall, future research on evolution of Ni hyperaccumulation among plants will benefit from experiments on hyperaccumulation ecology, improved understanding of Ni physiology, comparative data on the underlying genetic architecture of the trait (Pollard *et al.* 2002), additional phylogenetic studies on specific Ni-hyperaccumulating taxa and phylogenetic reconstruction of plant–Ni relationships at the scale of vascular plant diversification.

Accessory publications (available online)

Accessory publication consists of annotated NEXUS files (in .txt format) for the combined ITS and *trnL*–*F* DNA alignment (Fig. A1), trees resulting from analyses of ITS (Figs A2, A3) and *trnL*–*F* alone (Figs A4, A5) and trees resulting from analyses of combined data (Figs A6, A7).

Acknowledgements

We thank the curatorial staff of the State Herbarium of South Australia for their assistance with handling of specimens, as well as volunteer Ronda Atkinson for help in locating study material. Andrew Lowe, Fred Gurgel, Mike Gardner, Hugh Cross, Terry Bertozzi and Dean Cunningham are thanked for assistance in organising laboratory work. We thank Teresa Fowles and Lyndon Palmer of Waite Analytical Services (University of Adelaide, Australia) for assistance with development of tissue-sampling protocols for elemental analyses, and commentary on data interpretation. Fieldwork in Queensland was facilitated by Joy Brushe and Gordon Guymer. We are also grateful to James Beck, Robin Hopkins, Darren Crayn, Amanda Grusz, Carl Rothfels, Gwendolyn Williams, Kathleen Ferris and Kevin Wright for providing constructive criticism of this manuscript and earlier writings. This research was facilitated by an NSF EAPSI fellowship (OISE-0813227) awarded to DOB. The authors dedicate this work to the memory of George N. Batianoff.

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Appendix 1. Material examined

List of material used in the study, with taxon, collector, herbarium, locality and Ni assay data. Herbarium acronyms follow Holmgren *et al.* (1990). NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas., Tasmania; Vic., Victoria; WA, Western Australia. Ni concentration is given as ppm; results below reporting limit are given as a maximum using <symbol. †, new names being formally published by Barker (in press).

