

Multiple, Independent Colonizations of the Hawaiian Archipelago by the Family Dolichopodidae (Diptera)

Appendix S1. Taxonomic sampling, GenBank accession numbers, partitioning and supplementary trees.

TABLE S1A. TAXON SAMPLING AND GENBANK ACCESSION NUMBERS FOR *EURYNOGASTER* COMPLEX, *CONCHOPUS*, AND NON-HAWAIIAN ENDEMIC DOLICHOPODIDAE INCLUDED IN THIS STUDY. IN FINAL SUBMISSION, THE 1S WILL BE REPLACED BY GENBANK ACCESSION NUMBERS.

Genus	species	LabelName	Locality	ND2	COI	COII	12S	16S	CAD	EflaA	EflaB	Total
<i>Eurynogaster</i> complex specimens												
<i>Adachia</i>	<i>apicenigra</i>	<i>Ad.apicenigra</i> 107	HAWAII, Olaa Forest, Pole 44	1	1	1	1	1	1		1	7
<i>Adachia</i>	<i>hispida</i>	<i>Ad.hispida</i> 200978	HAWAII, Olaa Forest, Puu Unit, 4300'	1	1	1	1	1	1	1		7
<i>Adachia</i>	<i>n.sp.nr.hispida</i>	<i>Ad.sp.nr.hispida</i> 205015	KAUAI, Kawaikoi Stream, 3500', 18 May 2007, sweeping over stream	1	1	1	1	1	1	1	1	8
<i>Arciellia</i>	<i>dolichostoma</i>	<i>Ar.dolichostoma</i> 205016	KAUAI, Puu O Kila Road, 4080'	1	1	1	1	1	1	1	1	8
<i>Arciellia</i>	<i>dolichostoma</i>	<i>Ar.dolichostoma</i> 205017	KAUAI, Pihea Trail, 3600'	1	1	1	1	1	1	1	1	8
<i>Arciellia</i>	<i>dolichostoma</i>	<i>Ar.dolichostoma</i> 205359	MAUI, Haleakala NP, Kaupo Trail	1	1	1	1	1			1	6
<i>Arciellia</i>	<i>xanthopleura</i>	<i>Ar.xanthopleura</i> 205018	KAUAI, Pihea Trail, 3600'	1	1	1	1	1	1	1	1	8
<i>Arciellia</i>	<i>xanthopleura</i>	<i>Ar.xanthopleura</i> 147	KAUAI, Kokee SP, Nualolo Tr.			1	1	1	1		1	5
<i>Elmoia</i>	<i>bullata</i>	<i>El.bullata</i> 205260	HAWAII, Kohala State Forest, trail to Waimanu Stream	1		1	1	1	1	1	1	7
<i>Elmoia</i>	<i>saxatilis</i>	<i>El.saxatilis</i> 106	OAHU, Mt. Kaala		1	1	1	1	1		1	6
<i>Eurynogaster</i>	<i>sp.</i>	<i>E.sp</i> 135	MAUI, Waikamoi Forest Preserve, Heed Trail	1	1	1	1	1	1		1	7
<i>Eurynogaster</i>	<i>kauaiensis</i>	<i>E.kauaiensis</i> 131	KAUAI, Pihea Trail	1		1	1	1	1		1	6
<i>Eurynogaster</i>	<i>maculata</i>	<i>E.maculata</i> 205058_205380	MAUI, Paliku, crater wall, 6600'	1	1	1	1	1	1	1	1	8
<i>Eurynogaster</i>	<i>maculata</i>	<i>E.maculata</i> 132	OAHU, Poamoho Tr.	1	1	1	1	1	1		1	7
<i>Eurynogaster</i>	<i>n.sp.#1</i>	<i>E.n.sp.A.133</i>	HAWAII, Hakalau	1		1	1	1	1		1	6
<i>Eurynogaster</i>	<i>n.sp.#3</i>	<i>E.n.sp.C.128</i>	OAHU, Poamoho Tr.	1	1	1	1	1	1	1	1	8
<i>Eurynogaster</i>	<i>nr. cilifemorata</i>	<i>E.sp.nr.cilifemorata</i> 83	MAUI, East Maui Irrigation, Haiku Uka, Heed Trail	1	1	1	1	1	1	1	1	8
<i>Eurynogaster</i>	<i>paludis</i>	<i>E.paludis</i> 205025	MAUI, Pihea Trail, 3600'	1	1	1	1	1	1	1	1	8
<i>Eurynogaster</i>	<i>sp.</i>	<i>E.sp</i> 112	HAWAII, Olaa Forest, Pole 44	1	1	1	1	1	1	1		7
<i>Eurynogaster</i>	<i>sp. 2 nr. maculata</i>	<i>E.n.sp.B.105</i>	OAHU, Mt. Kaala			1	1	1	1		1	5

