

Supplementary materials

Forest disturbance increases functional diversity but decreases phylogenetic diversity of an arboreal tropical ant community

Supplementary Text 1.

Molecular methods for obtaining sequences of ant species and assembly of the phylogenetic tree

Genomic DNA was extracted using the Genomic DNAKit Tissue (Geneaid Biotech Ltd., New Taipei City, Taiwan) following the manufacturer's protocol, and primers and laboratory protocols follow published studies (Folmer et al., 1994; Ward & Downie, 2005; Brady et al., 2006). Sequencing of both DNA strands was carried out by the company Macrogen (South Korea) and the edition and alignment of sequences were conducted in Geneious R6.1. Dataset alignment was carried out using the Clustal W algorithm (Thompson et al., 1994) with the following parameters: cost matrix with gap open cost 16 and gap extend cost 8. With the exception of one single individual of *Lordomyrma* sp. for which we could not obtain molecular data (and thus excluded it from all further analyses in this study), we assembled molecular data for all the 127 remaining species. Specifically, we obtained both COI and Wg sequences for 112 of 127 species (also including sequences from Klimes et al., 2022; GenBank numbers with OK prefix in Table S1) Furthermore, we gathered missing COI and/or Wg for a further 4 species from the GenBank database (sequence numbers KR829145, KJ861847, HQ207477 and DQ353316), while the remaining 11 species were represented by a single gene (6 COI, 5 Wg; 9% of species). All ant specimens and DNA vouchers are deposited at the Institute of Entomology, Biology Centre of Czech Academy of Sciences, České Budějovice. All DNA sequences are available in GenBank. In addition, COI sequences are also deposited in BOLD (Barcode of Life) under the 'Ants of Papua New Guinea (ASPNA)' project (sample codes starting with HP0, PK-EE, and MJ prefix). All ant taxa names, sample codes and GenBank sequence numbers are listed in Table S1.

The concatenated and single-gene datasets consisting of the 127 taxa and partitioned by codon positions of COI and *wingless* were analysed in RAxML v8.1.11 (Stamatakis, 2014) and MrBayes v3.2.3 (Ronquist et al., 2012). Four Hymenopteran outgroup taxa were used to root the phylogeny, following COI and Wg sequence numbers downloaded from GenBank (in brackets): *Apis mellifera* (OP890239, AY703618), *Vespula* sp. (DQ353368, DQ353143), *Chypotes* sp. (DQ353285, DQ353144), and *Odontophotopsis* sp. (Wg only: DQ353146). We constrained the phylogenetic relationships among ant subfamilies following the comprehensive ant-family phylogeny of Moreau & Bell (2013). This approach was necessary because our molecular dataset consisted of two fast-evolving gene fragments, thus deep nodes were expected not to be fully resolved. Maximum

Likelihood analyses in RAxML v8.1.11 were carried out under the 'rapid bootstrapping' algorithm with 1,000 iterations. We set the GTRGAMMA model for each partition and we searched for the best-scoring tree using the command '-f a'. We computed an extended majority rule consensus tree from 1,000 bootstraps trees using the command '-J'. Bayesian Inference through MrBayes v3.2.3 consisted of two independent runs each for 50 million generations, sampling every 5,000 generations. The nucleotide substitution scheme 'mixed + gamma' (Huelsenbeck et al., 2004) was set to each partition. We confirmed convergence of chains after applying a burn-in of 25% by checking that the final average standard deviation of split frequencies was below 0.01, PSRFs were close to 1.0, ESS values higher than 200, and log probabilities reached stationary distribution. We summarized the MCMC sampled trees using the 50% majority rule consensus approach. All phylogenetic analyses were carried out through CIPRES (Miller et al., 2010). To visualise the phylogeny with community data we uploaded data to iTOL v.4.1 and finally edited in Inkscape v.0.92. For further analyses, after checking the tree topology congruence between the RAxML and MrBayes outputs, we imported our concatenated MrBayes phylogeny into R v3.4.0, removed the outgroups and created a phylogenetic distance matrix using the function *cophenetic* implemented in the 'stats' package. The phylogeny was square root transformed before community analyses following the recommendation of Letten and Cornwell (2015).

Table S1. List of the 127 species with gathered molecular information. The COI and Wg columns refer to sequence numbers available in GenBank for the mitochondrial gene fragment cytochrome c oxidase I (659 bp) and the nuclear gene fragment wingless (Wg, 409 bp). For more details about the taxa and samples, see the main text and Supplementary text1 above. Note that all associated online datasets and R-codes to our study are based on the species codes, while full ant species names are referred here. Species that are considered as non-native in PNG are marked by asterisk.

