

Supplementary material

A genome-wide approach for uncovering evolutionary relationships of Australian *Bactrocera* species complexes (Diptera: Tephritidae)

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Supplementary Material 1 – Sample information Collection methods and locality data

Sample collection

Infested fruit collection

1) Detailed sampling history (See table S1 for sample details)

A multitude of fruits (particularly *Terminalia petiolaris*) were sampled in Broome from the south of the main township (-18.003, 122.208) to '12 Miles'/Roebuck (-17.863, 122.365) over one week of surveying. All fruits (~15 kg) were placed at temperatures under 10 °C to slow down development. Subsequently, the fruits were then packed into an esky (Australian for "portable cooler" or "ice chest") prior to transporting to the Department of Agriculture and

Fisheries (DAFWA) in Perth to be processed (See fruit processing for further details). Adults from Broome were transported to Canberra at generation 1.

Flies from Mareeba were obtained from a shipment of guavas, mangoes and cashews (>20 kg) from Mareeba in February 2016, while in Sydney, flies were collected from infested loquats and mulberries in November 2016.

2) Fruit processing

Where not stated in the sampling history, fruits were transported/freighted back to Canberra laboratories to be processed. In general, fruits were either placed directly on fine vermiculite, or onto a net or wire mesh, or onto a tray with drainage separated from the fine vermiculite. The drainage trays were employed to avoid drenching the vermiculite. Vermiculite were generally lightly moisten with a spray bottle to reduce pupal mortality from dehydration (HULTHEN AND CLARKE 2006). Fruits were incubated between 24-26 °C. In general, vermiculite were gently sieved and placed into cages every 10 days post fruit collection at least twice to avoid to uncover as much pupae as possible yet avoiding adult eclosion in vermiculite holding trays. Adults (at most 3 days after eclosion) were identified by taxonomical features (Drew, 1989), where a subset of live adults were frozen after next generation eggs were collected.

Lure trapping

Three different lure traps were employed across this study, although not all were used in any given one time. lures from BioTrap Australia Pty Ltd: (1) male attracting Cue lure or 4-[4-(acetyloxy)phenyl]-2-butanone; as wafers (2g cue lure) or soaked wicks (4g cue lure), (2) male attracting Methyl eugenol (ME) or 1,2-Dimethoxy-4-(prop-2-en-1-yl)benzene soaked wicks, and (3) non-sex specific protein baits, containing 96% hydrolysed protein. One wafer, one soaked wick or 10 ML of protein bait were placed inside one Bio Trap V1 (trap). No insecticide were applied to the traps to ensure samples were alive at the time of inspection.

1) Darwin

10 cue lure and 10 protein bait traps were set up in an L-shaped perimeter around mango trees spanning approximately 100 m each side centring at -12.42078°, 130.92278°. Lures were monitored for a week on a daily basis. Flies were stored in absolute ethanol on site and species-identified in Canberra.

2) Cape Tribulation

A total of nine spots were utilised close to the James Cook University's Daintree Rainforest Observatory centring at -16.10391°, 145.44918°. Two cue lure and two ME lure were deployed at each spot one day prior to inspection. Traps were only inspected once only. Flies were placed into a BugDorm cage (32.5³ cm³) and transported alive to Mareeba to be identified to species. Once flies were identified, they were immediately preserved in absolute ethanol. From trap inspection to species identification, which spanned a timeframe of about 48 hours, mortality occurred at the beginning and during transit prior to species identification, and these were prioritised less for DArTseq unless there were insufficient alive samples of that species.

3) Malaysia

ME lure traps were deployed within Universiti Putra Malaysia (UPM) in early 2017. Flies collected from traps were immediately stored in absolute ethanol.

References

- Drew RAI 1989 The tropical fruit flies (Diptera: Tephritidae: Dacinae) of the Australasian and Oceanian regions. *Memoirs of the Queensland Museum* 26, 1-521.
- Hulthen, A. D., and A. R. Clarke, 2006 The influence of soil type and moisture on pupal survival of *Bactrocera tryoni* (Froggatt) (Diptera : Tephritidae). *Australian Journal of Entomology* 45: 16-19.

Table S1– Details of specimens included in the DArTseq runs

Species	Location	Latitude	Longitude	Collection method	Number included	
					Male	Female
<i>B. abscondita</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	1	
<i>B. aeruginosa</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. alyxiae</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. breviaculeus</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. bryoniae</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	4	
<i>B. endiandrae</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. laticaudus</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. rufofuscola</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	1	
<i>B. silvicola</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	1	
<i>B. striginifinis</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. frauenfeldi</i>	Cairns	-16.85579°	145.74616°	Fruit		1
<i>B. pallida</i>	Cairns	-16.90031°	145.74977°	Fruit	1	1
<i>B. carambolae</i>	Malaysia	3.00030°	101.71260°	Trap	2	
<i>B. dorsalis</i>	Malaysia	3.00030°	101.71260°	Trap	2	
<i>B. umbrosa</i>	Malaysia	3.00030°	101.71260°	Trap	2	
<i>B. jarvisi</i>	Darwin	-12.42078°	130.92278°	Trap		2
<i>B. aquilonis</i>	Broome	-17.96016°	122.22740°	Fruit	3	2
<i>B. neohumeralis</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	2	
<i>B. tryoni</i>	Cape Tribulation	-16.10391°	145.44918°	Trap	5	0
	Mareeba (Walkamin)	-17.13869°	145.42858°	Fruit	8	8
	Sydney	-33.90718°	151.15394°	Fruit	5	6

Supplementary Material 2 – Additional genetic results

Table S2.1 Total sequencing and SNP number after each filtering step for each of the analyses (all individuals for genetic clustering, species with only one individual removed (for SVDQuartets and Maximum Likelihood analyses, and SNAPP analysis).

