

# Family Ties: A Case of Study within Myrtoideae

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**Abstract:** *Phylogenetic relationships are important to explain clade evolutionary history, but they are frequently difficult to identify. Myrtaceae family has been shown as potentially good case - study to resolve several phylogenetic questions regarding its family history and evolution. The Myrtaceae (Myrtales order) contains over 5500 species within 144 genera, distributed predominantly in Southern Hemisphere. Several Myrtaceae taxa are known for their economic importance and notable representation in the humid pleotropical forests. The family includes two subfamilies, Psiloxiloideae and Myrtoideae. Interestingly, the Myrtoideae subfamily has a marked disparity in taxa number among its tribes that it has never been explained. Moreover, it includes species with different fruit type (fleshy, dry fruits) and this peculiarity has been previously considered to explain the subfamily diversification, but to no avail. A more highly comprehensive matrix of the BKMMST clade within Myrtoideae was generated and newly analysed. The results showed that considering mainly certain character state (molecular, fruit type, habitus) has been possible provided a new interpretation of family evolution. Fruit types and habitus traits were mapped and different Myrtoideae tribes were spatially and temporally compared. The conclusions represent an added important step to explain the phylogenetic relationships of this complicated family and evaluate a new evolutionary prospective.*

**Keywords:** Phylogenetic relationship, clade evolutionary history, ancestral character reconstruction, BKMMST clade, Myrtaceae, phylogenetic tree

## 1. Introduction

The Myrtales is considered the third most species - rich Angiosperm order, with species present in many different habitats, having high flower variety and fruit type (Dahlgren and Thorne 1984). It includes nine families *sensu* APG IV, but most without a clear phylogeny (Dahlgren and Thorne 1984; Stevens 2001; APG IV 2016; Berger et al.2016).

The Myrtaceae is nested within the order and has been intensively studied (Johnson and Briggs 1984; Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010; Thornhill et al.2015). However, only a few morphological factors were assessed initially and occurred in a poor phylogenetic resolution of this moderately sized family (Johnson and Briggs 1984). New taxa and molecular inputs were evaluated, only the main singular Myrtaceae clades were individuated and largely supported (Wilson et al.2001). Although the combination of morphological and molecular information has since resulted in a low congruence between them, several analyses have revealed an intense homoplasy within the family (Gadek et al.1996; Wilson et al.2001, 2005).

The family is composed of about 144 genera and over 5500 species and it is divided into two subfamilies, Psiloxiloideae and Myrtoideae, and 17 tribes (Wilson et al.2005; Wilson 2011). It is distributed predominantly in the Southern Hemisphere (Wilson et al.2001; Biffin et al.2010; Wilson 2011; Thornhill et al.2015), where its taxa occupy a wide range of diverse habitats, from moist tropical and subtropical forests to dry savannahs, from damp - wet to sandy soils and from coastal or lowland to mountain areas (Wilson 2011). The family is particularly well known for its economic importance (e. g. essential oils in *Eucalyptus* spp., several aromatic species in *Syzygium cumini*, edible fruit of *Psidium guajava* and ornamental use of *Callistemon* spp.). The Myrtaceae also represent an important component of humid

tropical forests; they are widely distributed in humid Pleotropical forests, with species and lineage diversity centred in the Australasian region (Craven 2001; Fig.1).

In this family, taxa have either fleshy or dry fruit; consequently, in the past, this distinction was used to manage the taxonomy of the group (McVaugh 1968; Biffin et al.2010). Traditionally, the fleshy fruit character was thought to have originated only once in Myrtaceae evolutionary history, but recently, more data have suggested that this state has multiple, separate origins within the same family (Johnson and Briggs 1984; Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010).

The Myrtaceae is a very old family, placed in the middle - late Cretaceous (Biffin et al.2010; Thornhill et al.2015; Berg et al.2016). Recently, it was shown that plants characterised by a deep - time origin might also display a large disparity in their lineage's taxa number (Nee et al.1992; McPeck and Brown 2007; Ricklefs 2007; Linder 2008; Rabosky 2009; Gehrke and Linder 2011).

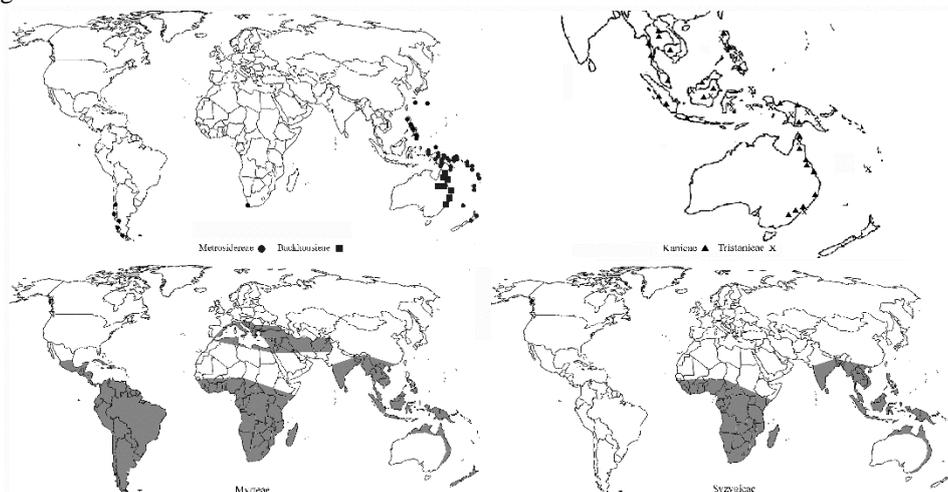
The BKMMST group (Backahousieae, Kaniae, Metrosidereae, Myrteae, Syzygieae, Tristanieae tribes) (Biffin et al.2010) forms an interesting clade within the Myrtoideae subfamily, as it represents most of the family diversity (c.3550 species and 68 genera) (WCSP 2020), and it is the only group to encompass fleshy as well as dry fruited taxa. The BKMMST group is composed of very large tribes, such as the Myrteae, estimated at c.2500 species and 51 genera. Syzygieae, a monogeneric tribe with c.1.100 - 1300 species (Parnell et al.2006; WCSP 2020), which contrast severely with very small tribes like Tristanieae, with c.41 species divided into four genera, and Backahousieae, with 13 species and consistent of one genus only (Wilson et al.2005; Harrington et al.2012). To explain the high taxa variation within the family, any potential positive correlations between Myrtoideae's hyper - diverse taxa and

their main characters' innovations have been thoroughly investigated, but in spite of these efforts no successful resolution has been obtained (Moore and Donoghue 2007; Bernardini 2013; Marazzi et al.2019).

Within the Myrtaceae family there are elevated traits of homoplasy and the taxa information freely available are not enough explicit to circumscribe each singular taxon. However, while the family exhibits remarkable life form diversity (Wilson et al.2001; Biffin et al.2010; Wilson 2011; Fahey et al.2019), there is only a limited amount of information about the evolution of the BKMMST traits that might have influenced growth, survival, reproducibility and evolutionary turnover frequencies. To address this shortfall, there is an urgent need for additional information

(morphological, ecological and geographical distribution) on different taxa.

Therefore, in this study, a new collated dataset of the BKMMST clade was examined, which comprised new taxa also from a wider biogeographical area, including Africa, New Caledonia, New Guinea, New Zealand and the Pacific area. The ancestral states of selected characters (fruit type, habitus trait) were reconstructed and geographically mapped. Furthermore, the same data of traits were also used to determine any potential pattern in between these taxa characters, as between the same features and their environmental, geographical distribution.



**Figure 1:** BKMMST clade geographical distribution: a) Metrosidereae and Backhousieae (Mapp by Bernardini 2013); b) Kanieae and Tristanieae (Mapp by Bernardini 2013); c) Myrteae (by Thornhill 2015); d) Syzygieae (by Thornhill 2015)

## 2. Materials & Methods

### 2.1 Phylogeny

A new improved matrix that targets specifically the BKMMST clade (Biffin et al.2010) was generated. It was composed of 218 taxa and 6 genes (ETS, ITS, MATK, NDHF, RPL16, PSBA - TRNH; 5418 base pairs). Fifteen taxa were employed as outgroups, because considered closer to the BKMMST cluster (Thornhill et al.2015): *Psiloxylon mauritanium* and *Heteropyxis natalensis*, both taxa in the Psiloxiloideae subfamily; from Myrtoideae, the following taxa were selected: *Xanthostemon chrysanthus* (Xanthostemoineae), *Lophostemon confertus* (Lophostemoneae), *Osbornia octodonta* (Osborneae), *Melaleuca viridiflora*, *Calothamnus validus*, *Beaufortia orbifolia* (Melaleuceae), *Syncarpia glomulifera* (Syncarpieae), *Allosyncarpia ternata*, *Eucalyptopsis papuana*, *Stockwellia quadrifida*, *Arillastrum gummiferum*, *Eucalyptusperriniana*, *Angophora hispida*, and *Corymbia variegata* (Eucalypteae).

Sequences selected in Myrtaceae were aligned using MAFFT v.7.471 (Kato and Standley 2013) and implemented visually in Aliview (Larsson 2014). All the sequences considered were listed in Supporting information S1. Each BKMMST tribe (*sensu* Wilson et al.2005) was fully represented in the resulting dataset with the highest number of genera compared to any previous ones. In this

study, a total of 202 taxa in BKMMST clade were used compared to 63 in Biffin et al. (2010) and 165 BKMMST taxa in Thornhill et al. (2015). Furthermore, the proportions of the selected genera reflected the size of any tribe as well as of the group's geographical distribution.

Each DNA partition was initially evaluated independently by phylogenetic analysis with RAXML v.8 (Stamatakis 2014). Furthermore, to confirm congruence among the genes used in this matrix, the incongruence length difference (ILD) test (Farris et al.1994) was run in PAUP\* v.4.0b10 (Swofford 2003) with the following settings: random stepwise sequence addition, TBR branch swapping and 100 replicates. The null hypothesis of congruence was discarded with a threshold of  $p < 0.01$  (Li et al.2015).

The final combine matrix was examined with two different evolutionary analyses and three programs: the maximum likelihood (ML) approach and the Bayesian Inference (BI) method. For the first investigation, it was used RAXML v.8 software (Stamatakis 2014) with bootstrap support (BS) and the PhyML vers.3.0 algorithm (Guindon et al.2010), applying a conservative and strong aLTR SH - like support (ALTR). The RAXML analysis was produced through the CIPRES portal (<http://www.phylo.org/subsections/portal/>) with a GTRCAT model and a separate partition for each gene. It was run for 1000 rapid bootstraps, employing the default setting. Meanwhile, the PhyML v.3.0 test was executed on the GITHUB platform (GITHUB.com) with an

SPR heuristic search into the BioNJ starting tree and employing the GTR model of evolution and SH - like branch supports.

For the Bayesian Inference (BI) method, it was used the program MrBayes v.3.2.6 (Ronquist and Huelsenbeck 2003), inclusive of posterior probability (PP) nodes support. The MrBayes was performed through the CIPRES portal, and the best - fitting nucleotide substitution model was estimated for each singular DNA region using Modeltest v.3.7 (Posada and Crandall 1998; Posada and Buckley 2004) under the Akaike information criterion (Akaike 1973). The model selected for each chloroplast is GTR+G; meanwhile, the nuclear genes are under the GTR+G+I model.

In order to approximate the posterior probability distribution, four independent algorithms Markov chain Monte Carlo (MCMC) were run twice for 20 million generations and sampled every 1000th generation with 25% of the 'burn - in' discarded. Convergence between the runs and the length of the burn - in fraction was verified using the "sump" command in MrBayes and Tracer vers.1.5 (Rambaut and Drummond 2009). The posterior distribution of trees was summarised using the half - compact consensus tree from MrBayes. The consensus tree and posterior probability (PP) values were visualised with Figtree vers.1.4 (Rambaut 2012).

