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Final Report

What is at risk? Identifying rainforest refugia and hotspots of plant genetic diversity in the Wet Tropics bio-region



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Sandra Abell-Davis, Daniel J. Metcalfe, Maurizio Rossetto,
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Australian Government
Department of the Environment

 **Reef &
Rainforest**
RESEARCH CENTRE

What is at risk? Identifying rainforest refugia and hotspots of plant genetic diversity in the Wet Tropics bio-region

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Acronyms and Abbreviations Used In This Report

AGRF	Australian Genome Research Facility
AICc	Akaike information criterion
ALA	Atlas of Living Australia
alt	altitude
AM	Arbuscular mycorrhizal fungi
approx.	Approximately
ATH	Australian Tropical Herbarium
BF	Mt. Bartle Frere
BK	Mt. Bellenden Ker
c.	approximately
CIPRES	Cyberinfrastructure for Phylogenetic Research
CSIRO	Commonwealth Scientific and Industrial Research Organisation
CU	Carbine Uplands
dbh	diameter at breast height
DNA	deoxyribonucleic acid
DRO	Daintree Rainforest Observatory
GR	genus richness
ha	hectare
HR	Herberton Range
iBOL	International Barcode of Life
IPCC	Intergovernmental Panel on Climate Change
ITS	internal transcribed spacer
IUCN	International Union for Conservation of Nature
km	kilometre
m	metre
Ma	million years ago
masl	metres above sea level
matK	maturase K gene
MAXENT	maximum entropy modeling program
NERP	National Environment Research Program
no.	number
NSW	New South Wales
P	Pleistocene
p	proportion
Pal	Palaeocene
PCNM	principle coordinates neighbour matrices
PD	phylogenetic diversity
Pli	Pliocene
rbcl	RuBisCO large subunit gene
TP	Thornton Peak
trnH-psbA	<i>trnH-psbA</i> intergenic spacer region
ycf1	yeast cadmium factor gene

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Introduction

Australia's tropical rainforest in far north Queensland (Figure 1) is internationally renowned for preserving one of the most complete and continuous records of earth's evolutionary history, and harbours much of the remaining Gondwanan flora that was once widespread across the continent. Little is known however, about the spatial distribution of this evolutionary history within the region, particularly for plants and fungi. A general and well-supported assumption in the literature to date has been that the upland flora of the region is primarily Gondwanan. This would suggest that if current climate change projections are accurate in predicting an upward elevational shift in distribution for many species as global temperatures increase then Australia's ancient Gondwanan relict flora is at risk. This study addresses this concern by first asking the question - Where are the hotspots of evolutionary history for plants in the Wet Tropics bioregion? Are they restricted to the uplands? Or are there other environmental or historical factors that can explain their distribution? We assessed this question by using phylogenetic diversity (PD), which measures evolutionary distinctiveness, as a broad scale measure of genetic diversity across the NE Qld rainforests. We then take an in depth look into the historical patterns that have shaped the extant plant biodiversity patterns in the region and test for independent lines of evidence for the general picture identified from the PD analysis. Lastly we focus specifically on the mountaintop flora and provide a threat assessment for the endemic plants that are restricted to northeast Queensland's mountaintop environments and conducted systematic fungal inventories to characterise the poorly documented mountaintop fungal flora.



Figure 1: The Wet Tropics bioregion and the current extent of rainforest and vine thickets (black)

This report is divided into two parts each with nested subprojects. Part I (rainforest biodiversity hotspots) reports on a region-wide analysis of patterns of genetic diversity across the NE Qld rainforests which provides a broad picture of their evolutionary history. It is followed by three case studies with a finer focus that provide additional support for this broad picture and give further depth to our understanding of historical and evolutionary processes in the region. Part II (mountaintop biodiversity) reports on a focussed study of the biodiversity and threats posed to one ecosystem in the Wet Tropics – the mountaintop rainforest – thought to be one of the Australian environments most threatened by climate change (Williams et al., 2012).

Part I: Rainforest biodiversity and history

Identifying hotspots of evolutionary history

Measures of biological diversity underpin priority setting of areas for conservation by Federal and State government agencies in Australia. The most commonly used measure is taxonomic richness (the number of species per unit area). Phylogenetic diversity is believed to be an inherently superior measure because it accounts for evolutionary 'distinctiveness' but its intractability, due to the paucity of available phylogenetic information for most taxa, means taxonomic richness is frequently used as its proxy. However, there is considerable debate over whether taxonomic richness is a good proxy. This study investigated the relative performance of taxonomic richness and phylogenetic diversity measures for conservation priority setting in the Wet Tropics rainforest context. We used the results to identify and map areas of high biodiversity significance and investigated correlations with environmental and ecological variables. A summarised version of this work is included here. For a complete description of the background, methods, and results of this study see Costion et al. (2014).

Key Objectives

- 1.) Identify hotspots of evolutionary history (PD) in NE Queensland rainforest floras and explore correlations between these and taxonomic richness and endemism.
- 2.) Test the performance of PD relative to taxonomic richness and endemism measures for estimating biodiversity and make recommendations as to the most efficient method to use for conservation priority-setting
- 3.) Relate patterns of PD to environmental variables to infer evolutionary and ecological drivers

Deepening the story – additional lines of evidence

After identifying the primary factors which best explain the overall patterns of phylogenetic diversity in the Queensland Wet Tropics (taxonomic richness, richness of Sahul-derived or "Gondwanan" taxa, and the co-occurrence of postulated rainforest refugia) we then further explored this hypothesis of the evolution of Australia's north eastern tropical rainforest through three sub-projects:

- 1.) An assessment of the contribution of northern hemisphere plant lineages to the assembly of the WT flora (Dispersal to Australia: the Sahul-Sunda floristic exchange);
- 2.) An assessment of the genetic diversity within WT species (Immigrant lineages: evidence from genetic diversity within species); and
- 3.) An assessment of the origins of the Australian species of one pan-tropical genus (Evolutionary origins of the Australian *Bulbophyllum* (Orchidaceae))

1. Dispersal to Australia: the Sahul-Sunda floristic exchange

The incursion of Asian plant lineages into the Wet Tropics bioregion is believed to have played a role in the evolution of diversity of Australia's tropical rainforests however, no studies to date have documented in detail the timing of this important chapter of Australia's evolutionary history. This section summarises a meta-analysis of molecular chronograms that characterize for the first time the Sahul-Sunda floristic exchange (rate and polarity) and interpret it within the context of Earth history and the ecology of the region. A summarized version of this study is included here. For a complete description of the background, methods, and results of this study see Crayn et al. (2014). This study investigated the dynamics of the exchange of plant lineages

between the Sahul and Sunda shelves through time, specifically through the following questions.

- 1.) When did the exchange begin and was it constant through time?
- 2.) Was there a directional bias in the exchange?
- 3.) What is the relationship between exchange dynamics and possible causal factors, such as Earth history (changing configurations of land and sea) and dispersal mechanism?

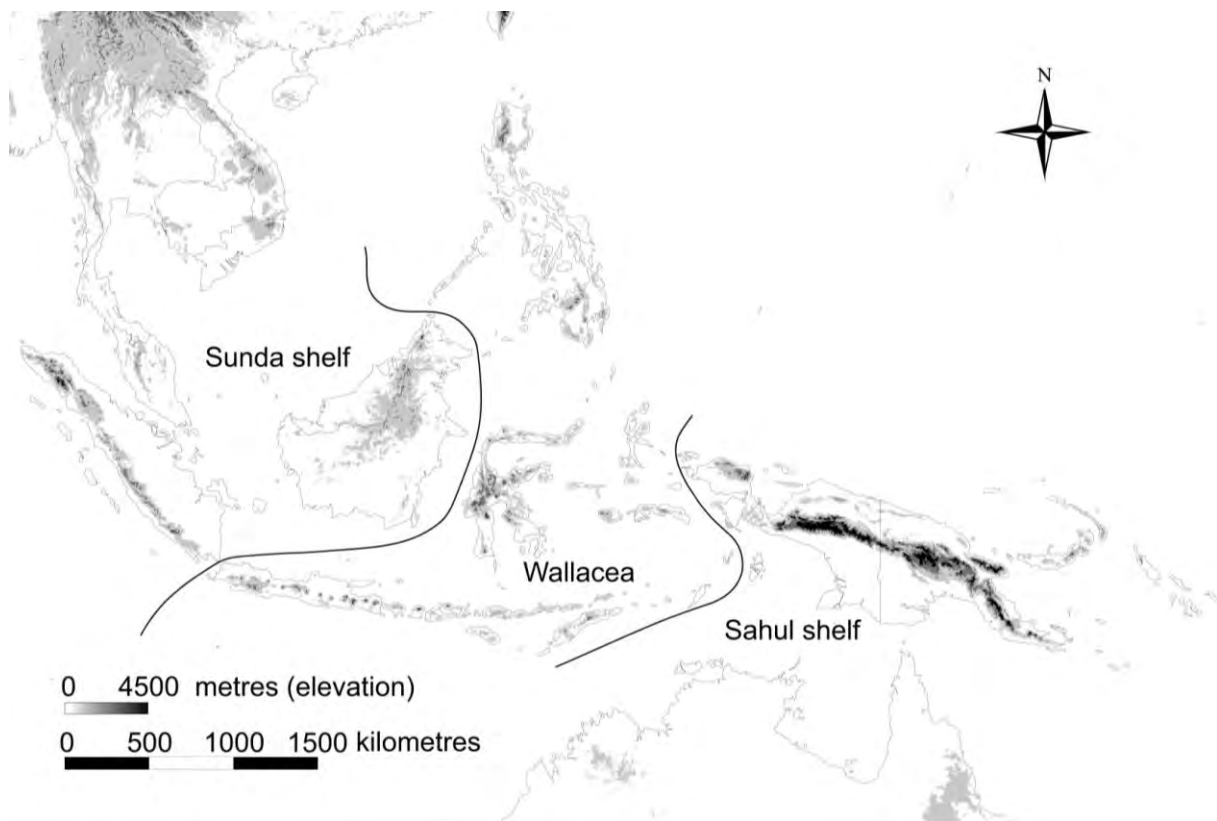


Figure 2: The Southeast Asian region showing the approximate positions of the margins of the Sahul and Sunda shelves, which define the three biogeographical areas used to study Cenozoic intercontinental dispersal dynamics: Sahul, Sunda and Wallacea (From Crayn et al. 2014).

2. Immigrant lineages: evidence from genetic diversity within species

If the extant plant species that comprise the current rainforests of the Queensland Wet Tropics are an admixture of ancient Sahul shelf derived (Gondwanan) species and Sunda shelf derived (Asian) species than one might expect that the more recently arrived species should have less genetic variation whereas the Sahul species having evolved over millennia in their current location should be more genetically diverse. Island biogeography theory (MacArthur and Wilson, 1967) predicts that during a colonizing event, a species goes through a bottleneck, where only a portion of the genetic variation represented by that species establishes in the new geographic location. This subset of genetic variation of the colonizing species then slowly evolves through time into a species or lineage of species divergent from its ancestor. We tested for evidence of this biological process by investigating the variation within species using DNA barcodes for 500 plant species of tropical north Queensland. We specifically investigated whether there were correlations between the degree of genetic variation within species and their origin from the

Sunda or Sahul shelf. In addition we further tested for correlations between floristic origin and life history traits of plant species. Are there common life history traits shared by established immigrant species from the Sunda shelf or similarly by Sahul derived species?

3. Evolutionary origins of Australian *Bulbophyllum* (Orchidaceae)

The genus *Bulbophyllum* Thouars with over 2,000 species is the largest genus in the orchid family (Orchidaceae) and one of the largest genera of flowering plants worldwide. A total of 33 species of *Bulbophyllum* orchids occur in Australia, which are distributed across mountaintops and upland regions of the east coast mesic zone. The highest diversity is found on mountaintops of the Wet tropics bioregion where 23 species (69% of Australian species) occur. Of these, 14 (60%) are endemic to the bioregion based on current taxonomic knowledge. However, little is known of the evolutionary origins of these mountaintop species. While previous work has identified divergent Madagascan (Fischer *et al.*, 2007) and Neotropical (Smidt *et al.*, 2011) lineages, little is known of the evolutionary relationships among Asian and Australasian taxa occurring across the Sunda and Sahul regions. Are the Australian species of *Bulbophyllum* ancient descendants derived from Sahul? Are they immigrants from the Sunda shelf? Or is there another explanation for their origin that does not fit into the general Sahul-Sunda floristic exchange model outlined in previous sections? A phylogenetic analysis of Australia's *Bulbophyllum* orchids based on molecular data was undertaken to shed light on these questions and improve our understanding of the evolutionary origins of these mountaintop species. In addition to addressing these broader intellectual questions this project aimed to improve practical knowledge of this genus in Australia. The appropriate taxonomic treatment of groups such as the putative new genus '*Spilorchis*' (represented here by a single species, *Bulbophyllum weinthalii*) is yet to be confirmed. Further more, species limits within several assemblages of closely related species which co-occur across mountaintops throughout the Wet Tropics bioregion have remained unclear to date hindering accurate taxonomic classification, biodiversity estimates, and effective conservation management. This sub-project aimed to address these knowledge gaps by delimiting the Australian species of this genus using the most up to date phylogenetic methods.

Part II: Mountaintop biodiversity and threat assessment

The mountains of the Wet Tropics and Cape York Peninsula represent cool islands in a sea of warmer (lowland) climates and harbour a very rich biota with high levels of endemism. The plants and fungi of these mountains are especially vulnerable to global warming as upward species' range shifts leave them nowhere to go. Studies on genetic diversity in mountain fauna have provided the underpinnings of informed management strategies for these groups. But almost nothing is known about the within-species diversity (e.g. genetic diversity) of the co-occurring plants and fungi and findings from faunal studies cannot be extrapolated because long-lived and immobile plants will likely respond to environmental change very differently. Furthermore, for fungi, which are critically important for ecosystem function, we lack the most basic knowledge of which species occur in these threatened landscapes. We aimed to address these major knowledge gaps by: 1) determining the location and relative importance of high altitude refugia for plants in the Wet Tropics Bioregion and 2) documenting the fungal biodiversity of the mountaintops. This baseline data will help determine exactly what is at risk, predict likely responses of the flora to future climate change, and support evidence-based conservation and management decision-making for these tropical mountain ecosystems.

Key Objectives

- 1.) Identify the location of high altitude refugia and their relative importance by assessing diversity and threat to mountain endemic plant species across their known range
- 2.) Systematically survey the mountaintop fungal flora and catalogue their taxonomic richness
- 3.) Discover and describe new taxa of mountaintop fungi and plants

Methodology

Part I: Rainforest biodiversity and history

Identifying hotspots of evolutionary history

We utilized presence/absence of genera, elevation, and GPS location data from the CSIRO plot network of 238, 0.1 hectare plots spanning the Wet Tropics bioregion (Graham 2006). A DNA sequence was then generated from leaf tissue for one species per genus present in the plot network (Appendix 3). The plastid locus *rbcLa* was chosen due to its universal amplification success across angiosperm orders. A total of 585 new *rbcLa* sequences were generated and deposited in GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>). Sequences for a small percentage of genera (73) were obtained from the existing GenBank database. This dataset was used as the base alignment for the phylogenetic tree from which phylogenetic diversity (PD) values were derived. Multiple phylogenetic trees were constructed from this database and the PD values from each of the final trees were strongly correlated against each other suggesting that the results were independent of the phylogenetic method used to generate the tree and subsequent calculation of PD. We then selected one tree and used Biodiverse (Laffan *et al.*, 2010) to calculate PD and the data from the 0.1 hectare plots was then amalgamated into grid cells to identify richness of PD across the bioregion.

We examined the relationship between genus richness (GR) and PD by first plotting GR against PD per taxonomic unit then performed linear regression at four spatial scales (0.1 Ha, 0.0625°, 0.125°, and 0.25°). We then accounted for affects of spatial autocorrelation using spatial eigenvector mapping through generated through Principal Coordinates Neighbour Matrices (PCNM) (Diniz-Filho & Bini, 2005). To visualise the geographic distribution of any remaining components of PD that could not be described by either GR or spatial autocorrelation, we mapped the residuals from the best out of several competing regression models (selected based on lowest AICc score). This map enabled a visual assessment of any geographic patterns evident in the distribution of PD that could be attributed to the analysed environmental and historical variables.

Explaining the patterns of PD – historical factors

After mapping the residuals and identifying a clear geographic pattern an explanation for this pattern was required. To test whether this pattern could be attributed to patterns of historical biogeography, more specifically the incursion of plant lineages into Australia from Asia, a published dataset of that assigned a biogeographic origin to all the Wet Tropics plant genera (Richardson *et al.*, 2012) was utilised. Percent of each floristic element per plot was then calculated. We then added two predictor variables (altitude (alt)) and the proportion of species within each plot that were determined to be from Sahul lineages (p(Sahul)) in another round of model fitting based on AICc scores. We then used Spearman's rank correlation test comparing the percent Sahul genera per plot, p(Sahul), and the rainforest stability index modeled for the Wet Tropics bioregion during the Quaternary to one hectare resolution (Hilbert *et al.*, 2007) to test for a direct correlation between the percent Sahul (Gondwanan) species per site and the persistence of rainforest during glacial maxima (rainforest refugia).

Deepening the story: Additional lines of evidence

The Sahul-Sunda floristic exchange

We designed an analysis to independently test the validity of the historical pattern identified by our PD results. To do this we started by defining three biogeographical areas: Sunda, Sahul and Wallacea (Figure 2) and compiled a database of dated molecular phylogenies that were a) published and b) from plant lineages that contained nodes showing a geographical disjunction between Sunda and Sahul. These were obtained via a comprehensive literature review. For each disjunct node we determined the direction of the biogeographical transition resulting from dispersal/migration events between Sahul and Sunda, and their age. The ages of each disjunct node were determined directly from the published chronograms. All of the studies included used fossils to calibrate molecular evolutionary rates (either directly or secondarily) and included estimates of their uncertainty.

To determine the approximate timing of this historical event we plotted the number of disjunctions against the approximate minimum overwater distance between the currently emergent landmarks on Sahul and Sunda since 40 Ma. This distance was determined using measurements on scaled graphical depictions of plate tectonic reconstructions of the region (Hall, 2002). Finally, we investigated the relationship between dispersal mode (zoochory or non-zoochory) and dispersal success between the Sahul and Sunda shelves by reconstructing the dispersal mode for each disjunct node under Fitch parsimony in Mesquite (Maddison & Maddison, 2011).

Immigrant lineages: Evidence from genetic diversity within species

We utilised data from a current International Barcode of Life (iBOL) project containing DNA barcode data from the three plastid loci *rbcl*, *matK*, and *trnH-psbA* for 500 species spanning tropical Queensland, each with multiple DNA samples collected per species from geographically distant localities within their range. Some of these species showed infraspecific variation between samples collected at geographically distant localities in north Queensland. For these species we measured total genetic variation by counting total nucleotide base pair mutations per species and then tested whether there was a significant difference in average infraspecific variation per species for Sahul derived and Sunda derived species. We tested for correlations between the variable species and life history trait data across all species. We then partitioned the data into Sunda and Sahul species and re-tested for correlations between the life history traits and the species with infraspecific variation from different biogeographic origins (Sunda and Sahul). Specifically we tested for correlations between the Sunda derived plants and fruit size, fruit length, leaf size, and tree height.

Origins of the Australian *Bulbophyllum* (Orchidaceae) species

Genetic barcodes were collected for two gene regions (nuclear ITS, plastid *ycf1*) from all Australian *Bulbophyllum* orchids with an additional gene region (plastid *matK*) collected for section *Adelopetalum* and the putative new genus '*Spilorchis*', thought to be closely related to the *Adelopetalum* group. A data set of 149 genetic barcodes for 33 species was obtained. To infer evolutionary origins of Australian *Bulbophyllum* species, a phylogenetic analysis was conducted on ITS sequences generated for Australian species in addition to 277 sequences obtained from GenBank from *Bulbophyllum* species occurring across their pan-tropical distribution. A phylogenetic tree was reconstructed based on the ITS sequence data using a Maximum Likelihood approach as implemented in the software RAxML (Stamatakis, 2014) was produced through the CIPRES science gateway (Miller et al., 2010). To infer relationships among closely related species within section *Adelopetalum* and the relationship with '*Spilorchis*', a

Bayesian analysis of a three loci concatenated alignment (ITS, *ycf1*, *matK*) was conducted using MrBayes 3.2 (Ronquist *et al.*, 2012).

Part II: Mountaintop biodiversity and threat assessment

Mountaintop refugia and threat assessment

For this study we identified plant species that are endemic to the Wet Tropics bioregion and which are restricted to areas 1000 metres above sea level (masl). We identified a total of 32 Queensland Wet Tropics mountaintop species by querying all known herbarium records in the bioregion above 1,000 metres. Several of these species were excluded from our modelling analysis due to lack of sufficient occurrence data leaving a total of 19 species of mountaintop endemic woody trees and shrubs for analysis.

