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Electronic supplementary material, tables S1-S6.

Table S1. *Pseudomyrmex* species and populations sequenced, and specimen codes for vouchers.

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Table S1. *Pseudomyrmex* species and populations sequenced, and specimen codes for vouchers. Complete collection data can be found by searching for the specimen code on AntWeb (www.antweb.org). All vouchers are deposited in the Bohart Museum of Entomology, University of California, Davis (UCDC).

Species	Sample_Name	Collection_Locality	Voucher_Specimen_Code
<i>Pseudomyrmex_depressus</i>	<i>Pseudomyrmex_depressus_D0119</i>	Bolivia: Santa Cruz	CASENT0221016
<i>Pseudomyrmex_evitus</i>	<i>Pseudomyrmex_evitus_D0226</i>	Mexico: Veracruz	CASENT0106120
<i>Pseudomyrmex_evitus</i>	<i>Pseudomyrmex_evitus_D1306</i>	Costa Rica: Heredia	INBIOCRIO01271961
<i>Pseudomyrmex_feralis</i>	<i>Pseudomyrmex_feralis_D0316</i>	Guatemala: Sacatepéquez	CASENT0106121
<i>Pseudomyrmex_ferrugineus</i>	<i>Pseudomyrmex_ferrugineus_D0347</i>	Belize: Orange Walk	CASENT0220557
<i>Pseudomyrmex_ferrugineus</i>	<i>Pseudomyrmex_ferrugineus_D0622</i>	Mexico: Oaxaca	CASENT0220555
<i>Pseudomyrmex_flavicornis</i>	<i>Pseudomyrmex_flavicornis_D0621</i>	Guatemala: Santa Rosa	CASENT0220573
<i>Pseudomyrmex_flavicornis</i>	<i>Pseudomyrmex_flavicornis_D0671</i>	Costa Rica: Guanacaste	CASENT0005786
<i>Pseudomyrmex_haytianus</i>	<i>Pseudomyrmex_haytianus_D1204</i>	Dominican Republic: Cibao Nordeste	CASENT0220790
<i>Pseudomyrmex_janzeni</i>	<i>Pseudomyrmex_janzeni_D0620</i>	Mexico: Nayarit	CASENT0221012
<i>Pseudomyrmex_laevifrons</i>	<i>Pseudomyrmex_laevifrons_D1238</i>	Ecuador: Napo	CASENT0221017
<i>Pseudomyrmex_micans</i>	<i>Pseudomyrmex_micans_D0507</i>	Peru: San Martín	CASENT0221019
<i>Pseudomyrmex_mixtecus</i>	<i>Pseudomyrmex_mixtecus_D0348</i>	Mexico: Guerrero	CASENT0220607
<i>Pseudomyrmex_mixtecus</i>	<i>Pseudomyrmex_mixtecus_D0351</i>	Mexico: Oaxaca	CASENT0221008
<i>Pseudomyrmex_nigrocinctus</i>	<i>Pseudomyrmex_nigrocinctus_D0613</i>	Nicaragua: Granada	CASENT0221011
<i>Pseudomyrmex_nigrocinctus</i>	<i>Pseudomyrmex_nigrocinctus_D1219</i>	Costa Rica: Guanacaste	CASENT0005795
<i>Pseudomyrmex_obtusus</i>	<i>Pseudomyrmex_obtusus_D0204</i>	Venezuela: Barinas	CASENT0221018
<i>Pseudomyrmex_particeps</i>	<i>Pseudomyrmex_particeps_D0628</i>	Costa Rica: Puntarenas	CASENT0220618
<i>Pseudomyrmex_particeps</i>	<i>Pseudomyrmex_particeps_D1307</i>	Costa Rica: San José	CASENT0794062
<i>Pseudomyrmex_peperi</i>	<i>Pseudomyrmex_peperi_D0346</i>	Guatemala: Sacatepéquez	CASENT0220623
<i>Pseudomyrmex_peperi</i>	<i>Pseudomyrmex_peperi_D0623</i>	Mexico: Oaxaca	CASENT0220624
<i>Pseudomyrmex_perboscii</i>	<i>Pseudomyrmex_perboscii_D0116</i>	Bolivia: Santa Cruz	CASENT0221015
<i>Pseudomyrmex_satanicus</i>	<i>Pseudomyrmex_satanicus_D0260</i>	Panama: Colón	CASENT0220626
<i>Pseudomyrmex_spinicola</i>	<i>Pseudomyrmex_spinicola_D0129</i>	Costa Rica: Guanacaste	CASENT0005800
<i>Pseudomyrmex_spinicola</i>	<i>Pseudomyrmex_spinicola_D0604</i>	Nicaragua: Granada	CASENT0221009
<i>Pseudomyrmex_spinicola</i>	<i>Pseudomyrmex_spinicola_D0605</i>	Colombia: Bolívar	CASENT0221010
<i>Pseudomyrmex_veneficus</i>	<i>Pseudomyrmex_veneficus_D0345</i>	Mexico: Jalisco	CASENT0220644
<i>Pseudomyrmex_veneficus</i>	<i>Pseudomyrmex_veneficus_D0624</i>	Mexico: Sinaloa	CASENT0221013
<i>Pseudomyrmex_veneficus</i>	<i>Pseudomyrmex_veneficus_D1305</i>	Mexico: Michoacán	CASENT0794061