	All species for IQtree genetic clustering analyses	IQtree - ind. species removed	SNAPP analyses
Raw reads per individual	~1.1 million		
Avg. reads per 60–70 bp DNA fragment	46.7 reads		
Total SNPs identified	22,714		
Number of individuals	32	28	28
SNPs left after filtering:			
Loci call rate	(85%) 2574	(85%) 4641	(85%) 1748
Ind. removed - ind call rate	(85%) <i>T. termitoxena</i> and all <i>B. strigifinis</i>	(80%) none	(90%) none
Filter reproducibility = 1	2277	4153	1459
Filter by minor allele frequency	1864	2433	762
Filter SNPs on same DNA fragment	1222	1874	578

Table S2.1. Nei's genetic distance on SNP data used in SVDQuartets/Maximum likelihood analyses

	alyxae	jarvisi	laticaudus	aeruginosa	breviaculeus	bryoniae	neohumeralis	endiandroe	aquilonis	tryoni	pallida	dorsalis	carambolae
jarvisi	0.209												
laticaudus	0.282	0.199											
aeruginosa	0.347	0.284	0.269										
breviaculeus	0.208	0.120	0.224	0.277									
bryoniae	0.322	0.242	0.259	0.331	0.258								
neohumeralis	0.203	0.102	0.217	0.278	0.117	0.244							
endiandroe	0.264	0.194	0.218	0.247	0.206	0.267	0.184						
aquilonis	0.220	0.113	0.228	0.293	0.131	0.258	0.025	0.201					
tryoni	0.223	0.116	0.236	0.302	0.133	0.265	0.025	0.209	0.025				
pallida	0.379	0.296	0.317	0.382	0.298	0.331	0.303	0.302	0.296				
dorsalis	0.247	0.176	0.199	0.250	0.182	0.207	0.180	0.185	0.190	0.198	0.149		
carambolae	0.232	0.168	0.190	0.249	0.175	0.203	0.171	0.176	0.181	0.190	0.171	0.057	
umbrosa	0.406	0.329	0.323	0.360	0.352	0.377	0.338	0.298	0.349	0.357	0.440	0.312	0.300

Table S2.2 Fst on all species SNP dataset (SNP data with used in genetic clustering analyses). Note that Fst cannot be calculated between species represented by a single individuals.

	alyxiae	jarvisi	laticaudus	rufofuscula	silvicola	aeruginosa	abscondita	breviaculeus	bryoniae	neohumeralis	endiandroe	aquilonis	tryoni	pallida	dorsalis	carambolae	umbrosa
jarvisi	0.146																
laticaudus	0.150	0.095															
rufofuscula	0.157	0.068	0.029														
silvicola	0.176	0.099	0.109														
aeruginosa	0.191	0.145	0.128	0.140	0.157												
abscondita	0.152	0.071	0.094	NA	NA	0.145											
breviaculeus	0.146	0.087	0.105	0.099	0.136	0.147	0.111										
bryoniae	0.183	0.131	0.129	0.135	0.156	0.172	0.138	0.138									
neohumeralis	0.146	0.065	0.102	0.101	0.131	0.145	0.110	0.084	0.129								
endiandroe	0.163	0.111	0.106	0.107	0.121	0.137	0.100	0.119	0.135	0.114							
aquilonis	0.149	0.070	0.101	0.095	0.119	0.144	0.101	0.086	0.131	0.019	0.114						
tryoni	0.155	0.074	0.105	0.101	0.128	0.149	0.111	0.082	0.132	0.016	0.120	0.019					
pallida	0.205	0.162	0.156	0.161	0.193	0.201	0.176	0.171	0.172	0.167	0.169	0.166	0.168				
dorsalis	0.158	0.107	0.100	0.086	0.108	0.143	0.095	0.116	0.128	0.110	0.107	0.112	0.117	0.120			
carambolae	0.149	0.095	0.092	0.053	0.091	0.140	0.068	0.106	0.112	0.101	0.097	0.106	0.106	0.127	0.055		
umbrosa	0.238	0.191	0.185	0.204	0.213	0.202	0.203	0.197	0.214	0.193	0.185	0.193	0.201	0.250	0.191	0.184	
fraunfeldi	0.171	0.103	0.111	NA	NA	0.163	NA	0.142	0.158	0.131	0.129	0.126	0.135	0.203	0.113	0.097	0.217

Table S2.3 Nei's genetic distance on SNP data used in Bayesian SNAPP analyses

	alyxiae	jarvisi	laticaudus	aeruginosa	breviaculeus	bryoniae	neohumeralis	endiandroe	aquilonis	tryoni	pallida	dorsalis	carambolae	umbrosa
jarvisi	0.248													
laticaudus	0.286	0.170												
aeruginosa	0.347	0.246	0.234											
breviaculeus	0.240	0.135	0.191	0.251										
bryoniae	0.362	0.250	0.248	0.323	0.267									
neohumeralis	0.226	0.098	0.169	0.240	0.114	0.241								
endiandroe	0.267	0.168	0.165	0.215	0.181	0.237	0.156							
aquilonis	0.240	0.107	0.179	0.248	0.123	0.252	0.027	0.166						
tryoni	0.256	0.117	0.193	0.267	0.140	0.265	0.032	0.181	0.029					
pallida	0.396	0.298	0.289	0.373	0.314	0.347	0.299	0.281	0.282	0.330				
dorsalis	0.268	0.168	0.154	0.226	0.179	0.215	0.162	0.149	0.169	0.189	0.153			
carambolae	0.261	0.162	0.150	0.228	0.176	0.207	0.162	0.142	0.167	0.190	0.177	0.047		
umbrosa	0.372	0.265	0.255	0.275	0.294	0.340	0.258	0.228	0.270	0.286	0.375	0.243	0.242	