Niche modelling was used to infer distributions of suitable climates for each species (based on current, observed species distributions), under current and future climates scenarios using MAXENT ver. 3.3.3 (Phillips *et al.*, 2006). We used suitable climate as a surrogate for habitat suitability to be consistent with the IUCN Red List terminology. To assess the impact of predicted climate change the distribution of suitable climate was modelled for the years 2040, 2060 and 2080. Climatic conditions were simulated by CSIRO's Mk3.5 climate model (Gordon *et al.*, 2010) using three future CO₂ emission scenarios, A1B, A2, B1 (IPCC special report, 2000).

Total suitable habitat was calculated in hectares for each species under each emission scenario and year, and then re-calculated for each species using only data within each species current range based on herbarium records. We then calculated "percent declines" in suitable habitat for each species and emission scenario where 99% decline equals a reduction in extent to 0.01 of current. We then assessed the threatened status of each species using the IUCN Red List Criterion (IUCN, 2001) A3(c), where a population decline can be inferred over 10 years or three generations (whichever is longer).

Fungal inventory

Four 0.5 Ha (100 m x 50 m) plots were chosen from the CSIRO plot network (Graham 2006) in which to conduct seasonal systematic surveys of macro-fungi biodiversity. The individual plots were chosen for their altitude, forest type and access (road) (Figure 4):

1. Oliver Creek (c. 20 masl (included as lowland comparison (warm/wet climate)), complex mesophyll vine forest, type 1a (floristic variant) very wet lowland, 16° 08' S 145° 26' E
2. Mt Lewis (1100 m elevation), simple microphyll vine-fern forest, type 9 cloudy wet highland, 16° 31' S 145° 16' E
3. Mt Baldy (1100 masl), simple microphyll vine-fern forest, type 9 cloudy wet highland, 17° 19' S 145° 26' E
4. Mt Haig (1100 masl, simple microphyll vine-fern forest, Type 9 cloudy wet highland, 17° 05' S 145° 35' E.

Each CSIRO plot is divided into sixteen sub-plots, labelled A through to P (Figure 5) and arranged in a four by four layout, distinguishable by plot designation marked on the trees in each sub-plot. All trees in each sub-plot with a diameter at breast height (DBH) ≥ 10 cm have been previously identified and the DBH recorded by CSIRO staff.

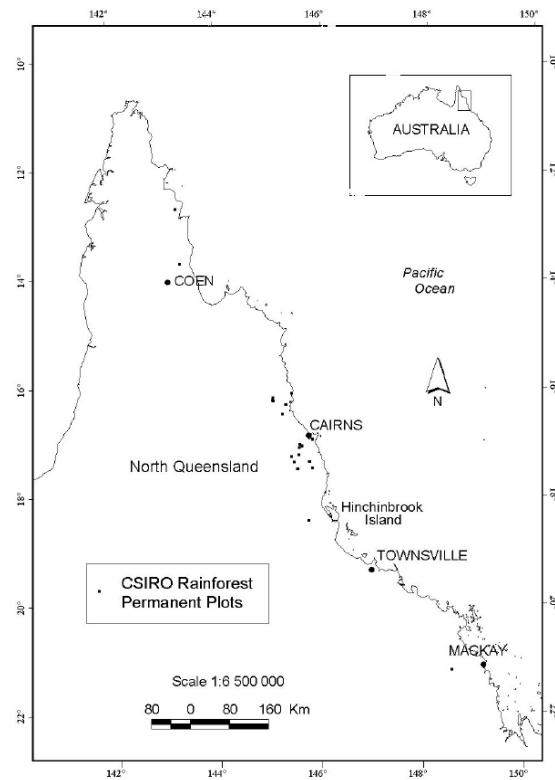


Figure 3: CSIRO permanent plot system. From Graham (2006).

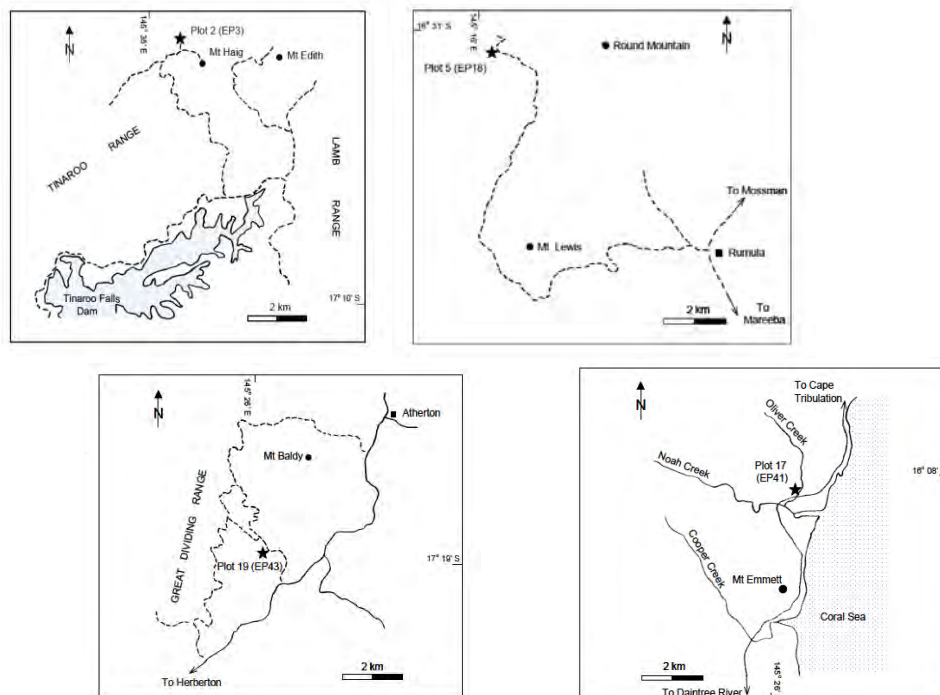


Figure 4: CSIRO Permanent Plots chosen for fungi survey. L to R: Mt Haig, Mt Lewis, Mt Baldy, Oliver Creek (from Graham, 2006).

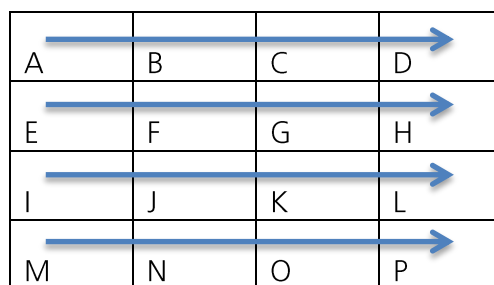


Figure 5: Transects through sub-plots of CSIRO plots.



Figure 6: Surveying for macro-fungi along transect (Photo: Ms Arianna Proia.)

From July 2012-March 2014, three dry season and four wet season surveys of macro-fungi were conducted in four plots (as above). Four, 100 m², transects were surveyed at each plot, one transect through each of four adjacent sub-plots (Figure 5) (Figure 6). In March 2014, a further lowland survey at the Daintree Rainforest Observatory (DRO) was conducted due to the inaccessibility of mountaintop sites.

Surveys were conducted as close to rainfall events as possible. Macro-fungi with pilei or fruiting bodies of less than 10 mm in diameter were excluded. Collections were processed and dried and determinations made to genus.

Results and Discussion

Part I: Rainforest biodiversity and history

Identifying hotspots of evolutionary history

Plant Phylogenetic Diversity (PD) in the Wet Tropics is concentrated in two primary areas (Figure 7, blue): the southern Cairns-Cardwell lowlands (hotspot 1) and the Daintree region (hotspot 2). Moderately high PD values are found in the Paluma range, and the northern edge of the Black Mountain Corridor. Low PD is observed between the two hotspots, and north and south of them (Figure 1, yellow). Hotspots of genus richness (GR) however are nearly identical (Figure 8) thus mapping PD alone merely shows the same result as mapping taxonomic (genus) richness. We then investigated if there were hidden patterns masked by GR through a series of model tests and regression analyses.

After the effects of GR and spatial autocorrelation were accounted for, a total of 12.5% observed variation in PD from our point data (0.1 Ha) remained unexplained. We mapped this 12.5% variation (PD residuals) and three spatial patterns were revealed:

- Areas with high PD but lower PD than expected based on GR (negative residuals), notably the Daintree region (hotspot 2);
- Areas with low PD but higher PD than expected (positive residuals), notably the Black Mountain Corridor and areas north and south of PD hotspots 1 and 2;
- Areas with high PD but higher than expected (positive residuals) notably the Cairns-Cardwell lowlands (hotspot 1) and the Paluma range.

Location	PD	Floristic affinity	Rainforest history
Daintree (PD hotspot 1)	High	Sahul	Refugium
Cairns-Cardwell (PD hotspot 2)	High	Sunda	Unstable area
Atherton-Bellenden Ker uplands	Low	Sahul	Refugium

Table 1: List of phylogenetic diversity (PD), Sunda/Sahul lineage hotspots, and major rainforest refugia

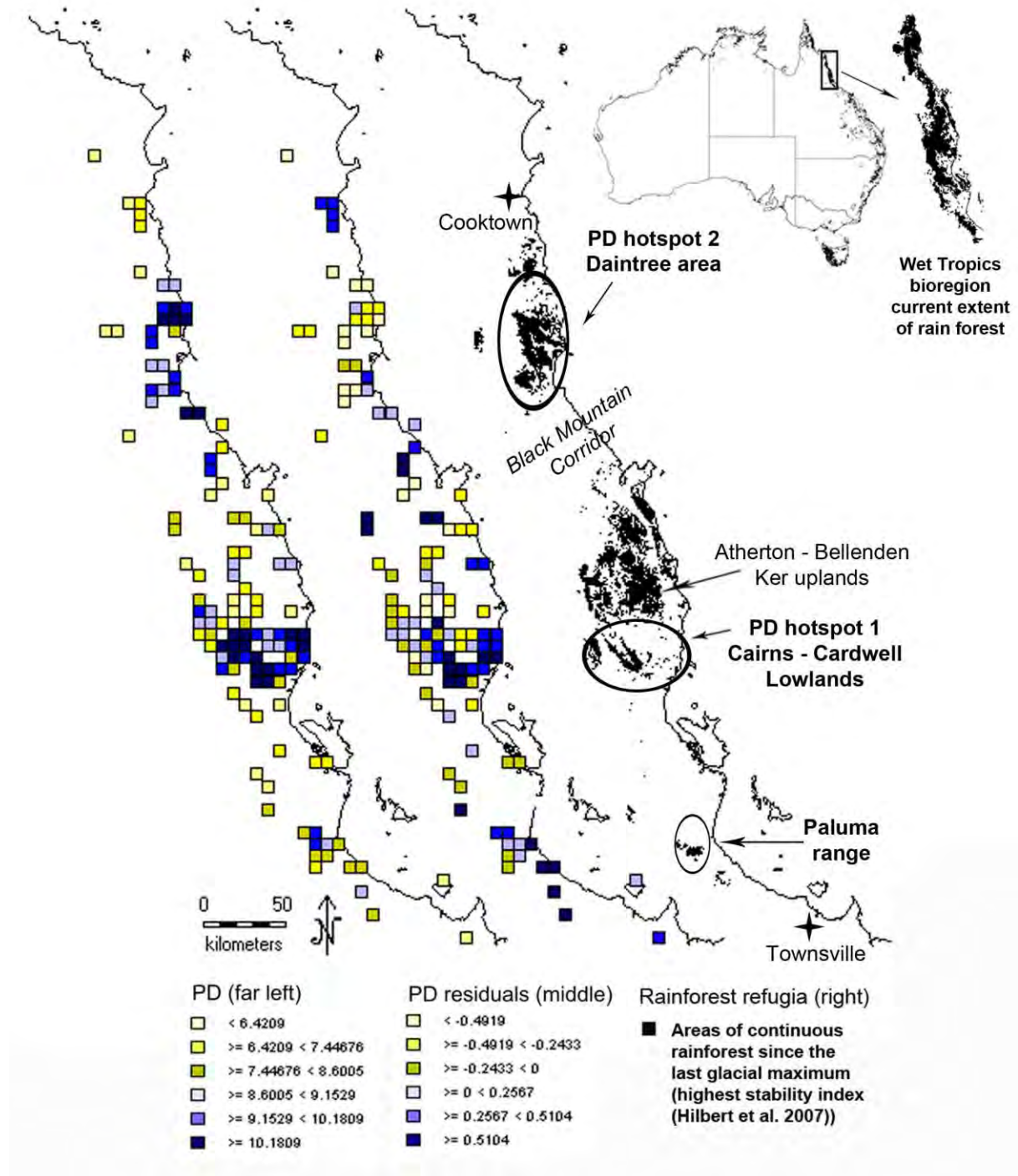


Figure 7: Phylogenetic diversity (PD) (left) and residuals of PD (middle) indicated by color-coded scale bar at 0.0625° grid cell resolution. Shaded areas (right) have maintained stable rainforest habitat since the last glacial maximum (From Costion *et al.* 2014).

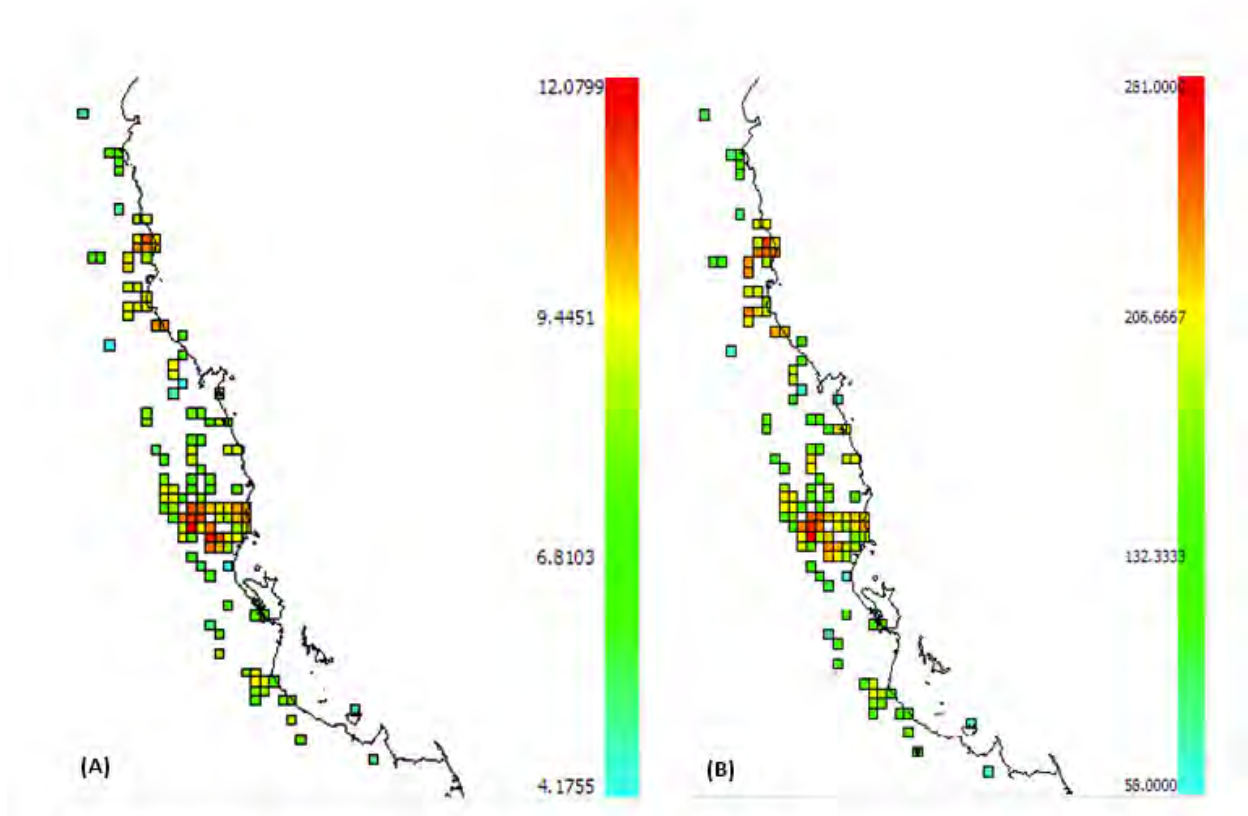


Figure 8: Phylogenetic diversity (A) and richness of genera (B) indicated by color-coded scale bar at 0.0625° grid cell resolution (From Costion et al., 2014)

Most interesting in this spatial pattern is that the two primary PD hotspots, the Daintree region and the Cairns-Cardwell lowlands are different, which suggests different evolutionary and/or ecological processes have shaped their biodiversity. We then tested for additional variables to explain the remaining 12% of PD not explained by GR and spatial auto-correlation in another round of model fitting.

Out of 61 candidate models of different combinations of explanatory variables, the model with the highest statistical support included GR, spatial filters (spatial auto-correlation), and the percent Sahul taxa per site. This means that the third variable, Sahul taxa per site, can explain the spatial pattern of the residuals (Figure 7), which was essentially the variation in PD after GR and spatial filters were removed. When then tested for a correlation between Sahul taxa per site and the rainforest stability index (Hilbert et al. 2007, Figure 7) and found a statistically significant positive correlation.

The statistical correlation between hotspots of PD and hotspots of taxonomic richness (GR) initially suggested that both of these areas may be significant long-term rainforest refugia. The linear regression residuals however showed that there were significant differences in these two hotspots. Cairns-Cardwell lowlands (Hotspot 1) has a higher concentration of established Sunda lineages and the Daintree region (hotspot 2) conversely is richer in Sahul lineages. Our results indicate that areas with higher PD than expected based on GR are positively correlated with areas that are rich in Sunda derived lineages.

This story developed further when we found a correlation between the percent Sahul species per site and the level of rainforest stability throughout the Quaternary period. Rainforest areas that were less stable throughout the Quaternary have a higher proportion of immigrant

lineages. Figure 7 shows areas of continuous rainforest during the Quaternary (Hilbert *et al.*, 2007). PD hotspot 1 (Cairns-Cardwell lowlands) overlaps with large areas of low stability (white). These areas are currently rainforest but were not consistently covered by rainforest vegetation over the last interglacial cycle. The only high stability areas (black) found within Hotspot 1 are significantly fragmented and smaller compared to the larger refugia areas directly to the north (Atherton Tablelands) and in hotspot 2 (Daintree). Hotspot 2 (Daintree) is notably intact with a high proportion of high stability areas and lower concentration of introduced lineages. The Black Mountain Corridor, the Cooktown area north of hotspot 2, and the region from the Paluma range south to Townsville are all mostly low stability and high PD residual areas with a high concentration of introduced lineages. The most striking example of these correlating patterns is found in the high stability area (black) north of hotspot 1 (Figure 7). This area, mostly upland habitat stretching from the Atherton Tablelands to the Bellenden Ker and Lamb ranges, is characterized by having low PD but a richness of Sahul lineages, or in other words a strong ‘Gondwanan character’.

These results illustrate the limitations of using diversity measures (species or phylogenetic) without historical interpretation. The Queensland Wet Tropics has two primary large rainforest refugia or high stability zones, the Daintree area and the Atherton-Bellenden Ker uplands. These refugia are rich in Sahul lineages giving them their iconic ‘Gondwanan’ character, but one is a diversity hotspot rich in species whereas the other does not stand out as a biodiversity hotspot within the bioregion on our analysis (but see Mokany *et al.*, 2014). Queensland’s Wet Tropics bioregion is also home to two major plant diversity hotspots, the Cairns-Cardwell lowlands and the Daintree region, which is comprised of both lowland and upland habitat. The Daintree region (PD hotspot 2) is well supported to be a long standing ancient rainforest refugium while the Cairns-Cardwell lowlands (PD hotspot 1) is diverse due to the intermixing of refugial Sahul species and immigrant species from the Sunda shelf (Asia). Our results indicate that the iconic ‘Gondwanan’ flora is not restricted to the uplands, but indeed one of its two largest existing refugia, the Daintree region, includes lowland habitat.

PD has recently been promoted for its use in guiding conservation policy to identify priority areas. Our study brings up important questions pertinent to this emerging field of work. Simply choosing a site or a series of sites that maximise PD can miss fundamental evolutionary stories and/or underlying processes that can explain the distribution of PD. In this case, understanding the distribution of PD after removing the effects of taxonomic richness is more informative than merely identifying the hotspots of PD alone. If conservation prioritisation in the Queensland Wet Tropics were based purely on PD hotspots without historical interpretation, it is possible that Australia’s largest remaining tropical rainforest refugium (the Atherton-Bellenden Ker uplands, Figure 7) would be down-ranked. Advocates of PD promote the use of PD complementarity (Faith 2004) which is argued would avoid this scenario if this methodology was properly implemented in policy.

