



Proposed plant host test list for assessing the risk of biological control agents for *Clidemia hirta* (L.) D. Don.

D.F. Comben, J.T. Callander, T. Taylor and M.D. Day

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Background

The following proposed plant host list is for the testing of potential biological control agents of *Clidemia hirta* (L.) D. Don (Melastomataceae). Post-release evidence from other countries suggests a promising outlook for biological control of *C. hirta* in Australia. Seven agents have already been released in Hawaii for this purpose, with six of these becoming established (Nakahara et al. 1992). *Liothrips urichi* Karny (Thysanoptera: Phlaeothripidae) is the first candidate biological control species proposed to undergo testing in Australia. The thrips have been released as a biological control agent for *C. hirta* in Fiji (1930), the Solomon Islands (1938, 1973 and 1975), Hawaii (1953), Palau (1960 and 1972), and American Samoa (1974) (Conant 2009). *Liothrips urichi* has established in all but the Solomon Islands and appears to be effective in open, sunny areas (Conant 2009). Host specificity of this insect has been demonstrated both within its native range and within countries where it has been introduced as a biological control of *C. hirta* (Table 1).

The plant host list put forward here was developed within a centrifugal phylogenetic framework (Table 2). This theory posits that the traits that make a plant host species desirable to an herbivore species are phylogenetically preserved (Briese 2005). Host-specific herbivore species are, therefore, less likely to recognise a plant species as an acceptable host as its phylogenetic separation from their primary host increases. In the context of biological control, candidate herbivore species are tested for herbivory and completion of life cycle stages on the most closely related host species to the target weed that are available. Under the centrifugal phylogenetic theory, if the candidate herbivore species can be shown to be unwilling to feed or unable to develop on close relatives of the target weed species, there is an acceptably low chance of it feeding on more distant relatives. Thus, the candidate is deemed suitably host-specific for release into a new environment. This theory has informed the host specificity testing of biological control agents in one form or another for the past 40+ years, and is now strongly supported by the data produced by host-specificity testing and post-release monitoring (Gilbert et al. 2012).

The number of Australian native Melastomataceae species presented here has been determined by consulting published literature and cross-checking results against the accepted plant nomenclature presented in the Australian Plant Consensus (Whiffin 1990; National Species List n.d.). Likewise, the intra- and interfamilial relationships of Melastomataceae and Memecylaceae have been determined from published molecular phylogenetic studies (Clausing and Renner 2001; Berger et al. 2016). Exotic Melastomataceae species numbers present in Australia were determined by searching the Atlas of Living Australia (ALA) for records of the family 'Melastomataceae' (Atlas of Living Australia n.d.). Total permitted horticultural Melastomataceae species in Australia and their naturalisation status were derived from Randall (2007).

The genus *Clidemia* contains around 150 species, none of which (apart from *C. hirta*) are found in Australia (Mabberley 1987; Atlas of Living Australia n.d.). *Clidemia* falls within the Miconieae clade of the family Melastomataceae (Order Myrtales) (Clausing and Renner 2001; Michelangeli et al. 2004). Melastomataceae has historically been divided into three subfamilies and 13 tribes (Renner 1993). A molecular phylogeny has revised the tribes into eight clades which have been assigned a name in this document that best suits their tribal association (Fig. 2 and 3) (Clausing and Renner 2001). Melastomataceae is a pantropical family, consisting of over 5,000 species spread across 165 genera (Christenhusz and Byng 2016). It is closely related to its sister taxon Memecylaceae, which has been considered at different times to be monophyletic, a subfamily within Melastomataceae or within Myrtaceae (Clausing and Renner 2001). In this host test list, we treat Memecylaceae as a subfamily within Melastomataceae and will refer to it hereafter as Memecyloideae (Fig. 2).

There are 11 recognised Melastomataceae species native to Australia (four endemics) (Fig. 2) (Maxwell 1981; Whiffin 1990; Bodegom and Veldkamp 2001; Meyer 2001; Hosking et al. 2011; Field 2012; National Species List n.d.). None of these species fall within the Miconieae clade with *C. hirta* (Fig. 2) (Clausing and Renner 2001). All 11 species are mostly confined to the wet tropics of the northern coast of Western Australia, the Northern Territory and Queensland, but the range of two species (*Melastoma affine* D. Don and *Memecylon*

pauciflorum Blume) also extend further south along the east coast into south-east Queensland and northern New South Wales (Whiffin 1990; Atlas of Living Australia n.d.). Thus far, *C. hirta* has invaded areas around Julatten and Wooroonooran National Park in far north Queensland, broadly sympatric with eight of the eleven native Australian Melastomataceae species (Breaden et al. 2012; Atlas of Living Australia n.d.). The other three native species have ranges that fall within the potential future range of *C. hirta* under a climate-matching model produced by the CSIRO (Fig. 1) (H. Murphy, CSIRO).