Table S2.4 Fst on SNP data used in SVDQuartets/Maximum likelihood analyses

	alyxiae	jarvisi	laticaudus	aeruginosa	breviaculeus	bryoniae	neohumeralis	endiandroe	aquilonis	tryoni	pallida	dorsalis	carambolae
jarvisi	0.931												
laticaudus	0.972	0.925											
aeruginosa	0.981	0.959	0.983										
breviaculeus	0.961	0.882	0.966	0.980									
bryoniae	0.984	0.953	0.983	0.995	0.979								
neohumeralis	0.932	0.823	0.937	0.962	0.888	0.956							
endiandroe	0.955	0.908	0.951	0.969	0.941	0.970	0.906						
aquilonis	0.909	0.795	0.917	0.941	0.865	0.940	0.424	0.895					
tryoni	0.952	0.870	0.960	0.973	0.922	0.979	0.552	0.938	0.477				
pallida	0.980	0.956	0.983	0.990	0.978	0.992	0.962	0.970	0.938	0.973			
dorsalis	0.938	0.877	0.920	0.952	0.910	0.943	0.884	0.906	0.868	0.912	0.912		
carambolae	0.931	0.877	0.927	0.947	0.914	0.946	0.886	0.904	0.863	0.913	0.921	0.688	
umbrosa	0.987	0.963	0.985	0.993	0.985	0.995	0.965	0.974	0.949	0.979	0.992	0.956	0.958

Table S2.5 Fst on SNP data used in Bayesian SNAPP analyses

	alyxiae	jarvisi	laticaudus	aeruginosa	breviaculeus	bryoniae	neohumeralis	endiandroe	aquilonis	tryoni	pallida	dorsalis	carambolae
jarvisi	0.930												
laticaudus	0.962	0.903											
aeruginosa	0.981	0.950	0.972										
breviaculeus	0.963	0.893	0.955	0.982									
bryoniae	0.983	0.954	0.977	0.998	0.987								
neohumeralis	0.935	0.813	0.904	0.962	0.895	0.960							
endiandroe	0.950	0.892	0.923	0.961	0.938	0.968	0.902						
aquilonis	0.909	0.773	0.884	0.921	0.846	0.927	0.434	0.860					
tryoni	0.931	0.836	0.912	0.953	0.897	0.958	0.582	0.902	0.444				
pallida	0.978	0.957	0.980	0.994	0.982	0.995	0.968	0.967	0.933	0.957			
dorsalis	0.934	0.860	0.873	0.943	0.909	0.944	0.868	0.876	0.838	0.879	0.912		
carambolae	0.940	0.864	0.891	0.947	0.919	0.945	0.884	0.878	0.844	0.890	0.928	0.633	
umbrosa	0.982	0.950	0.969	0.996	0.984	0.998	0.962	0.972	0.932	0.964	0.994	0.939	0.956