Species (or morphospecies) name	Subfamily	Genus	Species code	COI	Wg	Sample name in the alignment (SampleCode GenusCode SpeciesCode)
<i>Anochetus cato</i> Forel, 1901	Ponerinae	<i>Anochetus</i>	ANOC001	PP069609	PP063881	HP0093_d02_Anochetus_ANOC001
<i>Anonychomyrma</i> cf. <i>scrutator</i> (Smith F., 1859)	Dolichoderinae	<i>Anonychomyrma</i>	ANON001	PP069610	PP063882	HP0184_HP0182B_Anonyc_ANON001
<i>Anonychomyrma minuta</i> (Donisthorpe, 1943)	Dolichoderinae	<i>Anonychomyrma</i>	ANON002	PP069611	PP063883	PK_EE109_Anonychomyrma_ANON002
<i>Anoplolepis gracilipes</i> (Smith F., 1857)*	Formicinae	<i>Anoplolepis</i>	ANOP001	PP069612	PP063884	HP0742_Anoplolepis_ANOP001
<i>Aphaenogaster</i> sp. 1 aff. <i>dromedaria</i> (Emery, 1900)	Myrmicinae	<i>Aphaenogaster</i>	APHA001	PP069613	PP063885	HP0733_Aphaenogaster_APHA001
<i>Brachyponera croceicornis</i> (Emery, 1900)	Ponerinae	<i>Brachyponera</i>	PACH006	PP069658	PP063923	HP0159_Brachyponera_PACH006
<i>Camponotus (Myrmamblys)</i> sp. 20 aff. <i>janeti</i> Forel, 1895	Formicinae	<i>Camponotus</i>	CAMP020	-	PP063896	HP0701_Camponotus_CAMP020
<i>Camponotus (Myrmamblys)</i> sp. 11 aff. <i>pictostriatus</i> Karavaiev, 1933	Formicinae	<i>Camponotus</i>	CAMP011	PP069623	OK104536	HP0032_Camponotus_CAMP011
<i>Camponotus (Myrmamblys)</i> sp. 7 aff. <i>trajanus</i> Forel, 1912	Formicinae	<i>Camponotus</i>	CAMP007	PP069620	PP063891	HP0059_Camponotus_CAMP007
<i>Camponotus (Tanaemyrmex)</i> cf. <i>chloroticus</i> Emery, 1897	Formicinae	<i>Camponotus</i>	CAMP012	PP069624	OK104537	PKEE142_Camponotus_CAMP012
<i>Camponotus (Tanaemyrmex)</i> cf. <i>variegatus</i> (Smith, F., 1858)	Formicinae	<i>Camponotus</i>	CAMP018	OK046729	OK104544	HP0741_Camponotus_CAMP018
<i>Camponotus (Tanaemyrmex)</i> <i>dorycus confusus</i> Emery, 1887	Formicinae	<i>Camponotus</i>	CAMP016	PP069626	OK104539	HP0094_Camponotus_CAMP016
<i>Camponotus anezkae</i> Klimes & McArthur, 2014	Formicinae	<i>Camponotus</i>	CAMP022	PP069628	-	HP0617_Camponotus_CAMP022
<i>Camponotus wanangus</i> Klimes & McArthur, 2014	Formicinae	<i>Camponotus</i>	CAMP003	PP069616	PP063887	HP0208_Camponotus_CAMP003
<i>Cardiocondyla obscurior</i> Wheeler, 1929*	Myrmicinae	<i>Cardiocondyla</i>	CARD001	DQ353316	PP063897	RA0330_HP0039_Cardio_CARD001
<i>Carebara atoma</i> Emery, 1900	Myrmicinae	<i>Carebara</i>	CARE002	PP069629	PP063898	HP0654_Carebara_CARE002
<i>Carebara crassiuscula</i> (Emery, 1900)	Myrmicinae	<i>Carebara</i>	CARE006	-	PP063899	PKEE060_Carebara_CARE006
<i>Chronoxenus rossi</i> Donisthorpe, 1950	Dolichoderinae	<i>Chronoxenus</i>	BOTH001	PP069614	PP063886	PK_EE125_Chronoxenus_BOTH001
<i>Colobopsis aruensis</i> Karavaiev, 1933	Formicinae	<i>Colobopsis</i>	CAMP004	PP069617	PP063888	HP0030_Colobopsis_CAMP004
<i>Colobopsis</i> cf. <i>macrocephala</i> (Erichson, 1842)	Formicinae	<i>Colobopsis</i>	CAMP010	PP069622	PP063893	HP0097_Colobopsis_CAMP010
<i>Colobopsis conithorax</i> Emery, 1914	Formicinae	<i>Colobopsis</i>	CAMP006	PP069619	PP063890	HP0006_Colobopsis_CAMP006
<i>Colobopsis quadriceps</i> (Smith F., 1859)	Formicinae	<i>Colobopsis</i>	CAMP013	PP069625	PP063894	HP0041_Colobopsis_CAMP013