In the present study, we considered only parametric and non - parametric node values with high resolution: only BS and ALT values from 85% to 100% and a PP credibility ranging between 0.95 - 1 were assessed as strongly supportive for the phylogenetic relation (Li et al.2015).

All three node' confidences (PP, ALTR, BS) were reported on the phylogenetic tree at tribe level; meanwhile, only the high PP value was displayed at the tips. Furthermore, taxa with conflicting gene resolution (e. g. *Lindsayomyrtus racemoides*, *Syzygium kubiniense* and *Psidium guajava*) were excluded from the analyses.

## 2.2 DNA extraction

The DNA was extracted from c.0.3 g of silica gel dry material using a modified CTAB extraction protocol of Doyle and Doyle (1997). This was followed by a purification step involving a CsCl - ethidium bromide gradient ultracentrifugation (1.55 g/ml) and dialysis.

Three plastid DNA regions (MATK, NDHF and RPL16) and one nuclear ribosomal DNA region (ITS) were selected and processed (Kew Gardens laboratory). The primers AB101F and AB102F were used for ITS (Douzery et al.1999), XF and 5R for *matK* ([www.kew.org/barcoding/](http://www.kew.org/barcoding/)), 927F and 2110R for *ndhF* ([www.kew.org/barcoding/](http://www.kew.org/barcoding/)) and F71 and R1516 for *rpl16* (Shaw et al.2005).

PCR products were purified using the Nucleospin® Extract II minicolumn kit (Macherey - Nagel, Düren), according to the manufacturer's protocol. Sequencing reactions were carried out with the BigDye Terminator vers.3.1 Cycle Sequencing Kit™ (Applied Biosystems Inc.) following the manufacturer's protocol. All amplifications were performed on the GeneAmp 9700 PCD system (Applied Biosystems

Inc.). Sequences were analysed on an ABI 3730 Genetic Analyzer (Applied Biosystems Inc.).

## 2.3 Time evolution

Calibrating a phylogenetic tree is a fundamental step towards understanding the evolutionary history of lineages, and it is often required as a base for several evolutionary analyses. To understand clearly whether there were any significant age differences in the BKMMST lineages from the main geographical distribution (Neotropics, Australasia and Africa).

The dated phylogeny of the entire matrix (218 taxa) was generated using the real - time algorithm in MEGA vers. X (Kumar et al.2018) and each taxon was coloured in accordance to its geography (Supporting information S2).

## 2.4 Character state in the BKMMST matrix

The states of selected characters (fruit types, habitus) were described for any taxa included in the current matrix. The relative states for both characters (as reported at the present - time) were plotted on a world map using Tableau 2020.2 ([www.tableau.com](http://www.tableau.com)). A visual comparison between the maps was engaged to report any potential interesting pattern in between the states described. Moreover, it was checked any potential inter - correlation between the characters selected and their geography.

## 2.5 Ancestral character reconstruction (ACR)

ACR has been widely used to evaluate the evolution of character states along a phylogenetic tree to understand the evolutionary history of biological entities. The most likely ancestral character state was hypothesised at each internal node on the dated phylogenetic tree generated.

Two discrete characters were analysed: fruit types (number of seeds with its mesocarp class) and habitus trait. The future fruit types was used to predict the seeds survival of a specie and its temporal and spatial colonisation ability, while the habitus trait of an adult plant is indicative of its capacity to access light resources and to disperse diaspores. Fruit type states were sourced from the literature (Supporting information S3) and consist of berry (fleshy fruit with many seeds), drupe (fleshy fruit with 1 or 2 seeds), and capsule (dry fruits with many seeds). The habitus states were scored as: Phanerophyte (P), Nanophanerophyte - Phanerophyte (Np - P), Nanophanerophyte (Np), Climbing (Cl), Chamaephyte - Nanophanerophyte (Ch - Np), Hemicryptophyte - Chamaephyte (H - Ch), following the WCSP (2020) list.

ACR was performed in Mesquite vers.3.61 (Maddison and Maddison 2019), selecting the parsimony method option and the unordered state model. The Mesquite program could not include all the taxa (218) from the main matrix; therefore, a subgroup of only 76 taxa was selected. Although, all BKMMST clades, their full geographical distribution and the related character states were represented. The tips of the resulting dated tree were pruned in R program (R Core Team 2020) to preserve the phyla - relations and branch lengths of the taxa. Phylogenetic uncertainty was taken into account

using 1000 cut, dated trees. The ancestral character state hypotheses for each node were shown on the cut ultrametric tree, with the percentage of trees reconstructed for that particular state within the entire 1000 input tree.

### 3. Results

#### 3.1 Phylogeny

All the reconstructed phylogenetic trees resulted in the same outcome (Fig.2). The BKMMST group was identified by one deep node that was strongly supported (PP = 1, ALTR =

98, BS = 90) and the clade evolved firstly from a Kanieae monophyletic cluster (K). A distinct node was evident between Myrteae and the combined BMST clade (PP = 0.99, ALTR = 98, BS = 84). The BMST clade was also strongly supported (PP = 1, ALTR = 97, BS = 71), and inside this clade, it was possible to distinguish two groups: Syzygieae, which is closely related to Backousieae (PP = 0.99, ALTR = 100, BS = 87) and Metrosiderae, that it is assumed to be closely related to Tristanieae (PP = 1, ALTR = 99, BS = 79). The unplaced Syncarieae (in the outgroups) has been considered closely related to Eucalypteae (BS = 100).

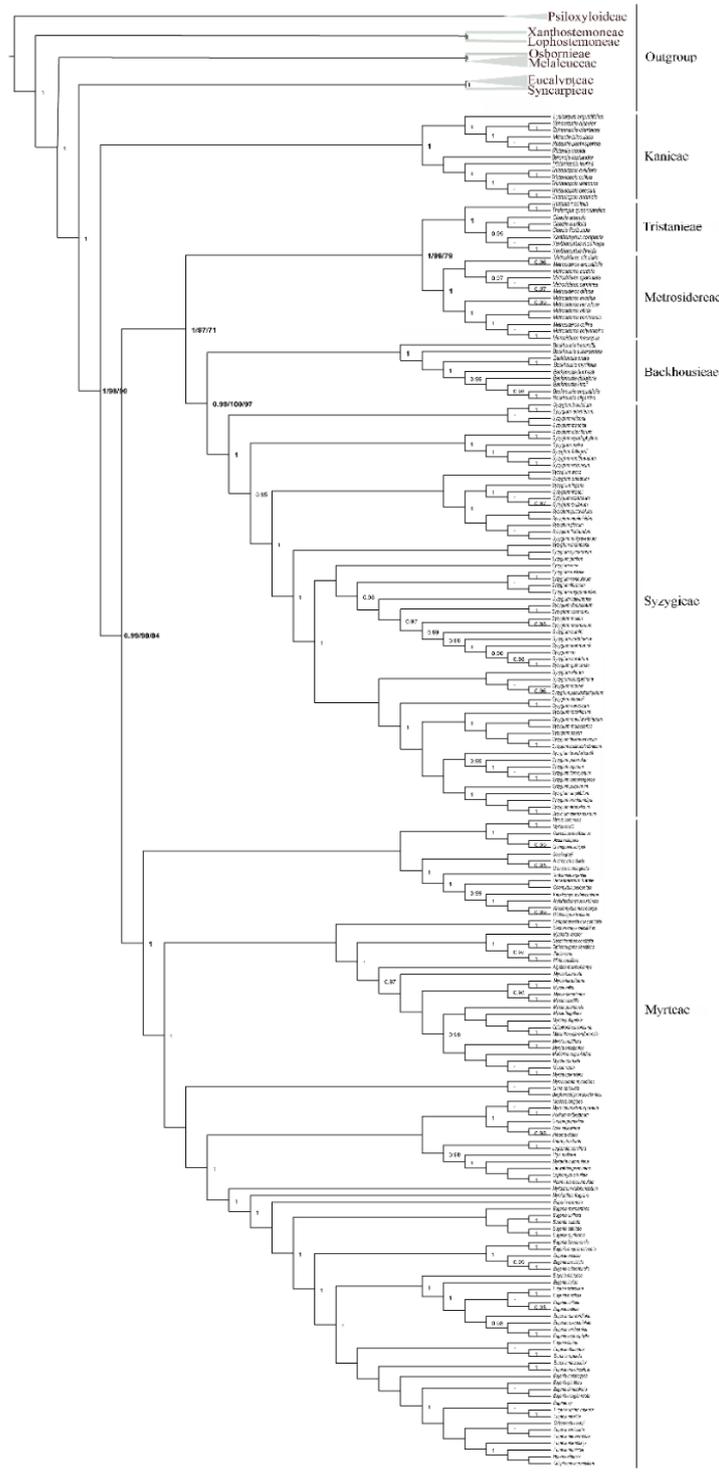
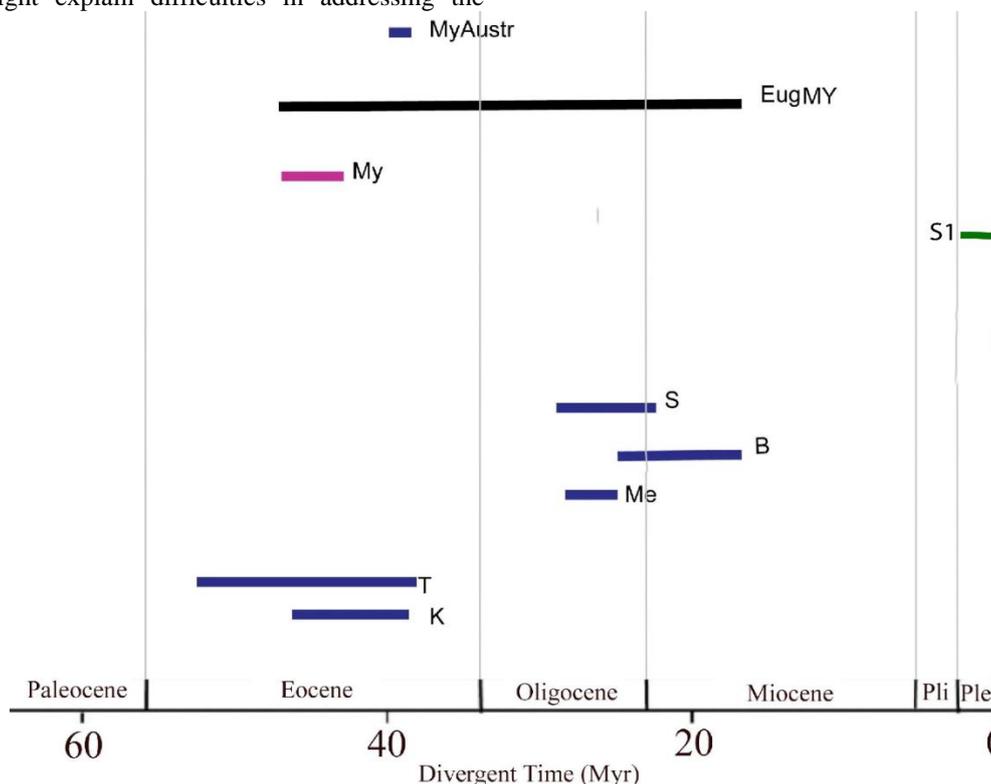


Figure 2: Phylogenetic tree with only high supports at node

**BKMMST time in geographical space** Tree time analyses suggested Myrteae, Tristanieae and Kaieae to be the oldest tribes, with all their crown nodes estimated at Eocene (Fig.3; S2). Syzygieae and Metrosidereae crown nodes appeared in Oligocene, while the Backhousieae node evolved mainly during the Miocene. A very short origin time occurred in between each singular clade. As a consequence, this particularity might explain difficulties in addressing the

phylogenetic relationships among these monophyletic groups. Most of the BKMMST tribes are centred in Australasia with a few taxa in Africa; only Myrteae taxa are focused in the new world, with some exceptions in Australasia and Africa (Figs.1 and 3; Tab.1).