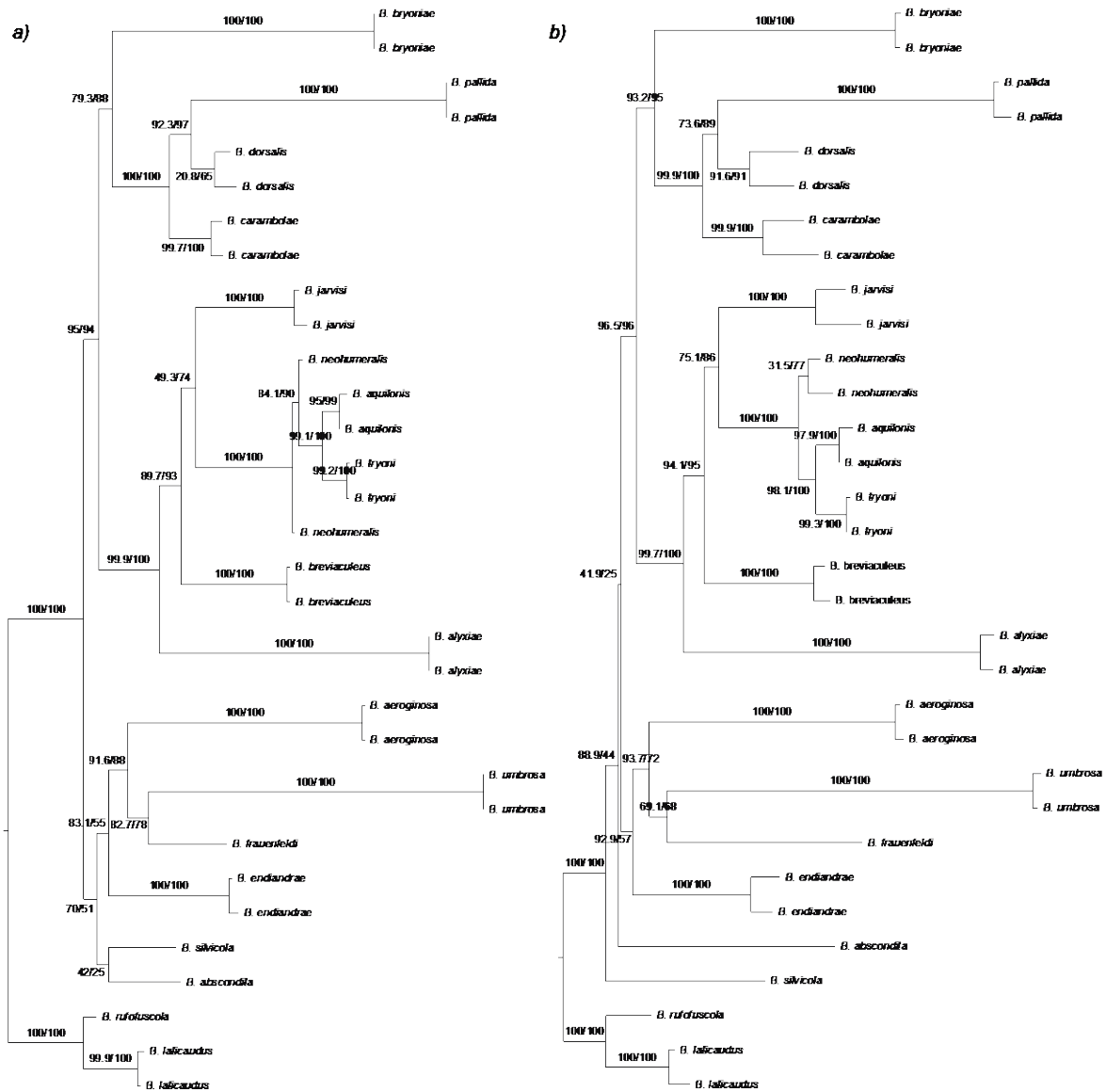


Figure S2.1. Phylogenetic analyses of SNP datasets that included species represented by a single individual. All methods followed IQtree parameters in main text. In (a), SNP data used for genetic clustering analyses was used, which incorporated alleles where minor allele frequency was set to 4 alleles out of 32 individuals ($2n = 64$). In (b), minor allele frequency was set to 2 alleles out of 32 individuals. Note the low support values at most nodes leading to a species represented by a single individual, the low support at nodes deeper in the phylogeny, and topological changes due to the minor allele frequency settings. In (a), no private alleles are present in species represented by a single individual, and therefore share all SNPs with other species. In (b), the low minor allele frequency means all SNPs present in one homozygous or two heterozygous individuals are included in the analysis. This likely introduces population genetic “noise” and artificial sharing of SNPs between distantly related individuals due to convergent mutations, confounding phylogenetic analyses.

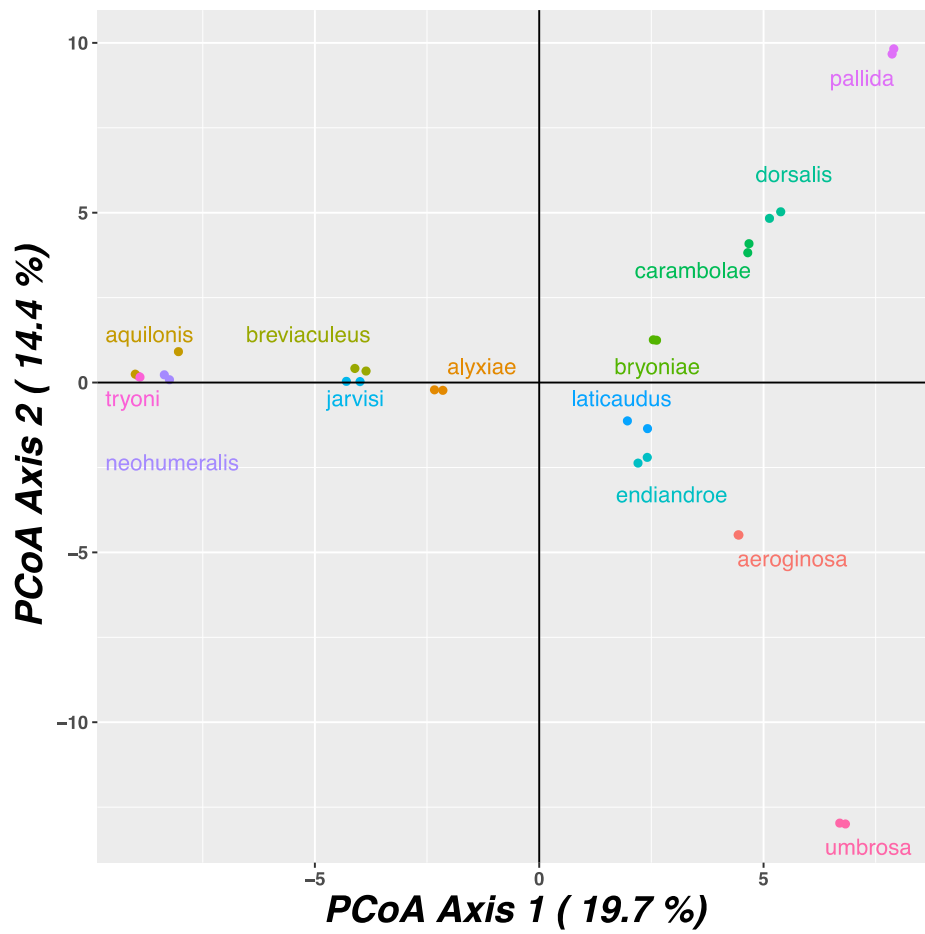


Fig. S2.2 Principal components analysis on SNP data used in SVDQuartets/Maximum likelihood analyses