Our study emphasizes that understanding the fundamental processes that have shaped the evolutionary history of a bioregion is an essential component for people facing difficult conservation decisions. This knowledge should be used in conjunction with maps of raw biodiversity data. Without it, such biodiversity maps may actually mask evidence of these important historical processes. Understanding how biodiversity patterns came about allows policy makers to make more informed decisions and certainly better equips them to plan for future climate change.

Figure 9 outlines a generalized summary of our methodology so that it can be applied in other regions. We advocate using PD in conjunction with statistical analyses that can identify and explain patterns and explanatory variables that are otherwise hidden by taxonomic richness.

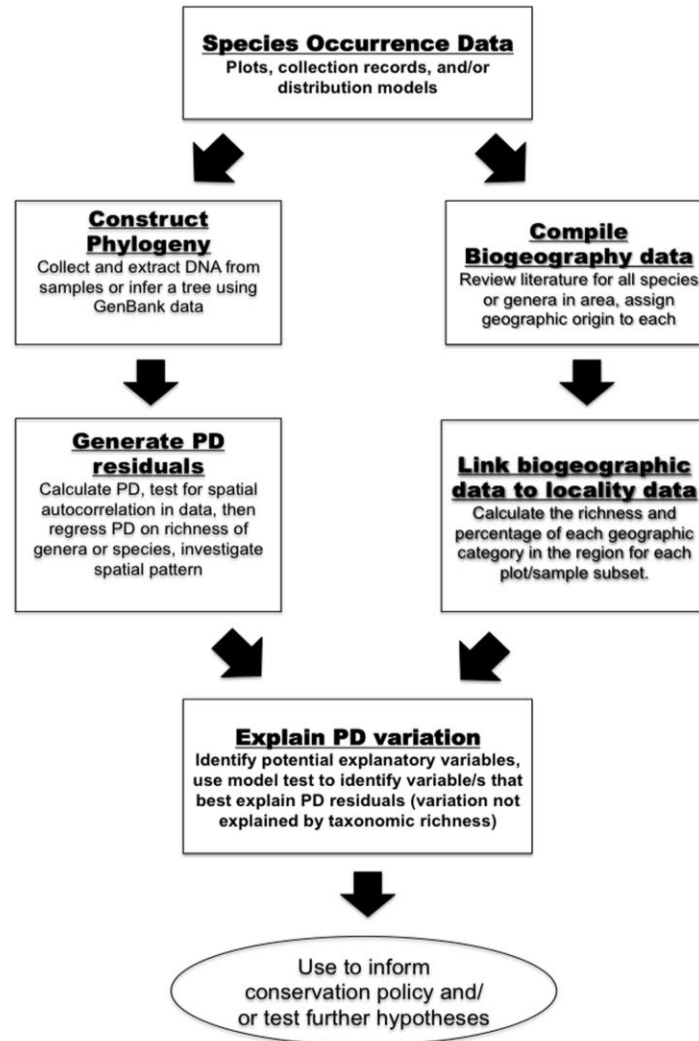


Figure 9: Summary of our methodology combining phylogenetic diversity (PD) and historical biogeography data (From Costion et al., 2014).

The Sunda Sahul floristic exchange

If our PD results can pick up a significant signal of Sunda lineages in Australia and their influence on diversity values in one of its biodiversity hotspots then there should also be other sources of evidence for this continental scale process. Indeed, our comprehensive literature review of molecular dated phylogenies relevant to this biogeographic region provided substantial support for this story.

Figure 10 shows the chronological distribution of all the sampled nodes that show a Sahul-Sunda disjunction and the inferred error around the ages. They are ordered from the oldest to the youngest. Disjunctions ranged from c. 19 Ma to c. 1 Ma. Precision varied widely from as little as $\pm 15\%$ of the inferred age (e.g. *Cleistanthus*) to $\pm 100\%$ (*Hypserpa*) as a result of various factors such as uncertainty in the age of fossils used for calibrating molecular clocks, calibration methods, resolution on phylogenetic trees, etc.

Figure 11 shows the plotted disjunctions in 2 Ma bins and the plotted distance between the Sahul and Sunda shelves through time. The earliest disjunct node (c. 32 Ma) marks onset of the

Sunda – Sahul floristic exchange, and coincides with the Sunda and Sahul shelves having approached to within approx. 500 km of each other. However, few disjunctions occurred between 32 and 20 Ma (when the shelves had approached to within approx. 100 km) which suggests that long distance dispersal was not important in the assembly of these two floras. In regards to the rate of exchange, the disjunctions (=dispersals/migrations) occurred at the rate of 1-3 per 2 Ma between 20 and 14 Ma. Subsequently the rate sharply increased, coincident with the shelves effectively merging.

We were also interested in determining whether there was a polarity in the exchange of plant lineages between the two continents and we found a statistically significant proportion of these disjunct nodes (68%) were of Sunda (or Asia) origin, indicating eastward dispersal across Wallacea is more frequent than chance (by a factor of about 2.4).

The propagule type of lineages that successfully dispersed was also found to be an important. We found a highly significant difference between the proportion of disjunct nodes on which propagule type optimised as fleshy (indicative of zoochory, or dispersal by animal means), and the proportion of zoochorous species in the source flora. Thus zoochory is strongly associated with successful dispersal.

These results indicate that dispersal of plant lineages between Sahul and Sunda was low until approx. 20 Ma when the two continents were approximately 100 km apart. When the two shelves effectively merged (c. 12 Ma) dispersal sharply increased as the distance required for birds and bats (or other dispersal vectors) to move between landmasses was minimised, allowing lineages to arrive into Australia from Asia (and vice versa to a lesser extent) via a stepping stone dispersal model.

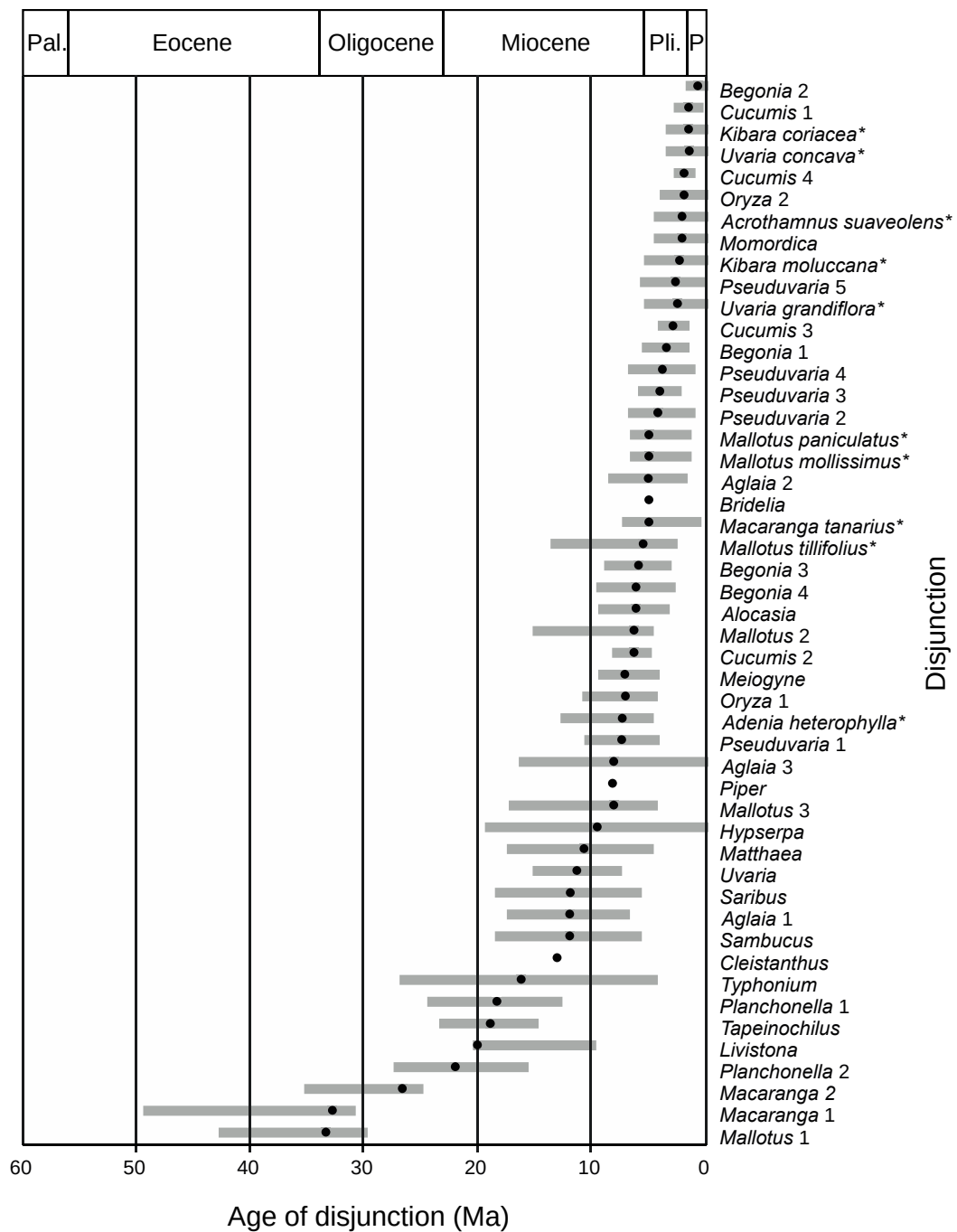


Figure 10: A plot of the minimum ages of 49 Sahul-Sunda disjunct clades of angiosperms for the study of Cenozoic intercontinental dispersal dynamics, arranged from oldest (left) to youngest. The error bars indicate the uncertainty around the minimum age estimates as determined by the original published analyses. *Infraspecific disjunction. Pal., Palaeocene; Pli., Pliocene; P., Pleistocene (From Crayn et al., 2014).

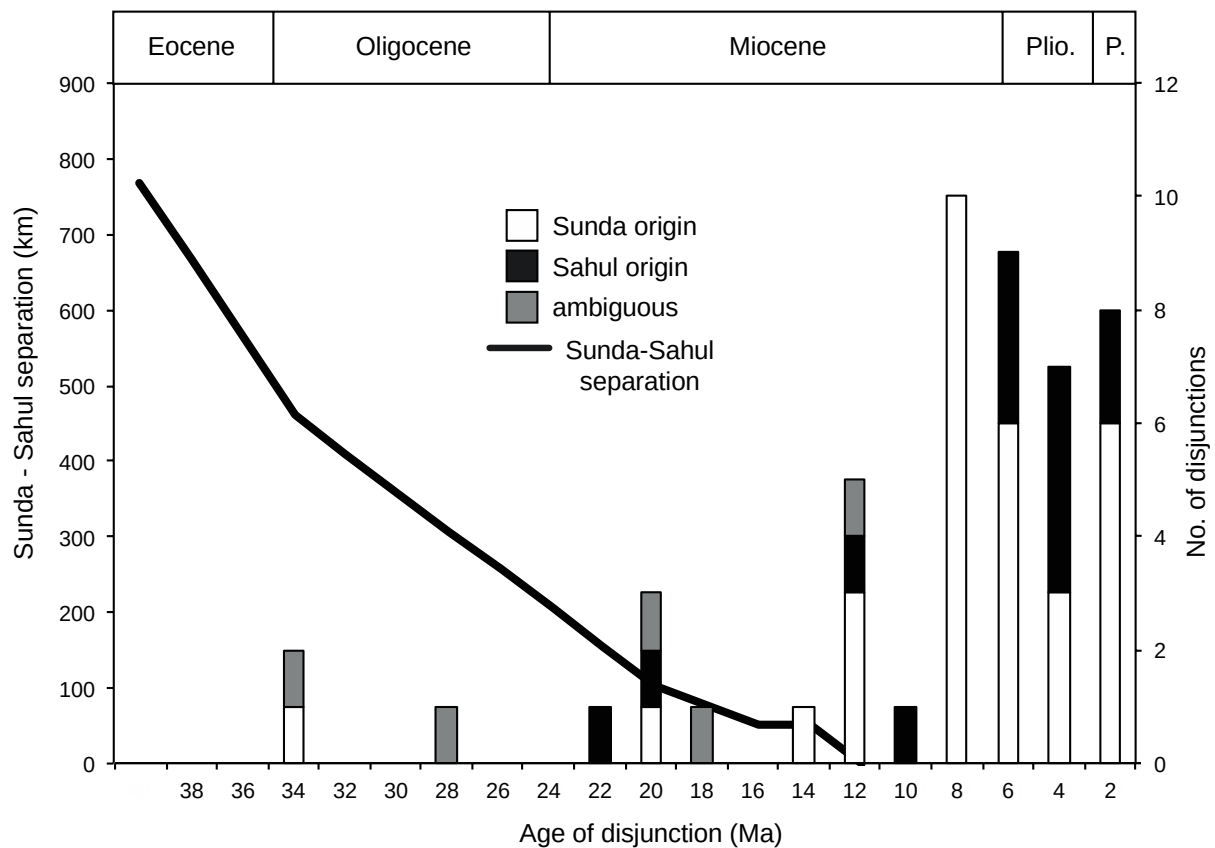


Figure 11: A frequency histogram showing the number of angiosperm disjunctions per 2 Myr time bin for the study of Cenozoic intercontinental dispersal dynamics across Sahul, Sunda and Wallacea. The histogram bars are shaded to show the proportion of disjunctions within that time bin for which the source area optimized as Sunda (white), Sahul (black) or ambiguous (grey). The line indicates the approximate minimum distance (km) between Sunda and Sahul landmasses (based on Hall, 2002). Pli., Pliocene; P., Pleistocene (from Crayn *et al.* 2014).

Immigrant lineages: Evidence from genetic diversity within species

Among the c. 500 species sampled, c. 100 species show infraspecific variation across north Queensland (Appendix 4). Since our sampling method was random and based on a limited number of samples per species we could not investigate the influence of specific biogeographic barriers on the distribution of genetic diversity as is routinely done for population genetics studies. We focused instead on drawing correlations between the variable and non-variable species and correlations between variable species and life history traits. Our first analysis assessed all species sampled against a database of life history traits for Australia's rainforest species. This analysis initially showed no significant patterns.

A second analysis was run after partitioning the dataset into Sahul and Sunda species, which yielded clear patterns: Sahul species showed higher amount of genetic variation than Sunda species. The Sunda species are expected to have less genetic variation since they are derived from a colonization event as a consequence of range expansion.

In addition the Sunda species tended to have larger leaf area, smaller fruits, shorter stature, and better dispersal ability than the Sahul species. These traits characterise 'pioneer' species, i.e.

species that dominate the early stages of ecological succession, such as after disturbance. Indeed, the Sunda species tend to be concentrated in areas where habitat was less stable through time. This model is consistent with global trends of biotic interchange (Vermeij 1991), which indicate that invasions of a biota are more successful where there has been a major disturbance in the recipient biota. These results and interpretations are currently being refined and the complete dataset, methods and results for this study will be published elsewhere.

Origins of *Bulbophyllum* (Orchidaceae) in Australia

Phylogenetic analysis of ITS sequence data confirms Asian and Australasian *Bulbophyllum* species represent a lineage which is divergent from African, Neotropical and Malagasy lineages (Figure 12). Species endemic to the Wet Tropics mountaintops, shown with light blue branches in Fig. 12, are found nested within the larger Asian and Australasian lineage. These relationships indicate that the *Bulbophyllum* species of the Wet Tropics mountaintops represent several distinct lineages derived from multiple migration events into Australia from the north. Some species are shown as single branches such as *Bulbophyllum evasum* and *Bulbophyllum bayelei*, both found in rainforests of the Wet Tropics and Cape York Peninsula. These species are the only representatives of their lineages occurring within Australia and are more closely related to species occurring outside Australia than to other Australian species. The sections *Monanthes*, *Cirrhopetalum*, *Polymeres*, *Minutissima* and *Oxysepala* are each represented by a cluster of at least two Australian species, nested within the greater Asian/Australasian lineage. These results indicate species radiations have occurred in Australia within several lineages, with radiations of *Polymeres*, *Monanthes*, and *Oxysepala* centered in the Wet Tropics bioregion.

A notable result of the phylogenetic analysis was the placement of species from section *Adelopetalum* in a sister position to the greater Asian/Australasian lineage (Figure 12). This phylogenetic pattern indicates an early divergence for the *Adelopetalum* lineage and an independent evolutionary history from the remaining Asian and Australasian taxa. Interestingly the group occupies a southern Sahul distribution across Australia, New Caledonia, Norfolk Island, Lord Howe Island and New Zealand, while all other *Bulbophyllum* sections are also represented by taxa in the northern Sahul (Papua New Guinea) and Sunda region. Most species of the *Adelopetalum* lineage are endemic to Australia, with a widespread species, *Bulbophyllum argyropus*, also occurring on Norfolk Island, Lord Howe Island and New Caledonia. A single species, *Bulbophyllum tuberculatum*, is endemic to New Zealand. Several closely related species are endemic to mountaintops of the Wet Tropics providing further evidence of species radiations that have occurred in this region. Whereas phylogenetic analysis of the single nuclear gene region (ITS) was able to give an indication of the evolutionary origins of the section it was unable to resolve relationships between closely related species within it. Further molecular evidence is required to resolve species limits within section *Adelopetalum*.

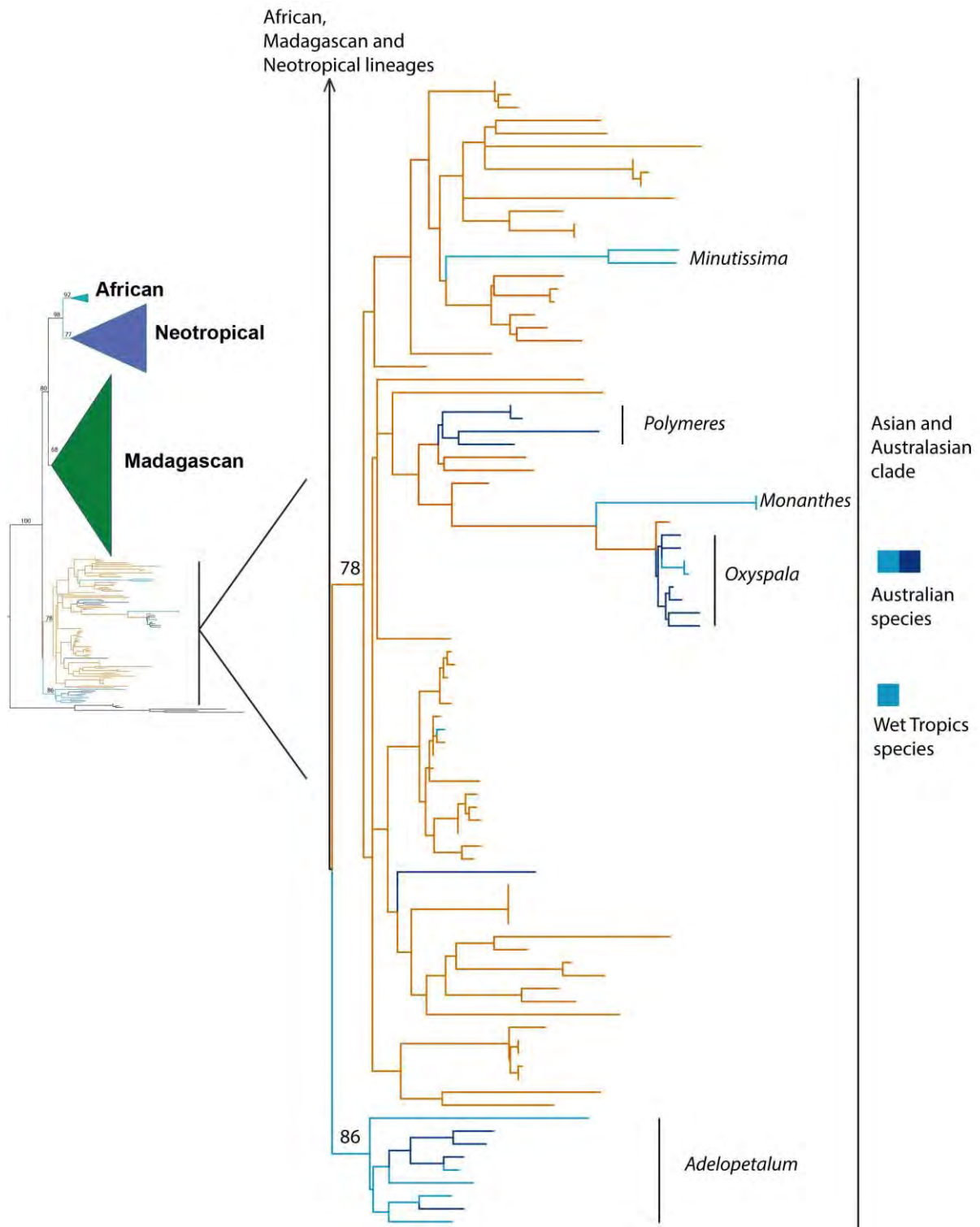


Figure 12: Evolutionary relationships in *Bulbophyllum* (Orchidaceae) based on DNA sequence data (ITS) with the Asian and Australasian clade enlarged. Australian species are indicated by blue branches with Wet Tropics species indicated by light blue branches. Bootstrap support is shown above major clade nodes.