**Figure 3:** Temporal and geographical origin of BKMMST. Each bar represents a tribe crown age. The nodes are gathered with 95% interval credibility. Neotropics = pink line, Africa = green line, mix origin in South Hemisphere = black line, Southeast Asia = blue line. K = Kanieae, T = Tristanieae, B = Backhousieae, Me = Metrosidereae, S = Syzygieae EastAsia, S1 = Syzygieae in Africa, My = Myrtaceae, My Austr = Australiasin Myrtaceae. The large fleshy - fruited genus *Eugenia* (Myrteae) is highly diversified in South America, with some species in Africa and few in Asia. EugMy = All species of the genus *Eugenia* (Myrteae).

**Table 1:** Time origin of BKMMST main tribes as retrieved in this paper

Tribe	Time mean	95%interval
Backhousieae	20.98	15.93 - 25.62
Kanieae	42.01	39.06 - 46.91
Metrosidereae	29.86	25.3 - 30.48
Myrteae	41.66	41.66 - 44.48
Syzygieae	31.24	28.17 - 34.65
Tristanieae	44.32	37.25 - 52.73
Australian Myrteae	37.13	35.63 - 37.15
Eugenia	27.55	17.63 - 44.48
Syzigium_Africa	1.22	0.15/9.88

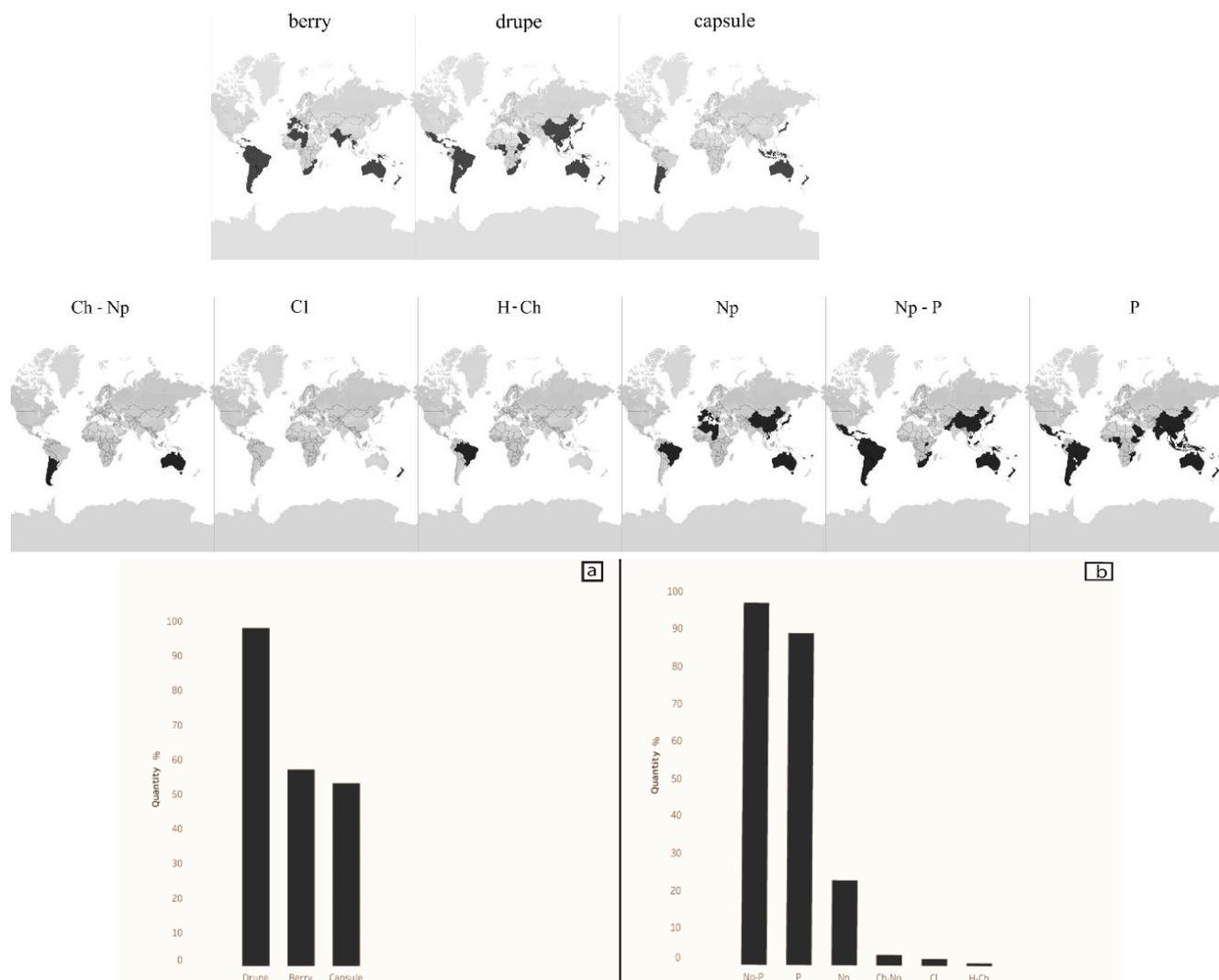
**Comparison of fruit and habitus states**

Taxa with berry and drupe fruits were shown to have a similar geographical distribution throughout the Southern

Hemisphere, although in south - eastern Asia only drupe fruits were confirmed (Fig.4)

Most of the selected taxa had fleshy fruits, where the drupe type was dominant (97% of all taxa selected), followed by berry (57% of all taxa selected) and then capsular (53% of all taxa selected) fruit types (Fig.4 a).

Of the habitus states across the group, the mixed state of phanerophyte with nanophanerophyte (P - NP, 97%) is the major one, followed by phanerophyte only state (P, 89% of all taxa) and the singular nanophanerophyte only state (Np, 23%), whilst the remaining habitus states was set around 6% of all BKMMST taxa employed (Fig.4 b).



**Figure 4:** Distribution of fruit type and habitus states in each taxon from the matrix at modern time with character states chart bar. Each state was plotted on a world map (using Tableau 2020.2 by <https://www.tableau.com>). The mapped states of both characters were compared in between to report any potential pattern. The percentage of BKMMST taxa with diverse fruit types (a) and habitus (b). Habitus state codes: Ch= Chamaephyte; Np= Nanophanerophyte; H= Hemicryptophyte; P= Phanerophyte; Cl = Climbing.

#### ACR - Character evolution fruit type

The capsule fruit type was hypothesised at the origin of BKMMST clade (Fig.5). In the earlier Oligocene, a new fruit state appeared, the berry fruit type, which coexisted with the capsular types through to the earlier Miocene. During the Miocene, the berry fruit type was inherited by many descendant generations, predominantly within the Myrteae. In the Miocene, capsular fruit types were mostly replaced with a novel state, the drupe fruit type, which was mainly dominant in the Syzygieae. In addition, the capsular fruit types were mainly located at the node between Syzygieae and Backahousieae, but the same state was

maintained only in Backahousieae. The capsule status was also inherited and maintained in both the Metrosidereae and Tristanieae. It is interesting to remark the occurrence of the berry fruit inside *Xanthomirtus* taxon (Tristanieae; Wilson et al.2001) because any other taxa in the same tribe are capsular. Kanieae has remained capsular fruits since the Paleocene. In the very early Miocene, drupe fruit also expanded within the Myrteae, simultaneously with the berry type, to become until nowadays the two principal fruit types in this tribe.

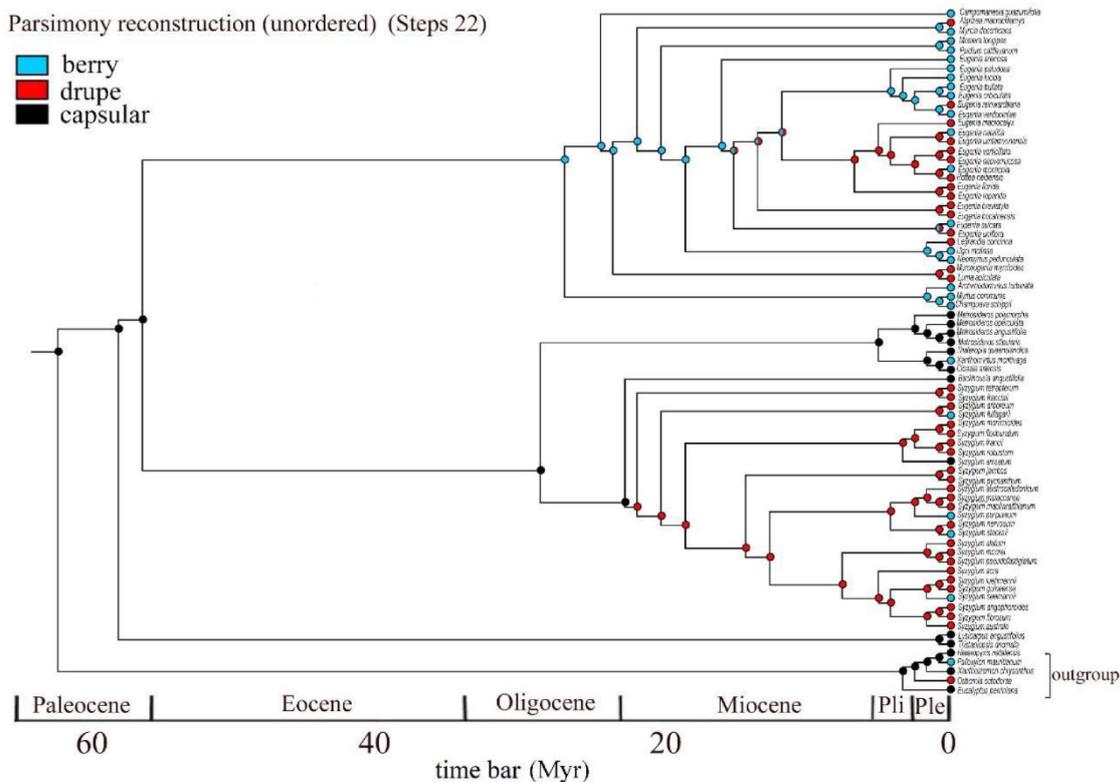


Figure 5: ACR of fruit types in BKMMST with time bar in Myr. Blue dots = Berry; red dots = drupe, black dots = capsule

ACR - Character evolution habitus

The first BKMMST taxa were inferred to be “phanerophyte - only” state, then it has changed into an imprecise status, a mix of phanerophyte or nanophanerophyte, which was assumed to be the main typical BKMMST habitus from late Eocene. The innovative “nanophanerophyte - only” state was found to have occurred only at the tree tips, in nearly all

the tribes, with the singular exclusion of the Tristanieae. Moreover, some lineages were shown to recover the “phanerophyte” state during the Miocene (e. g., most of the Syzygieae and Kanieae taxa). The same state was also retrieved more recently in a few Myrteae and Tristanieae taxa (Fig.6).