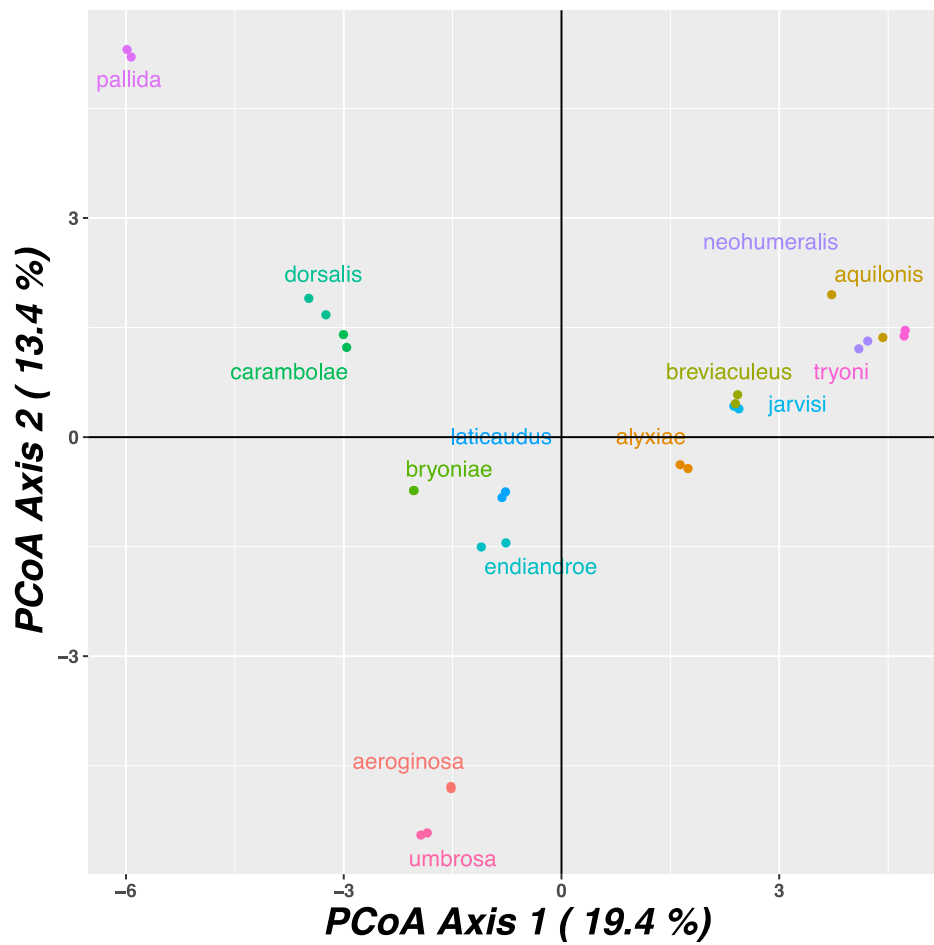


Fig. S2.3 Principal components analysis on SNP data used in Bayesian SNAPP analyses