Phylogenetic analysis of section *Adelopetalum* based on three genetic markers (ITS, *ycf1*, *matK*) shows highly supported well-resolved relationships at the species level (Figure 13). Relationships

can be inferred from the phylogenetic analysis with confidence as nearly all groupings receive maximum statistical support with posterior probabilities for clades equal to 1. Phylogenetic analysis shows the putative new genus '*Spilorchis*' (represented by *Bulbophyllum weinthalii*) is nested within the *Adelopetalum* lineage. Although morphologically distinct with large flowers, the data presented here suggest instead that this entity is best considered part of *Bulbophyllum* section *Adelopetalum* rather than as a distinct genus.

The evolutionary relationships of four species endemic to mountaintops across central Queensland, Wet Tropics Bioregion and Cape York Peninsula are resolved. The closest relative of the extremely rare Wet Tropics endemic, *Bulbophyllum boonjee*, is *B. bracteatum*, distributed across mountaintops in southeastern Queensland and northern NSW. Results confirm *B. lilianae*, *B. lageniforme* and *B. newportii*, which co-occur across mountaintops of the Wet tropics region are closely related to *B. exigium*, which occurs across mountaintops of southeast Queensland and NSW. The genetic evidence presented here support current species limits among the morphologically similar, co-occurring species *B. lilianae*, *B. lageniforme* and *B. newportii*. The strongly supported results in the phylogenetic reconstruction shows that each of these three species form a genetically distinct lineage.

Phylogenetic relationships revealed among Australian *Bulbophyllum* species provide an example of the complex evolutionary origins and diversity of plant species occurring across mountaintops of Cape York Peninsula and Wet Tropics bioregion. Within this highly diverse genus we found additional support for the overall trend observed from the PD study. Australian species of *Bulbophyllum* are a mix of older Sahul species and species migrated into Australia from Asia through multiple dispersal events, with several lineages showing evidence of active diversification into new species within the Wet Tropics bioregion. Further work is required to establish the timing of these events and a more precise origin for each of the lineages identified, but already we can see that even within one genus present in Australia, that the collision of the Sunda and Sahul shelves has played an important role in the complex origins of the biodiversity of the Wet Tropics bioregion. While addressing this larger question we also were able to resolve species limits of taxa that previously were unclear and conclude that '*Spilorchis*' is part of *Bulbophyllum* section *Adelopetalum*.

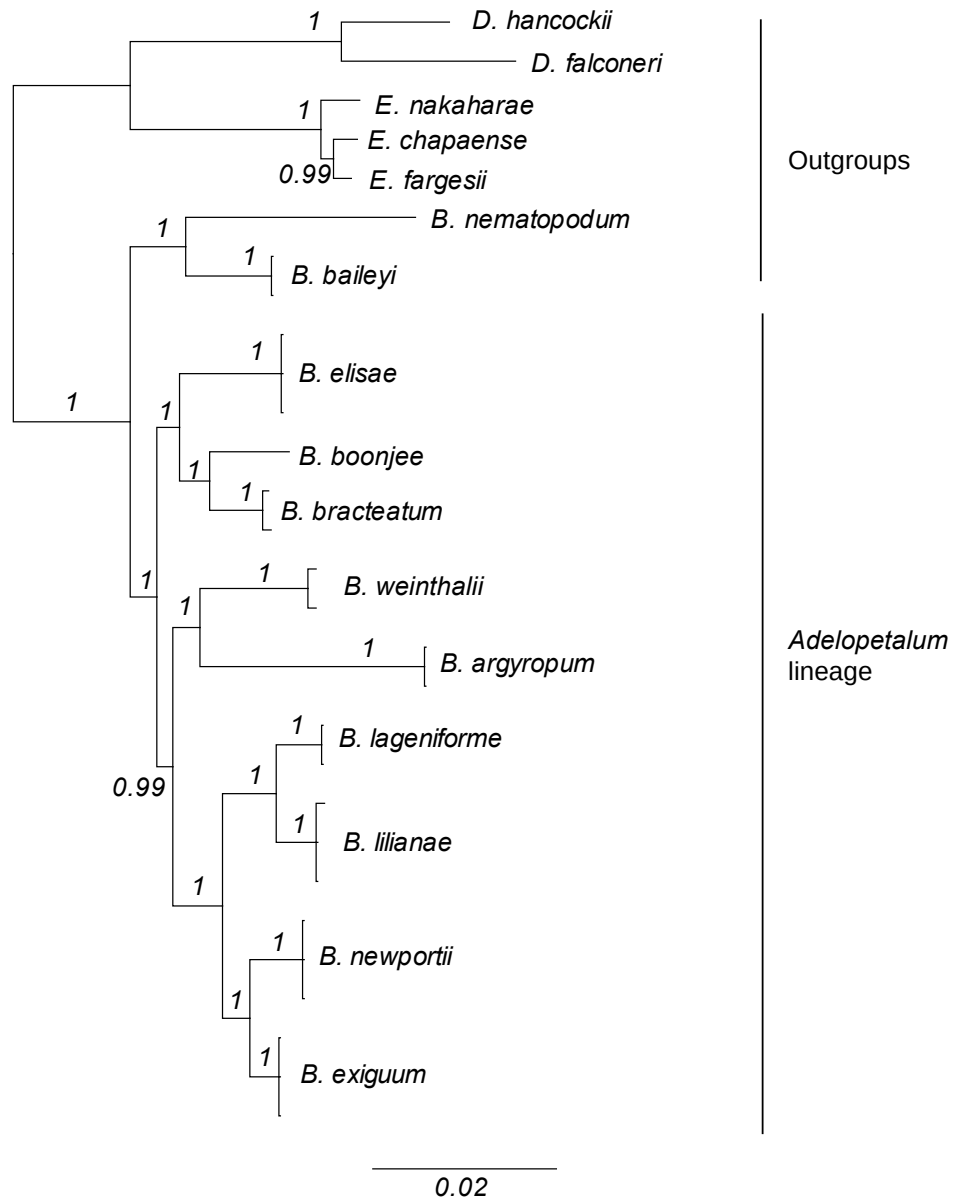


Figure 13: Phylogenetic tree based on Bayesian analysis of a concatenated alignment of one nuclear (ITS) and two plastid (*ycf1*, *matK*) genetic markers. Each taxon is represented by one to three individuals. Posterior probability values are shown above the nodes.

Part II: Mountaintop biodiversity and threat assessment

Mountaintop threat assessment

We identified seven hotspots of mountaintop endemic plant species diversity in the Wet Tropics bioregion. The 19 species (Table 2) discussed in this report are concentrated at these locations (Table 3, Figure 14). These seven hotspots may also be considered future refugia since each of them is predicted to maintain some suitable habitat in at least one of the climate scenarios by 2080. Three of the areas, Carbine Uplands, Mount Bartle Frere, and Mount Bellenden Ker, have local endemics, which are restricted to that locality only. The Carbine Uplands (including Mt. Lewis) stand out as containing 68% of the regional mountaintop endemics, six of which are locally endemic.

Table 2: List of mountaintop species modelled with current known range, BF = Mt. Bartle Frere, BK = Mt. Bellenden Ker, CU = Carbine Uplands, F = Mt. Finnigan, HR = Herberton Range, TP = Thornton Peak, WT = Windsor Tableland, WTB = Wet Tropics Bioregion

Species no.	Family	Species	Current range
1	Proteaceae	<i>Austromuelleria valida</i> B.Hyland	CU
2	Lauraceae	<i>Cinnamomum propinquum</i> F.M.Bailey	BK, BF
3	Lauraceae	<i>Cryptocarya bellendenkerana</i> B.Hyland	WTB
4	Ebenaceae	<i>Diospyros</i> sp. Mt Spurgeon	BK, BF, CU
5	Elaeocarpaceae	<i>Elaeocarpus linsmithii</i> Guymer	BK, BF, CU
6	Elaeocarpaceae	<i>Elaeocarpus</i> sp. Mt Misery	CU, WT
7	Cunoniaceae	<i>Eucryphia wilkiei</i> B.Hyland	BF
8	Myrtaceae	<i>Micromyrtus delicata</i> A.R.Bean	HR
9	Thymeleaceae	<i>Phaleria biflora</i> (C.T.White) Herber	CU, TP
10	Sapotaceae	<i>Planchonella</i> sp. Mt Lewis	CU
11	Escalloniaceae	<i>Polyosma</i> sp. Mt Lewis	CU
12	Solanaceae	<i>Solanum eminens</i> A.R.Bean	BK
13	Symplocaceae	<i>Symplocos graniticola</i> Jessup	CU, F
14	Symplocaceae	<i>Symplocos oresbia</i> Jessup	CU, TP, F
15	Symplocaceae	<i>Symplocos bullata</i> Jessup	CU
16	Myrtaceae	<i>Syzygium fratris</i> Craven	BF
17	Winteraceae	<i>Tasmannia</i> sp. Mt Bellenden Ker	BK, BF
18	Myrtaceae	<i>Uromyrtus metrosideros</i> (F.M.Bailey) A.R.Scott	WTB
19	Rutaceae	<i>Zieria alata</i> Duretto & P.I.Forst.	CU

Table 3: Number of Wet Tropics endemic plant species (and local endemics restricted to that locality) for each of the seven mountaintop hotspots.

Locality	Elevation (max. masl)	No. of endemic species
Mt. Finnigan	1,148	4
Thornton Peak	1,338	4
Windsor Tableland	1,356	2
Carbine Uplands	1,383	13 (6)
Lamb Ranges	1,308	2
Mt. Bellenden Ker	1,590	6 (1)
Mt. Bartle Frere	1,622	7 (2)



Figure 14: The seven mountaintop endemic species hotspots

A large and rapid decline in total extent of suitable climate/suitable habitat is projected for all species (Table 3, Figure 15) with an average decline by 2040 of 93% per species across all climate scenarios. The general pattern is strikingly similar for all three climate scenarios. Figure 15 and Table 3 show the best-case of the three potential climate scenarios for each species at each time interval. By 2040 all species are at risk with the projected habitat decline for four species suggesting they may qualify for **Endangered** status (IUCN red list criteria) because they show a $\geq 50\%$ decline in suitable habitat, for 13 suggesting qualification for **Critically Endangered** status ($\geq 80\%$ decline), and for two potentially **Extinct** (no suitable habitat remaining). In the best case scenario for all species by 2080, only six species are projected to have a maximum of 3%-1% of their current habitat remaining, whereas the other 13 species are projected to have no suitable habitat.

Table 4: Best case out of three climate scenarios of decline in total hectares from current suitable habitat for each mountaintop endemic species. Color-coding indicates relevant IUCN Red Listing status:

		Endangered		Critically Endangered		Extinct	
Species no.	Current ha	2040		2060		2080	
		ha	% decline	ha	% decline	ha	% decline
1	45918	14166	69%	486	97%	0	100%
2	42828	162	99%	42	99%	0	100%
3	77880	17070	88%	5496	93%	2334	97%
4	50742	8754	83%	276	99%	0	100%
5	50742	12642	75%	3750	93%	1590	97%
6	74802	8112	91%	162	99%	0	100%
7	4296	84	98%	0	100%	0	100%
8	54318	0	100%	0	100%	0	100%
9	26280	210	99%	0	100%	0	100%
10	23724	1152	95%	90	99%	0	100%
11	74988	7746	90%	78	99%	0	100%
12	1794	0	100%	0	100%	0	100%
13	72714	26406	64%	11142	85%	318	99%
14	67482	4368	94%	588	99%	12	99%
15	44040	1938	96%	36	99%	0	100%
16	4740	222	95%	6	99%	0	100%
17	31620	5160	84%	1668	95%	960	97%
18	78330	28824	64%	11052	86%	2778	97%
19	48282	2862	94%	0	100%	0	100%

Of the seven mountaintop hotspots or future refugia some suitable habitat is projected to be retained at Bellenden Ker, Bartle Frere, Carbine Uplands, Thornton Peak, and Mount Finnigan under all three emissions scenarios, whereas Windsor Tableland habitat is only retained in scenario A2, and the Lamb Ranges and Black Mountain are retained in only scenario B1. Most alarming is the loss of habitat in the largest and most species rich hotspot, the Carbine Uplands, which is projected to be reduced to tiny fragments under all three emissions scenarios.

These results do not take into consideration dispersal probabilities between the current populations and other habitats with suitable climate conditions determined by the model. If the model projections are correct, at least one of the six species projected to persist until 2080, *Symplocos graniticola*, will require for survival either a natural dispersal event to another mountaintop or a assisted relocation program because it is not currently known from the only area in which suitable habitat is projected to remain in 2080. We also tested whether it was possible for species to disperse to locations outside of the Wet Tropics bioregion. Modelling using Australia wide environmental layers were imprecise due to very low-resolution climate data, thus identification of suitable habitat outside of the Wet Tropics was deemed unreliable.

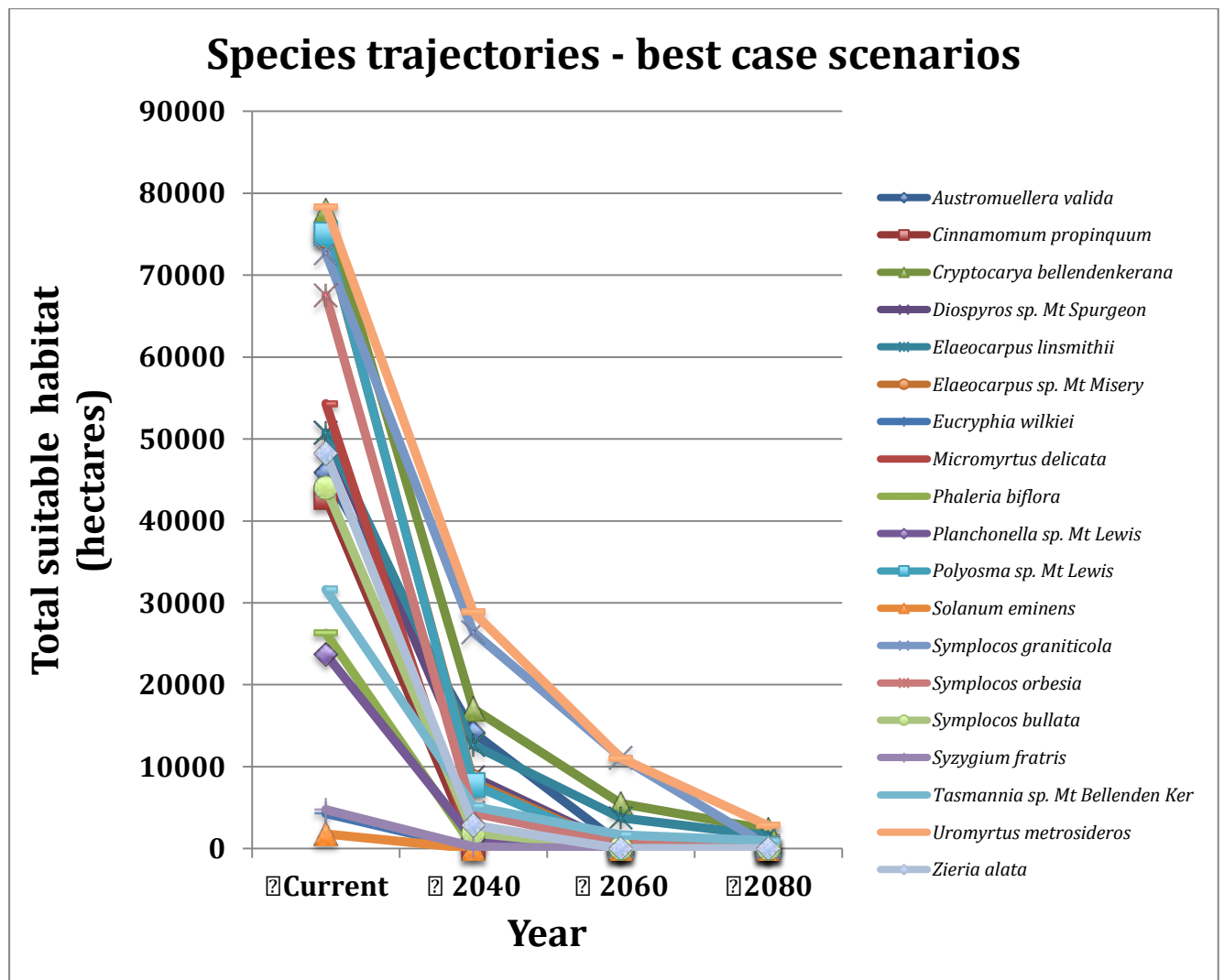


Figure 15: Best-case trajectories for decline in suitable habitat in the Wet Tropics for 19 mountaintop endemic plant species modelled over three, 20-year intervals using a 'best-case' global greenhouse gas emissions scenarios (IPCC4).

The closest area south of the Wet Tropics higher than 1000 masl is Mt. Elliot, located close the southern Wet Tropics bioregion boundary. Mt. Elliot is a potential refuge for the species modelled in our study due to its close proximity. Further work and climate modelling should be

considered a pertinent follow up to this study to assess whether Mt. Elliot is likely to maintain a suitable climate for these and other important Wet Tropics mountaintop species.

The results of this study should be regarded as preliminary. For many of these species the underlying data upon which species distribution modelling is undertaken are limited. For several species fewer than 10 records were available to estimate the climatic niche. Furthermore, decisions regarding the appropriate conservation status to be afforded these species (IUCN Red List criteria) depend not only on accurate distribution models, but also on detailed knowledge of the species' generation time (defined as the mean age of all reproductive individuals). These data don't exist for any of the modelled species. Thus, more research is needed, specifically (1) systematic surveys of the mountaintops to improve our knowledge of the distribution and abundance of the impacted species, and (2) the establishment of long term monitoring plots to estimate ecological, demographic and life history parameters.

Prospects

In the face of climate change, species may (1) acclimate (through physiological plasticity); (2) adapt (through natural selection); (3) migrate (through dispersal to suitable habitat elsewhere); or (4) go extinct (Feeley et al. 2012). Each of the first three responses, and the likelihood that they can mitigate against the fourth (extinction) are discussed in turn below.

Acclimation: Little is known about the potential of these species to acclimate to climate change. Previous research has suggested that Wet Tropics plants may be relatively water conservative due to past extinction of sensitive species and/or selection for drought tolerance under past severe climate cycles such as occurred throughout the Pleistocene. Furthermore, increased atmospheric CO₂ may help to improve water use efficiency by decreasing plant transpiration rates. Thus, acclimation of mountaintop species to reduced water availability may plausibly mitigate some of the effects of climate change. However, this speculative hypothesis requires experimental testing of mountaintop endemic species' responses to increased CO₂, increased temperature and decreased water availability. Studies on seedlings may be the most profitable due to the importance of this life stage to species' persistence in the wild and the relative tractability of experimental greenhouse manipulations compared with those on the adult stages of long-lived woody species.

Adaption: Mountaintop woody plant species are expected to have small population sizes and therefore adaptive mutations may, under powerful selection, become fixed in a relatively small number of generations. However, plants are long-lived, and their mean generation times may be a decade or more therefore it is expected that adaptive evolution will occur slowly in the studied species relative to other organisms with short generation times. Furthermore, adaptive evolution requires effective pollination and seed dispersal services, which may be also affected by climate change impacts on the faunal species which provide these services. Thus, adaptive evolutionary responses to environmental change through natural selection are unlikely to occur over the time frame required to significantly mitigate against the projected impacts.

Migration: The next closest potential refuge area to the south is Eungella National Park, which is roughly 500 km from the southern most Wet Tropics mountaintop habitat. If suitable habitat exists here in the future a long distance dispersal event or assisted relocation would be required. The next nearest areas with significant upland terrain are the Border Ranges and Nightcap National Park (Queensland-New South Wales border) some 1,400 km south. North of the Wet Tropics bioregion there is no upland terrain > 800 masl thus dispersal across the Torres Strait to the highlands of New Guinea approximately 900 km away would be required. The likelihood of any of the species in this study naturally dispersing to suitable habitat outside of the Wet Tropics (even if suitable habitat were to exist) without human-assisted translocation is minimal. Furthermore, establishment and long term survival of the dispersing species requires that all of

its ecological needs are satisfied, including those fulfilled by its associated faunal (pollinators and seed dispersers) and fungal (mycorrhizae and endophytes) partners. Therefore it seems highly unlikely that natural dispersal and establishment can mitigate against extinction of these species in the wild, especially when the short time frames of the projected declines are considered. Human assisted translocation is an alternative, but such measures are highly risky and controversial, and rarely succeed.