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**Dolichopodidae
specimens**

<i>Chrysotus</i>	<i>longipalpis</i>	<i>Ch.longipalpis</i> 205060	OAHU, Manoa Cliff Trail, 1800'	1	1	1	1	1	1	1	7	
<i>Chrysotus</i>	<i>longipalpis</i>	<i>Ch.longipalpis</i> 205379	OAHU, Honolulu Watershed FR, Manoa Cliffs Trail	1	1	1	1	1	1	1	7	
<i>Chrysotus</i>	<i>sp</i>	<i>Ch.sp</i> 173	MARQUESAS, HIVA OA	1	1		1				3	
<i>Chrysotus</i>	<i>sp nr.longipalpis</i>	<i>Ch.sp.nr.longipalpis</i> 205030	MAUI, Kahanaiki Gulch, 2100'	1	1		1	1	1		6	
<i>Chrysotus</i>	<i>sp.nr.longipalpis</i>	<i>Ch.sp.nr.longipalpis</i> 85	MAUI, Puu Kukui, Kahanaiki Gulch	1	1	1	1	1	1		6	
<i>Condylostylus</i>	<i>sp.</i>	<i>Condylostylus.sp</i> 164	OAHU, Maunaloa Beach Rocks	1	1		1	1	1	1	6	
<i>Dolichopus</i>	<i>exsul</i>	<i>D.exsul</i> 205024	KAUAI, Pihea Trail, 3500'	1	1	1	1	1	1	1	8	
<i>Dolichopus</i>	<i>exsul</i>	<i>D.exsul</i> 205034	MAUI, Puu Kukui Trail, 2900- 3700'	1	1	1	1	1	1	1	8	
<i>Dolichopus</i>	<i>exsul</i>	<i>D.exsul</i> 205232	HAWAII, Kau FR, Alahi Spring	1	1	1	1	1	1	1	8	
<i>Dolichopus</i>	<i>exsul</i>	<i>D.exsul</i> 205282	HAWAII, Kohala Mountains	1	1	1	1	1	1	1	8	
<i>Dolichopus</i>	<i>exsul</i>	<i>D.exsul</i> 169	OAHU, Poamoho	1		1	1	1	1	1	6	
<i>Hercostom</i>	<i>indonesianus</i> GB	<i>Hercostom.indonesianus</i> GB			1		1	1			3	
<i>Tachytrechus</i>	<i>angustipennis</i>	<i>T.angustipennis</i> 205026	KAUAI, Kumuwela Trail, 3500'	1	1	1	1	1	1	1	8	
TOTALS				49	47	52	53	55	50	24	47	377
% complete				0.88	0.84	0.93	0.95	0.98	0.89	0.43	0.84	

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APPENDIX S1: GENBANK ACCESSION NUMBERS, PARTITIONING AND SUPPLEMENTARY TREES

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TABLE S1B. SUMMARY OF DATA PARTITIONS AND NUCLEOTIDE MODELS DETERMINED FOR EACH PARTITION, SELECTED USING BIC IN PARTITIONFINDER (LANFEAR ET AL., 2012).