Table S2. Statistics for genome assembly and for the matrix of 95% completeness (matrix of loci present in 95% or more of the 29 taxa).

Taxon Name	Total Reads	Total Contigs	Total Contigs Cov (X)	Total Contigs Mean Length	UCE Contigs	UCE Contigs Mean Length	UCE Contigs Cov (X)
Pseudomyrmex_depressus_D0119	4,177,608	47,794	6.8	325.8	2,238	683.1	62.4
Pseudomyrmex_evitus_D0226	5,185,896	47,381	8.0	342.1	2,216	692.2	72.3
Pseudomyrmex_evitus_D1306	10,052,990	106,752	7.8	326.8	2,244	561.7	93.1
Pseudomyrmex_feralis_D0316	4,552,328	43,721	6.8	388.6	2,128	874.9	47.9
Pseudomyrmex_ferrugineus_D0347	4,050,932	34,185	8.2	403.3	2,150	788.4	53.2
Pseudomyrmex_ferrugineus_D0622	5,274,142	63,852	5.9	363.7	2,181	870.4	52.8
Pseudomyrmex_flavicornis_D0621	2,492,388	21,351	6.6	418.9	2,071	895.9	30.6
Pseudomyrmex_flavicornis_D0671	1,552,550	11,919	8.1	417.3	2,090	733.0	29.3
Pseudomyrmex_haytianus_D1204	877,552	6,724	11.7	372.4	2,062	503.5	29.5
Pseudomyrmex_janzeni_D0620	3,720,456	38,634	6.4	378.6	2,138	875.3	45.0
Pseudomyrmex_laevifrons_D1238	3,285,488	19,703	9.6	334.6	1,999	394.2	46.7
Pseudomyrmex_micans_D0507	1,226,322	7,343	11.4	472.3	1,995	615.3	26.5
Pseudomyrmex_mixtecus_D0348	4,864,762	53,065	6.1	346.4	2,209	802.3	54.0
Pseudomyrmex_mixtecus_D0351	3,405,860	26,128	8.6	405.8	2,124	824.4	51.7
Pseudomyrmex_nigrocinctus_D0613	8,292,460	136,982	5.8	351.4	2,279	901.5	92.0
Pseudomyrmex_nigrocinctus_D1219	2,957,482	24,323	7.4	412.8	2,124	926.0	41.1
Pseudomyrmex_obtusus_D0204	5,199,232	43,711	8.9	365.1	2,192	685.7	73.2
Pseudomyrmex_particeps_D0628	7,328,318	97,259	6.4	337.0	2,261	827.9	97.0
Pseudomyrmex_particeps_D1307	7,821,658	109,666	5.9	357.5	2,214	960.9	70.7
Pseudomyrmex_peperi_D0346	4,383,700	36,829	8.2	376.4	2,167	788.1	59.8
Pseudomyrmex_peperi_D0623	3,592,532	28,856	7.9	410.3	2,117	953.5	54.6
Pseudomyrmex_perboscii_D0116	7,343,272	94,894	6.4	351.4	2,237	901.7	82.6
Pseudomyrmex_satanicus_D0260	3,556,360	30,046	7.2	472.4	2,080	843.6	31.1
Pseudomyrmex_spinicola_D0129	4,093,956	33,108	7.7	401.2	2,166	832.9	49.7
Pseudomyrmex_spinicola_D0604	5,363,720	63,292	5.7	371.6	2,185	806.5	46.9
Pseudomyrmex_spinicola_D0605	5,679,366	61,065	6.9	370.6	2,217	736.3	68.6
Pseudomyrmex_veneficus_D0345	5,653,168	66,234	5.3	352.7	2,207	789.7	41.4
Pseudomyrmex_veneficus_D0624	9,267,862	128,380	6.0	343.9	2,230	949.3	86.3
Pseudomyrmex_veneficus_D1305	5,118,118	30,727	10.2	341.1	2,129	500.1	57.9
MEAN		4,840,361	52,204	7.5	376.3	2,160	776.5
MIN		877,552	6,724	5.3	325.8	1,995	394.2
MAX		10,052,990	136,982	11.7	472.4	2,279	960.9
Matrix		#Loci	Total Length	Mean Align Length	Align CI	Min Align Length	Max Align Length
Ferr-29T-F95		1,672	1,321,987	790.66	10.01	259	1,509
							Informative Sites
							58,173