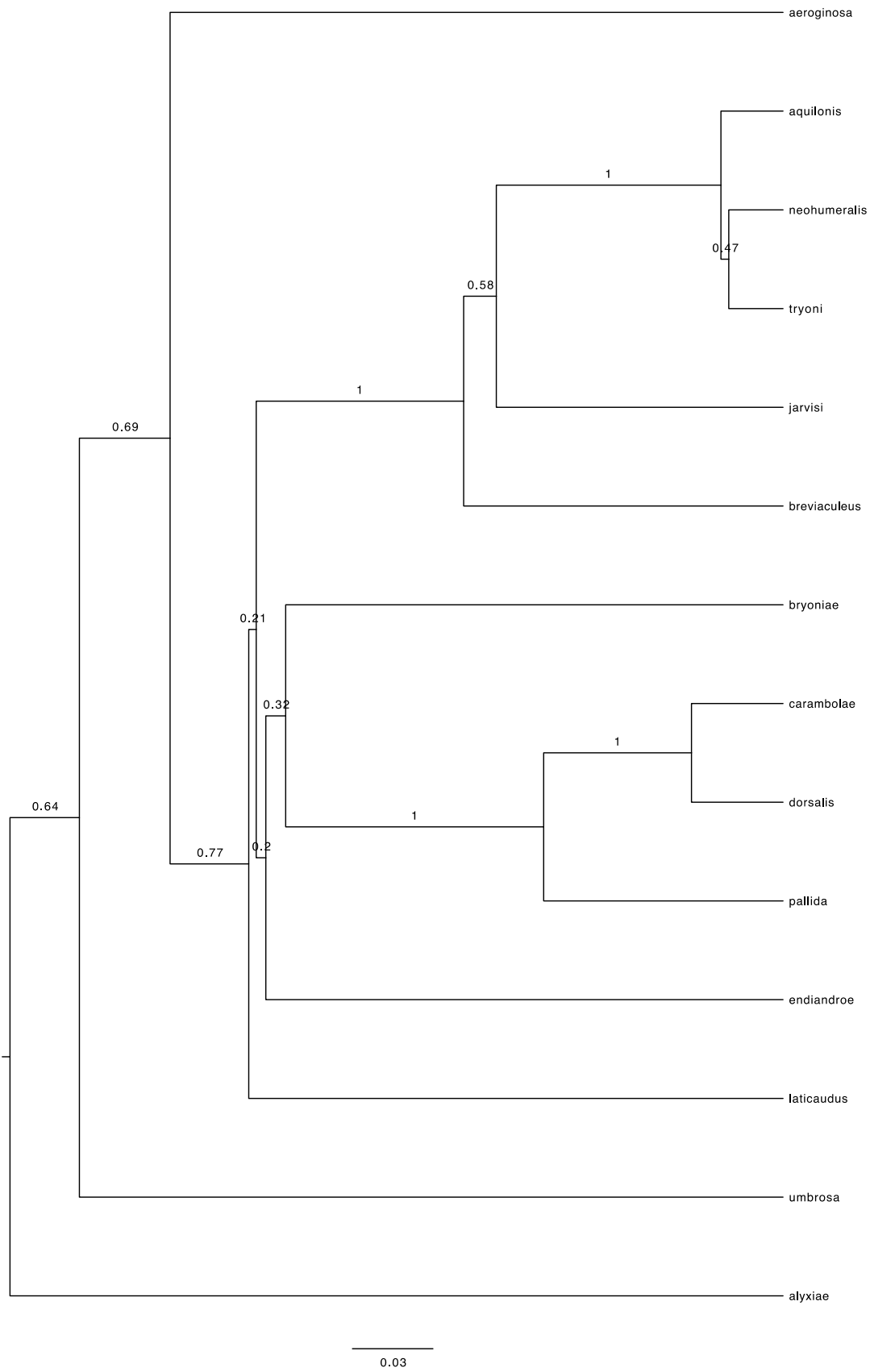


Fig. S2.5 Resulting phylogeny from Bayesian SNAPP species tree analysis

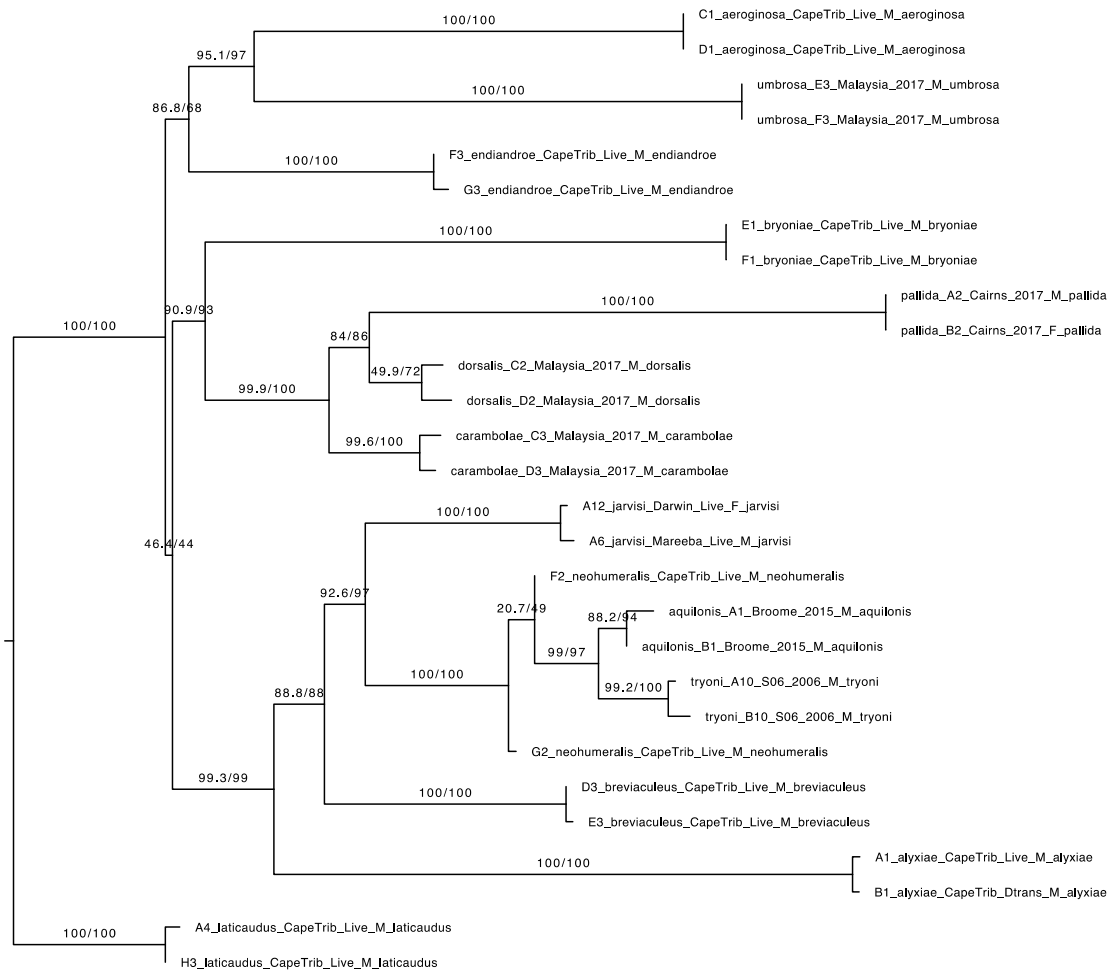


Fig. S2.6 IQtree phylogeny of SNP data used in Bayesian SNAPP analyses. Although this demonstrates an overall similar topology to the full IQtree analyses, many nodes lose support. This suggests that the number of SNPs able to be analysed in SNAPP in a reasonable time frame (three weeks) do not contain sufficient information to resolve the topology.

Table S1. Genbank accession numbers, specimen codes, DNA vouchers and region of origin for the specimens used in this study
 All vouchers are deposited in the South Australian Museum except those indicated by ^ which are deposited in the Queensland Museum, and those indicated by Ω obtained from Genbank. Shaded boxes represent missing data.