Although the fate of these species cannot be known with certainty, we advocate a pro-active response to these alarming predictions. Conservation of the upland endemic flora *in situ* depends on global political and social action to limit greenhouse gas emissions. *Ex situ* conservation plans for each of the impacted species is a potential insurance policy against failure to achieve this change. Australia has several public botanical garden facilities with the capacity to host a “threatened mountaintop species” living collection. Such initiatives should be explored. Furthermore, depositing suitable material of these species in seed banks and tissue banks for tissue culture are also relatively low cost measures to preserve some of the natural genetic diversity (Primack and Miller-Rushing, 2009; Seaton *et al.*, 2010).

Fungal biodiversity inventory

A total of 753 (639 rainforest) macro-fungi observations and collections in 106 genera (82 rainforest) were made between July 2012 and March 2014 (Table 5) (Figure 17), increasing the number of macro-fungal collections from the Wet Tropics region by 21%, rainforest mountaintops of the Wet Tropics by 96% and Wet Tropics upland areas (> 1000 masl) by 66%.

New and Notable Records

Twelve genera, representing ten families, are new records for the Wet Tropics region (Table 5) and another twelve genera were new records for the mountaintop sites of the region (Table 5). The new records represent the divisions Basidiomycota and Ascomycota and a number are known to form mycorrhizal associations or are plant pathogens.

Three specimens could not be identified to genus and likely represent genera new to science. These all have smooth hymenial surfaces and may belong to the Stereaceae or Amylostereaceae, fungal families comprising a range of pathogenic and saprophytic species.

Thirty-seven of the previously recorded genera were known from five or fewer Wet Tropics records and another ten were known from ten or fewer Wet Tropics records (Table 5). While species determinations are as yet unavailable, it is expected that some to many of the collections will be species new to science.

The collections were dominated by genera of Basidiomycetes. The most commonly collected mushroom species were *Marasmius* and *Mycena* and the most commonly collected non-gilled genera were *Ganoderma*, *Stereum* and *Polyporus*. Other mushroom genera, for example *Hygrocybe*, *Laccaria*, *Psathyrella*, were seen less frequently and more strictly in the wet season surveys. Other non-gilled genera such as *Clavuliniopsis* were also collected in wet season surveys only.

Analysis of the results of this project collated with the existing record data (source: Atlas of Living Australia, ALA) shows a total of at least 383 species of macrofungi in 295 genera and 88 families recorded in the Wet Tropics. The majority of existing collections are only determined to genus and at least 84 genera have no single determination to species.

The surveys of mountaintop sites in the Wet Tropics conducted in this project added significantly to the understanding of the macro-fungi of the region, adding 12 new genus records to the

region and nearly doubling the collections from mountaintop sites. In addition, one third of the genera had only been previously collected between one and five times and 43% of the genera between six and ten times. That these advances were achieved in years of relatively poor production of fruiting bodies indicates that the macro-fungi of the region are under-collected and their biodiversity is poorly understood. This is confirmed by collection of three putative new genera. Two of these specimens are macroscopically similar to a common genus, *Stereum*, which suggests that a proportion of the previous collections of *Stereum* and other genera may be incorrectly determined and that the historical collection data may not accurately describe the true species richness of the fungi of the Wet Tropics. It also indicates new genera and species are yet to be described from new and old collections.



Figure 16: Photos of selected fungi collected during the surveys. *Ganoderma* sp. (upper left), *Geastrum* sp. (upper right), *Microporus* sp. (lower left), and *Mycena* sp. (lower right). (Photographs: K. Bransgrove and Gary W. Wilson.)

Table 5: Genera of macro-fungi collected during Wet Tropics surveys 2012-2014. * 1-5 previous collections; ** 6-10 previous collections; § new record for the Wet Tropics; ❖ New record for Wet Tropics mountaintops (> 1000 masl)

Division	Family	Genus
Ascomycota	Heliotaceae	<i>Chlorociboria</i> Seaver ex C.S. Ramamurthi, Korf & L.R. Batra §
Ascomycota	Heliotaceae	<i>Hymenoschyphus</i> Gray *
Ascomycota	Pyronemataceae	<i>Scutellinia</i> (Cooke) Lambotte *
Ascomycota	Sarcoscyphaceae	<i>Cookeina</i> Kuntze **❖
Ascomycota	Sarcoscyphaceae	<i>Phillipsia</i> Berk. §
Ascomycota	Xylariaceae	<i>Hypoxylon</i> Bull. **
Ascomycota	Xylariaceae	<i>Xylaria</i> Hill ex Schrank
Basidiomycota	Agaricaceae	<i>Cystoderma</i> Fayod §
Basidiomycota	Agaricaceae	<i>Macrolepiota</i> Singer
Basidiomycota	Agaricomycetes	<i>Cotylidia</i> P. Karst. §
Basidiomycota	Amanitaceae	<i>Amanita</i> Pers.
Basidiomycota	Auriculariaceae	<i>Auricularia</i> Bull.
Basidiomycota	Boletaceae	<i>Austroboletus</i> (Corner) Wolfe
Basidiomycota	Boletaceae	<i>Boletus</i> L.
Basidiomycota	Boletaceae	<i>Fistulinella</i> Henn. *
Basidiomycota	Boletaceae	<i>Phylloporus</i> Quél.
Basidiomycota	Boletaceae	<i>Pulveroboletus</i> Murrill
Basidiomycota	Boletaceae	<i>Strobilomyces</i> Berk.
Basidiomycota	Boletaceae	<i>Tylopilus</i> P. Karst.
Basidiomycota	Cantharellaceae	<i>Cantharellus</i> Adans. ex Fr.
Basidiomycota	Clavariaceae	<i>Clavaria</i> Vaill. ex L.
Basidiomycota	Clavariaceae	<i>Clavulinopsis</i> Overeem *
Basidiomycota	Clavariaceae	<i>Ramariopsis</i> (Donk) Corner *
Basidiomycota	Cordycipitaceae	<i>Isaria</i> Pers. *
Basidiomycota	Corticaceae	<i>Corticium</i> Pers. *
Basidiomycota	Cortinariaceae	<i>Cortinarius</i> (Pers.) Gray
Basidiomycota	Cortinariaceae	<i>Dermocybe</i> (Fr.) Wünsche *
Basidiomycota	Entolomataceae	<i>Claudopus</i> Gillet
Basidiomycota	Entolomataceae	<i>Clitopilus</i> (Fr. ex Rabenh.) P. Kumm. *
Basidiomycota	Entolomataceae	<i>Entoloma</i> (Fr. ex Rabenh.) P. Kumm.
Basidiomycota	Entolomataceae	<i>Leptonia</i> (Fr.) P. Kumm. ❖
Basidiomycota	Entolomataceae	<i>Nolanea</i> (Fr.) P. Kumm.
Basidiomycota	Fomitopsidaceae	<i>Climacocystis</i> Kotl. & Pouzar §
Basidiomycota	Fomitopsidaceae	<i>Fomitopsis</i> P. Karst.
Basidiomycota	Fomitopsidaceae	<i>Phaeolus</i> (Pat.) Pat. §
Basidiomycota	Ganodermataceae	<i>Amauroderma</i> Murrill *❖
Basidiomycota	Ganodermataceae	<i>Ganoderma</i> P. Karst.
Basidiomycota	Geastraceae	<i>Geastrum</i> Pers. *❖
Basidiomycota	Gloeophyllaceae	<i>Gloeophyllum</i> P. Karst. *
Basidiomycota	Gloeophyllaceae	<i>Lenzites</i> Fr.
Basidiomycota	Gomphaceae	<i>Ramaria</i> Fr. ex Bonord.
Basidiomycota	Hydnangiaceae	<i>Laccaria</i> Broome
Basidiomycota	Hydnodontaceae	<i>Trechispora</i> P. Karst. *
Basidiomycota	Hygrophoraceae	<i>Hygrocybe</i> (Fr.) P. Kumm.

Basidiomycota	Hymenochaetaceae	<i>Coltricia</i> Gray
Basidiomycota	Hymenochaetaceae	<i>Hymenochaete</i> Lév. ❖
Basidiomycota	Hymenochaetaceae	<i>Phellinus</i> Quél.
Basidiomycota	Inocybaceae	<i>Crepidotus</i> (Fr.) Staude **
Basidiomycota	Inocybaceae	<i>Inocybe</i> (Fr.) Fr.
Basidiomycota	Lachnaceae	<i>Lachnum</i> Retz. §
Basidiomycota	Lachnocladiaceae	<i>Lachnocladium</i> Lév. ❖
Basidiomycota	Marasmiaceae	<i>Campanella</i> Henn. *
Basidiomycota	Marasmiaceae	<i>Gerronema</i> Singer *❖
Basidiomycota	Marasmiaceae	<i>Hydropus</i> Kühner ex Singer *
Basidiomycota	Marasmiaceae	<i>Marasmius</i> Fr.
Basidiomycota	Marasmiaceae	<i>Tetrapyrgos</i> E. Horak §
Basidiomycota	Marasmiaceae	<i>Trogia</i> Fr. *
Basidiomycota	Meruliaceae	<i>Bjerkandera</i> P. Karst. *❖
Basidiomycota	Meruliaceae	<i>Cymatoderma</i> Jungh.
Basidiomycota	Meruliaceae	<i>Podoschypa</i> Pat.
Basidiomycota	Mycenaceae	<i>Filoboletus</i> Henn.
Basidiomycota	Mycenaceae	<i>Mycena</i> (Pers.) Roussel
Basidiomycota	Mycenaceae	<i>Xeromphalina</i> Kühner & Maire **
Basidiomycota	Omphalotaceae	<i>Anthracoophyllum</i> Ces. **
Basidiomycota	Omphalotaceae	<i>Gymnopus</i> (Pers.) Roussel *
Basidiomycota	Omphalotaceae	<i>Marasmiellus</i> Murrill
Basidiomycota	Omphalotaceae	<i>Micromphale</i> Gray §
Basidiomycota	Omphalotaceae	<i>Omphalotus</i> Fayod **
Basidiomycota	Paxillaceae	<i>Paxillus</i> Fr. *
Basidiomycota	Peniophoraceae	<i>Peniophora</i> Cooke *❖
Basidiomycota	Physalacriaceae	<i>Armillaria</i> (Fr.) Staude **
Basidiomycota	Physalacriaceae	<i>Cryptotrama</i> Singer *
Basidiomycota	Physalacriaceae	<i>Hymenopellis</i> R.H. Petersen *
Basidiomycota	Physalacriaceae	<i>Oudemansiella</i> Speg. *
Basidiomycota	Pleurotaceae	<i>Hohenbuehelia</i> Schulzer **
Basidiomycota	Polyporaceae	<i>Corioloopsis</i> Murrill
Basidiomycota	Polyporaceae	<i>Datronia</i> Donk *
Basidiomycota	Polyporaceae	<i>Fomes</i> (Fr.) Fr. **
Basidiomycota	Polyporaceae	<i>Hexagonia</i> Fr.
Basidiomycota	Polyporaceae	<i>Lentinus</i> Fr. ❖
Basidiomycota	Polyporaceae	<i>Microporellus</i> Murrill *
Basidiomycota	Polyporaceae	<i>Microporus</i> P. Beauv.
Basidiomycota	Polyporaceae	<i>Pachykytospora</i> Kotl. & Pouzar §
Basidiomycota	Polyporaceae	<i>Panus</i> Fr.
Basidiomycota	Polyporaceae	<i>Polyporus</i> P. Micheli ex Adans.
Basidiomycota	Polyporaceae	<i>Pycnoporus</i> P. Karst.
Basidiomycota	Polyporaceae	<i>Trametes</i> Fr.
Basidiomycota	Polyporus	<i>Nigrofomes</i> Murrill *
Basidiomycota	Psathyrellaceae	<i>Coprinellus</i> P. Karst. *
Basidiomycota	Psathyrellaceae	<i>Psathyrella</i> (Fr.) Quél.
Basidiomycota	Pterulaceae	<i>Pterula</i> Fr. *
Basidiomycota	Russulaceae	<i>Lactarius</i> Pers.
Basidiomycota	Russulaceae	<i>Russula</i> Pers.
Basidiomycota	Sarcosomataceae	<i>Plectania</i> Fuckel *❖
Basidiomycota	Sclerodermataceae	<i>Scleroderma</i> Pers. *
Basidiomycota	Stereaceae	<i>Stereum</i> Hill ex Pers.

Basidiomycota	Strophariaceae	<i>Gymnopilus</i> P. Karst.
Basidiomycota	Strophariaceae	<i>Hypholoma</i> (Fr.) P. Kumm. **
Basidiomycota	Strophariaceae	<i>Pholiota</i> (Fr.) P. Kumm. *
Basidiomycota	Thelephoraceae	<i>Thelephora</i> Ehrh. ex Willd. *❖
Basidiomycota	Tricholomataceae	<i>Conchomyces</i> Overeem *
Basidiomycota	Tricholomataceae	<i>Melanoleuca</i> Pat. §
Basidiomycota	Tricholomataceae	<i>Omphalina</i> Qué. *
Basidiomycota	Tricholomataceae	<i>Resupinatus</i> Nees ex Gray *
Basidiomycota	Tricholomataceae	<i>Rimbachia</i> Pat. §
Basidiomycota	Tubariaceae	<i>Tubaria</i> (W.G. Sm.) Gillet *

Timing of collections

The largest numbers of collections were made in months associated with the wet-season (high rainfall and temperatures), particularly March 2014, and very few collections were made in any of the dry-season surveys (Figure 17). This was expected as fruiting-body production in the forests of the Wet Tropics, rainforest and sclerophyll, is aligned with the precipitation of the wet-season rather than autumnal preparation for winter as in temperate climates.

The collections from dry season surveys were dominated by woody persistent genera remaining from the last precipitation event e.g. *Ganoderma* spp., *Pycnoporus sanguineus*, *Stereum* spp., *Microporus xanthopus*, *Polyporus* spp., and *Microporellus* spp. These taxa were also commonly collected during wet season surveys. The collections from wet season surveys were dominated by *Mycena* and *Marasmius*. The yield of wet season surveys was inconsistent with respect to quality and quantity of collections due to fluctuations in precipitation, temperature and relative humidity and because mushroom genera decompose within days of genesis.

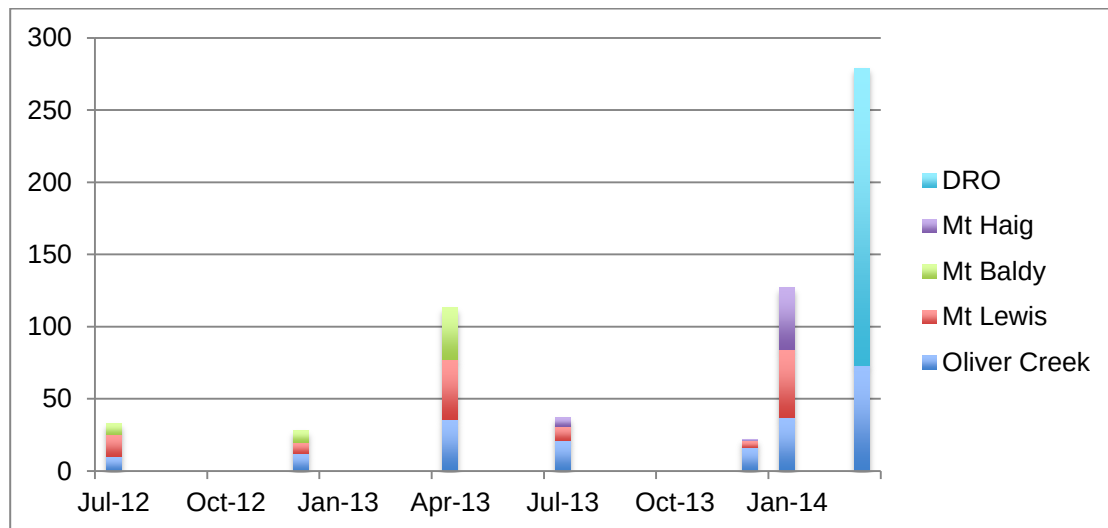


Figure 17: Number of macro-fungi (rainforest) collections per site and date.

The Oliver Creek lowland plot yielded significantly more collections in the winter (dry season) survey of 2013 than either of the two mountaintop sites (Figure 5). In this season, the mountaintop plots yielded only remnants of dry bracket fungi, primarily *Ganoderma*, *Polyporus*

and *Stereum* whereas the lowland plot yielded a small number of mushroom collections, primarily *Marasmius* and *Mycena*, active bracket fungi and the ascomycete *Cookeina*.

This difference in fruiting was attributed to consistently higher day- and night-time temperatures at Oliver Creek (c. 20 masl) than Mt Lewis or Mt Haig (1100 masl). This is consistent with research which has shown that as ambient and soil temperature increases, so does the abundance of fungi in the soil and production of fruiting-bodies (Kausarud et al., 2009; Castro et al., 2010). It suggests that as global temperatures increase greater fruiting activity of macro-fungi and macro-fungal will occur. As precipitation is also an important factor governing fruiting abundance and timing, it is likely that fruiting will be seen 'out of season' more regularly.

Site differences

Few differences in abundance and genus richness were seen between any of the sites. Slightly more diversity was noted at Mt Lewis (1100 masl) and Oliver Creek (20 masl) compared with the remaining mountaintop sites. This was not expected as the abundance and diversity of the mountaintop sites, chosen for similarity of elevation and forest type, were expected to be more similar to each other than to the lowland plot, which is a very different vegetation community. The lack of diversity in the mountaintop plots is thought to be an artefact of the surveys being completed in a number of years of poor fruiting-body production and the ephemeral nature of fungal fruiting bodies. The similarity of collections between Mt Lewis (1100 masl) and Oliver Creek (20 masl) in 2013 may indicate that the distribution of macro-fungi across the Wet Tropics is reasonably uniform and is not affected by altitudinal differences of the region. This suggests that the fungal flora of the mountaintops may be much more resilient to the effects of climate than what is projected for plant species.

Collections of fruiting bodies at Oliver Creek in March 2014 were approximately 100% greater than collected at the site in any of the remaining seasons. This was due to consistent precipitation and warm temperatures. In addition, fruiting body production in March 2014 was the best season seen during the project. Due to the inaccessibility of mountaintop sites in March 2014, another lowland site (DRO) was collected. The higher number of collections at the DRO is primarily due to a much larger area being surveyed over two visits.

Ecto-mycorrhizal (ECM) fungi

Arbuscular mycorrhizal fungi (AM fungi) dominate the mycorrhizal relationships formed with plants in tropical forests (Haug, 2005) and are usually considered to be the near sole mycorrhizal partner of trees in tropical rainforests (Peay et al., 2010; McGuire, 2008). Maps detailing the distribution of mycorrhizal relationships in Australian ecosystems do not distinguish between forest types and show that Australian tropical and sub-tropical forests form relationships with both AM and ecto-mycorrhizal (ECM) fungi. ECM relationships are thought to be of higher host specificity than AM fungi, found in forests of lower species richness and driven by low nitrogen availability. Their absence from tropical rainforests is often assumed. A study of the ECM of the species rich Dipterocarp forests of Sarawak showed that 86% of the root tips collected were colonised by ECM fungi and that the ECM species richness was in the range of that of temperate forests well-known for their relationships with ECM fungi (Peay et al., 2010).

We found a dominance of ECM fungi fruiting bodies in wet sclerophyll and sclerophyll forests, which was expected. There is considerably less woody debris in these habitats than in rainforests and therefore the wood-rotting saprophytes are fewer in number and produce fewer fruiting bodies. However, fruiting bodies of ECM fungi were also found in the rainforest both mountaintop and lowland, which was not as expected. Records for mountaintops (previous collections, source: Atlas of Living Australia) also show this trend. This indicates a more

significant role for ECM fungi in Wet Tropics rainforests than previously thought and that the assumption of dominance of AM fungi in Wet Tropics rainforests needs to be re-assessed.

A larger role for ECM fungi in rainforest mycorrhizal relationships may be further evidence that the Wet Tropics fungal flora will be more resilient to climate change than plants. ECM fungi survive through periods of drought, seasonal or extended, in sclerophyll forest systems. In addition, AM fungi are found in primary forests and in restoration sites (Haug, 2005) indicating rainforest species moving up in altitude in response to climate change will have access to AM fungal partners as they migrate. How this will affect the persistence of existing rainforest plant communities or the re-assembly of novel plant communities remains unknown. There has been no study of the AM or ECM fungi of the rainforests of the Wet Tropics to establish a benchmark of diversity and abundance of both mycorrhizal groups in these ecosystems. Further work that monitors changes in abundance and community structure of AM and ecto-mycorrhizal communities may provide key indicators for changes in response to climate change for both plants and fungi.