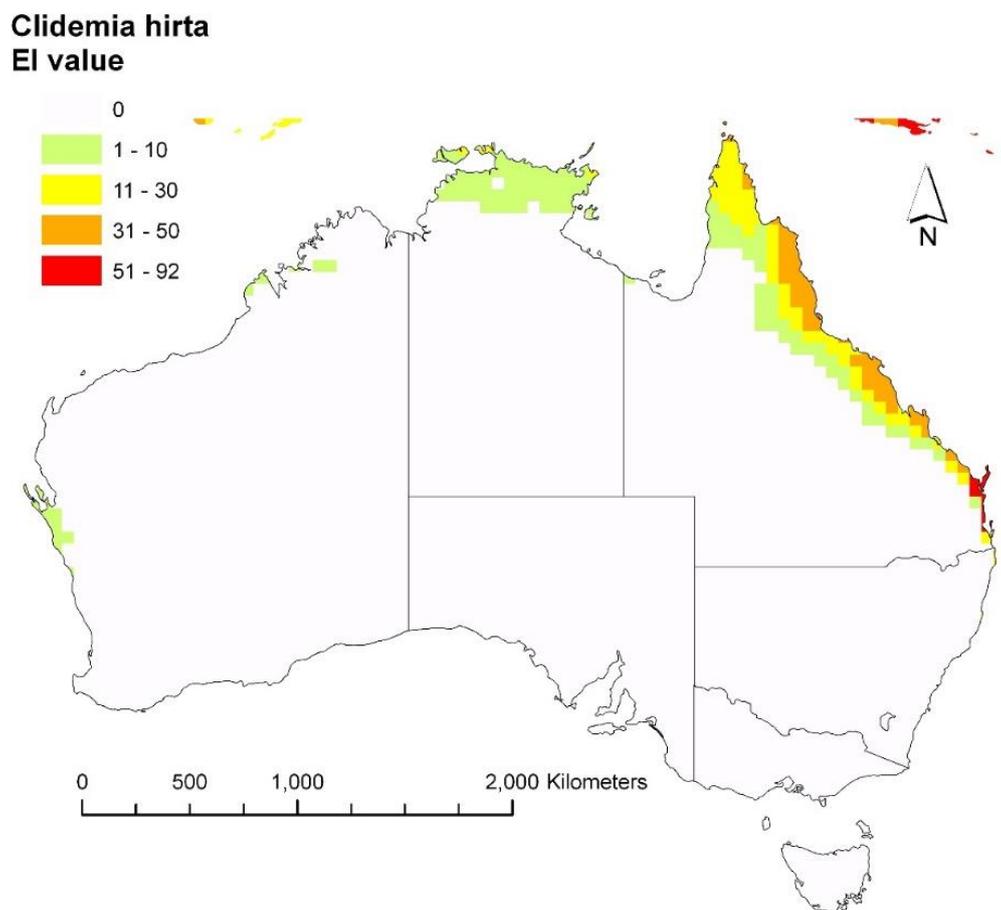


Fig. 1. The potential distribution, based on climatic suitability, of *C. hirta* using CLIMEX (H. Murphy, CSIRO). Red areas are the most climatically suitable habitats progressing through to green areas for least suitable and white for unsuitable.

In addition to the native Melastomataceae taxa, the ALA shows occurrence records indicating the presence of another 13 exotic Melastomataceae species in Australia (Atlas of Living Australia n.d.), seven of which are considered weeds. Four of the weedy species,

Miconia calvescens DC., *M. racemose* (Aubl.) DC., *M. nervosa* (Smith) Triana and *M. ciontricha* L.Urbe, are targeted for eradication under a national cost-share eradication programme. They also fall within the Miconieae clade, making them the closest phylogenetic relatives of *C. hirta* in Australia (Fig. 2) (Michelangeli, Penneys et al. 2004). In total, a further 72 Melastomataceae species are permitted for horticultural cultivation in Australia (Randall 2007), although most of these species are currently unavailable for purchase. The most ubiquitous ornamental Melastomataceae species in Australia are the *Tibouchina* s.l. Six common “*Tibouchina*” species are included in the test list but, due to taxonomic revisions, are placed in the genera *Pleroma*, *Andesanthus* and *Chaetogastra* (Guimarães et al. 2019). Two further permitted horticultural species (*Tetrazygia coriacea* Urb. and *Leandra xanthocoma* (Naudin) Cogn.) also fall within the Miconieae clade, but there are no records of these being grown in Australia (Clausing and Renner 2001). Other horticultural species may also sit within this clade but were excluded from previous phylogenetic studies.