<i>Colobopsis rotunda</i> Klimes & McArthur, 2014	Formicinae	<i>Colobopsis</i>	CAMP014	OK046730	OK104538	HP0084 Colobopsis CAMP014
<i>Colobopsis</i> sp. 17 aff. <i>polynesica</i> (Emery, 1896)	Formicinae	<i>Colobopsis</i>	CAMP017	PP069627	PP063895	HP0114 Colobopsis CAMP017
<i>Colobopsis</i> sp. 5 aff. <i>conithorax</i> Emery, 1914	Formicinae	<i>Colobopsis</i>	CAMP005	PP069618	PP063889	HP0017 Colobopsis CAMP005
<i>Colobopsis</i> sp. 8 aff. <i>sanguinifrons</i> Viehmeyer, 1925	Formicinae	<i>Colobopsis</i>	CAMP008	PP069621	PP063892	HP0016 Colobopsis CAMP008
<i>Colobopsis triangulata</i> Klimes & McArthur, 2014	Formicinae	<i>Colobopsis</i>	CAMP019	OK046731	OK104542	HP0213 Colobopsis CAMP019
<i>Colobopsis vitrea</i> (Smith F., 1860)	Formicinae	<i>Colobopsis</i>	CAMP001	PP069615	OK104531	MJ14769 HP0181 Colob CAMP001
<i>Crematogaster</i> cf. <i>irritabilis</i> Smith, F., 1860	Myrmicinae	<i>Crematogaster</i>	CREM014	PP069641	PP063909	B LEWE09 60 HP0669 Crem CREM014
<i>Crematogaster elysii</i> Mann, 1919	Myrmicinae	<i>Crematogaster</i>	CREM002	PP069632	PP063900	HP0040 Crematogaster CREM002
<i>Crematogaster emeryi</i> Forel, 1907	Myrmicinae	<i>Crematogaster</i>	CREM010	PP069638	PP063906	PKEE108 Crematogaster CREM010
<i>Crematogaster flavicornis</i> Emery, 1897	Myrmicinae	<i>Crematogaster</i>	CREM016	PP069642	PP063910	HP0169 Crematogaster CREM016
<i>Crematogaster flavitarsis</i> Emery, 1900	Myrmicinae	<i>Crematogaster</i>	CREM005	PP069635	PP063903	HP0073 Crematogaster CREM005
<i>Crematogaster obnigra</i> Mann, 1919	Myrmicinae	<i>Crematogaster</i>	CREM018	PP069644	PP063912	HP0644 Crematogaster CREM018
<i>Crematogaster polita</i> Smith F., 1865	Myrmicinae	<i>Crematogaster</i>	CREM003	PP069633	PP063901	HP0180 Crematogaster CREM003
<i>Crematogaster</i> sp. 11 aff. <i>fritzi</i> Emery, 1901	Myrmicinae	<i>Crematogaster</i>	CREM011	PP069639	PP063907	PKEE135 Crematogaster CREM011
<i>Crematogaster</i> sp. 15 aff. <i>flavicornis</i> Emery, 1897	Myrmicinae	<i>Crematogaster</i>	CREM015	PP069643	PP063911	PKEE143 d02 Crematogaster CREM015
<i>Crematogaster</i> sp. 4	Myrmicinae	<i>Crematogaster</i>	CREM004	PP069634	PP063902	HP0080 Crematogaster CREM004
<i>Crematogaster</i> sp. 6	Myrmicinae	<i>Crematogaster</i>	CREM006	PP069636	PP063904	PKEE032 Crematogaster CREM006
<i>Crematogaster</i> sp. 7 aff. <i>fritzi</i> Emery, 1901	Myrmicinae	<i>Crematogaster</i>	CREM007	PP069637	PP063905	HP0183 Crematogaster CREM007
<i>Crematogaster tarsata</i> Smith, F. 1865	Myrmicinae	<i>Crematogaster</i>	CREM013	PP069640	PP063908	NA0122 PKEE157 Cremat CREM013
<i>Diacamma rugosum</i> (Le Guillou, 1842)	Ponerinae	<i>Diacamma</i>	DIAC001	PP069645	PP063913	HP0053 Diacamma DIAC001
<i>Dilobocondyla cataulacoidea</i> (Stitz, 1911)	Myrmicinae	<i>Dilobocondyla</i>	DILO001	PP069646	PP063914	PKEE156 Dilobocondyla DILO001
<i>Echinopla</i> sp. 1 aff. <i>australis</i> Forel, 1901	Formicinae	<i>Echinopla</i>	ECHI001	OK046733	OK104543	HP0735 Echinopla ECHI001
<i>Echinopla</i> sp. 2 aff. <i>australis</i> Forel, 1901	Formicinae	<i>Echinopla</i>	ECHI002	PP069647	PP063915	HP0204 Echinopla ECHI002
<i>Hypoconera</i> cf. <i>confinis</i> Roger, 1860	Ponerinae	<i>Hypoconera</i>	HYPO002	PP069648	PP063916	HP0067 Hypoconera HYPO002
<i>Hypoconera sabrone</i> Donisthorpe, 1941	Ponerinae	<i>Hypoconera</i>	HYPO003	PP069649	-	B OHWE09 13 Hypoconera HYPO003
<i>Leptomymex fragilis</i> (Smith F., 1859)	Dolichoderinae	<i>Leptomymex</i>	LEPM001	PP069650	HQ207477	HP0128 CASENT0012050 Lept LEPM001
<i>Monomorium floricola</i> (Jerdon, 1851)*	Myrmicinae	<i>Monomorium</i>	MONO001	PP069651	PP063917	HP0100 Monomorium MONO001
<i>Monomorium intrudens</i> Smith F., 1894*	Myrmicinae	<i>Monomorium</i>	MONO002	PP069652	PP063918	PKEE144 Monomorium MONO002
<i>Monomorium pharaonis</i> (Linnaeus 1758)*	Myrmicinae	<i>Monomorium</i>	MONO004	PP069654	KJ861847	HP0022 CASENT0137619 Mon MONO004
<i>Monomorium</i> sp. 3	Myrmicinae	<i>Monomorium</i>	MONO003	PP069653	PP063919	HP0115 Monomorium MONO003