Summary and Conclusions

Part I: Rainforest biodiversity hotspots

This project identified important hotspots of evolutionary history in the Wet Tropics bioregion, specifically the Daintree region and the Cairns-Cardwell lowlands. These two regions have very different evolutionary histories that can explain their richness of biodiversity. The Daintree region is a rainforest refugium that has maintained continuous rainforest through major historical Earth changes including the last glacial maximum. The Cairns-Cardwell lowlands owes its richness of biodiversity to an inter-mixing of biotas from ancient Sahul ('Gondwana') and the Sunda shelf (Asia).

This floristic exchange was initiated approximately 20 Ma and its intensity correlated with the distance between the Sunda and Sahul shelves. The majority of lineages that arrived in Australia were fleshy-fruited species that may have been dispersed by birds and bats. These lineages radiated within Australia to become distinct species, but being better dispersors maintained a lower genetic diversity within bioregion compared to the more ancient Sahul (Gondwanan) species. Evidence suggests that the immigrant taxa established more successfully in areas that were not continuous rainforest through time. Having life history traits associated with pioneer species and that their concentration is higher outside supported refugia, it is likely that they acted as pioneer species colonizing more open and/or disturbed areas that retreated during glacial periods or in the areas that refugia re-expanded during warming periods.

The evidence of this trend can be found even within specific lineages. Our case study of the Orchidaceae genus *Bulbophyllum* exemplifies the complexity of the evolutionary history of mountaintops of the Cape York Peninsula and Wet Tropics Bioregion. The diversity of *Bulbophyllum* species occurring in this region is derived from several distinct lineages including a more ancient Sahul derived lineage and several more recent migrations from Asian lineages. Several of these lineages actively diversified after arriving in Australia, with species radiations centered in the Wet tropics region, suggesting that the renowned high biodiversity rates of the bioregion is partially owed to this inter-continental plant immigration into Australia.

Our study highlights the importance of identifying processes that shape current biodiversity patterns in order to better interpret them and make informed conservation decisions.

Part II: Mountaintop biodiversity and threat assessment

We identified seven important mountaintop areas that contain significant endemic plant diversity in the Wet Tropics bioregion. Our results predict a dismal future for all mountaintop endemic species with habitat declining by a minimum of 64% by 2040 and by a minimum of 97% by 2080. At least 13 of the 19 species investigated are projected to go extinct if unable to acclimate to novel climatic conditions. Given these projections, all 19 species may qualify for Critically Endangered Status under the IUCN Red List Criteria. We strongly advocate both follow research and follow up action plans, which may include:

- ~ Research on other potential refugia such as Mt. Elliot just south of the Wet Tropics bio-region boundary
- ~ Experimental research on the acclimation potential of seedlings of these species to changing temperature and moisture consistent with climate change projections
- ~ Collection of seeds and tissue for seed and tissue banks
- ~ Propagation and maintenance of *ex situ* populations in public botanical garden facilities

- ~ Systematic surveys of mountaintop endemic species to improve knowledge of their distribution and abundance
- ~ Studies of genetic diversity in threatened mountaintop plant species.

The first systematic fungal survey of the mountain environments of northeast Queensland has been completed. It is clear the region is still under-collected and species descriptions are required but we now have a better understanding of the current fungal flora of this environment, which may change under projected climate change conditions. This work has highlighted the need to understand the mycorrhizal partners of the rainforests of the Wet Tropics, at all altitudes, and will form the basis of a published checklist of the fungi of northeast Queensland and future fungal inventories and is a key study for advancing knowledge on tropical fungi in Australia.

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Outputs from this project

Appendix 1: List of publications

Peer reviewed scientific papers:

- Baba Y, Crayn DM. (2012). *Elaeocarpus hylobroma* (Elaeocarpaceae): a new species endemic to mountain tops in northeast Queensland, Australia. *Kew Bulletin* **67**: 743–750. DOI: 10.1007/s12225-012-9398-9
- Costion C, Edwards W, Ford AJ, Metcalfe DJ, Cross HB, Harrington MG, Richardson JE, Hilbert DW, Lowe AJ, Crayn DM. (2014). Using phylogenetic diversity to identify ancient rainforest refugia and diversification zones in a biodiversity hotspot. *Diversity and Distributions* In Press: DOI: 10.1111/ddi.12266
- Crayn D, Costion C, Harrington M. (2015). The Sahul-Sunda floristic exchange: dated molecular phylogenies document post-Miocene intercontinental dispersal dynamics. *Journal of Biogeography* **42**: 11–24. DOI:10.1111/jbi.12405
- Kooyman RM, Rossetto M, Sauquet H, Laffan SW. (2013). Landscape patterns in rainforest phylogenetic signal: Isolated islands of refugia or structured continental distributions? *PloS One* **8**, e80685. DOI: 10.1371/journal.pone.0080685
- Kooyman RM, Wilf P, Barreda VD, Carpenter RJ, Jordan GJ, Sniderman JMK, Allen A, Brodribb TJ, Crayn D, Feild TS, Laffan SW, Lusk CH, Rossetto M, Weston PH. (2014). Paleo-Antarctic rainforest into the modern Old World tropics: The rich past and threatened future of the “southern wet forest survivors”. *American Journal of Botany* **101**: 2121–2135 DOI: 10.3732/ajb.1400340
- Largent DL, Bergemann SE, Abell-Davis SE, Kluting KL, Cummings GA. (2013). Three new *Inocephalus* species with cuboid basidiospores from New South Wales and Queensland, Australia. *Mycotaxon* **123**: 301–319. DOI: 10.5248/123.301
- Largent DL, Bergemann SE, Abell-Davis SE, Kluting KL, Cummings GA. (2013). Five *Leptonia* species from New South Wales and Queensland, Australia. *Mycotaxon* **125**: 11–35. DOI: 10.5248/125.11
- Richardson JE, Costion CM, Muellner AN. (2012). The Malesian Floristic Interchange. In *Biotic Evolution and Environmental Change in Southeast Asia* (eds. D.J Gower, J.E. Richardson, B.R. Rosen, L. Rüber, S.T. Williams), pp. 138–163. Cambridge University Press.

Appendix 2: List of conference presentations

- Abell-Davis S, Nuske SJ, Crayn DM, May TM (2014) Connecting the codes: matching environmental sequence data to vouchered sequestrate ectomycorrhizal fungi in Australia. 10th International Mycological Congress, Thailand.
- Bransgrove K, Abell-Davis S, Crayn D, Summerell B. (2012) Biodiversity and Host Specificity of the Fungal Endophytes of the Wet Tropics. Australian Mycological Society (AMS), Cairns. [oral]
- Bransgrove K, Abell-Davis S, Crayn D, Summerell B. (2013) Mountaintop fungal endophytes of the wet tropics, Queensland: biodiversity, host specificity, biogeography and systematics. Systematics Without Borders, Australasian Systematic Botany Society and the Society of Australasian Systematic Biologists, Sydney NSW [oral]. Winner, Pauline Ladiges prize for best student presentation.
- Bransgrove K, Abell-Davis S, Crayn D, Summerell B. (2013) Biodiversity and host specificity of the fungal endophytes of the wet tropics of north-east Queensland, Australia. 9th International Flora Malesiana symposium, Bogor, Indonesia [oral].
- Bransgrove K, Abell-Davis S. (2012) Fungal Endophytes of the Rainforest of North-East Queensland, Australia. British Mycological Society (BMS) 'Fungal Interactions' Conference, Alicante, Spain. [poster]
- Costion C, Crayn D, Lowe A (2011). Tree DNA barcoding of the Australian Wet Tropics: species delineation and diversity estimation. XVIII International Botanical Congress, Melbourne VIC [oral].
- Costion C, Edwards W, Ford A, Metcalfe D, Cross H, Harrington M, Richardson JE, Lowe A, Crayn D. (2013) Layers in the landscape: The SE Asian flora in NE Queensland. South East Asian Gateway Evolution (SAGE) 2013, Berlin, Germany [oral].
- Costion C, Simpson L, Pert P, Crayn D. (2014) Vanishing with the clouds: climate change projections infer rapid declines of mountain top endemic plants of tropical northeast Queensland, Australia. Association for Tropical Biology and Conservation (ATBC) 'The Future of Tropical Biology and Conservation Conference', Cairns QLD [oral].
- Crayn D, Costion C, Harrington M. (2011). Laurasian invasion? Phylogenetics and the origins of the Australian tropical rainforest flora. XVIII International Botanical Congress, Melbourne VIC [oral].
- Crayn D, Costion C, Harrington M, Thornhill A. (2013) Historical dynamics of the Sahul-Sunda floristic exchange and the impact on northern Australian biodiversity. Systematics Without Borders, Australasian Systematic Botany Society and the Society of Australasian Systematic Biologists, Sydney NSW [oral].
- Crayn D, Harrington M, Costion C. (2012) Plant dispersal across Wallacea: dated molecular phylogenies reveal the dynamics of the Sahul-Sunda floristic exchange. Australian Systematic Botany Society 2012 Conference, Perth WA [oral].
- Crayn D, Harrington M, Costion C. (2013) Who wins when north and south collide? The historical dynamics of intercontinental floristic exchange across Wallacea. South East Asian Gateway Evolution (SAGE) 2013, Berlin, Germany [oral].

- Crayn D, Harrington M, Costion C. (2013) Who wins when north and south collide? The historical dynamics of intercontinental floristic exchange across Wallacea. Southern Connections 2013 Conference, Dunedin, New Zealand [oral].
- Crayn DM, Costion C, Bransgrove K, Abell-Davis S, Simpson L, Schulte K, Metcalfe D, Rossetto M, Lowe A, Williams S. (2013) What is at risk? Identifying rainforest refugia and hotspots of plant genetic diversity in the Wet Tropics and Cape York Peninsula. National Environmental Research Program (NERP) Tropical Ecosystems Hub Conference, Cairns [oral].
- Crayn DM, Costion C, Harrington M. (2013) The Sahul-Sunda floristic exchange: dated molecular phylogenies document post-Miocene intercontinental dispersal. 9th International Flora Malesiana Symposium, Bogor, Indonesia [oral].
- Schulte K, Micheneau C. (2014) Next-generation tropical biodiversity science and conservation – opportunities and challenges. Association for Tropical Biology and Conservation (ATBC) 'The Future of Tropical Biology and Conservation Conference', Cairns QLD [oral].
- Schulte K, Micheneau C. (2013) Rapid species identification and discovery in the age of next generation sequencing – opportunities and challenges. Bushblitz Symposium – Adding to Australia's biodiversity picture, Canberra [oral].
- Simpson L, Clements M, Crayn D, Schulte K. (2013) What is at risk? Phylogeography and taxonomy of orchids endemic to Queensland's mountaintop biodiversity hotspots. Systematics Without Borders, Australasian Systematic Botany Society and the Society of Australasian Systematic Biologists, Sydney NSW [oral].
- Simpson L, Clements M, Costion C, Pert P, Crayn D, Schulte K. (2014) What is at risk? Climate impacts on Australia's Wet Tropics mountaintop plant diversity. Australasian Systematic Botany Society conference, Palmerston North, New Zealand
- Simpson L (2012) What is at risk? Phylogeography and taxonomy of orchids endemic to Australia's Wet Tropics mountaintop biodiversity hotspots. Australian Systematic Botany Society conference, Perth WA [poster]
- Simpson L. (2013) What is at risk? Phylogeography and taxonomy of orchids endemic to Queensland's mountaintop biodiversity hotspots. PhD confirmation seminar, JCU, Cairns [oral].

Appendix 3: List of species from the PD study sequenced and accessioned into GenBank

Family	Taxon	GenBank Accession
Acanthaceae	<i>Graptophyllum excelsum</i>	KF496794
Acanthaceae	<i>Hypoestes floribunda</i>	KF496829
Acanthaceae	<i>Pseuderanthemum variabile</i>	KF496479
Acanthaceae	<i>Ruellia</i> sp.	KF496849
Actinidiaceae	<i>Saurauia andreana</i>	KF496654
Alseuosmiaceae	<i>Crispiloba disperma</i>	KF496297
Amaranthaceae	<i>Achyranthes aspera</i>	KF496324
Amaranthaceae	<i>Deeringia amaranthoides</i>	KF496554
Amaryllidaceae	<i>Proiphys</i> sp.	KF496655
Anacardiaceae	<i>Blepharocarya involucrigera</i>	KF496621
Anacardiaceae	<i>Buchanania arborescens</i>	KF496482
Anacardiaceae	<i>Euroschinus falcatus</i>	KF496522
Anacardiaceae	<i>Pleiogynium timorense</i>	KF496354
Anacardiaceae	<i>Rhus taitensis</i>	KF496709
Anacardiaceae	<i>Semecarpus australiensis</i>	KF496691
Annonaceae	<i>Cananga odorata</i>	KF496508
Annonaceae	<i>Desmos polycarpus</i>	KF496673
Annonaceae	<i>Fitzalania bidwillii</i>	KF496666
Annonaceae	<i>Goniothalamus australis</i>	KF496833
Annonaceae	<i>Haplostichanthus submontanus</i> subsp. <i>sessiliflorus</i>	KF496689
Annonaceae	<i>Meiogyne verrucosa</i>	KF496325
Annonaceae	<i>Melodorum uhrri</i>	KF496615
Annonaceae	<i>Miliusa horsfieldii</i>	KF496583
Annonaceae	<i>Mitrephora diversifolia</i>	KF496459
Annonaceae	<i>Murraya paniculata</i>	KF496528
Annonaceae	<i>Polyalthia nitidissima</i>	KF496317
Annonaceae	<i>Pseuduvaria froggattii</i>	KF496500
Annonaceae	<i>Uvaria concava</i>	KF496609
Annonaceae	<i>Xylopia maccrae</i>	KF496441
Apiaceae	<i>Centella asiatica</i>	KF496513
Apiaceae	<i>Oenanthe javanica</i>	KF496630
Apocynaceae	<i>Alstonia muelleriana</i>	KF496562
Apocynaceae	<i>Alyxia spicata</i>	KF496374
Apocynaceae	<i>Carissa ovata</i>	KF496589
Apocynaceae	<i>Cerbera floribunda</i>	KF496566
Apocynaceae	<i>Dischidia nummularia</i>	KF496800
Apocynaceae	<i>Gymnanthera oblonga</i>	KF496681
Apocynaceae	<i>Heterostemma acuminatum</i>	KF496783
Apocynaceae	<i>Hoya australis</i> subsp. <i>tenuipes</i>	KF496867

Apocynaceae	<i>Ichnocarpus frutescens</i>	KF496505
Apocynaceae	<i>Kopsia arborea</i>	KF496808
Apocynaceae	<i>Marsdenia longipedicellata</i>	KF496340
Apocynaceae	<i>Melodinus baccellianus</i>	KF496707
Apocynaceae	<i>Neisosperma poweri</i>	KF496737
Apocynaceae	<i>Parsonsia velutina</i>	KF496418
Apocynaceae	<i>Secamone elliptica</i>	KF496437
Apocynaceae	<i>Tabernaemontana pandacaqui</i>	KF496736
Apocynaceae	<i>Tylophora williamsii</i>	KF496291
Apocynaceae	<i>Wrightia laevis</i>	KF496532
Aquifoliaceae	<i>Ilex</i> sp. (<i>Gadgarra</i>)	KF496854
Aquifoliaceae	<i>Sphenostemon lobosporus</i>	KF496342
Araceae	<i>Alocasia brisbanensis</i>	KF496352
Araceae	<i>Epipremnum pinnatum</i>	KF496862
Araceae	<i>Gymnostachys anceps</i>	KF496572
Araceae	<i>Pothos longipes</i>	KF496718
Araceae	<i>Raphidophora australiana</i>	KF496472
Araceae	<i>Rhaphidospora cavernarum</i>	KF496516
Araceae	<i>Typhonium wilbertii</i>	KF496356
Araliaceae	<i>Cephalalaria cephalobotrys</i>	KF496546
Araliaceae	<i>Mackinlaya confusa</i>	KF496711
Araliaceae	<i>Motherwellia haplosciadea</i>	KF496676
Araliaceae	<i>Polyscias australiana</i>	KF496639
Araliaceae	<i>Schefflera bractescens</i>	KF496723
Araucariaceae	<i>Agathis robusta</i>	KF496614
Arecaceae	<i>Archontophoenix alexandrae</i>	KF496290
Arecaceae	<i>Arenga australasica</i>	KF496714
Arecaceae	<i>Calamus moti</i>	KF496468
Arecaceae	<i>Hydriastele wendlandiana</i>	KF496611
Arecaceae	<i>Laccospadix australasicus</i>	KF496387
Arecaceae	<i>Licuala ramsayi</i>	KF496308
Arecaceae	<i>Linospadix</i> sp.	KF496444
Arecaceae	<i>Livistona benthamii</i>	KF496442
Arecaceae	<i>Normanbayi normanbayi</i>	KF496846
Arecaceae	<i>Oraniopsis appendiculata</i>	KF496832
Arecaceae	<i>Ptychosperma elegans</i>	KF496601
Argophyllaceae	<i>Argophyllum cryptophlebum</i>	KF496493
Aristolochiaceae	<i>Aristolochia thozetii</i>	KF496713
Aristolochiaceae	<i>Pararistolochia australopithecus</i>	KF496751
Asparagaceae	<i>Cordyline cannifolia</i>	KF496576
Asparagaceae	<i>Kuntheria pedunculata</i>	KF496385
Asparagaceae	<i>Lomandra</i> sp. (Bellenden Ker)	KF496864
Asparagaceae	<i>Pleomele angustifolia</i>	KF496804
Asparagaceae	<i>Romnaldia ophiopogonoides</i>	KF496520
Asparagaceae	<i>Schelhammera multiflora</i>	KF496524
Asteraceae	<i>Adenostemma macrophyllum</i>	KF496661

Asteraceae	<i>Cyanthillium cinereum*</i>	KF496312
Atherospermataceae	<i>Daphnandra repandula</i>	KF496591
Atherospermataceae	<i>Doryphora aromatica</i>	KF496677
Atherospermataceae	<i>Dryadodaphne trachyphloia</i>	KF496366
Austrobaileyaceae	<i>Austrobaileya scandens</i>	KF496678
Balanopaceae	<i>Balanops australiana</i>	KF496463
Bignoniaceae	<i>Deplanchea tetraphylla</i>	KF496405
Bignoniaceae	<i>Pandorea pandorana</i>	KF496377
Bignoniaceae	<i>Tecomanthe sp.</i> (Roaring Meg)	KF496788
Bixaceae	<i>Cochlospermum gillivraei</i>	KF496487
Boraginaceae	<i>Cordia dichotoma</i>	KF496651
Boraginaceae	<i>Ehretia laevis</i>	KF496326
Boraginaceae	<i>Heliotropium sp.</i>	KF496613
Boryaceae	<i>Borya septentrionalis</i>	KF496791
Burseraceae	<i>Canarium australasicum</i>	KF496579
Burseraceae	<i>Garuga floribunda</i>	KF496577
Calycanthaceae	<i>Idiospermum australiense</i>	KF496448
Capparaceae	<i>Capparis arborea</i>	KF496688
Cardiopteridaceae	<i>Citronella smythii</i>	KF496665
Casuarinaceae	<i>Allocasuarina torulosa</i>	KF496457
Casuarinaceae	<i>Gymnostomaustralianum</i>	KF496820
Celastraceae	<i>Cassine melanocarpa</i>	KF496632
Celastraceae	<i>Celastrus subspicatus</i>	KF496763
Celastraceae	<i>Denhamia viridissima</i>	KF496400
Celastraceae	<i>Elaeodendron melanocarpum</i>	KF496416
Celastraceae	<i>Euonymus globularis</i>	KF496455
Celastraceae	<i>Hedraianthera porphyropetala</i>	KF496376
Celastraceae	<i>Hexaspora pubescens</i>	KF496836
Celastraceae	<i>Hippocratea barbata</i>	KF496424
Celastraceae	<i>Hypsophila dielsiana</i>	KF496422
Celastraceae	<i>Maytenus disperma</i>	KF496380
Celastraceae	<i>Perrottetia arborescens</i>	KF496358
Celastraceae	<i>Salacia chinensis</i>	KF496393
Celastraceae	<i>Siphonodon membranaceus</i>	KF496595
Clusiaceae	<i>Calophyllum sil</i>	KF496871
Clusiaceae	<i>Garcinia sp.</i> Davies Creek (J.G.Tracey 14745)	KF496847
Clusiaceae	<i>Mesua sp.</i>	KF496496
Combretaceae	<i>Macropteranthes montana</i>	KF496587
Combretaceae	<i>Terminalia sericocarpa</i>	KF496633
Commelinaceae	<i>Aneilema acuminatum</i>	KF496588
Commelinaceae	<i>Commelina ensifolia</i>	KF496644
Connaraceae	<i>Rourea brachyandra</i>	KF496534
Convolvulaceae	<i>Bonamia dietrichiana</i>	KF496556
Convolvulaceae	<i>Erycibe coccinea</i>	KF496730
Convolvulaceae	<i>Ipomoea velutina</i>	KF496622
Convolvulaceae	<i>Merremia peltata</i>	KF496716