Taxon	Origin	Specimen code	DNA Voucher	Genbank Accession No. (COI)	Genbank Accession No. (EF1αF2)	Genbank Accession No. (wg)
<i>Anillomyrma decacrema</i>	Asia		^Ω CAS:ENT:0235147		KJ859694	KJ861768
<i>Anillomyrma sp.</i>	Africa		^Ω CAS:ENT:0280595		KJ859693	KJ861767
<i>Erromyrma latinodis</i>	Australia	latiTERC50	SAMA32-034929	KJ847490	KJ847521	KJ847552
<i>Monomorium aithoderum</i>	Australia	PL5	SAMA32-034893	KJ847507, KJ847508	KJ847511	
<i>Monomorium albipes</i>	Australia	QM52091	SAMA32-034894	KJ847470		KJ847535
<i>Monomorium antarcticum</i>	New Zealand	PL6	SAMA32-034895	KJ847471	KJ847512	KJ847536
<i>Monomorium antipodum</i>	New Zealand	PL7	SAMA32-034896	KJ847473	KJ847513	KJ847538
<i>Monomorium bicorne</i>	Australia	SAM32-03911	SAMA32-003911	KJ847474		
<i>Monomorium bifidum</i>	Australia	TERC24	SAMA32-034897	KJ847475		KJ847539
<i>Monomorium c.f. antipodum</i>	Australia	CJB170_06	SAMA32-034898	KJ847472		KJ847537
<i>Monomorium capeyork (rothsteini complex)</i>	Australia	TERC4	SAMA32-034952	KC572926		
<i>Monomorium centrale</i>	Australia	KSS8	SAMA32-034899	KJ847476		KJ847540

<i>Monomorium decuria</i>	Australia	PL3	SAMA32-034900	KJ847477		KJ847541
<i>Monomorium eremum</i> (rothsteini complex)	Australia	KSS98	SAMA32-034959	KC573009		
<i>Monomorium euryodon</i>	Australia	SAM32-03449	SAMA32-003449	KJ956898		
<i>Monomorium fastidium</i>	Australia	ANA09-24	SAMA32-034901	KJ956899		
<i>Monomorium fieldi</i>	Australia	TERC12	SAMA32-034902	KJ956900		
<i>Monomorium fieldi</i>	Australia	TERC31	SAMA32-034903	KJ847479		
<i>Monomorium fieldi</i>	Australia	KSS16	SAMA32-034904	KJ847480	KJ847515	KJ847543
<i>Monomorium fieldi</i>	Australia	TERC59	SAMA32-034905	KJ956901		
<i>Monomorium fieldi</i>	Australia	TERC62	SAMA32-034906	KJ956902		
<i>Monomorium fieldi</i>	Australia	160p3	SAMA32-034907	KJ956903		
<i>Monomorium fieldi</i> (donisthorpei-form)	Australia	150p2	SAMA32-034908	JQ846285, KJ847509		
<i>Monomorium fieldi</i> (donisthorpei-form)	Australia	217p3	SAMA32-034909	JQ846286, KJ956895		
<i>Monomorium fieldi</i> (donisthorpei-form)	Australia	334p3	SAMAA32-035166	JQ846287, KJ956896		
<i>Monomorium fieldi</i> (donisthorpei-form)	Australia	428p3	SAMA32-034911	JQ846288, KJ956897		
<i>Monomorium fieldi</i> (nigrius-form)	Australia	228p3	SAMA32-034912	JQ846297, KJ956912		
<i>Monomorium fieldi</i> (nigrius-form)	Australia	240p3	SAMA32-034913	JQ846305, KJ956913		
<i>Monomorium fieldi</i> (sp. 18)	Australia	146p2	SAMA32-035167	JQ846312, KJ956923		
<i>Monomorium floricola</i>	Africa	TERC36	SAMA32-034915	KJ847481	KJ847516	KJ847544
<i>Monomorium gilberti</i>	Australia	ANA001	SAMA32-034916	KJ956904		
<i>Monomorium humilior</i> (rothsteini complex)	Australia	KSS83	SAMA32-034956	KC572944		
<i>Monomorium humilior</i> (rothsteini complex)	Australia	KSS85	SAMA32-034957	KC572946	KJ847530	KJ847563
<i>Monomorium insolescens</i>	Australia	TERC23	SAMA32-034917	KJ847485		
<i>Monomorium junodi</i>	Africa	TERC49	SAMA32-034918	KJ847486	KJ847519	KJ847548
<i>Monomorium kiliani</i>	Australia	QM31414	^QM31414	KJ956906		
<i>Monomorium kiliani</i>	Australia	ANA09_9	SAMA32-034920	KJ847487		KJ847549
<i>Monomorium kilianrobi</i>	Australia	ANA09_10	SAMA32-034921	KJ847488		KJ847550