<i>Monomorium</i> sp. 5	Myrmicinae	<i>Monomorium</i>	MONO005	PP069655	PP063920	HP0071_Monomorium_MONO005
<i>Nylanderia nuggeti</i> Donisthorpe, 1941	Formicinae	<i>Nylanderia</i>	PARA007	PP069664	PP063929	PKEE090_Nylanderia_PARA007
<i>Nylanderia</i> sp. 5 aff. <i>vaga</i> (Forel, 1901)	Formicinae	<i>Nylanderia</i>	PARA005	PP069662	PP063927	HP0111_Nylanderia_PARA005
<i>Odontomachus testaceus</i> Emery, 1897	Ponerinae	<i>Odontomachus</i>	ODON002	PP069656	PP063921	HP0739_Odontomachus_ODON002
<i>Oecophylla smaragdina</i> (Fabricius, 1775)	Formicinae	<i>Oecophylla</i>	OECO001	PP069657	PP063922	PKEE147_Oecophylla_OECO001
<i>Overbeckia papuana</i> Klimes, 2022	Formicinae	<i>Overbeckia</i>	CAMP021	OK046732	OK104541	HP0177_Overbeckia_CAMP021
<i>Paraparatrechina minutula</i> (Forel, 1901)	Formicinae	<i>Paraparatrechina</i>	PARA003	PP069661	PP063926	HP0002_Paraparatrechina_PARA003
<i>Paraparatrechina pallida</i> Donisthorpe, 1947	Formicinae	<i>Paraparatrechina</i>	PARA001	PP069659	PP063924	HP0013_Paraparatrechina_PARA001
<i>Paraparatrechina</i> sp. 10	Formicinae	<i>Paraparatrechina</i>	PARA010	PP069665	PP063930	HP0162_Paraparatrechina_PARA010
<i>Paraparatrechina</i> sp. 2	Formicinae	<i>Paraparatrechina</i>	PARA002	PP069660	PP063925	HP0063_Paraparatrechina_PARA002
<i>Paraparatrechina</i> sp. 6	Formicinae	<i>Paraparatrechina</i>	PARA006	PP069663	PP063928	HP0112_d02_Paraparatrechina_PARA006
<i>Parasyscia</i> cf. <i>flavaclavata</i> Donisthorpe, 1938	Dorylinae	<i>Parasyscia</i>	CERA001	PP069630	-	HP0118_Cerapachys_CERA001
<i>Parasyscia desposyne</i> Wilson, 1959	Dorylinae	<i>Parasyscia</i>	CERA002	PP069631	-	MJ9214_Cerapachys_CERA002
<i>Pheidole</i> cf. <i>distincta</i> Donisthorpe, 1943	Myrmicinae	<i>Pheidole</i>	PHEI018	PP069672	PP063937	PKEE139_Pheidole_PHEI018
<i>Pheidole hospes</i> Smith, F. 1865	Myrmicinae	<i>Pheidole</i>	PHEI004	PP069668	PP063933	HP0160_Pheidole_PHEI004
<i>Pheidole sexspinosa biroi</i> Emery, 1900	Myrmicinae	<i>Pheidole</i>	PHEI030	PP069676	PP063941	HP0171_Pheidole_PHEI030
<i>Pheidole</i> sp. 1	Myrmicinae	<i>Pheidole</i>	PHEI001	PP069666	PP063931	PKEE030_Pheidole_PHEI001
<i>Pheidole</i> sp. 13 aff. <i>tricolor</i> , Donisthorpe, 1949	Myrmicinae	<i>Pheidole</i>	PHEI013	PP069670	PP063935	HP0740_Pheidole_PHEI013
<i>Pheidole</i> sp. 14 aff. <i>gambogia</i> Donisthorpe, 1948	Myrmicinae	<i>Pheidole</i>	PHEI014	PP069671	PP063936	HP0082_Pheidole_PHEI014
<i>Pheidole</i> sp. 2 aff. <i>sexspinosa biroi</i> Emery, 1900	Myrmicinae	<i>Pheidole</i>	PHEI002	PP069667	PP063932	HP0138_Pheidole_PHEI002
<i>Pheidole</i> sp. 24 aff. <i>amber</i> Donisthorpe, 1941	Myrmicinae	<i>Pheidole</i>	PHEI024	PP069673	PP063938	HP0052_Pheidole_PHEI024
<i>Pheidole</i> sp. 25 aff. <i>sexspinosa biroi</i> Emery, 1900	Myrmicinae	<i>Pheidole</i>	PHEI025	PP069674	PP063939	HP0075_Pheidole_PHEI025
<i>Pheidole</i> sp. 26	Myrmicinae	<i>Pheidole</i>	PHEI026	PP069675	PP063940	HP0090_Pheidole_PHEI026
<i>Pheidole</i> sp. 7 aff. <i>gambogia</i> Donisthorpe, 1948	Myrmicinae	<i>Pheidole</i>	PHEI007	PP069669	PP063934	HP0106_Pheidole_PHEI007
<i>Philidris</i> cf. <i>cordata</i> (Smith F., 1859)	Dolichoderinae	<i>Philidris</i>	PHIL001	PP069677	PP063942	PK_EE133_Philidris_PHIL001
<i>Philidris</i> sp. 2	Dolichoderinae	<i>Philidris</i>	PHIL002	PP069678	PP063943	HP0154_Philidris_PHIL002
<i>Philidris</i> sp. 3	Dolichoderinae	<i>Philidris</i>	PHIL003	PP069679	PP063944	PK_EE155_Philidris_PHIL003
<i>Podomyrma</i> sp. 2 aff. <i>basalis</i> Smith F., 1859	Myrmicinae	<i>Podomyrma</i>	PODO002	PP069680	PP063945	PKEE045_Podomyrma_PODO002
<i>Podomyrma</i> sp. 3 aff. <i>laevifrons</i> Smith F., 1859	Myrmicinae	<i>Podomyrma</i>	PODO003	PP069681	PP063946	HP0046_Podomyrma_PODO003
<i>Polyrhachis (Aulacomyrma) pallipes</i> Donisthorpe, 1948	Formicinae	<i>Polyrhachis</i>	POLY021	PP069696	-	PKEE146_Polyrhachis_POLY021