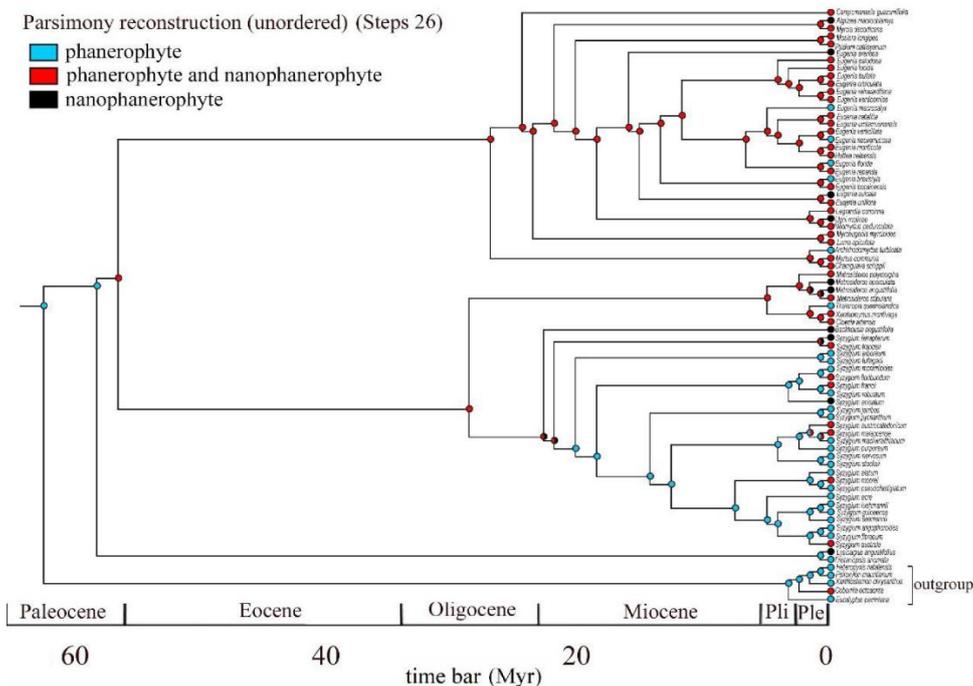


Figure 6: Habitus ancestral reconstruction of BKMMST with time bar in Myr. Blue dot = Phanerophyte; red dot = Phanerophyte and nanophanerophyte; black dot = only nanophanerophyte.

## 4. Discussion

### Phylogeny

For the first time, the BKMMST clade was fully phylogenetically resolved at deep nodes, with each tribe confirmed as monophyletic (Fig.2; Support information S4). Interestingly, it has been noticed that the tribes inside the clade evolved with very short branch length, underling the strong linkage from them. It was thought that the small character differences among these taxa might have been responsible for the many difficulties in producing a completely resolved evolutionary tree for the BKMMST group.

Branches were supported well, according to the non - parametric ALTR and parametric PP values, but often the same nodes had small bootstrap (BS) values. These contrasting confidence results were already identified in previous molecular studies (Biffin et al.2010; Bernardini 2013; Thornhill et al.2015). Differences between ALTR, PP and BS confidences could still indicate a lack of resolution in the evolutionary signal for specific phylogenetic parts (Anisimova et al.2011). As consequence, parametric support may better explain the actual situation.

It was suggested that a low Myrtaceae node support might result from an incomplete sequence coverage of the markers used in older publications (Thornhill et al.2015). Although an impaired gene set was adopted also in this study, the results achieved do not totally confirm the assumption. In most recent studies, it has been stressed that the Myrtaceae cluster received a higher confidence respect to previous molecular investigations (Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010) as a possible consequence of applying different methodologies (Berget al.2016). Therefore, in this study, a clearer resolution of the controversial clade BKMMST might have been reached because of the better samples proposed and as a possible consequence of the improved analyses used.

### Divergence time estimation

Myrtaceae were dated around late Cretaceous (83.6 - 87.5 Ma) (Berg et al.2016), and the extensive fossil records found in Antarctica, Australia, New Zealand, India, Eurasia, North America and South America have suggested that the family had an almost cosmopolitan distribution during and probably prior Eocene. Several recent studies (Sytsma et al.2004, Crisp and Cook 2009) have proposed a massive extinction event in South America that has possibly reduced the number of Myrtaceae taxa, probably because of the family early pantropical distribution.

During the Palaeocene - Eocene era, two important events occurred, the collision between the African and Eurasian plates and the increase in global temperatures, which allowed the expansion of tropical species towards northeaster latitudes. This expansion from the tropics is indicated by the presence of Myrtaceae fossils in Colorado (Manchester et al.1998) and Europe (Collison 1983). In addition, the data suggest that the majority of BKMMST tribes originated during the Eocene, when global temperatures peaked and South America was still connected with Australia across the Antarctica peninsula (Renner et

al.2001; Davies et al.2004). A period of climatic cooling followed, from the end of Eocene to Miocene, forcing the ranges of megathermal taxa to shrink back to lower latitudes into refuge sites such as Central America, Caribbean, East to Southeast Asia and Africa (Richardson et al.2001; Smedmark and Anderberg 2007).

The origin time of the BKMMST clade in Myrtoideae indicated here is consistent with previous studies (Biffin et al.2010; Thornhill et al.2015). It was also demonstrated that the development of each singular clade occurred in very narrow evolutionary timescale (Fig.3; S2). This evolutionary rapidity might explain the difficulties experienced in targeting the phylogenetic relationships among BKMMST clades.

During Miocene and Pliocene, the African forests suffered higher climate oscillations than the Australasian and the Neotropical ecosystems. From c.16 Ma onwards, the southeast African continent experienced uplift and a gradual temperature decrease that could explain an expansion of woodlands and savannah vegetation and a reduction of lowland rainforest (van Zinderen Bakker and Mercer 1986; Jacobs 2004). Generally, the African Myrtoideae groups might have evolved more recently and were characterised by less taxa compared to Australasian and Neotropical clades (e. g. *Eugenia*, *Syzygium*, *Metrosideros*). Such reduction in taxa diversity could be indicative of the unfavourable climate fluctuations during Miocene and Pliocene, which resulted either limited diversification or extinction of older Myrtaceae taxa. Therefore, in tropical area, the taxa diversification often has been explained better as the result of recent dispersal events that are typical of the post - Eocene era (Renner et al.2001; Michalak et al.2010).

### Characters evolution

The selected characters generally accumulated changes from the Miocene on (Figs.5 and 6). Previous findings reported a lack of correlation between selected characters with the hyper - taxa diversification of any BKMMST clade. While the fruit types presented highly distinct states, the habitus diverse classes were not so well defined. The character, only phanerophyte is exclusively of tall trees, the state only nanophanerophyte is typical of taxa developing only short trunk, woody bushes or few herbs (Fig.4), but many BKMMST taxa had a mix state, being able to develop either tall or short life forms.

However, here the familial states tested could be linked to ecological attributes, such as climate fluctuation and geological uplift, as resulted by matching this data results with geological era story.

In this paper, it was noted that the BKMMST habitus was characterised by a mix of mainly woody states with tall trees (over 5 m, Phanerophyte) and low trees (less than 5 m, Nanophanerophyte), with only a very few herbaceous species (Fig.6). Normally, large woody life - forms require much more resources than bushes and herbaceous taxa. Here, the results might confirmed that at principle, there were many new environments with abundant resources (nutrients, light), to be colonized. Later on, with advances in evolutionary time, the same supplies availability were

reduced, likely led to a shift from Phanerophyte to mainly Nanophanerophyte plants and more specialist plants, such as Chamaephyte, Hemicryptophyte and Climbing woody life - forms. Furthermore, these results suggested that taxa distribution and resources availability might have been very important for the preservation of older states in Myrtaceae and eventually allowing a faster adaptation to new environmental demands. Syzigieae, focused in Australiasia but the tribe has also expanded into Africa, documented the latter situation clearly. Thus, probably the expansion of this clade into further areas, allowed both the selected traits to preserve the states longer during geological time, displaying a low frequency of character change.

In Angiosperms, a model of phylogenetic niche conservatism has been proposed often, by many researchers and the results obtained in this investigation seemed to support the idea that evolving new adaptations, for a changing environment, is less likely than migrate towards areas with similar ecological niches (Behling et al.2005; Donoghue 2008; Krebs et al.2011). Moreover, the rapid ecological changes (e. g. in climate and geography) occurred during Myrtoideae evolutionary history, could be addressed as responsible for any possible severe extinction event within the clade (Systma et al.2004; Wilson et al.2005; Crisp and Cook 2009).

#### Traits visualisation

The distributions of the two characters was analysed and it was possible to visualise coexistence between capsular fruits and Chamaephyte and/ or Nanophanerophyte (Ch - Np) life form. Both these features were present just in Australia and in the southern part of South America.

The habitus states which are classified as a mix of Nanophanerophyte and Phanerophyte (Np - P), only Phanerophyte (P) and most of the extant taxa allocated in the only Nanophanerophyte state (Np) were similarly distributed throughout the Southern Hemisphere (Fig.4).

## 5. Conclusion

The quality data concept was fully adopted in this study, consequentially a new exhaustive taxa sampling of the BKMMST group was analysed. All the clade tribes were represented and new taxa, never adopted before, were added. Each tribe size and its geographical range was considered entirely. The most appropriated BKMMST outgroups and genes were selected, not genuine DNA sequences and informations were discarded as new improved programs were applied.

It was emphasised that the origin time of any examined tribe was very close one each other, so each BKMMST tribe has appeared in a particularly short interval of time. This aspect might explain difficulties in underlining the phylogenetic relationships in the same group.

Wherefore, a new and more exhaustive matrix was evaluated that improved upon previous investigations and new programs were executed, which were more adapted to manage the larger datasets carefully. Hence the matrix resolved into a clearer phylogenetic BKMMST tree.

Finally, dramatic environmental changes, such as global temperature changes (cooling following the early Eocene, or more recent Miocene - Quaternary aridification in Australia and South America (Pole et al.20018), could have shaped Myrtaceae. More in - depth works on the ecological side and further taxa descriptions will be required in the future.

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- [73] [https://www.researchgate.net/profile/Neil - Ellwood - 2](https://www.researchgate.net/profile/Neil-Ellwood-2)
- S2 - Molecular dating. Calibration points table and phylogenetic dated tree.  
A correct estimation of molecular evolution rates among gene regions and lineages is important to reduce bias effect on age inference (Bell & Donoghue, 2005; Mulchay *et al.*, 2012).
- At first, the dating BEAST approach (Drummond & Rambaut, 2007), which does not assume rate autocorrelation among lineages, was also used. Although it was run several times with different settings, it failed each time to reach convergence and produce acceptable effective sample sizes (ESS). Similar problems were reported by other authors (eg. Buerki *et al.*, 2011), where the size and complexity of the data set was assumed to be the main reason for these failures.
- In this study, the failure of the program BEAST might be explained by the presence of high variable mutation rates, probably very different between the markers used and the large number of taxa employed. Therefore, more versatile dating programs are needed, to better fit datasets characterised by high substitution rates (Rabosky *et al.*, 2008).
- In this scenario, a fast and reliable dating algorithm is real time implemented in MEGA v. X (Kumar *et al.*, 2018). This software allowed to perform complicate analyses, transforming relative node ages into absolute times using calibration records.
- A time - tree was inferred by applying the RelTime method (Tamura *et al.*, 2012, 2018) to the resulting supplied

phylogenetic tree whose branch lengths were calculated using the Maximum Likelihood (ML) method and with the General Time Reversible substitution model.