<i>Monomorium laeve</i>	Australia	KSS63	SAMA32-034922	KJ847489	KJ847520	KJ847551
<i>Monomorium laeve</i> (sp. 23)	Australia	79p2	SAMA32-034923	JQ846314, KJ956907	[REDACTED]	
<i>Monomorium laeve</i> (sp. 23)	Australia	81p2	SAMA32-034924	JQ846315, KJ956908		
<i>Monomorium laeve</i> (sp. 24)	Australia	129p2	SAMA32-034925	JQ846318, KJ956909		
<i>Monomorium laeve</i> (sp. 24)	Australia	55p1	SAMA32-034926	JQ846317, KJ956910		
<i>Monomorium laeve</i> (sp. 33)	Australia	12p1	SAMA32-034927	JQ846322, KJ956911		
<i>Monomorium laeve</i> (sp. A)	Australia	3p1	SAMA32-034928	JQ846329, KJ956924		
<i>Monomorium leae</i> (dark form)	Australia	CJB245_06	SAMA32-034930	KJ847491		KJ847522
<i>Monomorium leae</i> (flavipes-form)	Australia	KSS24	SAMA32-034931	KJ847492	KJ847523	KJ847554
<i>Monomorium leae</i> (light form)	Australia	QM15899	SAMA32-034932	KJ847493	[REDACTED]	KJ847555
<i>Monomorium leae</i> (light form)	Australia	QM15798	SAMA32-034933	KJ847494	[REDACTED]	KJ847556
<i>Monomorium legulus</i>	Australia	ES36	SAMA32-034934	KJ847495	KJ847524	KJ847557
<i>Monomorium longinode</i>	Australia	BH004	SAMA32-034935	KJ847496	KJ847525	KJ847558
<i>Monomorium pharaonis</i>	Africa	TERC74	SAMA32-034936	KJ847499	KJ847528	KJ847561
<i>Monomorium rubriceps</i>	Australia	KSS19	SAMA32-034937	KJ956914	[REDACTED]	
<i>Monomorium rubriceps</i>	Australia	QM51880	SAMA32-034938	KJ847500		KJ847564
<i>Monomorium rubriceps</i>	Australia	ANA09	SAMA32-034939	KJ956915		
<i>Monomorium sordidum</i>	Australia	KSS10	SAMA32-034940	KJ956918		
<i>Monomroium smithii</i>	New Zealand	PL4	SAMA32-034968	KJ956917		
<i>Monomorium sordidum</i>	Australia	KSS6	SAMA32-034941	KJ956919		
<i>Monomorium sordidum</i>	Australia	KSS27	SAMA32-034942	KJ956920		
<i>Monomorium sordidum</i>	Australia	KSS42	SAMA32-034943	KJ956921		
<i>Monomorium sordidum</i>	Australia	KSS43	SAMA32-034944	KJ956922		
<i>Monomorium sordidum</i>	Australia	KSS49	SAMA32-034945	KJ847501		KJ847565
<i>Monomorium sordidum</i>	Australia	KSS84	SAMA32-034946	KJ847502	KJ847531	
? <i>Monomorium</i> sp.	Australia	QM31277	SAMA32-034947	KJ956905	[REDACTED]	

<i>?Monomorium</i> sp.	Australia	QM15787	SAMA32-034948	KJ847484	KJ847518	KJ847547
<i>?Monomorium</i> sp.	Australia	CJB30906	[^] QM- CJB30906	KJ956916		
<i>Monomorium</i> sp.	New Caledonia	TERC32	SAMA32-034950	KJ847483		KJ847546
<i>Monomorium</i> sp. (<i>forcipatum</i> group)	New Caledonia	TERC55	SAMA32-034951	KJ847498	KJ847527	KJ847560
<i>Monomorium</i> sp. (<i>rothsteini</i> complex)	Australia	KSS32	SAMA32-034954	KC572939	KJ847529	KJ847562
<i>Monomorium</i> sp. (<i>rothsteini</i> complex)	Australia	KSS66	SAMA32-034955	KC572943		
<i>Monomorium stictonotum</i>	Australia	MV002	SAMA32-034960	KJ956925		
<i>Monomorium stictonotum</i>	Australia	SAM32-0028	SAMA32-002802	KJ847503	KJ847532	
<i>Monomorium striatifrons</i>	Australia	SAM32-02892	SAMA32-002892	KJ956926		
<i>Monomorium subapterum</i> (<i>rothsteini</i> complex)	Australia	KSS88	SAMA32-034958	KC572951		
<i>Monomorium sydneyense</i>	Australia	KSS1	SAMA32-034961	KJ847504	KJ847533	KJ847566
<i>Monomorium sydneyense</i> (<i>carinatum</i> -form)	Australia	TERC30	SAMA32-034963	JQ846340, KJ956894		
<i>Monomorium sydneyense</i> (<i>carinatum</i> -form)	Australia	180p2	SAMA32-034964	JQ846332, KJ956893		
<i>Monomorium sydneyense</i> (<i>carinatum</i> -form)	Australia	223p3	SAMA32-034965	KJ956928		
<i>Monomorium tambourinense</i>	Australia	QM31247	SAMA32-034966	KJ847505		KJ847567
<i>Monomorium topend</i> (<i>rothsteini</i> complex)	Australia	KSS22	SAMA32-035022	KC572928		
<i>Sylophopsis fisheri</i>	Madagascar		^o CASENT0491610		KJ859766	KJ861842
<i>Sylophopsis sechellensis</i>	Australia	QM15141	SAMA32-034970	KJ847482	KJ847517	KJ847545
OUTGROUPS						
<i>Myrmica tahoensis</i>	N. America		^o RS219-02, ^o CASENT0106091, ^o PSWard#14767	GQ255190	EF013459	AY703629
<i>Myrmecaria brunnea</i>	Asia		^o RA0283	DQ353389		DQ353014
<i>Myrmecaria exigua</i>	Africa		^o CASENT0403455		EF013460	EF013727
<i>Solenopsis invicta</i>	S. America		^o CASENT0500523	DQ353293		DQ353039
<i>Stereomyrmex</i> sp.	Australia	KSS155	SAMA32-034969	KP224452	KP224453	KP224454
<i>Trichomyrmex destructor</i>	Asia	TERC73	SAMA32-034971	KJ847478	KJ847514	KJ847542
<i>Trichomyrmex mayri</i>	Asia	TERC76	SAMA32-034972	KJ847497	KJ847526	KJ847559