Program (# partitions)	Figure	Data partitions: nucleotide models selected by PartitionFinder
Dataset A Dolichopodidae Mr Bayes/ RAxML(11)	Figures 2, S1a & S1b in Appendix 1	Mr Bayes: COI_3, COII_3, ND2_3: GTR+I+G COI_1, COII_1: GTR+I+G EF1_2, COI_2, COII_2: GTR+I+G ND2_1: GTR+G ND2_2: GTR+G 12S, 16S: GTR+I+G CAD_3: HKY+I+G CAD_1, CAD_2: K80+I+G CADintron: GTR+I+G EF1_3: HKY+G EF1_1: F81+I+G RAxML: Each partition was run using the GTR+GAMMA model
Dataset B (<i>Eurynogaster</i> complex): Mr Bayes/ RAxML(11)	Figure 1 & Figure S1c-1 in Appendix 1	Mr Bayes: CAD_3: HKY+I CAD_1: GTR+G CAD_2, EF1A_2, ND_2: HKY+I+G CADintron, EF1Aintron1, EFAintron2: HKY+I EF1A_3, EF1B_3: HKY+G EF1A_1, EF1B_1: F81+I COI_2, COII_2, EF1B_2: F81+I+G EF1Bintron: F81 12S, 16S, ND2_1: GTR+I+G COI_3, COII_3, ND2_3: GTR+I+G COI_1, COII_1: GTR+G RAxML: Each partition was run using the GTR+GAMMA model
Dataset B (<i>Eurynogaster</i> complex): BEAST: Island calibrations (10)	Figures 1 & S2b in Appendix 2	CAD_3: HKY CAD_1, EF1A_1, EF1B_1: TrN+I CAD_2, EF1A_2, ND_2: HKY+I+G CADintron, EF1Aintron1, EF1Aintron2: HKY+I EF1A_3, EF1B_3: HKY+G COI_2, COII_2, EF1B_2: HKY+I+G EF1Bintron: HKY 12S, 16S, ND2_1: GTR+I+G COI_3, COII_3, ND2_3: GTR+I+G COI_1, COII_1: GTR+G
Dataset B (<i>Eurynogaster</i> complex): BEAST: Divergence rates (11)	Figures S2c & S2d in Appendix 2	COI: GTR+I+G CAD_3: HKY+I CAD_1, EF1A_2, EF1B_1: TrN+I CAD_2, EF1A_2, ND2_2: HKY+I+G CADintron, EF1Aintron1, EF1Aintron2: HKY+I EF1A_3, EF1B_3: HKY+G COII_2, EF1B_2: HKY+I EF1Bintron: HKY 12S, 16S, ND2_1: GTR+I+G COII_3, ND2_3: GTR+I+G COII_1: TrN+G

SUPPLEMENTARY TREES:

FIGURE S1A. COMBINED DOLICHOPODIDAE ANALYSIS (DATA SET A). Majority rule consensus tree summarizing Bayesian analysis, with the *Eurynogaster* complex and *Campsicnemus* collapsed. Bayesian posterior probabilities (Mr. Bayes) and bootstrap supports from the maximum likelihood analysis (RAxML) are displayed as boxes.