Table S3. Support for alternate phylogenetic placements of *Pseudomyrmex peperi*. All analyses of acacia ants and relatives yield the same species relationships except for the position of *P. peperi*, which appears in one of two places in the tree. Topology 1 has *P. peperi* as sister to all other members of the *P. ferrugineus* subgroup (as in Figures 1-3). Topology 2 has *P. peperi* situated one node shallower, as sister to the *P. ferrugineus* complex (as in Figure S2f). ML = maximum likelihood; BS = bootstrap support (as percentage); PP = Bayesian posterior probability. ML analyses were conducted with RAxML v.8.2.8, Bayesian analyses with ExaBayes v1.5. Species tree analyses employed ASTRAL (v4.8.0); “500 best loci” refers to those with the highest average bootstrap scores; “branch lengths” refers to a third ASTRAL analysis with a newer version (v4.10.8) which generates branch lengths in coalescent units but does not allow for species assignment.

Analysis	Topology	Support
ML, no partitioning	2	BS 59
ML, hcluster partitioning	2	BS 55
ML, kmeans partitioning	1	BS 100
ML, no partitioning, RY-coded	1	BS 86
Bayesian, no partitioning	2	PP 1.00
Bayesian, hcluster partitioning	1	PP 0.97
Bayesian, kmeans partitioning	2	PP 1.00
Species tree analysis, all 1,672 loci	1	BS 45
Species tree analysis, 500 best loci	1	BS 54
Species tree analysis, 500 best loci; branch lengths	1	BS 54

Table S4. Biogeographic model comparisons from BioGeoBEARS analyses of acacia ants and relatives.

Topology 1 has *Pseudomyrmex peperi* as sister to all other members of the *P. ferrugineus* subgroup (as in Figures 1-3). Topology 2 has *P. peperi* situated one node shallower, as sister to the *P. ferrugineus* complex (as in Figure S2f). Analysis 1 allowed all area possibilities; analysis 2 excluded range combinations containing areas DE (see text).