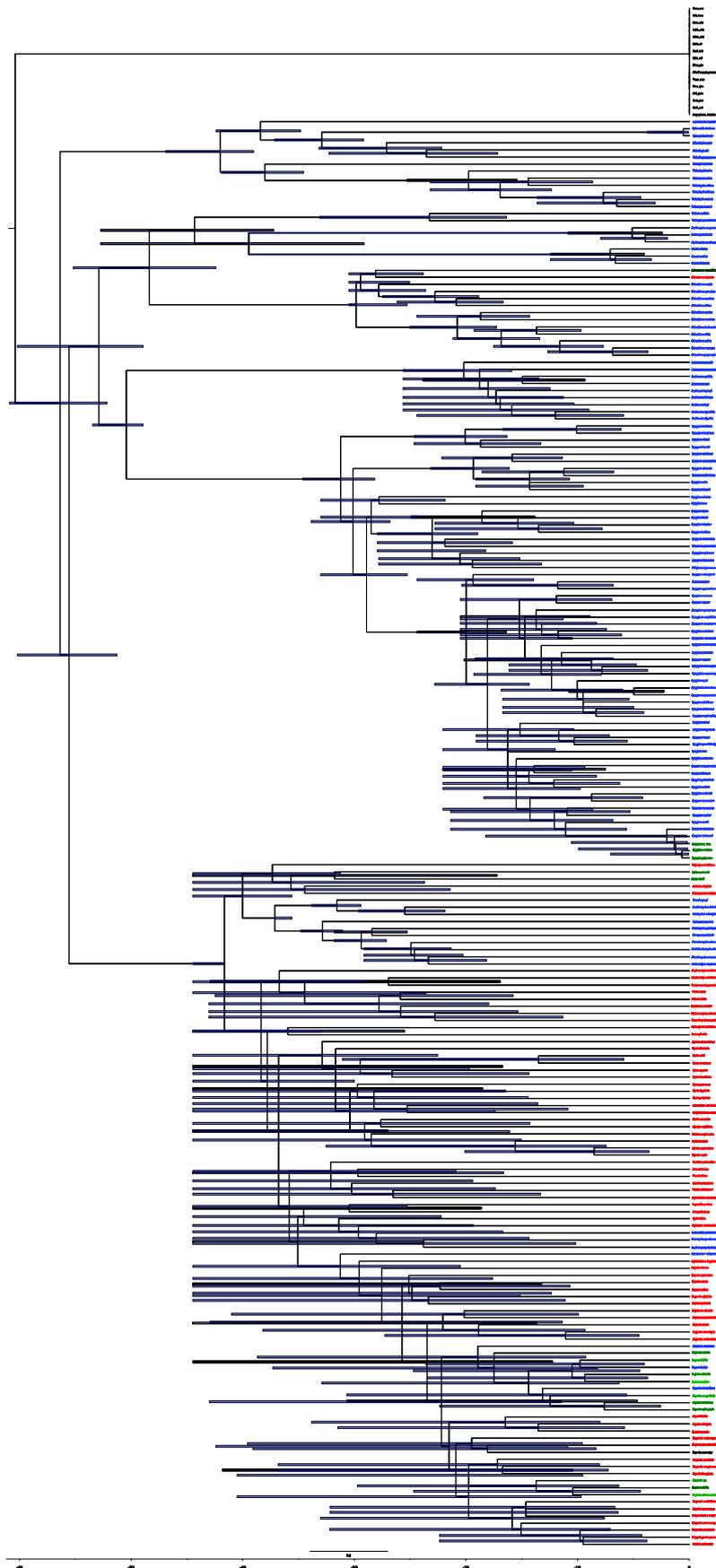
The time - tree was computed using five calibration constraints, setting minimum and maximum time boundaries on nodes (table1). A discrete Gamma distribution model was used to pattern evolutionary rate differences among sites (4 categories, +G). The final dataset consisted in 218 nucleotide sequences with a total of 5418 characters, and codon positions 1st+2nd+3rd+Noncoding, were included.

The phylogenetic tree was dated using five Myrtoideae fossils, and their placements were mostly based on previous studies (Sytsma et al., 2004; Biffin et al., 2010; Thornhill et al., 2015). In order to calibrate Myreae crown group, the fossil *Myrceugenelloxylon antarcticus* (Rabosky et al., 2008)

was selected and it was estimated Late Cretaceous to Mid - Eocene time. The basal Australian group in Myrteae was recovered, the clade was dated with *Myrtineoxylon maomingensis*, placed in South China, during Late Eocene (Oskolski et al., 2013). The New Zealand fossil spore *Myrtaceidites eugenioides* (Harris et al., 1965) of Early Eocene was used to constrain the nodes connecting Syzygia and Backhousieae. Metrosiderea crown clade was dated during period time from late - oligocene to early Miocene, with several fruit and leaves fossils, recovered in New Zealand (Tarran et al., 2017). *Tristaniandra alleyii* from the Eocene of South Australia suggest an affinity to tribe Kanieae Basinger et al., 2007 [72]). The calibration information from this study are summarised in table 1. Divergence - time results from the current study were similar to those obtained previously (Biffin et al., 2010, Thornhill et al., 2015).

**Calibration points** summarise the fossil name, relative time node, the node where the fossil was applied on and the fossil rate.

Fossil	Time (Myr)	Node	Rates
<i>Tristandria alleyi</i> .	48.6 - 40.4	Kanieae crown	Uniform distribution
<i>myrceugenelloxylon antarcticus</i>	99.6 - 37.2	Myrtea crown	Uniform distribution
Fruits and leaves	31.5 - 19	Metrosiderea crown	Uniform distribution
<i>Myrteloxylon maomingensis</i>	37.2 - 33.9	Australian Myrteae crown	Uniform distribution
<i>myrtaceidites eugenioides</i>	55.8 - 48.6	Backhousieae+ Syzygiae crown	Uniform distribution



**Dated tree** with color tips names. Red= South America, Blue=East Asia, Green=Africa. Bars on node represent 95% credibility intervals. Geographical area from WCSP, 2020. Time in Myr.

S1 - Taxa used with vouchers and accession number for each gene. Slash symbols indicated no molecular data adopted.

TAXA	ITS	MATK	NDHF	RPL16	ETS	TRNH - PSBA	Voucher
<i>Acca sellowiana</i> (O. Berg) Burret	AM489973	AY498783	–	–	AM234067	–	–
<i>Accara elegans</i> (DC.) Landrum	MF954013	MF954518	MF954431	NF954309	–	MF954271	–
<i>Algrizea macrochlamys</i> (DC.) Proença & Nic Lugh.	AM489976	–	–	–	AM234126	–	–
<i>Allosyncarpia ternata</i> S. T. Blake	AF390446	KC180806	KC180806	KC180806	DQ352477	AF190370	–
<i>Amomyrtus luma</i> (Molina) D. Legrand & Kausel	AM234073	KM065323	MF954434	–	AM489892	AM489811	–
<i>Angophora hispida</i> (Sm.) Blaxell	KM065051	KM065116	–	–	KT631415	–	–
<i>Archirhodomyrtus turbinate</i> (Schltr.) Burret	MF954015	–	MF954435	MF954312	–	MF954273	–
<i>Arillastrum gummiferum</i> (Brongn. & Gris) Panch. exBaill.	AF058454	AF368198	AY498765	–	DQ352479	–	–
<i>Austromyrtus dulcis</i> (C. T. White) L. S. Sm.	MF954016	AM489977	MF954436	–	AM489894	MH587032	–
<i>Backhousia angustifolia</i> F. Muell	KC134136	KM894680	–	–	–	KM895200	–
<i>Backhousia bancroftii</i> F. M. Bailey & F. Muell.	KC134137	KC134162	–	–	–	KC134150	–
<i>Backhousia citriodora</i> F. Muell	KM064898	KM065350	AY498768	–	–	KM895020	–
<i>Backhousia enata</i> A. J. Ford, Craven & J. Holmes	KC134139	KC134163	–	–	–	KC134152	–
<i>Backhousia hughesii</i> C. T. White	KC134140	KC134164	–	–	–	KC134153	–
<i>Backhousia kingii</i> Guymer	KC134142	–	–	–	–	KM895350	–
<i>Backhousia myrtifolia</i> Hook & Harv.	ZF 0266091	AF368200	DQ088472	DQ088408	–	KC134156	–
<i>Backhousia oligantha</i> A. R. Bean	KC134144	KM894720	–	–	–	KM895223	–
<i>Backhousia subargentea</i> (C. T. White) L. A. S. Johnson_ (C. T. White) M. G. Harr.	DQ088409	AF368202	DQ088473	DQ088409	–	–	–
<i>Barongia lophandra</i> P. G. Wilson & B. Hyland	In this study	In this study	In this study	–	–	–	Sankowsky 3890 (K)
<i>Beaufortia orbifolia</i> F. Muell	AF048888	AY521530	AY498771	–	–	–	–
<i>Blepharocalyx cruckshanksii</i> (Hook. & Arn.) Nied.	JN660857	AM489978	MF954437	JN660956	AM489895	AM489814	–
<i>Blepharocalyx salicifolius</i> (Kunth) O. Berg	AY521531	AY498772	–	–	AM234084	–	–
<i>Calothamnus validus</i> S. Moore	AF048856	AF184705	AY498773	–	–	–	–
<i>Calycolpus moritzianus</i> (O. Berg) Burret	–	–	–	KU945977	JQ730668	KU945999	–
<i>Calycorectes bergii</i> Sandwith	MN296376	–	–	–	–	KX248112	–
<i>Calyptranthes concinna</i> DC.	AM489980	KP722454	KU898502	AM489898	AM234103	AM489817	–
<i>Calyptrogenia grandiflora</i> Burret, Notizbl.	MF954024	–	MF954448	MF954322	–	MF954282	–
<i>Campomanesia guazumifolia</i> (Cambess.) O. Berg	AY521532	AY498777	–	AM489902	AM234076	AM489821	–
<i>Changuava schippii</i> (Standl.) Landrum	MF954027	GQ981963	MF954451	MF954325	–	GQ982182	–
<i>Cloezia artensis</i> (Montrouz.) P. S. Green	in this study	in this study	in this study	in this study	–	–	McPherson & Munzinger 18155 (MO)
<i>Cloezia buxifolia</i> Brongn. & Gris	in this study	in this study	in this study	–	–	–	LowryII, Munzinger & Pignal 6499 (MO)
<i>Cloezia floribunda</i> Brongn. & Gris	AF172767	AY521533	–	–	AY606255	–	–
<i>Corymbia variegata</i> (F. Muell.) K. D. Hill & L. A. S. Johnson/Corymbiacitriodora (Hook.) K. D. Hill & L. A. S. Johnson	DQ993141	AF368203	–	–	DQ352524	–	–
<i>Curitiba prismatica</i> (D. Legrand) Salywon & Landrum	MF954028	MF954524	MF954452	MF954326	–	MF954286	–
<i>Decaspermum humile</i> (G. Don) A. J. Scott	AY521534	AY498780	–	AM489905	AM234128	AM489824	–
<i>Eucalyptopsis papuana</i> C. T. White	–	AF368205	–	–	DQ352538	AF190371	–
<i>Eucalyptus perriniana</i> F. Muell. exRodway	AM234139	–	MF954455	MF954330	AM489907	–	–
<i>Eugenia adenocalix</i> DC.	MF954042	–	MF954470	MF954342	–	MF954300	–