<i>Polyrhachis (Campomyrma) xiphias</i> Smith, F. 1863	Formicinae	<i>Polyrhachis</i>	POLY029	PP069699	PP063961	NA0040_Polyrhachis_POLY029
<i>Polyrhachis (Cyrtomyrma) debilis</i> Emery, 1887	Formicinae	<i>Polyrhachis</i>	POLY004	PP069684	PP063949	HP0081_Polyrhachis_POLY004
<i>Polyrhachis (Myrma) biroi bidentata</i> Stitz, 1912	Formicinae	<i>Polyrhachis</i>	POLY007	PP069685	PP063950	HP0167_Polyrhachis_POLY007
<i>Polyrhachis (Myrma) rufofemorata</i> Smith F., 1859	Formicinae	<i>Polyrhachis</i>	POLY022	PP069697	PP063960	HP0161_Polyrhachis_POLY022
<i>Polyrhachis (Myrma) sericata</i> (Guérin-Méneville, 1838)	Formicinae	<i>Polyrhachis</i>	POLY002	PP069683	OK104540	HP0143_Polyrhachis_POLY002
<i>Polyrhachis (Myrmatopa) alpeha</i> Smith F., 1863	Formicinae	<i>Polyrhachis</i>	POLY008	PP069686	PP063951	HP0005_Polyrhachis_POLY008
<i>Polyrhachis (Myrmatopa) dolomedes</i> Smith F., 1863	Formicinae	<i>Polyrhachis</i>	POLY020	PP069695	PP063959	PKEE137_Polyrhachis_POLY020
<i>Polyrhachis (Myrmatopa) lombokensis</i> Emery, 1898	Formicinae	<i>Polyrhachis</i>	POLY019	PP069694	-	PKEE129_Polyrhachis_POLY019
<i>Polyrhachis (Myrmatopa) luteogaster</i> Kohout, 2012	Formicinae	<i>Polyrhachis</i>	POLY010	PP069688	PP063953	HP0044_Polyrhachis_POLY010
<i>Polyrhachis (Myrmatopa) menozzii</i> Karavaiev, 1927	Formicinae	<i>Polyrhachis</i>	POLY017	PP069693	PP063958	HP0103_Polyrhachis_POLY017
<i>Polyrhachis (Myrmatopa) sp. 14 (flavicornis-group)</i>	Formicinae	<i>Polyrhachis</i>	POLY014	PP069690	PP063955	HP0076_Polyrhachis_POLY014
<i>Polyrhachis (Myrmhopta) esuriens</i> Emery, 1897	Formicinae	<i>Polyrhachis</i>	POLY001	PP069682	PP063947	HP0122_Polyrhachis_POLY001
<i>Polyrhachis (Myrmhopta) mucronata</i> Smith F., 1859	Formicinae	<i>Polyrhachis</i>	POLY016	PP069692	PP063957	HP0117_Polyrhachis_POLY016
<i>Polyrhachis (Myrmhopta) sp. 23 aff. bubastes</i> Smith F., 1863	Formicinae	<i>Polyrhachis</i>	POLY023	PP069698	-	HP0145_Polyrhachis_POLY023
<i>Polyrhachis (Myrmhopta) sp. 3 aff. saevissima</i> Smith F., 1860	Formicinae	<i>Polyrhachis</i>	POLY003	-	PP063948	HP0191_Polyrhachis_POLY003
<i>Polyrhachis (Myrmhopta) waigeuensis</i> Donisthorpe, 1943	Formicinae	<i>Polyrhachis</i>	POLY015	PP069691	PP063956	HP0077_Polyrhachis_POLY015
<i>Polyrhachis (Myrmotherinax) queenslandica</i> Emery, 1895	Formicinae	<i>Polyrhachis</i>	POLY011	PP069689	PP063954	HP0070_Polyrhachis_POLY011
<i>Polyrhachis (Myrmotherinax) sp. 9 aff. neptunus</i> Smith F., 1865	Formicinae	<i>Polyrhachis</i>	POLY009	PP069687	PP063952	HP0042_Polyrhachis_POLY009
<i>Pseudolasius cf. breviceps</i> Emery, 1887	Formicinae	<i>Pseudolasius</i>	PSEU001	PP069700	PP063962	HP0729_Pseudolasius_PSEU001
<i>Rhytidoponera strigosa</i> (Emery, 1887)	Ectatomminae	<i>Rhytidoponera</i>	RHYT002	PP069701	-	PKEE166_Rhytidoponera_RHYT002
<i>Rogeria cf. stigmatica</i> Emery, 1897	Myrmicinae	<i>Rogeria</i>	ROGE001	PP069702	PP063963	HP0062_Rogeria_ROGE001
<i>Solenopsis papuana</i> Emery, 1900	Myrmicinae	<i>Solenopsis</i>	SOLE004	PP069703	PP063964	HP0092_Solenopsis_SOLE004
<i>Strumigenys cf. racabura</i> Bolton, 2000	Myrmicinae	<i>Strumigenys</i>	STRU003	PP069705	PP063966	HP0155_Strumigenys_STRU003
<i>Strumigenys snellingi</i> Bolton, 2000	Myrmicinae	<i>Strumigenys</i>	STRU005	-	PP063967	HP0163_Strumigenys_STRU005
<i>Strumigenys szalayi</i> Emery, 1897	Myrmicinae	<i>Strumigenys</i>	STRU002	PP069704	PP063965	HP0065_Strumigenys_STRU002
<i>Tapinoma cf. indicum</i> Forel, 1895*	Dolichoderinae	<i>Tapinoma</i>	TAPI002	PP069707	PP063969	HP0049_Tapinoma_TAPI002
<i>Tapinoma melanocephalum</i> (Fabricius, 1793)*	Dolichoderinae	<i>Tapinoma</i>	TAPI001	PP069706	PP063968	HP0036_Tapinoma_TAPI001
<i>Tapinoma sp. 3 aff. williamsi</i> (Wheeler 1935)	Dolichoderinae	<i>Tapinoma</i>	TAPI003	PP069708	PP063970	HP0038_Tapinoma_TAPI003
<i>Technomyrmex albicoxis</i> Donisthorpe, 1945	Dolichoderinae	<i>Technomyrmex</i>	TECH004	PP069712	PP063974	HP0109_Technomyrmex_TECH004
<i>Technomyrmex albipes</i> (Smith F., 1861)*	Dolichoderinae	<i>Technomyrmex</i>	TECH002	PP069710	PP063972	PK EE020_Technomyrmex_TECH002

<i>Technomyrmex cf. brunneus</i> Forel, 1895*	Dolichoderinae	<i>Technomyrmex</i>	TECH001	PP069709	PP063971	HP0033B <i>Technomyrmex</i> TECH001
<i>Technomyrmex difficilis</i> Forel 1892*	Dolichoderinae	<i>Technomyrmex</i>	TECH003	PP069711	PP063973	HP0037 <i>Technomyrmex</i> TECH003
<i>Technomyrmex gilvus</i> Donisthorpe, 1941	Dolichoderinae	<i>Technomyrmex</i>	TECH005	PP069713	PP063975	PK EE122 <i>Technomyrmex</i> TECH005
<i>Tetramorium cf. validisculum</i> Emery, 1897	Myrmicinae	<i>Tetramorium</i>	TETR003	PP069718	PP063980	PKEE105 <i>Tetramorium</i> TETR003
<i>Tetramorium kydelphon</i> Bolton, 1979	Myrmicinae	<i>Tetramorium</i>	TETR002	PP069717	PP063979	HP0025 <i>Tetramorium</i> TETR002
<i>Tetramorium pulchellum</i> Emery, 1897	Myrmicinae	<i>Tetramorium</i>	TETR012	PP069720	PP063982	HP0085 <i>Tetramorium</i> TETR012
<i>Tetramorium</i> sp. 16 aff. <i>pulchellum</i> Emery, 1897	Myrmicinae	<i>Tetramorium</i>	TETR016	PP069721	PP063983	HP0147 <i>Tetramorium</i> TETR016
<i>Tetramorium</i> sp. 6 aff. <i>validisculum</i> Emery, 1897	Myrmicinae	<i>Tetramorium</i>	TETR006	PP069719	PP063981	HP0110 <i>Tetramorium</i> TETR006
<i>Tetraoponera atra</i> Donisthorpe, 1949	Pseudomyrmecinae	<i>Tetraoponera</i>	TETP003	PP069716	PP063978	HP0135 <i>Tetraoponera</i> TETP003
<i>Tetraoponera laeviceps</i> (Smith F., 1859)	Pseudomyrmecinae	<i>Tetraoponera</i>	TETP001	PP069714	PP063976	HP0015 <i>Tetraoponera</i> TETP001
<i>Tetraoponera modesta</i> (Smith F., 1860)	Pseudomyrmecinae	<i>Tetraoponera</i>	TETP004	-	KR829145	CASENT0220746 <i>Tetraoponera</i> TETP004
<i>Tetraoponera nitida</i> (Smith F., 1860)	Pseudomyrmecinae	<i>Tetraoponera</i>	TETP002	PP069715	PP063977	HP0158 <i>Tetraoponera</i> TETP002
<i>Turneria cf. pacifica</i> Mann, 1919	Dolichoderinae	<i>Turneria</i>	TURN002	PP069608	PP063985	PK EE113 <i>Turneria</i> TURN002
<i>Turneria dahlia</i> Forel, 1901	Dolichoderinae	<i>Turneria</i>	TURN001	PP069722	PP063984	HP0099 <i>Turneria</i> TURN001
<i>Vollenhovia brachycera</i> Emery, 1897	Myrmicinae	<i>Vollenhovia</i>	VOLL001	PP069723	PP063986	PKEE130 <i>Vollenhovia</i> VOLL001