Cornaceae	<i>Alangium villosum</i> subsp. <i>polyosmoides</i>	KF496778
Corynocarpaceae	<i>Corynocarpus cribbianus</i>	KF496364
Costaceae	<i>Costus potierae</i>	KF496638
Cucurbitaceae	<i>Diplocyclos palmatus</i>	KF496491
Cucurbitaceae	<i>Momordica cochinchinensis</i>	KF496464
Cucurbitaceae	<i>Neoachmandra cunninghamii</i>	KF496401
Cucurbitaceae	<i>Neosalsomitra clavigera</i>	KF496842
Cucurbitaceae	<i>Trichosanthes pentaphylla</i>	KF496819
Cucurbitaceae	<i>Zehneria mucronata</i>	KF496369
Cunoniaceae	<i>Acsmithia davidsonii</i>	KF496590
Cunoniaceae	<i>Ceratopetalum succirubrum</i>	KF496503
Cunoniaceae	<i>Davidsonia pruriens</i>	KF496535
Cunoniaceae	<i>Geissois biagiana</i>	KF496295
Cunoniaceae	<i>Gillbeea adenopetala</i>	KF496454
Cunoniaceae	<i>Pseudoweinmannia lachnocarpa</i>	KF496758
Cunoniaceae	<i>Pullea stutzeri</i>	KF496606
Cunoniaceae	<i>Schizomeria whitei</i>	KF496494
Cupressaceae	<i>Callitris</i> sp.	KF496460
Cyperaceae	<i>Carex horsfieldii</i>	KF496637
Cyperaceae	<i>Cyperus gracilis</i>	KF496824
Cyperaceae	<i>Exocarya scleroides</i>	KF496341
Cyperaceae	<i>Hypolytrum nemorum</i>	KF496738
Cyperaceae	<i>Mapania macrocephala</i>	KF496498
Cyperaceae	<i>Paramapania parvibractea</i>	KF496334
Cyperaceae	<i>Rhynchospora corymbosa</i>	KF496719
Cyperaceae	<i>Scleria brownii</i>	KF496640
Dichapetalaceae	<i>Dichapetalum papuanum</i>	KF496761
Dilleniaceae	<i>Dillenia alata</i>	KF496868
Dilleniaceae	<i>Hibbertia scandens</i>	KF496426
Dilleniaceae	<i>Tetracera daemeliana</i>	KF496699
Dioscoreaceae	<i>Dioscorea alata</i>	KF496870
Droseraceae	<i>Drosera prolifera</i>	KF496415
Ebenaceae	<i>Diospyros hebecarpa</i>	KF496697
Elaeagnaceae	<i>Elaeagnus triflora</i>	KF496304
Elaeocarpaceae	<i>Aceratium ferrugineum</i>	KF496865
Elaeocarpaceae	<i>Elaeocarpus bancroftii</i>	KF496623
Elaeocarpaceae	<i>Peripentadenia phelpsii</i>	KF496571
Elaeocarpaceae	<i>Sloanea australis</i> subsp. <i>parviflora</i>	KF496841
Ericaceae	<i>Acrothamnus spathaceus</i>	KF496287
Ericaceae	<i>Dracophyllum sayeri</i>	KF496465
Ericaceae	<i>Leucopogon spathaceus</i>	KF496303
Ericaceae	<i>Paphia meiniana</i>	KF496403
Ericaceae	<i>Trochocarpa bellendenkerensis</i>	KF496384
Erythroxylaceae	<i>Erythroxylum ecarinatum</i>	KF496852
Escalloniaceae	<i>Polyosma alangiacea</i>	KF496735
Euphorbiaceae	<i>Alchornea thozetiana</i>	KF496641

Euphorbiaceae	<i>Aleurites moluccanus</i>	KF496724
Euphorbiaceae	<i>Baloghia parviflora</i>	KF496536
Euphorbiaceae	<i>Claoxylon tenerifolium</i>	KF496626
Euphorbiaceae	<i>Cleidion javanicum</i>	KF496299
Euphorbiaceae	<i>Codiaeum variegatum</i>	KF496627
Euphorbiaceae	<i>Croton insularis</i>	KF496848
Euphorbiaceae	<i>Dimorphocalyx australiensis</i>	KF496685
Euphorbiaceae	<i>Endospermum myrmecophilum</i>	KF496564
Euphorbiaceae	<i>Fontainea picrosperma</i>	KF496545
Euphorbiaceae	<i>Homalanthus novoguineensis</i>	KF496635
Euphorbiaceae	<i>Hylandia dockrillii</i>	KF496717
Euphorbiaceae	<i>Mallotus mollissimus</i>	KF496392
Euphorbiaceae	<i>Omphalea queenslandiae</i>	KF496563
Euphorbiaceae	<i>Rockinghamia angustifolia</i>	KF496526
Euphorbiaceae	<i>Wetria australiensis</i>	KF496664
Eupomatiaceae	<i>Eupomatia laurina</i>	KF496647
Fabaceae	<i>Abrus precatorius</i>	KF496667
Fabaceae	<i>Acacia celsa</i>	KF496481
Fabaceae	<i>Adenanthera pavonina</i>	KF496787
Fabaceae	<i>Albizia sp.</i>	KF496694
Fabaceae	<i>Archidendron grandiflorum</i>	KF496702
Fabaceae	<i>Archidendropsis sp.</i>	KF496712
Fabaceae	<i>Austrosteenisia sp.</i>	KF496413
Fabaceae	<i>Caesalpinia traceyi</i>	KF496612
Fabaceae	<i>Callerya pilipes</i>	KF496809
Fabaceae	<i>Calopogonium mucunoides</i>	KF496684
Fabaceae	<i>Canavalia papuana</i>	KF496866
Fabaceae	<i>Cassia queenslandica</i>	KF496815
Fabaceae	<i>Castanospermum australe</i>	KF496507
Fabaceae	<i>Cynometra iripa</i>	KF496756
Fabaceae	<i>Derris trifoliata</i>	KF496391
Fabaceae	<i>Desmodium tortuosum</i>	KF496394
Fabaceae	<i>Dioclea hexandra</i>	KF496408
Fabaceae	<i>Entada phaseoloides</i>	KF496514
Fabaceae	<i>Erythrina variegata</i>	KF496750
Fabaceae	<i>Erythrophleum chlorostachys</i>	KF496399
Fabaceae	<i>Flemingia parviflora</i>	KF496570
Fabaceae	<i>Intsia bijuga</i>	KF496786
Fabaceae	<i>Maniltoa lenticellata</i>	KF496825
Fabaceae	<i>Millettia pinnata</i>	KF496373
Fabaceae	<i>Ormosia ormondii</i>	KF496679
Fabaceae	<i>Pararchidendron pruinsum</i>	KF496772
Fabaceae	<i>Paraserianthes toona</i>	KF496288
Fabaceae	<i>Rhynchosia minima</i>	KF496856
Fabaceae	<i>Senna coronilloides</i>	KF496645
Fabaceae	<i>Storckia australiensis</i>	KF496449

Fabaceae	<i>Vandasina retusa</i>	KF496368
Flagellariaceae	<i>Flagellaria indica</i>	KF496381
Gentianaceae	<i>Fagraea cambagei</i>	KF496414
Gentianaceae	<i>Geniostoma rupestre</i> var. <i>australiana</i>	KF496575
Gesneriaceae	<i>Boea kinneari</i>	KF496760
Gesneriaceae	<i>Cyrtandra baileyi</i>	KF496462
Gesneriaceae	<i>Lenbrassia australiana</i>	KF496302
Goodeniaceae	<i>Scaevola enantophylla</i>	KF496512
Hamamelidaceae	<i>Neostrearia fleckeri</i>	KF496801
Hamamelidaceae	<i>Noahdendron nicholasii</i>	KF496309
Hamamelidaceae	<i>Ostrearia australiana</i>	KF496410
Hemerocallidaceae	<i>Dianella atraxis</i>	KF496710
Hernandiaceae	<i>Hernandia nymphaeifolia</i>	KF496470
Himantandraceae	<i>Galbulimima baccata</i>	KF496753
Hypoxidaceae	<i>Molineria capitulata</i>	KF496544
Icacinaeae	<i>Apodytes brachystylis</i>	KF496467
Lamiaceae	<i>Basilicum polystachyon</i>	KF496565
Lamiaceae	<i>Callicarpa longifolia</i>	KF496313
Lamiaceae	<i>Clerodendrum floribundum</i> var. <i>ovatum</i>	KF496552
Lamiaceae	<i>Faradaya splendida</i>	KF496602
Lamiaceae	<i>Glossocarya hemiderma</i>	KF496706
Lamiaceae	<i>Gmelina fasciculiflora</i>	KF496817
Lamiaceae	<i>Orthosiphon aristatus</i>	KF496653
Lamiaceae	<i>Plectranthus amicornum</i>	KF496704
Lamiaceae	<i>Premna serratifolia</i>	KF496428
Lamiaceae	<i>Vitex acuminata</i>	KF496336
Lamiaceae	<i>Viticipremna queenslandica</i>	KF496396
Lauraceae	<i>Beilschmiedia bancroftii</i>	KF496701
Lauraceae	<i>Cinnamomum laubatii</i>	KF496668
Lauraceae	<i>Cryptocarya angulata</i>	KF496458
Lauraceae	<i>Endiandra cowleyana</i>	KF496859
Lauraceae	<i>Lindera queenslandica</i>	KF496338
Lauraceae	<i>Litsea leefeana</i>	KF496321
Lauraceae	<i>Neolitsea dealbata</i>	KF496461
Lecythidaceae	<i>Barringtonia calyptrata</i>	KF496359
Lecythidaceae	<i>Planchonia careya</i>	KF496802
Linaceae	<i>Hugonia jenkinsii</i>	KF496383
Loganiaceae	<i>Strychnos minor</i>	KF496419
Loranthaceae	<i>Amyema villiflora</i> subsp. <i>tomentilla</i>	KF496740
Loranthaceae	<i>Amylothea dictyophleba</i>	KF496311
Loranthaceae	<i>Dendrophthoe vitellina</i>	KF496466
Loranthaceae	<i>Diplatia furcata</i>	KF496292
Lythraceae	<i>Lagerstroemia archeriana</i>	KF496670
Malvaceae	<i>Abelmoschus moschatus</i> subsp. <i>tuberosus</i>	KF496619
Malvaceae	<i>Abutilon oxycarpon</i>	KF496687
Malvaceae	<i>Argyrodendron peralatum</i>	KF496739

Malvaceae	<i>Bombax ceiba</i> var. <i>leiocarpum</i>	KF496596
Malvaceae	<i>Brachychiton acerifolius</i>	KF496450
Malvaceae	<i>Commersonia bartramia</i>	KF496759
Malvaceae	<i>Firmiana papuana</i>	KF496411
Malvaceae	<i>Franciscodendron laurifolium</i>	KF496807
Malvaceae	<i>Grewia papuana</i>	KF496779
Malvaceae	<i>Helicteres isora</i>	KF496517
Malvaceae	<i>Heritiera littoralis</i>	KF496435
Malvaceae	<i>Hibiscus tiliaceus</i>	KF496860
Malvaceae	<i>Kleinhovia hospita</i>	KF496484
Malvaceae	<i>Sterculia quadrifida</i>	KF496629
Malvaceae	<i>Thespesia populneoides</i>	KF496542
Malvaceae	<i>Trichospermum pleiostigma</i>	KF496599
Melastomataceae	<i>Melastoma affine</i>	KF496618
Melastomataceae	<i>Memecylon pauciflorum</i>	KF496398
Meliaceae	<i>Aglaia argentea</i>	KF496592
Meliaceae	<i>Anthocarapa nitidula</i>	KF496421
Meliaceae	<i>Chisocheton longistipitatus</i>	KF496370
Meliaceae	<i>Dysoxylum gaudichaudianum</i>	KF496781
Meliaceae	<i>Melia azedarach</i>	KF496754
Meliaceae	<i>Synoum glandulosum</i> subsp. <i>paniculosum</i>	KF496603
Meliaceae	<i>Toona ciliata</i>	KF496355
Meliaceae	<i>Turraea pubescens</i>	KF496790
Meliaceae	<i>Vavaea amicorum</i>	KF496432
Menispermaceae	<i>Carronia protensa</i>	KF496372
Menispermaceae	<i>Hypserpa smilacifolia</i>	KF496310
Menispermaceae	<i>Legnephora moorei</i>	KF496367
Menispermaceae	<i>Pachygone ovata</i>	KF496322
Menispermaceae	<i>Parapachygone longifolia</i>	KF496543
Menispermaceae	<i>Pleogyne australis</i>	KF496594
Menispermaceae	<i>Pycnarrhena novoguineensis</i>	KF496446
Menispermaceae	<i>Stephania japonica</i>	KF496796
Menispermaceae	<i>Tinospora smilacina</i>	KF496604
Monimiaceae	<i>Austromatthaea elegans</i>	KF496436
Monimiaceae	<i>Endressia wardellii</i>	KF496636
Monimiaceae	<i>Hedycarya loxocarya</i>	KF496729
Monimiaceae	<i>Kibara rigidifolia</i>	KF496574
Monimiaceae	<i>Levieria acuminata</i>	KF496510
Monimiaceae	<i>Palmeria scandens</i>	KF496477
Monimiaceae	<i>Stegantthera laxiflora</i>	KF496732
Monimiaceae	<i>Wilkiea angustifolia</i>	KF496597
Moraceae	<i>Antiaris toxicaria</i>	KF496469
Moraceae	<i>Ficus destruens</i>	KF496521
Moraceae	<i>Streblus glaber</i> subsp. <i>australianus</i>	KF496327
Moraceae	<i>Trophis scandens</i>	KF496675
Musaceae	<i>Musa banksii</i>	KF496696

Myristicaceae	<i>Horsfieldia australiana</i>	KF496315
Myristicaceae	<i>Myristica globosa</i>	KF496610
Myrtaceae	<i>Acmena resa</i>	KF496616
Myrtaceae	<i>Acmenosperma claviflorum</i>	KF496648
Myrtaceae	<i>Archirhodomyrtus beckleri</i>	KF496489
Myrtaceae	<i>Austromyrtus hillii</i>	KF496423
Myrtaceae	<i>Backhousia enata</i>	KF496323
Myrtaceae	<i>Callistemon viminalis</i>	KF496747
Myrtaceae	<i>Corymbia torelliana</i>	KF496869
Myrtaceae	<i>Decaspermum humile</i>	KF496348
Myrtaceae	<i>Eucalyptus pellita</i>	KF496742
Myrtaceae	<i>Eugenia sp.</i>	KF496789
Myrtaceae	<i>Gossia shepherdii</i>	KF496811
Myrtaceae	<i>Lenwebbia lasioclada</i>	KF496306
Myrtaceae	<i>Leptospermum wooroonooran</i>	KF496839
Myrtaceae	<i>Lindsayomyrtus racemoides</i>	KF496850
Myrtaceae	<i>Lithomyrtus obtusa</i>	KF496511
Myrtaceae	<i>Lophostemon suaveolens</i>	KF496643
Myrtaceae	<i>Melaleuca stenostachya</i>	KF496727
Myrtaceae	<i>Pilidiostigma sessile</i>	KF496525
Myrtaceae	<i>Rhodamnia blairiana</i>	KF496497
Myrtaceae	<i>Rhodomyrtus macrocarpa</i>	KF496509
Myrtaceae	<i>Ristantia gouldii</i>	KF496365
Myrtaceae	<i>Sphaerantia discolor</i>	KF496530
Myrtaceae	<i>Stockwellia quadrifida</i>	KF496584
Myrtaceae	<i>Syncarpia glomulifera</i>	KF496683
Myrtaceae	<i>Syzygium kuranda</i>	KF496573
Myrtaceae	<i>Thaleropia queenslandica</i>	KF496519
Myrtaceae	<i>Tristaniopsis exiliflora</i>	KF496649
Myrtaceae	<i>Waterhousea unipunctata</i>	KF496822
Myrtaceae	<i>Xanthostemon whitei</i>	KF496720
Nyctaginaceae	<i>Pisonia umbellifera</i>	KF496550
Ochnaceae	<i>Brackenridgea australiana</i>	KF496371
Olcaceae	<i>Ximenia americana</i>	KF496540
Oleaceae	<i>Chionanthus axillaris</i>	KF496397
Oleaceae	<i>Jasminum simplicifolium</i>	KF496748
Oleaceae	<i>Ligustrum australicum</i>	KF496755
Oleaceae	<i>Olea paniculata</i>	KF496329
Opiliaceae	<i>Opilia amentacea</i>	KF496431
Orchidaceae	<i>Anoectochilus yatesiae</i>	KF496538
Orchidaceae	<i>Apostasia stylidioides</i>	KF496553
Orchidaceae	<i>Appendicula australiensis</i>	KF496659
Orchidaceae	<i>Bulbophyllum gadgarrense</i>	KF496557
Orchidaceae	<i>Cadetia taylori</i>	KF496803
Orchidaceae	<i>Cepobaculum trilamellatum</i>	KF496773
Orchidaceae	<i>Cestichis bracteata</i>	KF496746

Orchidaceae	<i>Cymbidium madidum</i>	KF496417
Orchidaceae	<i>Dendrobium fleckeri</i>	KF496350
Orchidaceae	<i>Dienia ophrydis</i>	KF496652
Orchidaceae	<i>Eria kingii</i>	KF496445
Orchidaceae	<i>Grastidium baileyi</i>	KF496452
Orchidaceae	<i>Plectorrhiza brevilabris</i>	KF496695
Orchidaceae	<i>Rhychophoretia micrantha</i>	KF496705
Pandanaceae	<i>Freycinetia scandens</i>	KF496855
Pandanaceae	<i>Pandanus gemmifer</i>	KF496764
Paracryphiaceae	<i>Quintinia quatrefagesii</i>	KF496721
Passifloraceae	<i>Adenia heterophylla</i>	KF496339
Passifloraceae	<i>Passiflora kuranda</i>	KF496451
Pennantiaceae	<i>Pennantia cunninghamii</i>	KF496752
Philesiaceae	<i>Eustrephus latifolius</i>	KF496692
Philesiaceae	<i>Geitonoplesium cymosum</i>	KF496453
Philydraceae	<i>Helmholtzia acorifolia</i>	KF496541
Phyllanthaceae	<i>Actephila foetida</i>	KF496353
Phyllanthaceae	<i>Antidesma buniis</i>	KF496438
Phyllanthaceae	<i>Bischofia javanica</i>	KF496300
Phyllanthaceae	<i>Breynia stipitata</i>	KF496301
Phyllanthaceae	<i>Bridelia tomentosa</i>	KF496797
Phyllanthaceae	<i>Cleistanthus hylandii</i>	KF496529
Phyllanthaceae	<i>Flueggea leucopyrus</i>	KF496726
Phyllanthaceae	<i>Glochidion harveyanum</i>	KF496473
Phyllanthaceae	<i>Phyllanthus lamprophyllus</i>	KF496834
Phyllanthaceae	<i>Sauropus macranthus</i>	KF496502
Picrodendraceae	<i>Austrobuxus megacarpus</i>	KF496837
Picrodendraceae	<i>Choriceras tricornis</i>	KF496775
Picrodendraceae	<i>Dissiliaria surculosa</i>	KF496425
Picrodendraceae	<i>Sankowskyia stipularis</i>	KF496351
Picrodendraceae	<i>Whyanbeelia terrae-reginae</i>	KF496330
Piperaceae	<i>Peperomia hunteriana</i>	KF496734
Piperaceae	<i>Piper umbellatum</i>	KF496838
Pittosporaceae	<i>Auranticarpa papyracea</i>	KF496567
Pittosporaceae	<i>Bursaria incana</i>	KF496715
Pittosporaceae	<i>Pittosporum rubiginosum</i>	KF496296
Poaceae	<i>Ancistrachne uncinulata</i>	KF496582
Poaceae	<i>Centotheca lappacea</i>	KF496319
Poaceae	<i>Cyrtococcum oxyphyllum</i>	KF496382
Poaceae	<i>Entolasia stricta</i>	KF496605
Poaceae	<i>Garnotia stricta</i>	KF496708
Poaceae	<i>Ichnanthus pallens</i> var. <i>major</i>	KF496332
Poaceae	<i>Leptaspis banksii</i>	KF496490
Poaceae	<i>Lophatherum gracile</i>	KF496693
Poaceae	<i>Microlaena stipoides</i>	KF496828
Poaceae	<i>Mullerochloa moreheadiana</i>	KF496682