The sister taxa to Melastomataceae are the small families Crypteroniaceae, Alzateaceae, Rhynchocalycaceae, Oliniaceae and Penaeaceae which make up the CAROP clade of Myrtales (Fig. 3) (Clausing and Renner 2001; Berger, Kriebel et al. 2016). No species from any of these families are present in Australia (Silverstone-Sopkin and Graham 1986; Rourke 1995; Conti et al. 2002). The next closest related family after the CAROP clade is Myrtaceae, which is very well represented in Australia with over 1500 species recorded (George 1988; Berger, Kriebel et al. 2016). Myrtaceae is split into 17 tribes by Berger et al. (2016), 14 of which are represented in Australia. After Myrtaceae are the families Vochysaceae (not present in Australia), Lythraceae, Onagraceae and Combretaceae, in order of increasing phylogenetic distance from Melastomataceae (Berger, Kriebel et al. 2016).

Given the small number of Melastomataceae species available in Australia, a phylogenetically broad host-test list is required (Table 2). Host-testing will prioritise all available Melastomataceae species first. One Myrtaceae species from 13 of the 14 tribes native to Australia (the tribe Lindsayomyrteae is monospecific and difficult to acquire) have

been included in the test list as the next closest relatives of the target, with emphasis placed on species sympatric with the current invasive range of *C. hirta*. Finally, two species each have been included from the families Lythraceae, Onagraceae and Combretaceae, to ensure comprehensive coverage of Myrtales in Australia.

Any suggestions for plant species substitutions or additions are welcome, but we kindly ask that they be justified within the phylogenetic/evolutionary/ecological framework approach taken to develop the plant host-test list. QDAF reserves the right to substitute any of the species listed in Table 2 and replace them with a surrogate species of equal phylogenetic relatedness to the target. Feedback and comments on this proposed host-test list can be addressed to David Comben (david.comben@daf.qld.gov.au) or Jason Callander (Jason.callander@daf.qld.gov.au).