	Model		Likelihood-ratio test				AIC comparison				
	alt	null	alt LnL	null LnL	D	P-value	AIC1	AIC2	wt1	wt2	Ratio
Topology 1 Analysis 1	DEC+J	DEC	-36.01	-38.89	5.77	0.016	78.02	81.79	0.87	0.13	6.58
	DIVALIKE+J	DIVALIKE	-38.29	-40.46	4.33	0.037	82.58	84.92	0.76	0.24	3.21
	BAYAREALIKE+J	BAYAREALIKE	-41.78	-44.44	5.33	0.021	89.55	92.88	0.84	0.16	5.29
Topology 1 Analysis 2	DEC+J	DEC	-37.34	-43.56	12.44	0.0004	80.67	91.12	0.99	0.0054	185.1
	DIVALIKE+J	DIVALIKE	-38.88	-44.77	11.78	0.0006	83.76	93.54	0.99	0.0075	133
	BAYAREALIKE+J	BAYAREALIKE	-41.09	-47.18	12.17	0.0005	88.19	98.35	0.99	0.0062	161.2
Topology 2 Analysis 1	DEC+J	DEC	-35.45	-38.12	5.33	0.021	76.9	80.24	0.84	0.16	5.29
	DIVALIKE+J	DIVALIKE	-37.54	-39.34	3.59	0.058	81.09	82.67	0.69	0.31	2.21
	BAYAREALIKE+J	BAYAREALIKE	-41.31	-44.30	5.97	0.015	88.63	92.6	0.88	0.12	7.28
Topology 2 Analysis 2	DEC+J	DEC	-36.82	-42.80	11.95	0.0005	79.64	89.59	0.99	0.0069	144.9
	DIVALIKE+J	DIVALIKE	-38.21	-43.61	10.81	0.001	82.42	91.22	0.99	0.012	81.76
	BAYAREALIKE+J	BAYAREALIKE	-40.73	-47.05	12.64	0.0004	87.46	98.1	1	0.0049	204.6

Table S5. Biogeographic model comparisons from BioGeoBEARS analyses of domatia-bearing *Vachellia* and relatives. Analysis 1 allowed all area possibilities; analysis 2 excluded all disjunct continental areas, but all connected continental areas containing E were allowed; and analysis 3 disallowed all areas that included E except for widespread ranges: ABCDE, BCDE, ABCE, and CDE. Note that in analysis 3, the BAYAREALIKE analysis failed, due to the exclusion of necessary area transition states.

	Model		Likelihood-ratio test				AIC comparison				
	alt	null	alt LnL	null LnL	D	P-value	AIC1	AIC2	wt1	wt2	Ratio
Analysis 1	DEC+J	DEC	-64.78	-65.84	2.12	0.15	135.6	135.7	0.52	0.48	1.06
	DIVALIKE+J	DIVALIKE	-71.46	-72.08	1.24	0.27	148.9	148.2	0.41	0.59	0.68
	BAYAREALIKE+J	BAYAREALIKE	-68.11	-74.70	13.17	0.0003	142.2	153.4	1	0.0037	266.5
Analysis 2	DEC+J	DEC	-64.43	-65.51	2.17	0.14	134.9	135	0.52	0.48	1.09
	DIVALIKE+J	DIVALIKE	-72.02	-72.19	0.35	0.56	150	148.4	0.3	0.7	0.44
	BAYAREALIKE+J	BAYAREALIKE	-69.64	-81.04	22.8	1.8E-06	145.3	166.1	1	0.00003	32830
Analysis 3	DEC+J	DEC	-66.00	-67.20	2.41	0.12	138	138.4	0.55	0.45	1.23
	DIVALIKE+J	DIVALIKE	-73.55	-75.11	3.12	0.077	153.1	154.2	0.64	0.36	1.75
	BAYAREALIKE+J	BAYAREALIKE	81.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table S6. Ancestral trait estimation model comparisons for habitat and nesting analyses performed with the Ace function in APE. Models are ER (equal rates), SYM (symmetric rates) and ARD (all rates different); ER and SYM models are equivalent for a two-state character. For both traits, likelihood ratio tests favored the 1-parameter ER model over more complex models, strongly so for nesting behavior, marginally so for habitat.

Trait	Model		Likelihood-ratio test						
	alt	null	alt LnL	null LnL	DF alt	DF null	DF	D	P-value
Habitat	ARD	ER (=SYM)	-9.2389	-10.6583	2	1	1	2.8387	0.0920
Nesting	ARD	ER	-9.0058	-10.0806	6	1	5	2.1497	0.8281
	SYM	ER	-9.5891	-10.0806	3	1	2	0.9830	0.6117
	ARD	SYM	-9.0058	-9.5891	6	3	3	1.1667	0.7610