Poaceae	<i>Neololeba atra</i>	KF496362
Poaceae	<i>Oplismenus compositus</i>	KF496501
Poaceae	<i>Ottochloa nodosa</i>	KF496551
Poaceae	<i>Panicum mitchellii</i>	KF496857
Poaceae	<i>Pogonatherum crinitum</i>	KF496620
Poaceae	<i>Sacciolepis indica</i>	KF496561
Podocarpaceae	<i>Podocarpus grayae</i>	KF496658
Podocarpaceae	<i>Prumnopitys ladei</i>	KF496548
Podocarpaceae	<i>Sundacarpus amarus</i>	KF496700
Polygonaceae	<i>Persicaria barbata</i>	KF496757
Primulaceae	<i>Ardisia pachyrrhachis</i>	KF496642
Primulaceae	<i>Embelia australiana</i>	KF496298
Primulaceae	<i>Maesa dependens</i>	KF496293
Primulaceae	<i>Myrsine achradifolia</i>	KF496523
Primulaceae	<i>Rapanea achradifolia</i>	KF496767
Primulaceae	<i>Tapeinosperma pallidum</i>	KF496443
Proteaceae	<i>Alloxylon wickhamii</i>	KF496744
Proteaceae	<i>Athertonia diversifolia</i>	KF496433
Proteaceae	<i>Austromuellera trinervia</i>	KF496792
Proteaceae	<i>Banksia aquilonia</i>	KF496762
Proteaceae	<i>Buckinghamia celsissima</i>	KF496743
Proteaceae	<i>Cardwellia sublimis</i>	KF496657
Proteaceae	<i>Carnarvonia araliifolia</i> var. <i>montana</i>	KF496631
Proteaceae	<i>Catalepidia heyana</i>	KF496853
Proteaceae	<i>Darlingia darlingiana</i>	KF496617
Proteaceae	<i>Eidothea zoexylocarya</i>	KF496531
Proteaceae	<i>Gevuina bleasdalei</i>	KF496608
Proteaceae	<i>Grevillea baileyana</i>	KF496388
Proteaceae	<i>Helicia australasica</i>	KF496360
Proteaceae	<i>Hicksbeachia pilosa</i>	KF496533
Proteaceae	<i>Hollandaea sayeriana</i>	KF496672
Proteaceae	<i>Lasjia claudiensis</i>	KF496722
Proteaceae	<i>Lomatia fraxinifolia</i>	KF496331
Proteaceae	<i>Macaranga inamoena</i>	KF496314
Proteaceae	<i>Megahertzia amplexicaulis</i>	KF496390
Proteaceae	<i>Musgravea heterophylla</i>	KF496480
Proteaceae	<i>Neorites kevedianus</i>	KF496378
Proteaceae	<i>Opisthiolepis heterophylla</i>	KF496495
Proteaceae	<i>Placospermum coriaceum</i>	KF496818
Proteaceae	<i>Sphalmium racemosum</i>	KF496795
Proteaceae	<i>Stenocarpus davallioides</i>	KF496345
Putranjavaceae	<i>Drypetes</i> sp.	KF496568
Ranunculaceae	<i>Clematis pickeringii</i>	KF496518
Rhamnaceae	<i>Alphitonia excelsa</i>	KF496294
Rhamnaceae	<i>Colubrina asiatica</i>	KF496826
Rhamnaceae	<i>Emmenosperma alphitonioides</i>	KF496412

Rhamnaceae	<i>Gouania australiana</i>	KF496766
Rhamnaceae	<i>Rhamnella vitiensis</i>	KF496656
Rhamnaceae	<i>Sageretia hamosa</i>	KF496858
Rhamnaceae	<i>Schistocarpaea johnsonii</i>	KF496843
Rhipogonaceae	<i>Ripogonum album</i>	KF496404
Rhizophoraceae	<i>Carallia brachiata</i>	KF496851
Rosaceae	<i>Prunus turneriana</i>	KF496483
Rosaceae	<i>Rubus queenslandicus</i>	KF496782
Rousseaceae	<i>Abrophyllum ornans</i>	KF496798
Rubiaceae	<i>Aidia racemosa</i>	KF496555
Rubiaceae	<i>Antirhea</i> sp. (Mt Lewis)	KF496600
Rubiaceae	<i>Atractocarpus hirtus</i>	KF496686
Rubiaceae	<i>Bobea myrtoides</i>	KF496863
Rubiaceae	<i>Canthium lamprophyllum</i>	KF496741
Rubiaceae	<i>Coelospermum purpureum</i>	KF496476
Rubiaceae	<i>Cyclophyllum multiflorum</i>	KF496474
Rubiaceae	<i>Gardenia ovularis</i>	KF496827
Rubiaceae	<i>Gen.</i> (AQ124851) sp.	KF496812
Rubiaceae	<i>Genus</i> (Aq520454) sp. Shute Harbour	KF496598
Rubiaceae	<i>Geophila repens</i>	KF496703
Rubiaceae	<i>Guettarda speciosa</i>	KF496830
Rubiaceae	<i>Gynochthodes oresbia</i>	KF496409
Rubiaceae	<i>Ixora oreogena</i>	KF496844
Rubiaceae	<i>Lasianthus chrysoneurus</i>	KF496471
Rubiaceae	<i>Morinda reticulata</i>	KF496337
Rubiaceae	<i>Myrmecodia</i> sp.	KF496375
Rubiaceae	<i>Nauclea orientalis</i>	KF496634
Rubiaceae	<i>Neonauclea glabra</i>	KF496549
Rubiaceae	<i>Ophiorrhiza australiana</i>	KF496537
Rubiaceae	<i>Psychotria dallachiana</i>	KF496624
Rubiaceae	<i>Psydrax laxiflorens</i>	KF496320
Rubiaceae	<i>Randia tuberculosa</i>	KF496456
Rubiaceae	<i>Tarenna dallachiana</i>	KF496806
Rubiaceae	<i>Timonius singularis</i>	KF496771
Rubiaceae	<i>Uncaria cordata</i>	KF496420
Rubiaceae	<i>Wendlandia inclusa</i>	KF496349
Rutaceae	<i>Acronychia acidula</i>	KF496407
Rutaceae	<i>Bosistoa medicinalis</i>	KF496768
Rutaceae	<i>Brombya platynema</i>	KF496439
Rutaceae	<i>Citrus garrawayi</i>	KF496793
Rutaceae	<i>Clausena brevistyla</i>	KF496725
Rutaceae	<i>Dinosperma erythrococcum</i>	KF496427
Rutaceae	<i>Euodia hylandii</i>	KF496586
Rutaceae	<i>Flindersia bourjotiana</i>	KF496335
Rutaceae	<i>Geijera salicifolia</i>	KF496628
Rutaceae	<i>Glycosmis trifoliata</i>	KF496499

Rutaceae	<i>Halfordia kendack</i>	KF496289
Rutaceae	<i>Leionema ellipticum</i>	KF496578
Rutaceae	<i>Medicosma fareana</i>	KF496749
Rutaceae	<i>Melicope vitiflora</i>	KF496669
Rutaceae	<i>Micromelum minutum</i>	KF496344
Rutaceae	<i>Pitaviaster haplophyllus</i>	KF496305
Rutaceae	<i>Sarcomelicope simplicifolia</i>	KF496580
Rutaceae	<i>Zanthoxylum ovalifolium</i>	KF496650
Rutaceae	<i>Zieria madida</i>	KF496816
Salicaceae	<i>Baileyoxylon lanceolatum</i>	KF496361
Salicaceae	<i>Casearia costulata</i>	KF496406
Salicaceae	<i>Flacourtia</i> sp. (Shiptons Flat)	KF496810
Salicaceae	<i>Homalium circumpinnatum</i>	KF496333
Salicaceae	<i>Ryparosa kurrangii</i>	KF496539
Salicaceae	<i>Scolopia braunii</i>	KF496663
Salicaceae	<i>Xylosma terrae-reginae</i>	KF496731
Santalaceae	<i>Exocarpos latifolius</i>	KF496569
Santalaceae	<i>Korthalsella grayi</i>	KF496698
Santalaceae	<i>Notothixos subaureus</i>	KF496485
Santalaceae	<i>Santalum lanceolatum</i>	KF496821
Santalaceae	<i>Viscum articulatum</i>	KF496504
Sapindaceae	<i>Alectryon connatus</i>	KF496560
Sapindaceae	<i>Allophylus cobbe</i>	KF496861
Sapindaceae	<i>Arytera pauciflora</i>	KF496585
Sapindaceae	<i>Atalaya sericopetala</i>	KF496784
Sapindaceae	<i>Castanospora alphandii</i>	KF496547
Sapindaceae	<i>Cnesmocarpon dasyantha</i>	KF496307
Sapindaceae	<i>Cupaniopsis foveolata</i>	KF496625
Sapindaceae	<i>Diploglottis smithii</i>	KF496593
Sapindaceae	<i>Elattostachys microcarpa</i>	KF496745
Sapindaceae	<i>Ganophyllum falcatum</i>	KF496316
Sapindaceae	<i>Guioa acutifolia</i>	KF496733
Sapindaceae	<i>Harpullia rhyticarpa</i>	KF496363
Sapindaceae	<i>Jagera</i> sp.	KF496799
Sapindaceae	<i>Lepiderema largiflorens</i>	KF496475
Sapindaceae	<i>Mischarytera lautereriana</i>	KF496434
Sapindaceae	<i>Mischocarpus albescens</i>	KF496440
Sapindaceae	<i>Rhysotoechia florulenta</i>	KF496728
Sapindaceae	<i>Sarcopteryx reticulata</i>	KF496379
Sapindaceae	<i>Sarcotoechia cuneata</i>	KF496680
Sapindaceae	<i>Synima reynoldsiae</i>	KF496770
Sapindaceae	<i>Toechima erythrocarpum</i>	KF496835
Sapotaceae	<i>Chrysophyllum roxburghii</i>	KF496346
Sapotaceae	<i>Mimusops elengi</i>	KF496343
Sapotaceae	<i>Niemeyera prunifera</i>	KF496558
Sapotaceae	<i>Palaquium galactoxylum</i>	KF496660

Sapotaceae	<i>Planchonella euphlebia</i>	KF496581
Sapotaceae	<i>Pouteria pearsoniorum</i>	KF496674
Sapotaceae	<i>Sersalisia sessiliflora</i>	KF496488
Sapotaceae	<i>Vanroyena castanosperma</i>	KF496780
Scrophulariaceae	<i>Myoporum montanum</i>	KF496776
Simaroubaceae	<i>Ailanthus triphysa</i>	KF496357
Simaroubaceae	<i>Brucea javanica</i>	KF496805
Simaroubaceae	<i>Quassia baileyana</i>	KF496813
Smilacaceae	<i>Smilax glyciphylla</i>	KF496785
Solanaceae	<i>Lycianthes shanesii</i>	KF496662
Solanaceae	<i>Solanum viridifolium</i>	KF496395
Stemonuraceae	<i>Gomphandra australiana</i>	KF496486
Stemonuraceae	<i>Irvingbaileya australis</i>	KF496506
Symplocaceae	<i>Symplocos ampulliformis</i>	KF496430
Taccaceae	<i>Tacca leontopetaloides</i>	KF496814
Theaceae	<i>Ternstroemia cherryi</i>	KF496845
Thymelaeaceae	<i>Lethedon setosa</i>	KF496769
Thymelaeaceae	<i>Oreodendron biflorum</i>	KF496671
Thymelaeaceae	<i>Phaleria octandra</i>	KF496607
Thymelaeaceae	<i>Wikstroemia indica</i>	KF496831
Ulmaceae	<i>Aphananthe philippinensis</i>	KF496492
Ulmaceae	<i>Celtis paniculata</i>	KF496386
Ulmaceae	<i>Trema orientalis</i>	KF496774
Urticaceae	<i>Dendrocnide photinophylla</i>	KF496478
Urticaceae	<i>Elatostema reticulatum</i>	KF496402
Urticaceae	<i>Pipturus argenteus</i>	KF496559
Urticaceae	<i>Pouzolzia zeylanica</i>	KF496389
Urticaceae	<i>Procris pedunculata</i>	KF496690
Vitaceae	<i>Cayratia saponaria</i>	KF496515
Vitaceae	<i>Cissus hypoglauca</i>	KF496646
Vitaceae	<i>Leea indica</i>	KF496447
Winteraceae	<i>Bubbia queenslandiana</i>	KF496765
Winteraceae	<i>Tasmannia membranacea</i>	KF496777
Xanthophyllaceae	<i>Xanthophyllum octandrum</i>	KF496823
Zamiaceae	<i>Lepidozamia hopei</i>	KF496328
Zingiberaceae	<i>Alpinia modesta</i>	KF496318
Zingiberaceae	<i>Amomum dallachyi</i>	KF496429
Zingiberaceae	<i>Curcuma australasica</i>	KF496840
Zingiberaceae	<i>Hornstedtia scottiana</i>	KF496347
Zingiberaceae	<i>Tapeinochilos ananassae</i>	KF496527

Appendix 4: List of species showing infraspecific variation based on DNA barcode data

Order	Family	Species
Celastrales	Celastraceae	<i>Hippocratea barbata</i>
Celastrales	Celastraceae	<i>Siphonodon australis</i>
Ericales	Primulaceae	<i>Maesa dependens</i>
Ericales	Symplocaceae	<i>Symplocos ampulliformis</i>
Ericales	Symplocaceae	<i>Symplocos cochinchensis</i>
Escalloniales	Escalloniaceae	<i>Polyosma hirsuta</i>
Fabales	Fabaceae	<i>Acacia celsa</i>
Fabales	Fabaceae	<i>Archidendron ramiflorum</i>
Fabales	Fabaceae	<i>Castanospermum australe</i>
Fabales	Fabaceae	<i>Entada phaseoloides</i>
Fabales	Polygalaceae	<i>Xanthophyllum octandrum</i>
Gentianaceae	Rubiaceae	<i>Atractocarpus fitzalanii</i>
Gentianaceae	Rubiaceae	<i>Atractocarpus hirtus</i>
Gentianaceae	Rubiaceae	<i>Everistia vacciniifolia</i>
Gentianales	Apocynaceae	<i>Parsonsia lanceolata</i>
Gentianales	Apocynaceae	<i>Tabernaemontana pandacaqui</i>
Gentianales	Gentianaceae	<i>Fagraea fagraeacea</i>
Gentianales	Rubiaceae	<i>Ixora timorensis</i>
Lamiales	Acanthaceae	<i>Graptophyllum spinigerum</i>
Lamiales	Lamiaceae	<i>Glossocarya hemiderma</i>
Laurales	Lauraceae	<i>Beilschmiedia bancroftii</i>
Laurales	Lauraceae	<i>Cryptocarya bellendenderana</i>
Laurales	Lauraceae	<i>Cryptocarya densiflora</i>
Laurales	Lauraceae	<i>Cryptocarya lividula</i>
Laurales	Lauraceae	<i>Cryptocarya mackinnoniana</i>
Laurales	Lauraceae	<i>Cryptocarya melanocarpa</i>
Laurales	Lauraceae	<i>Cryptocarya saccharata</i>
Laurales	Lauraceae	<i>Endiandra impressicosta</i>
Laurales	Lauraceae	<i>Endiandra insignis</i>
Laurales	Lauraceae	<i>Endiandra leptodendron</i>
Laurales	Lauraceae	<i>Endiandra longipedicellata</i>
Laurales	Lauraceae	<i>Litsea leefeana</i>
Laurales	Monimiaceae	<i>Stegantthera laxiflora</i>
Laurales	Monimiaceae	<i>Stegantthera macooria</i>
Laurales	Monimiaceae	<i>Wilkiea angustifolia</i>
Laurales	Monimiaceae	<i>Wilkiea macrophylla</i>
Laurales	Monimiaceae	<i>Wilkiea sp.</i>
Magnoliales	Annonaceae	<i>Goniothalamus australis</i>
Magnoliales	Annonaceae	<i>Meiogyne cylindrocarpa</i>
Magnoliales	Annonaceae	<i>Meiogyne verrucosa</i>
Magnoliales	Annonaceae	<i>Melodorum leichhardtii</i>

Magnoliales	Annonaceae	<i>Melodorum unguiculatum</i>
Magnoliales	Annonaceae	<i>Miliusa traceyi</i>
Magnoliales	Eupomatiaceae	<i>Eupomatia laurina</i>
Magnoliales	Myristicaceae	<i>Horsfieldia australiana</i>
Magnoliales	Myristicaceae	<i>Myristica globosa</i>
Malpighiales	Euphorbiaceae	<i>Claoxylon tenerifolium</i>
Malpighiales	Euphorbiaceae	<i>Croton acronychioides</i>
Malpighiales	Phyllanthaceae	<i>Breynia cernua</i>
Malpighiales	Phyllanthaceae	<i>Breynia stipitata</i>
Malpighiales	Phyllanthaceae	<i>Glochidion harveyanum</i>
Malpighiales	Phyllanthaceae	<i>Glochidion sessiliflorum</i> var. <i>pedicellatum</i>
Malvales	Malvaceae	<i>Abutilon oxycarpum</i>
Malvales	Malvaceae	<i>Argyrodendron peralatum</i>
Malvales	Malvaceae	<i>Argyrodendron polyandrum</i>
Malvales	Malvaceae	<i>Brachychiton acerifolius</i>
Malvales	Malvaceae	<i>Brachychiton australis</i>
Myrtales	Myrtaceae	<i>Gossia floribunda</i>
Myrtales	Myrtaceae	<i>Gossia retusa</i>
Myrtales	Myrtaceae	<i>Gossia shepherdii</i>
Myrtales	Myrtaceae	<i>Leptospermum wooroonooran</i>
Myrtales	Myrtaceae	<i>Lindsayomyrtus racemoides</i>
Myrtales	Myrtaceae	<i>Rhodamnia blairiana</i>
Myrtales	Myrtaceae	<i>Rhodamnia sessiliflora</i>
Myrtales	Myrtaceae	<i>Rhodomyrtus macrocarpa</i>
Myrtales	Myrtaceae	<i>Sphaerantia discolor</i>
Myrtales	Myrtaceae	<i>Syzygium fibrosum</i>
Myrtales	Myrtaceae	<i>Syzygium johnsonii</i>
Myrtales	Myrtaceae	<i>Syzygium kuranda</i>
Oxalidales	Cunoniaceae	<i>Gillbeea adenopetala</i>
Pinales	Podocarpaceae	<i>Podocarpus grayae</i>
Proteales	Proteaceae	<i>Carnarvonina araliifolia</i>
Proteales	Proteaceae	<i>Helicia australasica</i>
Proteales	Proteaceae	<i>Lomatia fraxinifolia</i>
Rosaceae	Moraceae	<i>Ficus variegata</i>
Rosales	Cannabaceae	<i>Aphananthe philippinensis</i>
Rosales	Moraceae	<i>Streblus glaber</i>
Rosales	Moraceae	<i>Trophis scandens</i>
Rosales	Rhamnaceae	<i>Emmenosperma cunninghamii</i>
Sapindales	Burseraceae	<i>Canarium australasicum</i>
Sapindales	Meliaceae	<i>Aglaia brassii</i>
Sapindales	Meliaceae	<i>Dysoxylum klanderii</i>
Sapindales	Rutaceae	<i>Acronychia peninsularis</i>
Sapindales	Rutaceae	<i>Bosistoa brassii</i>
Sapindales	Rutaceae	<i>Brombya platynema</i>
Sapindales	Rutaceae	<i>Flindersia bourjotiana</i>
Sapindales	Rutaceae	<i>Flindersia brayleyana</i>

Sapindales	Rutaceae	<i>Medicosma sessiflora</i>
Sapindales	Rutaceae	<i>Melicope stipitata</i>
Sapindales	Sapindaceae	<i>Arytera divaricata</i>
Sapindales	Sapindaceae	<i>Cupaniopsis diploglottoides</i>
Sapindales	Sapindaceae	<i>Diploglottis harpullioides</i>
Sapindales	Sapindaceae	<i>Diploglottis smithii</i>
Sapindales	Sapindaceae	<i>Elattostachys microcarpa</i>
Sapindales	Sapindaceae	<i>Harpullia rhyticarpa</i>
Sapindales	Sapindaceae	<i>Rhysotoechia robertsonii</i>
Sapindales	Sapindaceae	<i>Sarcotoechia cuneata</i>
Sapindales	Simaroubaceae	<i>Ailanthus triphysa</i>
Unplaced	Boraginaceae	<i>Ehretia membranifolia</i>
Unplaced	Icacinaceae	<i>Apodytes brachystylis</i>