<i>Eugenia arenosa</i> Mattos	–	–	–	KJ187658	JQ033314	JQ033344	–
<i>Eugenia bimarginata</i> DC.	–	–	–	KJ187664	KJ187611	KJ469660	–
<i>Eugenia brevistyla</i> D. Legrand	KJ187614	MF954460	MG718641	–	KJ187667	KJ469663	–
<i>Eugenia bullata</i> Pancher ex Guillaumin	–	MF954461	MF954334	–	MF954034	MF954292	–
<i>Eugenia bunchosiiifolia</i> Nied.	MG707978	MG718642	MF954469	MF954341	–	–	–
<i>Eugenia buxifolia</i> Lam.	KU945987	KU945992	In this study	–	KU945979	KU946000	Byng 60 (K)
<i>Eugenia erythrophylla</i> Strey	JX517830	–	AY463125.	AY454145.	AY463139	–	–
<i>Eugenia excelsa</i> O. Berg	In this study	In this study	In this study	In this study	KJ187673	KJ469670	Byng 66 (K)
<i>Eugenia florida</i> DC.	KJ187622	MG718956	In this study	MH446205	KJ187674	KJ469671	Mazine 965 (ESA, K)
<i>Eugenia lucida</i> Lam.	–	–	AY463110	AY454132	AY487289	–	–
<i>Eugenia macrocalyx</i> Mart. ex B. D. Jacks.	JQ626398	–	–	–	FJ037852	KX248447	–
<i>Eugenia magnibracteolata</i> Mattos & D. Legrand	KX789271	MG718650	–	KX789329	–	KX789304	–
<i>Eugenia melanogyna</i> (D. Legrand) Sobral	KJ187624	MG718651	–	–	KJ187676	KJ469673	–
<i>Eugenia monticola</i> (Sw.) DC.	MF954037	KJ012591	MF954464	MF954337	–	MF954295	–
<i>Eugenia myrcianthes</i> Nied.	MG708033	MG718830	MF954475	MF954346	KU945982	MH446060	–
<i>Eugenia natalitia</i> Sond.	JX517466	–	AY463121	AY454141	AY463135	–	–
<i>Eugenia neoverrucosa</i> Sobral	–	–	–	KJ187680	KJ187628	KJ469676	–
<i>Eugenia oblongata</i> O. Berg	–	–	–	KJ18768	KJ187630	KJ469678	–
<i>Eugenia orbiculata</i> Lam.	–	–	AY463111	KJ187683.	KJ187631	KJ469679	–
<i>Eugenia paludosa</i> Pancher ex Brongn. & Gris	MF954038	–	MF954465.	MF954338	–	MF954296	–
<i>Eugenia pluriflora</i> DC.	KJ187636	MG718831	–	–	KJ187688	KJ469684	–
<i>Eugenia puberula</i> Nied. in H. G. A. Engler & K. A. E. Prantl	KX789282	–	–	KJ187665	KJ187612.	KJ469661	Duarte ESA 85677 (ESA, K)
<i>Eugenia pyriformis</i> Cambess.	–	–	In this study	AM489914	KJ187639	KJ469687	Mazine 1028 (ESA, K)
<i>Eugenia reinwardtiana</i> (Blume) A. Cunn. ex DC.	KM894685	–	AY463131	–	KU945989	KU946003	–
<i>Eugenia repanda</i> O. Berg	–	In this study	In this study	KJ187692	KJ187640	KJ469688	Lucas 273 (ESA, K)
<i>Eugenia roseopetiolata</i> N. Snow & Cable	–	MF954468	–	–	MF954040	MF954298	–
<i>Eugenia</i> sp. [AG3]	MN296363	–	–	MN887414	–	MN887384	–
<i>Eugenia stipitata</i> McVaugh	MF954043	–	MF954471	MF954343	KJ187698	MF954301	–
<i>Eugenia subglomerata</i> (Kuntze) Sobral	KJ187626	KF981335	–	–	KJ187678	KJ469674	–
<i>Eugenia subterminalis</i> DC.	MG708058	MG718958	–	–	KJ187700	KJ469696	–
<i>Eugenia sulcata</i> Sping ex Mart.	HM160097	HM160097	–	KJ187701	AM234089	KJ469697	–
<i>Eugenia tinifolia</i> Lam.	–	–	AY487287	AY454130	AY463108.	–	–
<i>Eugenia umtamvunensis</i> A. E. Van Wyk	JX517784	–	AY463128	AM489911	AY463142	–	–
<i>Eugenia uniflora</i> L.	DQ088457	AF21559	AY463105	AM489910	AY487284	KP719066	–
<i>Eugenia verdoorniae</i> A. E. Van Wyk	JX517398	–	AY463123.1	AY454143.	AY463137	–	–
<i>Eugenia verticillata</i> (Vell.) Angely	MG707998	MG718663	–	–	KJ187704	KJ469700	–
<i>Gossia grayi</i> N. Snow & Guymer	JN564152	–	–	–	AM234132	KM895411	–
<i>Heteropyxis natalensis</i> Harv.	KM064805	KM065121	AY498824	–	–	–	–
<i>Hottea neibensis</i> Alain	MF954046	–	MF954476	MF954347	–	MF954304	–
<i>Kanakomyrtus dawsoniana</i> N. Snow	–	MF954477	MF954348	–	HQ225445	MF954305	–
<i>Legrandia concinna</i> (Phil.) Kausel	AM234072	AM489990	MF954478	–	AM489921	AM489839	–
<i>Lenwebbia prominens</i> N. Snow & Guymer	MF954048	KM894619	–	–	AM234072	MF954306	–
<i>Lophomyrtus ballata</i> Burret	KM064781	AM489992	–	–	AM489923	AM489841	–
<i>Lophostemon confertus</i> (R. Br.) P. G. Wilson & J. T. Waterh.	AF390444	AY498794	AY498794	AM489925	AY498794	–	–
<i>Luma apiculata</i> (DC.) Burret	AY498795	AY498795	KX789340	AM489926	AM234101	KX789312	–
<i>Lysicarpus angustifolius</i> (Hook.) Druce	–	AF368210	AY498796	–	–	–	–
<i>Marlierea eugenioides</i> (Cambess.) D. Legrand	AM489996	HM160099	–	AM489929	AM234108	AM489845	–
<i>Melaleuca viridiflora</i> Sol. ex Gaertn.	AF294611	AY498798	–	–	–	EU410242	–
<i>Metrosideros angustifolia</i> (L.) Sm.	KM064919	KM065077	–	–	KM064687	–	–

<i>Metrosideros boninensis</i> (Hayata ex Koidz.) Tuyama	AF172734.	In this study	In this study	In this study	–	–	Chase 2455 (K)
<i>Metrosideros carminea</i> W. R. B. Oliv.	AF211498	AY521541	AY498799	–	KM064696	–	–
<i>Metrosideros collina</i> (J. R. Forst. & G. Forst.) A. Gray	KM065036	KM065294	In this study	EU605584	AF328068	–	Christenhusz (TUR, BM)
<i>Metrosideros cordata</i> (C. T. White & W. D. Francis) J. W. Dawson	JF950776	–	In this study	In this study	AY606240	–	Lucas 27 (K)
<i>Metrosideros diffusa</i> (G. Forst.) Sm.	KM064992	KM065382	AY498800	–	–	–	–
<i>Metrosideros excelsa</i> Sol. ex Gaertn	JF950777	KM065270	AM235426	AM235462	AF328052	–	–
<i>Metrosideros macropus</i> Hook. & Arn	AF172745	AF368212	AY498801	EU605503	AF328047	–	–
<i>Metrosideros nervulosa</i> C. Moore & F. Muell.	DQ088395}	DQ088535	AY498802	EU605481	AF328051	–	–
<i>Metrosideros nitida</i> Brongn. & Gris	AF172770	In this study	In this study	In this study	–	–	Jérémie & Tirel s. n. (K)
<i>Metrosideros operculata</i> Labill.	AF172733	In this study	In this study	In this study	AY606246	–	Bamps 6107
<i>Metrosideros polymorpha</i> Gaudich.	–	In this study	In this study	EU605532	AF328059	–	Chase 2872 (K)
<i>Metrosideros stipularis</i> Griseb.	AF368222	In this study	In this study	In this study	AM489969	AM489884	Cult. RBGE 1995–2370A (E)
<i>Mitranthes clarendonensis</i> (Proctor) Proctor	MF954049	KM065078	MF954482	MF954352	–	–	–
<i>Mitranthia bilocularis</i> P. G. Wilson & B. Hyland	AY521543	In this study	–	In this study	–	–	Sankowsky 3889
<i>Mosiera longipes</i> (O. Berg) Small	MF954051	–	MF954484	MF954354	–	MF954388	–
<i>Myrceugenia myrcioides</i> (Cambess.) O. Berg	–	JN660964	JN660964	AM489936	JN660915	AM489853	–
<i>Myrcia amazonica</i> DC.	JN091306	KP722437	–	JN091267	JN091214	JN091405	–
<i>Myrcia bicarinata</i> (O. Berg) D. Legrand	–	KU898370	–	AM489945	KU898313	–	–
<i>Myrcia coumete</i> (Aubl.) DC.	AM889731	–	–	AM489947	AM234123	GQ248348	–
<i>Myrcia decorticans</i> DC.	JN091308	KP722460	–	JN091273	KP722383	KX248905	–
<i>Myrcia flagellaris</i> (D. Legrand) Mattos	HM16009	KP722430	MF954360	–	AM234113	AM489836	–
<i>Myrcia guianensis</i> (Aubl.) DC.	KJ012690	–	–	–	JN091277	JN091415	–
<i>Myrcia laruotteana</i> Cambess.	AM490002	–	–	AM489939	AM234115	AM489856	–
<i>Myrcia multiflora</i> (Lam.) DC.	AM490003	KP722464	–	AM489941	KP722387	KP722294	–
<i>Myrcia pubipetala</i> Miq.	AM490001	KP722426	–	–	AM234114	AM489855	–
<i>Myrcia rupta</i> M. L. Kawas. & B. K. Holst	AM234124	AM889732	–	–	AM489948	AM489865	–
<i>Myrcia saxatilis</i> (Amshoff) McVaugh	AM490004.	HM160100	–	AM489943	AM234119	AM489860	–
<i>Myrcia selloi</i> (Spreng.) N. Silveira	JN091315	KP722436	–	JN091291	JN091240	JN091431	–
<i>Myrcia splendens</i> (Sw.) DC.	MF954059	HM446718	MF954491	–	JN091293	JN091433	–
<i>Myrcianthes fragrans</i> (Sw.) McVaugh	KJ187655	KJ772955	AY498803	–	KJ187708	KJ469705	–
<i>Myrciaria vexator</i> McVaugh	MF954063	AY521544	MF954495	MF954414	–	–	–
<i>Myrrhimum atropurpureum</i> Schott	MH716442	MH713607	MF954496	MF954415	–	MF954400	–
<i>Myrtastrum rufopunctatum</i> (Pancher ex Brongn. & Gris) Burret	–	MF954527	MF954497	MF954416	–	MF954401	–
<i>Myrteola nummularia</i> (Lam.) O. Berg	AM234068	AM490008	MF954498	MF954417	AM489954	AM489871	–
<i>Myrtus communis</i> L.	AF215593	AF215593	KX789342	AM489955	AF215628	KX789314	–
<i>Myrtus nivellei</i> Batt. & Trab.	–	–	–	FJ611325.	GU984339	HM014143	–
<i>Neomitranthes cordifolia</i> (D. Legrand) D. Legrand	AM489410	–	–	MF954418	AM489413	–	–
<i>Neomyrtus pedunculata</i> (Hook. f.) Allan	AM234144	AM490010	–	MF954370	–	–	–
<i>Octamyrtus pleiopetala</i> Diels	AM234130	–	MF954500	MF954371	AM489957	AM489873	–
<i>Osbornia octodonta</i> F. Muell	EF041844	AY498805	–	–	–	–	–
<i>Pilidiostigma tropicum</i> L. S. Sm.	MF954066	–	MF954501	–	–	MF954402	–
<i>Pimenta dioica</i> (L.) Merr.	KM065298	MF954502	MF954374.	AM489958	AM234081	AM489874	–
<i>Plinia cauliflora</i> (Mart.) O. Berg.	AM234093	AM490007	–	NC039395	AM489952	AM489869	–
<i>Plinia nana</i> Sobral	MF954068	–	MF954504	MF954375	–	MF954404	–
<i>Psidium cattleyanum</i> Afzel ex	HM160101	HM160101	–	AM489962	AM490014	AM489878	–