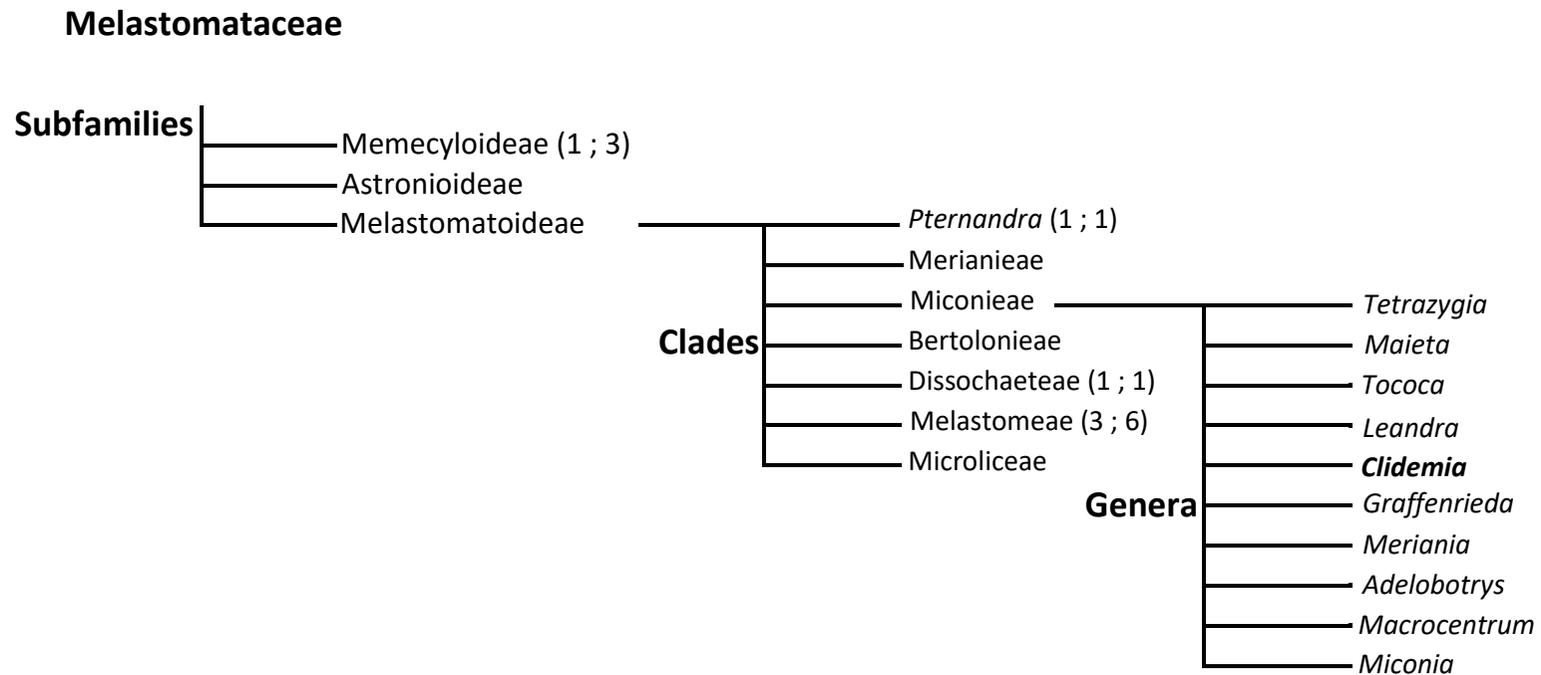


Fig. 2. A contracted dendrogram representing the phylogenetic pathway to the *Clidemia* genus within the Melastomataceae family based on the molecular phylogeny presented by Clausen & Renner (2001) and Michelangeli et al. (2004). Clades are named to best reflect their tribal identity as presented by Renner (1993). The phylogenetic divisions within clades are only given where they apply to *Clidemia*. Numbers in parentheses refer to the number of genera followed by the number of species within the group native to Australia.

Table 1. Previous studies of the host-specificity of *L. urichi*.**Study: Cook (1929)**

Field observations were made in Trinidad during which *L. urichi* was not observed on any other plants, including *Clidemia dentata* D.Don or *Clidemia neglecta* D.Don. Laboratory no-choice host specificity testing was conducted on the following crop species with no off-target damage recorded:

Family	Species	Common name
Dioscoreaceae	<i>Dioscorea</i> L. spp.	Yam
Araceae	<i>Colocasia esculenta</i> (L.) Schott	Taro
Arecaceae	<i>Cocos nucifera</i> L.	Coconut
Fabaceae		Dhal
Fabaceae	<i>Arachis hypogaea</i> L.	Peanut
Fabaceae	<i>Cicer arietinum</i> L.	Chickpea
Fabaceae	<i>Glycine max</i> (L.) Merr.	Soybean
Fabaceae	<i>Mimosa pudica</i> L.	Sensitive plant
Convolvulaceae	<i>Ipomoea batatas</i> (L.) Lam.	Sweet potato
Solanaceae	<i>Nicotiana</i> L. spp.	Tobacco
Bromeliaceae	<i>Ananas comosus</i> (L.) Merr.	Pineapple
Poaceae		Paragrass
Poaceae	<i>Saccharum</i> L. spp.	Sugarcane
Poaceae	<i>Paspalum virgatum</i> L.	
Poaceae	<i>Zea mays</i> L.	Maize
Euphorbiaceae	<i>Hevea brasiliensis</i> Müll.Arg.	Hevea rubber
Euphorbiaceae	<i>Manihot esculenta</i> Crantz	Cassava
Malvaceae	<i>Theobroma cacao</i> L.	Cacao
Malvaceae	<i>Gossypium</i> L. spp.	Cotton
Moraceae	<i>Artocarpus altilis</i> (Parkinson) Fosberg	Breadfruit
Musaceae	<i>Musa</i> L. spp.	Banana

Study: Taylor (1928)

Field observations were made in Trinidad during which *L. urichi* was not observed on any other Melastomataceae species. Laboratory no-choice host specificity testing was conducted on the following congeneric species with no off-target damage recorded:

Family	Species
Melastomataceae	<i>Clidemia neglecta</i> D.Don
Melastomataceae	<i>Clidemia postulata</i> DC.
Melastomataceae	<i>Clidemia spicata</i> (Aubl.)