Table S2 Ant traits used in this study. We present their proposed functional significance on current literature knowledge, and include measurement definitions mostly derived from Parr et al., 2017.

Trait	Functional significance	Measurement definition
Spinosity	Spines are defensive adaptations (Blanchard et al., 2020)	sum of petiolar and alitrunk spines
Sculpture	Increase in sculpture might harden cuticule and increases dehydration tolerance (Buxton et al., 2021)	Index 0 to 3, 0 indicating no sculpturing and 3 heavy cuticular sculpturing.
Head width	Correlates positively with bite force (Rühr et al., 2022), can be indicative of feeding mode (Weiser & Kaspari, 2006)	Distance across eyes in full face view (including protruding eyes)
Clypeus Length	Clypeus is important for liquid-feeding behaviour (Davidson et al., 2004)	Maximum length of clypeus along midline of head in full face view
Mandible Length	Mandible length is indicative of diet, with predators typically possessing longer mandibles (Gibb & Cunningham, 2013; Sosiak & Barden, 2021)	Maximum length of mandible from its basal insertion to tip
Eye Size	indicative of food searching behaviour with omnivores having largest eyes (Weiser & Kaspari, 2006); spatial niche, with larger eye size on arboreal ants (Sosiak & Barden, 2021); higher habitat complexity might select for smaller eye size (Guilherme et al., 2019)	Area calculated using two perpendicular measurements of eye width (maximum eye length and eye width)
Eye Position	Related to the hunting method (Fowler et al., 1991); and the component of the habitat occupied, with simpler habitat having a more dorsal eye position (Gibb & Parr, 2013)	The head width minus interocular distance in full face view. Head width measure see above. Interocular distance is the maximum distance between innermost margin of eyes in full face view.
Leg Length	Longer legs are indicative of foraging speed (Feener et al., 1988); predators have often shorter legs (Sosiak & Barden, 2021); longer legs enable thermoregulatory strategy (Sommer & Wehner, 2012); higher	Leg length is approximated as sum of the maximum length of the hind femur and hind tibia

Head Length	<p>environmental complexity might select for shorter legs (Weiser & Kaspari, 1999; but see Guilherme et al., 2019)</p> <p>Indicator of body size in this study, which is related to metabolism (Gibb et al., 2018); and microclimate (Kaspari, 1993); Higher habitat complexity selects for smaller body size (Guilherme et al., 2019); body size can be linked to the ants contribution to decomposition (Nooten et al., 2022); Indicator of diet, with predators having longer head length (Weiser & Kaspari, 2006)</p>	<p>The maximum longitudinal length from the most anterior part of the clypeus to the posterior cephalic margin, in full face view</p>
Polymorphism index	<p>More polymorphic ants have larger colony size, increased labour division and plasticity in functions for the ant colony (Wills et al., 2018; Ohyama et al., 2023)</p>	<p>The maximum head length of a species divided by the minimum head length (among all worker castes).</p>

Table S3 Characteristics of arboreal ant communities sampled in 0.4 ha of primary and 0.4 ha of secondary lowland rainforest in Papua New Guinea, and of their taxonomic, functional (FD) and phylogenetic (PD) diversity, with non-native species excluded from the dataset. (A) values on plot scale and (B) values on tree scale. Standardised effect sizes from null models (Rao Q SES, see Methods) near zero indicate random communities, while positive SES indicate community overdispersion (highlighted as light blue) and negative SES indicate clustering (highlighted as light orange). On plot scale, we give the p-values in comparison to the taxa-swap null model, while for the tree scale we test the distribution of all SES values against 0 with a Wilcoxon's signed-rank test. Significant overdispersion and clustering values as well as their respective p-values are highlighted in bold (alpha = 0.05).

A) Plot scale	Primary all	Secondary all	Primary visitors	Secondary visitors	Primary nesters	Secondary nesters
N of sampled trees	472	380	472	380	472	380
N of species occurrences	1660	848	997	469	662	662
Species richness	95	49	60	29	80	42
FD (Rao observed)	0.192	0.205	0.188	0.201	0.209	0.200
FD (Rao SES)	-1.211	-0.284	-0.923	-0.044	-1.294	-0.428
p value (null model)	0.092	0.398	0.195	0.481	0.092	0.359
decoupled FD SES	-0.303	0.975	-0.008	1.904	-1.039	-0.743
p value (null model)	0.474	0.844	0.593	0.951	0.146	0.252
PD (Rao Q observed)	0.529	0.489	0.514	0.455	0.538	0.483
PD (Rao Q SES)	-0.030	-1.526	0.269	-1.092	-0.655	-0.820
p value (null model)	0.529	0.053	0.659	0.120	0.250	0.196
decoupled PD (Rao Q SES)	-0.338	-1.566	-0.222	-1.486	-0.686	-1.128
p value (null model)	0.383	0.053	0.426	0.061	0.252	0.127