Sabine							
<i>Psiloxylon mauritianum</i> (BoutonexHook. f.) Baill.	EF026606	AF368215	AM235430	AM235466	–	–	–
<i>Rhodamnia argentea</i> Benth.	AY498810	AY463132	AY463132	–	AF368217	KM895308	–
<i>Rhodomyrtus macrocarpa</i> Benth.	AY498811	–	–	AM489965??	AY525137	KP095748	–
<i>Ristantia gouldii</i> P. G. Wilson & B. Hyland	In this study	AF368219	–	In this study	–	–	Sankowsky 3885 (K)
<i>Ristantia pachysperma</i> (F. Muell. & F. M. Bailey) P. G. Wilson & J. T. Waterh.	In this study	–	–	In this study	–	–	Sankowsky 3886 (K)
<i>Siphoneugena densiflora</i> O. Berg	AM489412	–	KP722444	MF954383	AM489572	KX789316	–
<i>Sphaerantia chartacea</i> P. G. Wilson & B. Hyland	HM160116/15	AY521547	–	In this study	–	–	Sankowsky 3888 (K)
<i>Sphaerantia discolor</i> P. G. Wilson & B. Hyland	In this study	–	–	In this study	–	–	Gray 848 (CNS)
<i>Stockwellia quadrifida</i> D. J. Carr, S. G. M. Carr & B. Hyland	AY525138	AY498812	–	–	DQ352539	HQ287696	–
<i>Syncarpia glomulifera</i> (Sm.) Nied.	AF368220	AY498813	–	–	–	–	–
<i>Syzygium acre</i> (Pancher ex Guillaumin) J. W. Dawson	EF026619	DQ088555	DQ088480	DQ088415	–	–	–
<i>Syzygium alatum</i> (Lauterb.) Diels	–	–	In this study	In this study	–	In this study	Barker 115 (K)
<i>Syzygium amplifolium</i> L. M. Perry	–	EF026620	DQ088556	DQ088481	–	DQ088416	–
<i>Syzygium angophoroides</i> (F. Muell.) B. Hyland	AY187106	AY187172	DQ088557	–	–	–	–
<i>Syzygium anisatum</i> (Vickery) Craven & Biffin	AF368195	DQ088471	–	–	M489812	AM489893	–
<i>Syzygium apodophyllum</i> (F. Muell.) B. Hyland	DQ088558	DQ088482	DQ088417	DQ088417	–	–	–
<i>Syzygium aqueum</i> (Burm. f.) Alston	AY187108	JF682809	DQ088559	DQ088483	MH826496	–	–
<i>Syzygium arboreum</i> (Baker f.) J. W. Dawson	DQ088560	DQ088484	DQ088418	DQ088418	–	–	–
<i>Syzygium aromaticum</i> (L.) Merr. & L. M. Perry	DQ088561	DQ088485	DQ088419	DQ088419	–	–	–
<i>Syzygium australe</i> (J. C. Wendl. ex Link) B. Hyland	AY187111	AY187177	AF368221	–	KM895253	–	–
<i>Syzygium austrocaledonicum</i> (Seem.) Guillaumin	–	EF026623	DQ088563	DQ088486	–	DQ088420	–
<i>Syzygium brackenridgei</i> (A. Gray) Müll. Stuttg	–	–	DQ088565	DQ088487	–	DQ088421	–
<i>Syzygium branderhorstii</i> Lauterb.	AY187115	AY187181	DQ088566	DQ088488	–	DQ088422	–
<i>Syzygium bullatum</i> (Brongn. & Gris) N. Snow & Byng	DQ088552	DQ088478	DQ088413	–	DQ088552	–	–
<i>Syzygium bungadinnia</i> (F. M. Bailey) B. Hyland	DQ088568	DQ088490	DQ088490	DQ088423.	–	AY187116.	–
<i>Syzygium buxifolium</i> Hook. & Arn.	DQ088569	DQ088491	DQ088424	DQ088424	HQ427087	–	–
<i>Syzygium championii</i> (Benth.) Merr. & L. M. Perry	KP093047	HQ415318	–	–	KP095752	–	–
<i>Syzygium claviflorum</i> (Roxb.) Wall. ex A. M. Cowan & Cowan	DQ088546	DQ088470	DQ088470	DQ088406	–	AY187103	–
<i>Syzygium cordatum</i> Hochst. ex Krauss	EF026625	JX517332	DQ088493	DQ088426	JQ279706	–	–
<i>Syzygium crebrinerve</i> (C. T. White) L. A. S. Johnson hide S. ramp	EF026627	DQ088574	DQ088495	DQ088428	KU564625	–	–
<i>Syzygium cumini</i> (L.) Skeels	JX856510	GU134997	AY498814	GQ870669	GU135395	–	–
<i>Syzygium decussatum</i> (A. C. Sm.) Biffin & Craven	DQ088547	DQ088474	DQ088410	DQ088410	–	–	–
<i>Syzygium fibrosum</i> (F. M. Bailey) T. G. Hartley & L. M. Perry	AY187123	AY187189	DQ088577	DQ088497	–	DQ088429	–
<i>Syzygium floribundum</i> F. Muell	AY187221	KM065373	DQ088531	DQ088453	–	AY187155	–
<i>Syzygium francii</i> (Guillaumin) N. Snow, Byng & Munzinger	–	EF026616	DQ088551	DQ088477	–	–	–
<i>Syzygium francisii</i> (F. M. Bailey) L. A. S. Johnson	DQ088578	DQ088498	DQ088498	–	KM895364	–	–
<i>Syzygium fullagarii</i> (F. Muell.) Craven	DQ088579	DQ088499	DQ088499	–	–	AY187127.	–
<i>Syzygium glenum</i> Craven	AY187096	AY187162	DQ088539	DQ088464	–	DQ088400	–
<i>Syzygium guineense</i> (Willd.) DC.	EF026628	DQ088581	DQ088500	DQ088432	–	–	–
<i>Syzygium gustavioides</i> (F. M.	AY187128	AY187194	DQ088582	DQ088501	–	DQ088433	–

Bailey) B. Hyland							
<i>Syzygium ingens</i> (F. Muell. ex C. Moore) Craven & Biffin	DQ088542	DQ088466	DQ088402	DQ088402	KM895091	–	–
<i>Syzygium jambos</i> (L.) Alston	JX856511	GU135056	KU060786	DQ088434	GU135387	AM489967	–
<i>Syzygium lateriflorum</i> Brongn. & Gris	DQ088585	DQ088504	DQ088435	DQ088435	–	–	–
<i>Syzygium laxeracemosum</i> (Guillaumin) J. W. Dawson	DQ088586	DQ088506	DQ088506	DQ088436	–	–	–
<i>Syzygium luehmannii</i> (F. Muell.) L. A. S. Johnson	AY187197	DQ088587	DQ088505	DQ088437	AY187131	KM895401	–
<i>Syzygium macilwraithianum</i> B. Hyland	AY187132	AY187198	DQ088588	DQ088507	–	–	–
<i>Syzygium maire</i> (A. Cunn.) Sykes & Garn. - Jones	EF026632	DQ088508	KM065310	DQ088438	AM489883	–	–
<i>Syzygium malaccense</i> (L.) Merr. & L. M. Perry	DQ088590	DQ088509	–	–	–	–	–
<i>Syzygium monimioides</i> Craven	DQ088544	DQ088468	DQ088404	DQ088404	–	–	–
<i>Syzygium moorei</i> (F. Muell.) L. A. S. Johnson	AY187135	AY187201	DQ088592	DQ088510	–	–	–
<i>Syzygium muelleri</i> (Miq.) Miq.	EF026634	DQ088593	DQ088511	DQ088439	–	–	–
<i>Syzygium mulgraveanum</i> (B. Hyland) Craven & Biffin	DQ088622	DQ088533	DQ088455	DQ088455	–	–	–
<i>Syzygium multipetalum</i> Pancher ex Brongn. & Gris	–	EF026635	DQ088594	DQ088512	–	DQ088440	–
<i>Syzygium nervosum</i> A. Cunn. ex DC.	DQ088595	DQ088513	DQ088513	–	–	AY187136	–
<i>Syzygium paniculatum</i> Gaertn.	DQ088598	DQ088515	DQ088515	–	–	AY187138.	–
<i>Syzygium pseudofastigiatum</i> B. Hyland	AY187206	DQ088600	DQ088516	–	AY187140	–	–
<i>Syzygium puberulum</i> Merr. & L. M. Perry	DQ088601	DQ088517	DQ088517	–	–	AY187141	–
<i>Syzygium purpureum</i> (L. M. Perry) A. C. Sm.	–	EF026639	DQ088602	DQ088518	–	DQ088442	–
<i>Syzygium pycnanthum</i> Merr. & L. M. Perry	–	EF026640	DQ088603	DQ088519	–	DQ088443	–
<i>Syzygium racemosum</i> (Blume) DC.	–	EF026641	DQ088604	DQ088520	–	DQ088444	–
<i>Syzygium robustum</i> Miq.	–	EF026618	DQ088553	DQ088479	–	DQ088414	–
<i>Syzygium salwinense</i> Merr. & L. M. Perry	KR532640	GU134997	DQ088601	DQ088446	KR533018	–	–
<i>Syzygium samarangense</i> (Blume) Merr. & L. M. Perry	–	KC815989	AY525141	AY498815	–	–	–
<i>Syzygium sayeri</i> (F. Muell.) B. Hyland	DQ088607	DQ088607	In this study	–	–	AY187143	Gadek s. n. (JCT)
<i>Syzygium seemannianum</i> Merr. & L. M. Perry	–	EF026642	DQ088608	DQ088521	–	DQ088445	–
<i>Syzygium seemannii</i> (A. Gray) Biffin & Craven	–	EF026613	DQ088548	DQ088475	–	DQ088411	–
<i>Syzygium</i> sp. = [syzy sp. BC 140]	EF026647	–	DQ088526	DQ088446	–	–	–
<i>Syzygium stocksii</i> (Duthie) Gamble	KY607864	KT936460	–	–	–	–	–
<i>Syzygium tetrapterum</i> (Miq.) Chantaran. & J. Parn.	–	EF026649	DQ088615	DQ088527	–	DQ088448	–
<i>Syzygium tierneyanum</i> (F. Muell.) T. G. Hartley & L. M. Perry	AY187147	AY187213	DQ088616	DQ088528	–	DQ088449	–
<i>Syzygium wesa</i> B. Hyland	DQ088617	DQ088529	DQ088529	DQ088450.	–	AY187150.1	–
<i>Syzygium wilsonii</i> (F. Muell.) B. Hyland	DQ088618	DQ088530	DQ088530	DQ088451	–	AY187153	–
<i>Thaleropia queenslandica</i> P. J. Wilson	AF368223	DQ088460	DQ088397	DQ088397	–	–	–
<i>Tristania neriifolia</i> (Sims) R. Br.	AF368224	DQ088461	AY498817	DQ088398	–	–	–
<i>Tristaniopsis anomala</i> (Merr.) P. G. Wilson & J. T. Waterh.	In this study	In this study	–	–	–	–	S.100612 (SAN)
<i>Tristaniopsis beccarii</i> (Ridl.) P. G. Wilson & J. T. Waterh.	In this study	In this study	In this study	In this study	–	–	Berhamen 727 (SAN)
<i>Tristaniopsis collina</i> P. G. Wilson & J. T. Waterh.	In this study	KM894817	In this study	–	–	–	NSW.210020 (SAN)
<i>Tristaniopsis exiliflora</i> (F. Muell.) P. G. Wilson & J. T. Waterh.	–	EF173072	–	–	–	–	–
<i>Tristaniopsis laurina</i> (Sm.) P. G.	–	AF184710	AY498818	–	–	–	–

Wilson & J. T. Waterh.							
<i>Tristaniaopsis whiteana</i> (Griff.) P. G. Wilson & J. T. Waterh.	In this study	In this study	In this study	In this study	-	-	Berhamen 778 (SAN)
<i>Ugni molinae</i> Turcz.	AY498819	Y498819	MF954384	AM489970	AM490018	AM489885	-
<i>Uromyrtus emarginata</i> (Pancher ex Baker f.) Burret	MF954077	MF954529	MF954514	MF954385	-	MF954413	-
<i>Xanthomyrtus compacta</i> Diels	AM234148.	-	MF954515	MF954386	AM489972	AM489887	-
<i>Xanthomyrtus flavida</i> (Stapf) Diels	In this study	In this study	In this study	In this study	-	-	Wilson SAN152562 (SAN)
<i>Xanthomyrtus montivaga</i> A. J. Scott	AM234147	-	MF954516	MF954387	AM489971	AM489886	-
<i>Xanthostemon chrysanthus</i> (F. Muell.) Benth.	AF368227	EU410135	-	-	-	-	-