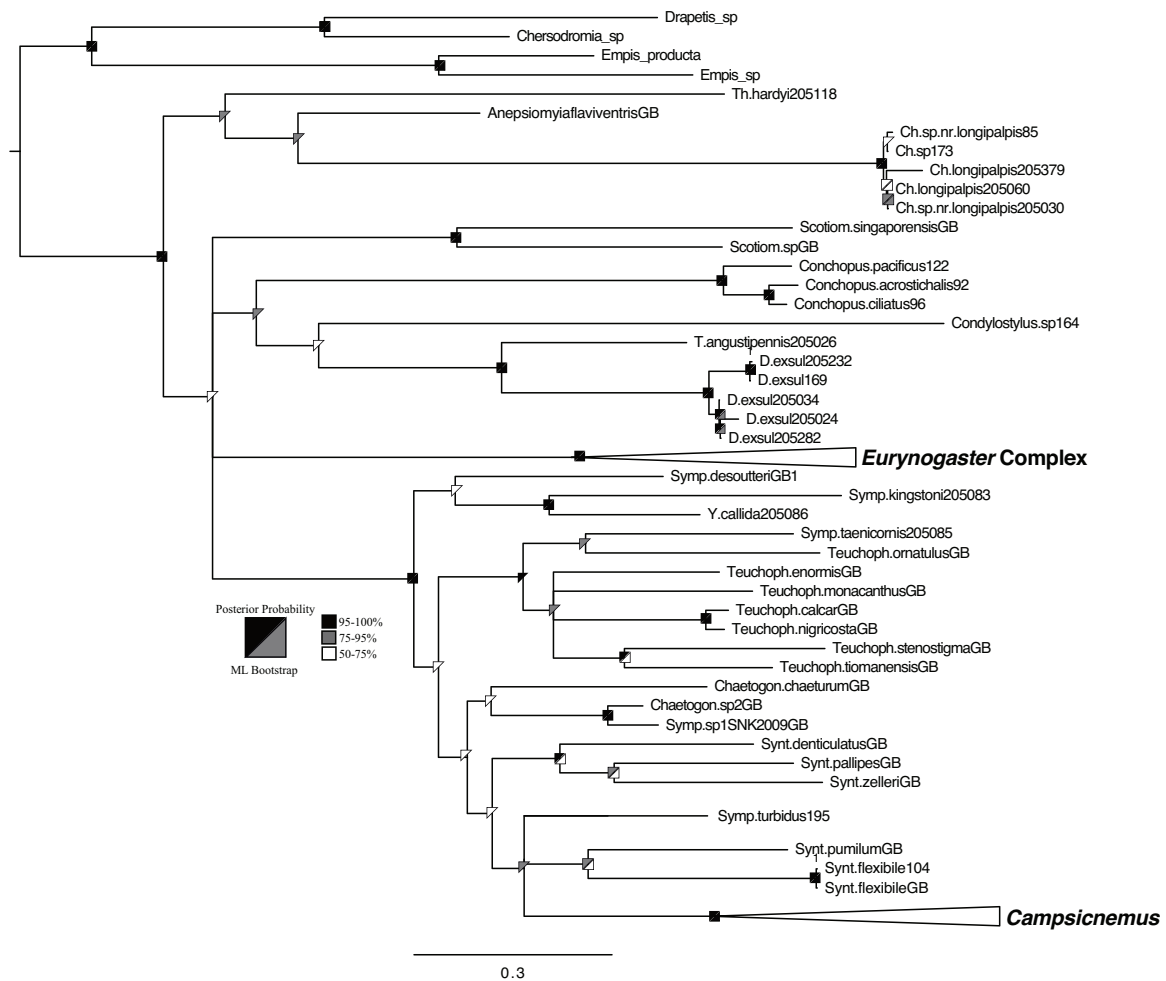


FIGURE S1B. MAXIMUM LIKELIHOOD ANALYSIS OF THE DOLICHOPODIDAE (DATA SET A).