B) Tree scale	Primary all	Secondary all	Primary visitors	Secondary visitors	Primary nesters	Secondary nesters
N of occupied trees	442	314	362	229	324	239
N of trees with ≥ 2 species	382	224	284	147	172	87
mean species richness	3.52	2.23	2.11	1.23	1.40	1.00
FD (Rao Q obs.)	0.142	0.147	0.132	0.135	0.130	0.137
FD (Rao Q SES)	-0.592	-0.198	-0.481	-0.120	-0.418	-0.059
p value (against 0)	<0.001	0.001	<0.001	0.458	<0.001	0.921
mean decoupled FD (Rao Q SES)	-0.162	0.572	0.033	1.019	-0.326	-0.327
p values (against 0)	<0.001	<0.001	0.322	<0.001	<0.001	<0.001
mean PD (Rao Q obs.)	0.408	0.347	0.372	0.307	0.344	0.325
mean PD (Rao Q SES)	0.088	-0.742	0.182	-0.665	-0.144	-0.229
p values (against 0)	0.007	<0.001	<0.001	0.006	0.438	0.065
mean decoupled SES PD	-0.108	-0.839	-0.063	-0.890	-0.136	-0.471
p value (against 0)	0.001	<0.001	0.271	<0.001	0.016	<0.001

Table S4. Blomberg's K of the traits used in this study. Blomberg's K signal indicates how strong a trait is predicted by its phylogeny, with values ranging from 0 (no phylogenetic signal) to >2 (i.e., strongly phylogenetically conserved trait), under the assumption of the Brownian Motion model of evolution. In addition, we give p-values for the test if a trait has a significant phylogenetic signal, which is the case for all.

Trait	Blomberg's K	p-value
Spinosity	1.74	0.001
Sculpture	0.60	0.010
Rel. Eye Size	1.19	0.001
Rel. Head width	1.06	0.001
Rel. Clypeus Length	2.40	0.001
Rel. Mandible Length	1.15	0.001
Rel. Eye Position	1.42	0.001
Rel. Leg Length	1.03	0.001
Head Length	1.39	0.001
Polymorphism index	1.13	0.001

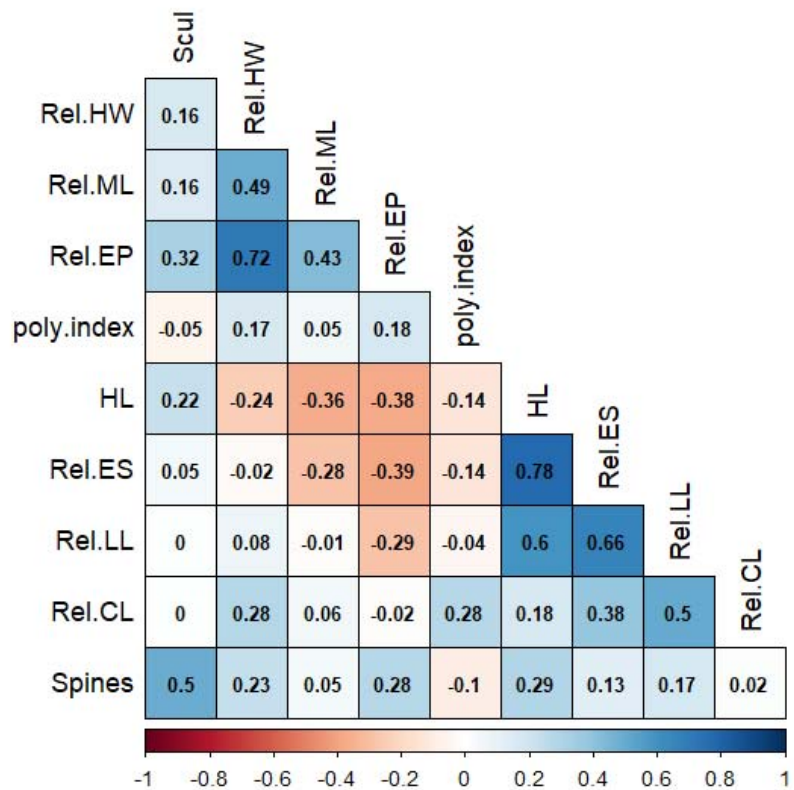


Fig. S1. Correlations between all traits used in this study. Given are spearman-rank coefficients, where more negative correlations are red while more positive correlations are blue. Trait abbreviations: Rel.HW = relative head width; Rel.ML = relative mandible length; Rel. EP: relative eye position; poly.index = polymorphisms index; HL = head length; Rel. ES = relative eye size; Rel. LL = relative leg length; Rel.CL = relative clypeus length.