Study: Cook (2001)

Field observations were made in American Samoa post-release during which *L. urichi* was not observed on any of the native Melastomataceae species there. In the course of these surveys, the following species were closely examined:

Family	Species
Melastomataceae	<i>Astronidium navigatorium</i> Christoph.
Melastomataceae	<i>Astronidium pickeringii</i> (A. Gray)
Melastomataceae	<i>Melastoma denticulatum</i> Labill.
Melastomataceae	<i>Medinilla samoensis</i> (Hoehreut.) Christoph.

Table 2. Host plant list for the testing of biological control agents for *C. hirta*. Total number of taxa native to Australia is listed under each family name, with the percentage of the total Australian native taxon represented on this list indicated in parentheses. ‘Status’ refers to the status of a particular species in Queensland (TW = target weed, N = native, O = ornamental, R = restricted, P = prohibited, E = environmental weed). ‘Range overlap with TW’ was determined using occurrence data obtained from the ALA (Atlas of Living Australia n.d.).

Family	Subfamily	Clade	Species	Status	Range overlap with TW	
Melastomataceae 6 gen. 11 spp. (45%)	Melastomoideae	Miconeae	<i>Clidemia hirta</i> (L.) D.Don	TW & R		
			<i>Miconia calvescens</i> D.	R		
			<i>Miconia nervosa</i> Triana	R		
			Dissochaeteae	<i>Miconia racemosa</i> (Aubl.) DC.	R	
				<i>Medinilla balls-headleyi</i> F.Muell.	N	x
			Melastomeae	<i>Medinilla myriantha</i> Merr.	O	
				<i>Andesanthus gleasonianus</i> (Wurdack) P.J.F.Guim. & Michelang.	O	
				<i>Centradenia floribunda</i> Planch.	O	
				<i>Chaetogastra laxa</i> (Desr.)	O	
				<i>Dissotis rotundifolia</i> (Sm.) Triana	E	
				<i>Melastoma affine</i> D.Don	N	x
				<i>Melastoma candidum</i> D.Don	E	
				<i>Melastoma cyanooides</i> Sm.	N	x
				<i>Pleroma mutabile</i> (Vell.) Triana	O	
				<i>Pleroma heteromallum</i> (D.Don) D.Don	O	
			<i>Pleroma granulorum</i> (Desr.) D.Don	O		
			<i>Pleroma urvilleanum</i> (DC.) P.J.F.Guim. & Michelang.	O		
		<i>Tristemma mauritianum</i> J.F.Gmel.	E			

	Memecyloideae	<i>Memecylon hylandii</i> Whiffin	N	x
		<i>Memecylon pauciflorum</i> Blume	N	x
Myrtaceae	Xanthostemoneae	<i>Xanthostemon chrysanthus</i> (F.Muell.)	N	x
75 gen. >1500 spp. (0.9%)	Lophostemoneae	<i>Lophostemon confertus</i> (R.Br.) Peter G.Wilson & J.T.Waterh.	N	x
	Osbornieae	<i>Osbornia octodonta</i> F.Muell.	N	x
	Melaleuceae	<i>Melaleuca quinquenervia</i> (Cav.) S.T.Blake	N	x
	Eucalypteae	<i>Stockwellia quadrifida</i> D.J.Carr, S.G.M. Carr & B.Hyland	N	x
	Syncarpieae	<i>Syncarpia glomulifera</i> (Sm.) Nied.	N	x
	Leptospermeae	<i>Leptospermum brachyandrum</i> (F.Muell.) Druce	N	x
	Chamelaucieae	<i>Baeckea frutescens</i> L.	N	x
	Myrteae	<i>Decaspermum humile</i> (G.Don) A.J.Scott	N	x
	Kanieae	<i>Ristantia gouldii</i> Peter G.Wilson & B.Hyland	N	
	Tristanieae	<i>Thaleropia queenslandica</i> (L.S.Sm.) Peter G. Wilson	N	x
	Backhousieae	<i>Backhousia bancroftii</i> F.M.Bailey	N	x
	Syzygieae	<i>Syzygium oleosum</i> (F.Muell.) B.Hyland	N	x
Lythraceae		<i>Cuphea hyssopifolia</i> Kunth	O	
8 gen. 24 spp. (8.3%)		<i>Punica granatum</i> L.	O	
Onagraceae		<i>Ludwigia peploides</i> (Kunth) P.H.Raven	-	x
2 gen. 17 spp. (11.8%)		<i>Oenothera biennis</i> L.	O	
Combretaceae		<i>Terminalia catappa</i> L.	O	
5 gen. 33 spp. (6%)		<i>Combretum indicum</i> L.	O	