S3 - Fruit type reported for each species

Taxa	Fruit Type with reference
<i>Algrizea macrochlamys</i> (DC.) Proença & Nic Lugh.	fleshy/drupe ( <a href="https://www.jstor.org/">https://www.jstor.org/</a> )
<i>Archirhodomyrtus turbinata</i> (Schltr.) Burret	fleshy/berry ( <a href="https://en.wikipedia.org/">https://en.wikipedia.org/</a> )
<i>Backhousia angustifolia</i> F. Muell	dry/capsule ( <a href="https://www.researchgate.net/publication/271078147">researchgate.net/publication/271078147</a> )
<i>Campomanesia guazumifolia</i> (Cambess.) O. Berg	fleshy/berry ( <a href="https://www.scielo.br/scielo.php">https://www.scielo.br/scielo.php</a> )
<i>Chamguava schippii</i> (Standl.) Landrum	fleshy/berry ( <a href="https://stricollections.org/portal/taxa/index.php">https://stricollections.org/portal/taxa/index.php</a> )
<i>Cloezia artensis</i> (Montrouz.) P. S. Green	dry/capsule ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Eucalyptus perriniana</i> F. Muell. ex Rodway	dry/capsule ( <a href="http://keyserver.lucidcentral.org/https://vicflora.rbg.vic.gov.au/">http://keyserver.lucidcentral.org/https://vicflora.rbg.vic.gov.au/</a> )
<i>Eugenia arenosa</i> Mattos	fleshy/ berry ( <a href="https://www.researchgate.net/publication/326465558">https://www.researchgate.net/publication/326465558</a> )
<i>Eugenia brevistyla</i> D. Legrand	fleshy/drupe ( <a href="https://www.earth.com/https://bioone.org/journals/Systematic-Botany/vol-37">https://www.earth.com/https://bioone.org/journals/Systematic - Botany/vol - 37</a> )
<i>Eugenia bullata</i> Pancher ex Guillaumin =Eug. Ro	fleshy/ berry ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Eugenia florida</i> DC.	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Eugenia lucida</i> Lam.	fleshy/drupe ( <a href="https://plants.jstor.org/compilation/">https://plants.jstor.org/compilation/</a> )
<i>Eugenia macrocalyx</i> Mart. ex B. D. Jacks.	fleshy/drupe ( <a href="https://www.researchgate.net/publication/304008230">https://www.researchgate.net/publication/304008230</a> )
<i>Eugenia monticola</i> (Sw.) DC.	fleshy/berry ( <a href="https://www.researchgate.net/">https://www.researchgate.net/</a> )
<i>Eugenia natalitia</i> Sond.	fleshy/berry ( <a href="https://www.zimbabweflora.co.zw/">https://www.zimbabweflora.co.zw/</a> )
<i>Eugenia neoverrucosa</i> Sobral	fleshy/drupe ( <a href="https://www.scielo.br/pdf/bn/v11n1/19.pdf">https://www.scielo.br/pdf/bn/v11n1/19.pdf</a> )
<i>Eugenia orbiculata</i> Lam.	fleshy/berry ( <a href="http://pages.intnet.mu/nathraj/eugor.html">http://pages.intnet.mu/nathraj/eugor.html</a> )
<i>Eugenia paludosa</i> Pancher ex Brongn. & Gris	fleshy/drupe ( <a href="https://endemia.nc/flore/fiche4223">https://endemia.nc/flore/fiche4223</a> )
<i>Eugenia puberula</i> Nied. in Engler & Prantl	flashy/drupe ( <a href="https://teses.usp.br/">https://teses.usp.br/</a> )
<i>Eugenia reinwardtiana</i> (Blume) A. Cunn. ex DC.	flashy/drupe ( <a href="https://cnas-re.uog.edu/">https://cnas - re. uog. edu/</a> )
<i>Eugenia repanda</i> O. Berg	flashy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Eugenia sulcata</i> Sping ex Mart.	fleshy/berry rounded ( <a href="http://www.bananasraras.org/">http://www.bananasraras.org/</a> )
<i>Eugenia umtamvunensis</i> A. E. Van Wyk	fleshy/drupe ( <a href="https://core.ac.uk/download/pdf/81992013.pdf">https://core.ac.uk/download/pdf/81992013.pdf</a> )
<i>Eugenia uniflora</i> L.	fleshy/drupe ( <a href="http://www.iucngisd.org/">http://www.iucngisd.org/</a> )
<i>Eugenia verticillata</i> (Vell.) Angely	fleshy/drupe ( <a href="http://tropical.theferns.info/viewtropical.php">http://tropical.theferns.info/viewtropical.php</a> )
<i>Eugenia verdoorniae</i> A. E. van Wyk	fleshy/ berry ( <a href="https://inaturalist.nz/taxa/192144">https://inaturalist.nz/taxa/192144</a> )
<i>Heteropyxis natalensis</i> Harv.	dry/capsule ( <a href="http://pza.sanbi.org/">http://pza.sanbi.org/</a> )
<i>Hottea neibensis</i> Alain	fleshy/drupe ( <a href="https://www.sciencedirect.com/science/article/pii/S1055790317300052">https://www.sciencedirect.com/science/article/pii/S1055790317300052</a> )
<i>Legrandia concinna</i> (Phil.) Kausel	flehy/drupe ( <a href="https://treesandshrubsonline.org/">https://treesandshrubsonline.org/</a> )
<i>Luma apiculata</i> (DC.) Burret	flehy/berry (Mora2017. pdf)
<i>Lysicarpus angustifolius</i> (Hook.) Druce	dry/ capsule ( <a href="http://www.npqtownsville.org.au/">http://www.npqtownsville.org.au/</a> )
<i>Metrosideros angustifolia</i> (L.) Sm.	dry/woody casule ( <a href="https://en.wikipedia.org/http://pza.sanbi.org/https://treesa.org/">https://en.wikipedia.org/http://pza.sanbi.org/https://treesa.org/</a> )
<i>Metrosideros operculata</i> Labill.	dry/capsule ( <a href="https://www.repository.naturalis.nl/document/565561">https://www.repository.naturalis.nl/document/565561</a> )
<i>Metrosideros polymorpha</i> Gaudich.	dry/capsule ( <a href="https://en.wikipedia.org/http://nativeplants.hawaii.edu/">https://en.wikipedia.org/http://nativeplants.hawaii.edu/</a> )
<i>Metrosideros stipularis</i> Griseb. Ex tepualia	dry/capsule (Wilson 2011)
<i>Mosiera longipes</i> (O. Berg) Small	flehy/berry ( <a href="https://books.google.it/">https://books.google.it/</a> )
<i>Myrceugenia myrcioides</i> (Cambess.) O. Berg	flehy/drupe ( <a href="https://www.scielo.br/pdf/bn/v11n1/19.pdf">https://www.scielo.br/pdf/bn/v11n1/19.pdf</a> )
<i>Myrcia decorticans</i> DC.	hairy fleshy ( <a href="http://www.biotaxa.org">www.biotaxa.org</a> )
<i>Myrtus communis</i> L.	fleshy/berry ( <a href="https://besjournals.onlinelibrary.wiley.com">https://besjournals.onlinelibrary.wiley.com</a> )
<i>Neomyrtus pedunculata</i> (Hook. f.) Allan	fleshy/berry ( <a href="https://www.nzpcn.org.nz/">https://www.nzpcn.org.nz/</a> )
<i>Osbornia octodonta</i> F. Muell	Fleshy/drupe ( <a href="https://books.google.it/">https://books.google.it/</a> )
<i>Psidium cattleianum</i> Sabine	fleshy/berry ( <a href="https://www.cabi.org/">https://www.cabi.org/</a> )
<i>Psiloxylon mauritianum</i> (Bouton ex Hook. f.) Baill.	fleshy/berry ( <a href="https://fr.wikipedia.org/https://www.ncbi.nlm.nih.gov/pmc">https://fr.wikipedia.org/https://www.ncbi.nlm.nih.gov/pmc</a> )
<i>Syzygium acre</i> (Pancher ex Guillaumin) J. W. Dawson	fleshy/drupe ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Syzygium alatum</i> (Lauterb.) Diels	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )

<i>Syzygium angophoroides</i> (F. Muell.) B. Hyland	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium anisatum</i> (Vickery) Craven & Biffin	dry/dry papery capsules ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Syzygium arboreum</i> (Baker f.) J. W. Dawson	flashy /drupe ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Syzygium australe</i> (J. C. Wendl. ex Link) B. Hyland	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Syzygium austrocaledonicum</i> (Seem.) Guillaumin	fleshy/drupe ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Syzygium fibrosum</i> (F. M. Bailey) T. G. Hartley & L. M. Perry	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Syzygium floribundum</i> F. Muell	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium francii</i> (Guill.) N. Snow, Byng & Munzinger	flesh/drupe ( <a href="http://endemia.nc/">http://endemia.nc/</a> )
<i>Syzygium francisii</i> (F. M. Bailey) L. A. S. Johnson	flashy/drupe drysh flesh ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium fullagarii</i> (F. Muell.) Craven	fleshy/berry (Craven and Biffin 2010)
<i>Syzygium guineense</i> (Willd.) DC.	dry /subwoody drupe ( <a href="http://pza.sanbi.org/">http://pza.sanbi.org/</a> )
<i>Syzygium jambos</i> (L.) Alston	fleshy/drupe ( <a href="http://www.efloras.org/">http://www.efloras.org/</a> )
<i>Syzygium luehmannii</i> (F. Muell.) L. A. S. Johnson	fleshy/drupe ( <a href="https://books.google.it/">https://books.google.it/</a> )
<i>Syzygium macilwraithianum</i> B. Hyland	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium malaccense</i> (L.) Merr. & L. M. Perry	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Syzygium monimioides</i> Craven	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium moorei</i> (F. Muell.) L. A. S. Johnson	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium nervosum</i> A. Cunn. ex DC.	fleshy/drupe ( <a href="https://books.google.it/">https://books.google.it/</a> )
<i>Syzygium pseudofastigiatum</i> B. Hyland	fleshy/drupe ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Syzygium purpureum</i> (L. M. Perry) A. C. Sm.	fleshy/berry (Craven and Biffin 2010)
<i>Syzygium pycnanthum</i> Merr. & L. M. Perry	fleshy/drupe ( <a href="http://tropical.theferns.info/">http://tropical.theferns.info/</a> )
<i>Syzygium robustum</i> Miq.	flashy/drupe ( <a href="https://www.earth.com/">https://www.earth.com/</a> )
<i>Syzygium seemannii</i> (A. Gray) Biffin & Craven	flashy/berry (Craven and Biffin 2010)
<i>Syzygium tetrapterum</i> (Miq.) Chantaran. & J. Parn.	flashy/drupe (Craven and Biffin 2010)
<i>Thaleropia queenslandica</i> P. J. Wilson	dry/ capsule ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )
<i>Tristaniopsis anomala</i> (Merr.) P. G. Wilson & J. T. Waterh.	dry/ capsule (Wilson 2011)
<i>Ugni molinae</i> Turcz.	fleshy/berry ( <a href="https://www.nzpcn.org.nz/flora/species">https://www.nzpcn.org.nz/flora/species</a> )
<i>Xanthomyrtus montivaga</i> A. J. Scott	fleshy/berry ( <a href="https://books.google.it/">https://books.google.it/</a> )
<i>Xanthostemon chrysanthus</i> (F. Muell.) Benth.	dry/capsule ( <a href="http://www.anbg.gov.au/">http://www.anbg.gov.au/</a> )

S4 - Comparison of BKMMST phylogenetic tree in latest studies