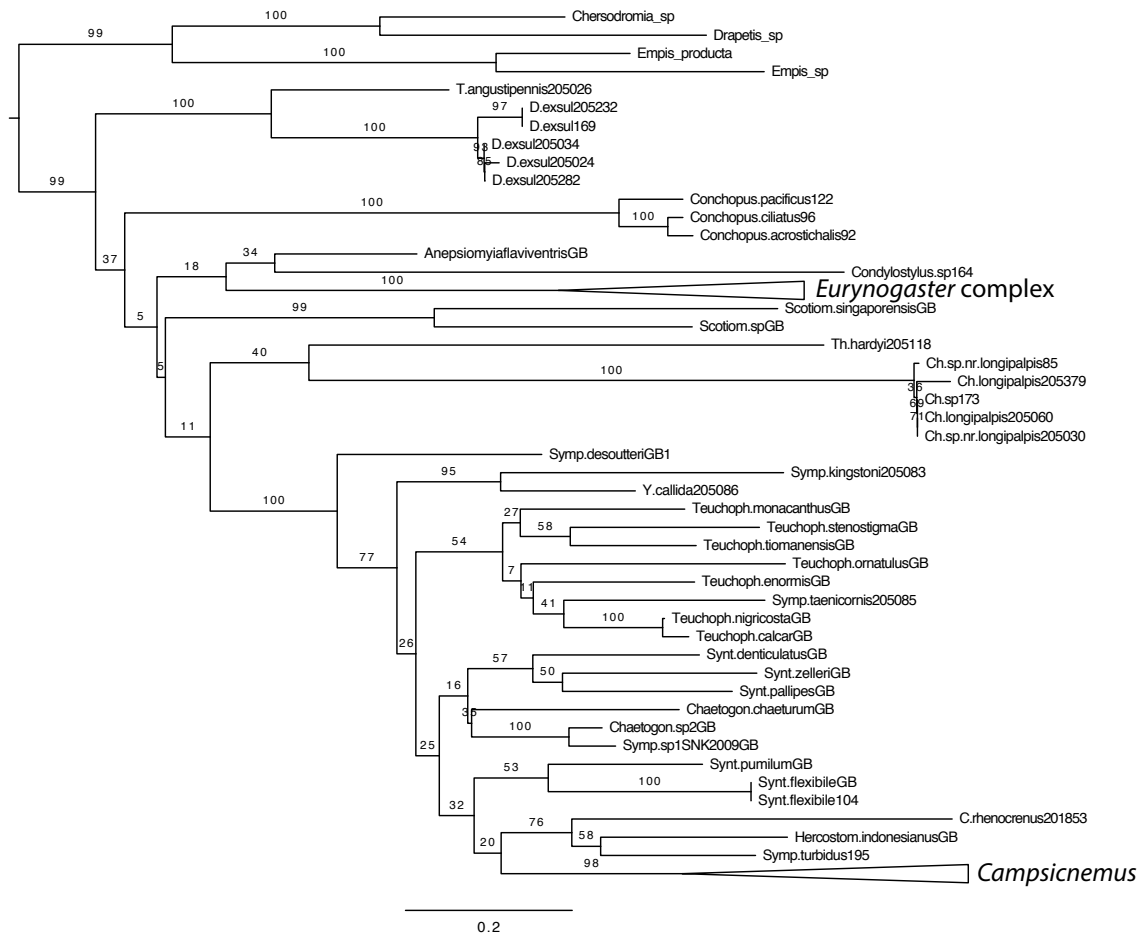


FIGURE S1C. Majority rule consensus tree summarizing Bayesian analysis of the *Eurynogaster* complex. Bayesian posterior probabilities (Mr. Bayes) and bootstrap supports from the maximum likelihood analysis (RAxML) are displayed as boxes. Islands that each specimen was collected from are shown next to each tip.