Macgregoria racemigera F.Muell. – J.B. Cleland, s.n. (AD), Giles Tank, WA; Ni < 6. *M. racemigera* – R.J. Chinnock 9683 (AD), 18.7 km E of Coondiner Pool, WA; Ni < 9; *Stackhousia annua* W.R.Barker – T. Hall 181 (AD), Warrenben NP, SA; Ni < 20. *S. aspericocca* Schuch. subsp. *aspericocca* – D. Hopton 235 (AD), Wanilla Conservation Park, SA; Ni < 4; *S. aspericocca* subsp. *aspericocca* – W.R. Barker 3652 (AD), W of Dergholm on road to Penola, Vic.; Ni < 6. †*S. aspericocca* Schuch. subsp. *muelleri* (Schuch.) W.R.Barker – D.E. Albrecht 5140 (AD), Portland–Nelson road, Vic.; Ni < 6. †*S. aspericocca* subsp. *muelleri* – D.E. Symon 13395 (AD), S of Cherry Gardens, SA; Ni < 10. †*S. aspericocca* subsp. *muelleri* – W.R. Barker 1418 (AD), SSW of Casterton, Vic.; Ni < 3. †*S. cartilaginea* W.R.Barker – H.J. Eichler 20268 (AD), near Shire of Esperance, WA; Ni < 7. *S. clementii* Domin – F.J. Badman 2349 (AD), E of Andamooka Opal Field, SA; Ni < 3. *S. clementii* Domin – W.R. Barker 2829 (AD), Tanami Desert, NW of The Granites, NT; Ni < 3; *S. dielsii* Pamp. – W.R. Barker 2181 (AD), NW Coastal Highway, N of Murchison River crossing, WA; Ni 1.29. *S. georgei* Diels – A.S. George 4489 (AD), E of Laverton, WA; Ni < 20. *S. georgei* – D.E. Symon 17024 (AD), Fraser Range Station, WA; Ni < 5. *S. georgei* – H.J. Eichler 21274 (AD), near Norseman, WA; Ni 2.21. *S. georgei* – P.G. Wilson 3111 (AD), near Londonderry, WA; Ni 4.08. *S. georgei* Diels – R.V. Smith 66/525 (AD), Queen Victoria Rock, WA; Ni < 6. *S. georgei* – W.R. Barker 7235 (AD), N of Paynes Find, WA; Ni < 2. *S. huegelii* Endl. – A.E. Orchard 4254 (AD), road to Nambung NP, WA; Ni < 4. *S. intermedia* Bailey – R.M. Barker 367 (AD), Daly River Rd off Stuart Hwy, NT; Ni < 6; †*S. lasiocarpa* W.R.Barker – S. Paust 757 (PERTH), S of Ravensthorpe, WA; Ni 5.48. †*S. lasiocarpa* – W.R. Barker 2212 (AD), Kalbarri NP, WA; Ni < 1. †*S. latzii* W.R.Barker – P.K. Latz 12870 (AD), Lake Mackay, NT; Ni < 2; *S. linariifolia* A.Cunn. – C.R. Alcock 800 (AD), Hundred of Hutchison, SA; Ni < 4. *S. linariifolia* A.Cunn. – E.N.S. Jackson 2317 (AD), Billiatt NP, SA; Ni < 3; †*S. macrantha* W.R.Barker – A.R. Bean 10891 (BRI), S of Warwick, Qld; Ni < 5. †*S. macrantha* (*S. macrantha* 1; Table 3, Figs 2–4) – A.R. Bean 11956 (BRI), State Forest 43, Qld; Ni < 5; †*S. macrantha* – A.R. Bean 18310 (AD), Burnett Hwy, N of Tansey, Qld; Ni < 5. †*S. macrantha* – D. Halford Q8067 (BRI), south slope of Mt McCamley, Qld; Ni < 10. †*S. macrantha* (*S. macrantha* 2; Table 3, Figs 2–4) – D. Halford Q8806 (BRI), N of Rossmoya, Qld; Ni < 7. †*S. macrantha* – E.R. Anderson 3846 (BRI), W of Ambrose, Qld; Ni < 7. †*S. macrantha* – I.G. Champion 1246 (BRI), Cape Palmerston NP, Qld; Ni < 7. †*S. macrantha* – N. Gibson 427 (BRI), Toondoon, Qld; Ni < 10. †*S. macrantha* – N. Gibson 937 (BRI), State Forest 60, Qld; Ni < 8. †*S. macrantha* – P. Grimshaw 2569 (BRI), State Forest 210, Qld; Ni < 10. *S. macrantha* – P.I. Forster 16156 (BRI), Timber Reserve 202, Qld; Ni < 7. †*S. macrantha* (*S. macrantha* 3; Table 3, Figs 2–4) – P.I. Forster 31822 (BRI), Forest Reserve 1344, Qld; Ni < 8. †*S. macrantha* (*S. macrantha* 4; Table 3, Figs 2–4) – P.R. Sharpe 5346 (BRI), Deepwater Ck NP, Qld; Ni < 9. †*S. macrantha* – R.D. Reeves 611 (BRI), E of Jim Crow Mountain, Qld; Ni 9.32. †*S. macrantha* – T. Eisen 39 (BRI), S of Mt Hope, Qld; Ni < 8. †*S. macrantha* (*S. macrantha* 