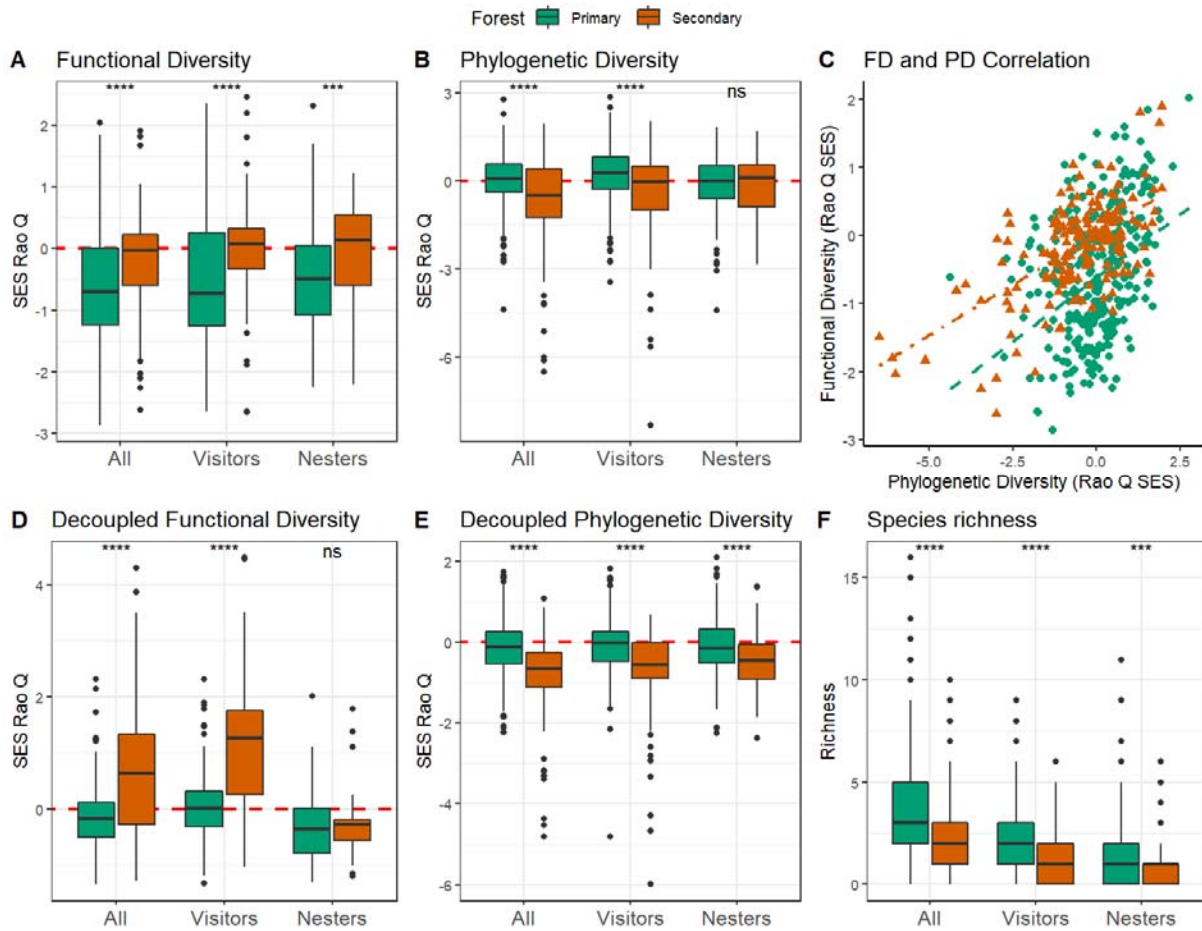


Figure S2. Arboreal ant functional diversity (A), phylogenetic diversity (B), the correlation between functional and phylogenetic diversity (C), the decoupled functional (D) and phylogenetic diversity (E) and the species richness (F) on tree scale after excluding all non-native species. Box-plots show median values per a tree with 25–75% quartiles and with whiskers representing 1.5 interquartile ranges for all species combined (All), for foraging species not nesting in a focal tree (Visitors) and nesting species (Nesters). Both forest types are shown in different colours (primary forest – green; secondary forest – orange) or symbols (in C: triangles denote primary forest, circles secondary forest). The values for individual ant communities are compared between the two forest types with a Kruskal-Wallis test, where stars indicate statistically significant differences (*** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$, ns $p > 0.05$). Standardised effect sizes (i.e., SES of Rao Q) are compared in A, B, D, and E where the dash horizontal line at 0 indicates random communities, while positive SES values indicate community overdispersion and negative values clustering. For mean observed and SES values and for tests of the statistical significance of the SES against null distribution, see Table S3.

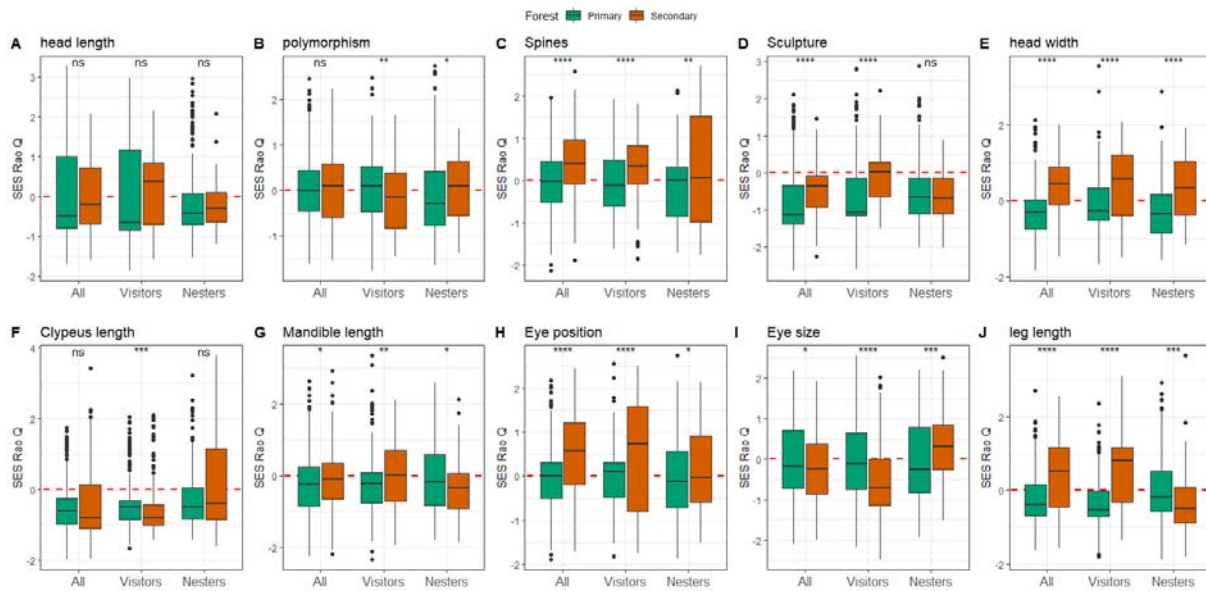


Figure S3. The SES Rao Q of ten individual traits, calculated from three different community matrices (all, visitors and nesters). Box-plots show median values per a tree with 25–75% quartiles and with whiskers representing 1.5 interquartile ranges for all species combined (All), for foraging species not nesting in a focal tree (Visitors) and nesting species (Nesters). Both forest types are shown in different colours (primary forest – green; secondary forest – orange). The values for individual ant communities are compared between the two forest types with a Kruskal-Wallis test, where stars indicate statistically significant differences (*** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$, ns $p > 0.05$). Standardised effect sizes (i.e., SES of Rao Q) are compared, so that the dash horizontal line at 0 indicates random communities, while positive SES values indicate community overdispersion and negative values clustering.

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