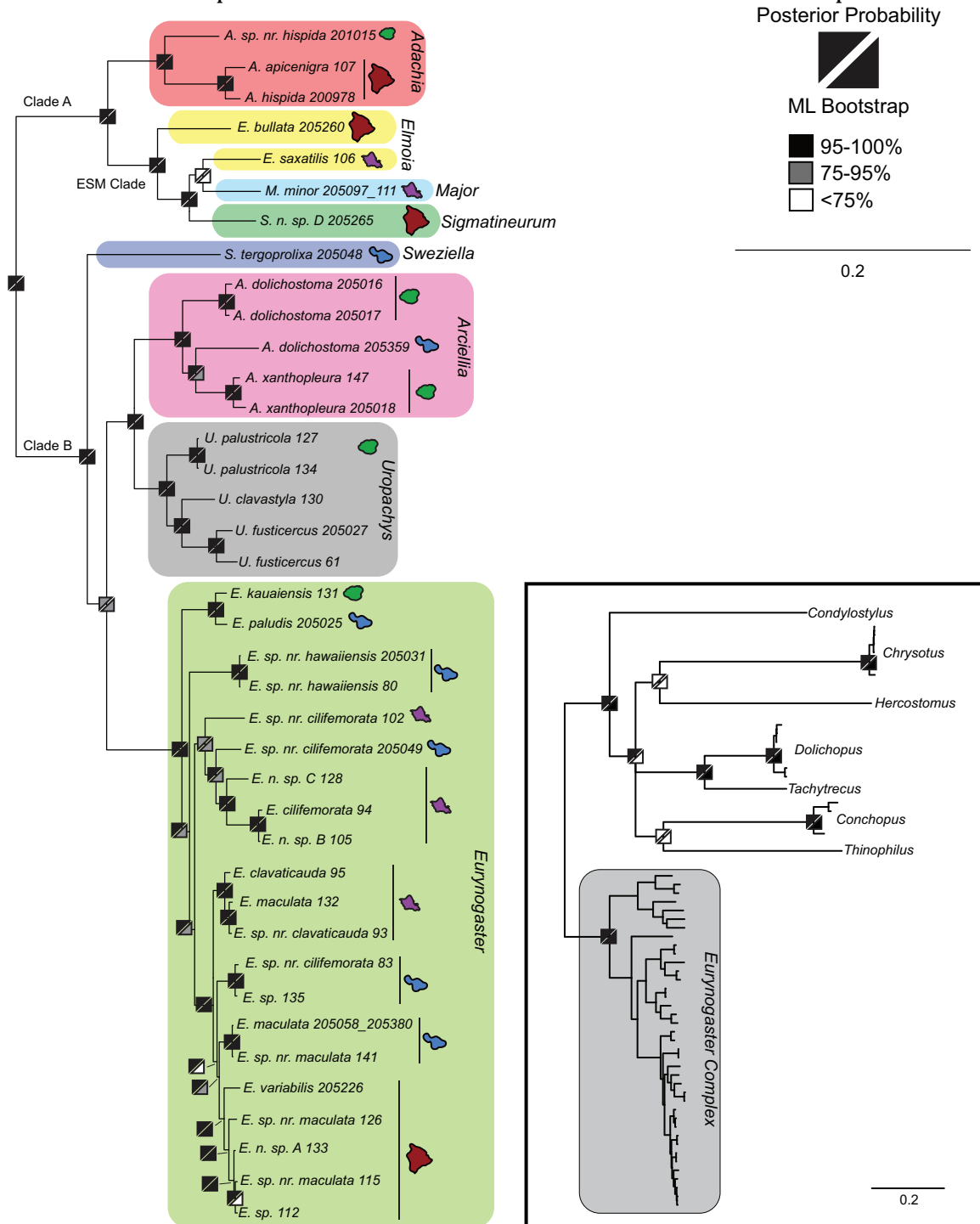
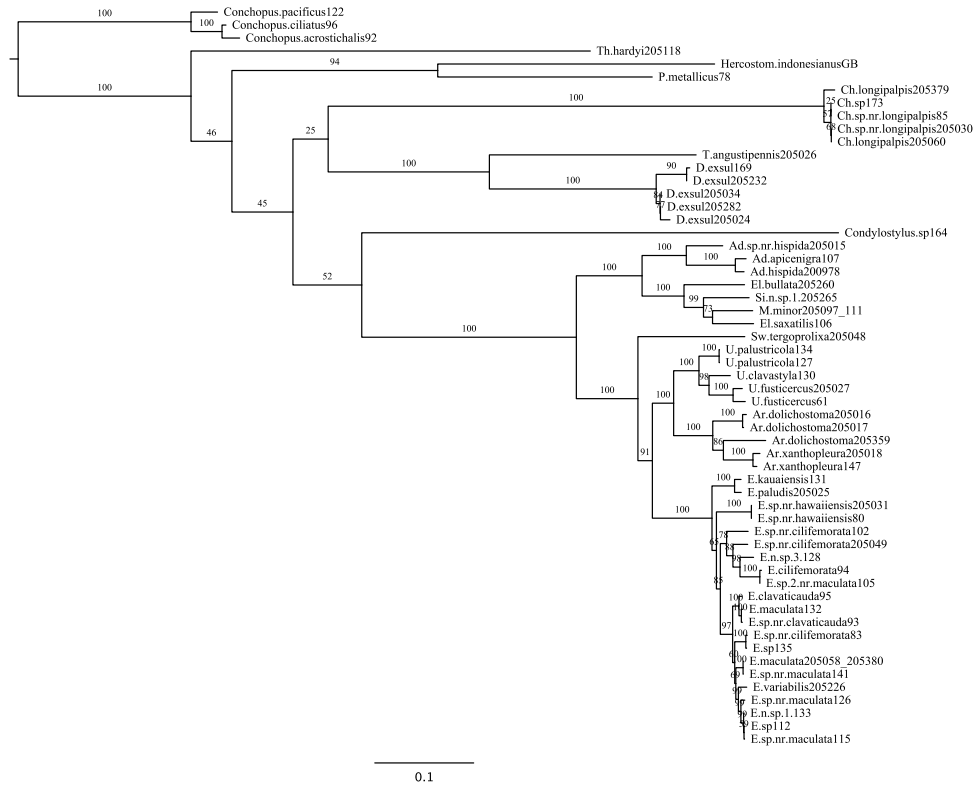


FIGURE S1D. COMBINED MAXIMUM LIKELIHOOD ANALYSIS OF ALL GENES (DATA SET B).