5; Table 3, Figs 2–4) – T. Ritchie, s.n. (BRI), W of Eidsvold, Qld; Ni < 20. *S. megaloptera* F.Muell. – P. Canty for NPWS 2022 (AD), SE of Immarna Siding, SA; Ni < 2. *S. megaloptera* – P.G. Wilson 8915 (AD), E of Depot Springs, WA; Ni 13.29. *S. megaloptera* – R.J. Chinnock 5117 (AD), SW of Yamarna, WA; Ni 4.41. *S. minima* Hook.f. – W.R. Barker 5796 (AD), Sphinx Ck, New Zealand; Ni < 10. †*S. monogyna* Labill. subsp. *maidenii* (Pamp.) W.R.Barker – L.A. Craven 1508 (CANB), Burrewarra Point, NSW; Ni < 5. *S. monogyna* Labill. subsp. *monogyna* – J.H. Ross 3502 (AD), Croajingalong NP, Vic.; Ni < 4. *S. monogyna* subsp. *monogyna* – W.R. Barker 1639 (AD), Brindibella Range, ACT; Ni < 4. *S. monogyna* subsp. *monogyna* – W.R. Barker 983 (AD), Holwell Gorge, Tas.; Ni < 9. *S. monogyna* subsp. *monogyna* – W.R. Barker 988 (AD), Rocky Cape, Tas.; Ni < 2. *S. muricata* Lindl. – T. Hall 400 (AD), Outalpa Station, SA; Ni < 5. †*S. nematomera* W.R.Barker – W.R. Barker 2443 (AD), Kamballup, WA; Ni < 6. *S. nuda* Lindl. – B.J. Lepschi 3981 (AD), Wyee, NSW; Ni < 4. *S. nuda* – P.R. Sharpe 5515 (BRI), Shoalwater Bay Military Reserve, Qld; Ni < 3. *S. occidentalis* Domin – A.A. Munir 5236 (AD), S of Goongarrie, WA; Ni 7.30. *S. occidentalis* – W.R. Barker 2118 (AD), NW Coastal Highway, WA; Ni < 8. †*S. oedipoda* W.R.Barker – W.R. Barker 2042 (AD), 9 km by road ESE of Gregory Range, WA; Ni < 2. *S. pubescens* A.Rich. – R.J. Chinnock 4373 (AD), Lake Magenta Rd, WA; Ni < 3. *S. pubescens* – W.R. Barker 2541 (AD), Mt Short, WA; Ni < 4. *S. pulvinaris* F.Muell. – H.J. Eichler 14686 (AD), Bogong High Plains, Vic.; Ni < 6. *S. scoparia* Benth. – A.S. George 7275 (PERTH), Mt Short, WA; Ni < 5. *S. scoparia* – G.J. Keighery 895 (PERTH), Middle Ironcap, WA; Ni < 6. *S. sp. Colliculate cocci* (W.R. Barker 6025) W.R.Barker (*Stackhousia* sp. 1; Tables 2, 3, Figs 2–4) – W.R. Barker 6825 (AD), Valentine Rockhole, WA; Ni < 5. *S. sp. McIvor River* (J.R. Clarkson 5201) Queensland Herbarium (*Stackhousia* sp. 2; Tables 2, 3, Figs 2–4) – J.R. Clarkson 7833 (AD), McIvor River near Starcke Station, Qld; Ni < 3. *S. sp. Puberulent* (N.G. Walsh 4835) W.R.Barker (*Stackhousia* sp. 3; Tables 2, 3, Figs 2–4) – N.G. Walsh 4835 (AD), Golden Beach, Vic.; Ni < 7. *S. sp. Sharply tuberculate cocci* (P.K. Latz 8376) W.R.Barker (*Stackhousia* sp. 4; Tables 2, 3, Figs 2–4) – P.K. Latz 8376 (AD), Rabbit Flat Road House, NT; Ni < 5. *S. sp. West Kimberley* (W.R. Barker 6856) W.R.Barker (*Stackhousia* sp. 5; Tables 2, 3, Figs 2–4) – W.R. Barker 6856 (AD), 10.8 km by road S of Pine Ck, NT; Ni < 4. *S. spathulata* Sieber ex Sprengel – I. Crawford 1106a (AD), Flinders I., Cameron Inlet, Tas.; Ni < 3. *S. spathulata* – N.N. Donner 11178 (AD), beach at Avoid Bay, SA; Ni < 2. *S. tryonii* Bailey (*S. tryonii* 3; Table 3, Figs 2–4) – D.O. Burge 1013a (AD), Canoona Ck watershed, Qld; Ni 19400. *S. tryonii* (*S. tryonii* 2; Table 3, Figs 2–4) – D.O. Burge 1013c (AD), Canoona Ck watershed, Qld; Ni 16400. *S. tryonii* (*S. tryonii* 1; Table 3, Figs 2–4) – D.O. Burge 1014b (AD), Ross Range, Qld; Ni 41000. *S. tryonii* – D.O. Burge 1016a (AD), Limestone Ck watershed, Qld; Ni 2500. *S. tryonii* (*S. tryonii* 4; Table 3, Figs 2–4) – D.O. Burge 1017a (AD), Oaky Ck watershed, Qld; Ni 30000. *S. tryonii* (*S. tryonii* 5; Table 3, Figs 2–4) – D.O. Burge 1018a (AD), Raspberry Ck Rd, Qld; Ni 14100. *S. tryonii* (*S. tryonii* 6;