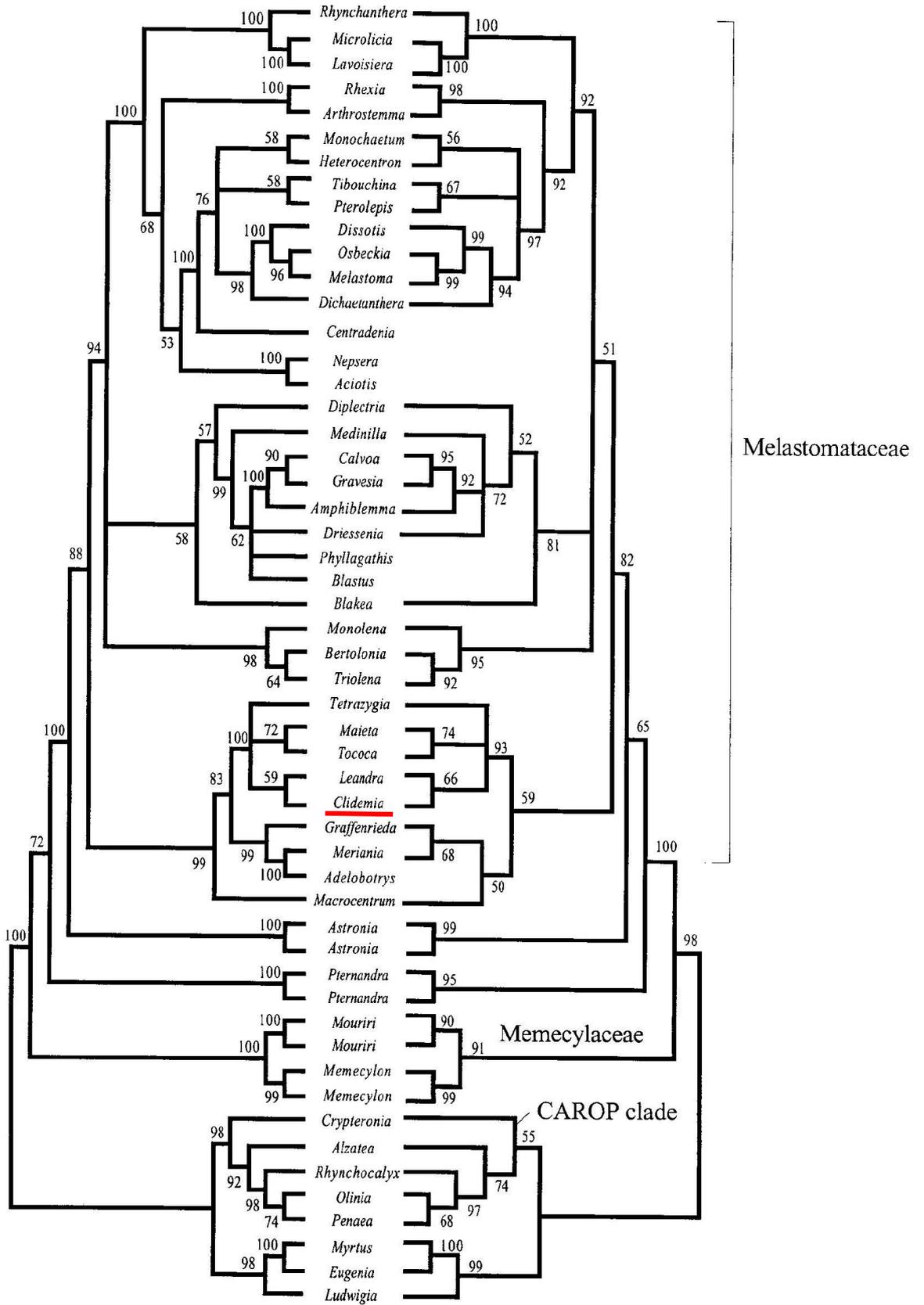


Fig. 3. Midpoint-rooted strict consensus of three equally parsimonious trees (left) and midpoint-rooted highest likelihood tree (right) from Clausen and Renner (2001). *Clidemia* is highlighted with red underlining.

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