Table 3, Figs 2–4) – *D.O. Burge 1019b* (AD), Marlborough Ck watershed, Qld; Ni 20000. *S. tryonii* (*S. tryonii* 7; Table 3, Figs 2–4) – *D.O. Burge 1020a* (AD), Pine Mountain Ck watershed, Qld; Ni 15800. *S. tryonii* – *G. Porter, s.n.* (BRI), South Percy I., Qld; Ni 21000. *S. tryonii* – *G.N. Batianoff 11394* (AD), S Percy I., Qld; Ni 35000. *S. tryonii* (*S. tryonii* 8; Table 3, Figs 2–4) – *G.N. Batianoff 11405* (BRI), near Chase Point, S Percy I., Qld; Ni 20000. *S. tryonii* – *G.N. Batianoff 91086* (BRI), Mount Slopeaway, Qld; Ni 16400. *S. tryonii* (*S. tryonii* 9; Table 3, Figs 2–4) – *G.N. Batianoff 98121* (BRI), Cawarral, Qld; Ni 10500. *S. tryonii* (*S. tryonii* 10; Table 3, Figs 2–4) – *J. Elsol, s.n.* (BRI), Kunwarara Magnesite Mine, Qld; Ni 8200. *S. tryonii* – *R.D. Reeves 645* (BRI), Princhester overpass, Qld; Ni 28000. *S. umbellata* C.Gardner & A.S.George – *R.J. Chinnock 6901* (AD), ridge W of No. 2 Oil Well, WA; Ni < 1. *S. viminea* Sm. – *A.R. Bean 13819* (BRI), Cooloola NP, Qld; Ni < 20. *S. viminea* (*S. viminea* 1; Table 3, Figs 2–4) – *G.S. Hope, s.n.* (CANB), Sundown Point, 10 km S of the Arthur River, Tas.; Ni < 20. *S. viminea* (*S. viminea* 2; Table 3, Figs 2–4) – *J. Brushe 1332* (BRI), Shoalwater Bay, Pine Mountain sector, Qld; Ni < 10. *S. viminea* – *M. Evans 2534* (CANB), Bungonia Lookdown, NSW; Ni < 9. *S. viminea* – *P.I. Forster 9252* (BRI), Biggenden–Maryborough road, Qld; Ni < 30. *S. viminea* – *R.L. Specht 810* (BRI), Upper Kandanga Ck, Qld; Ni 171.5. *S. viminea* – *W.D. Jackson 113* (HO), Corinna, Tas.; Ni < 20. *S. viminea* – *W.R. Barker 1584* (AD), Bogong Township, Vic.; Ni < 3. *S. virgata* Pamp. – *R.M. Barker 398* (AD), road to Middle Arm Jetty, NT; Ni < 4. *S. virgata* – *W.R. Barker 6874* (AD), Kakadu NP, NT; Ni < 7. †*Tripterococcus brachylobus* W.R.Barker – *A.S. George 15067* (AD), N of Crystal Springs, WA; Ni < 6. *T. brunonis* Endl. – *L. Haegi 977* (AD), Lake Johnston, WA; Ni < 3. *T. brunonis* (*T. brunonis* 1; Table 3, Figs 2–4) – *R. Bates 4282* (AD), 20 km N of Hyden, WA; Ni < 3. *T. brunonis* (*T. brunonis* 2; Table 3, Figs 2–4) – *W.R. Barker 2256* (AD), Brand Hwy to Dongara, WA; Ni < 2. †*T. paniculatus* W.R.Barker – *s.d. Hopper 4736* (AD), Ludlow Hithergreen Rd, WA; Ni < 4.