SUPPLEMENTARY TREES: INDIVIDUAL MAXIMUM LIKELIHOOD GENE TREES:

FIGURE S1E. COI

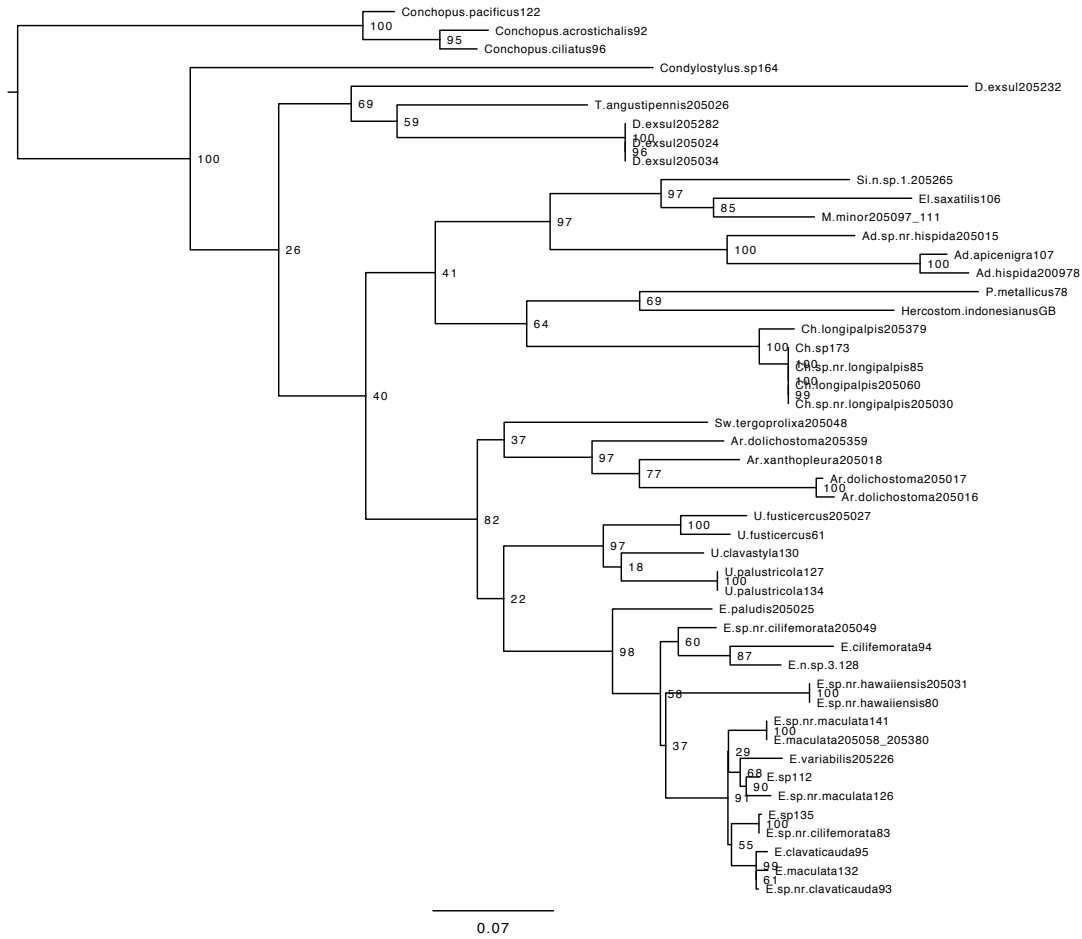


FIGURE S1F. COII

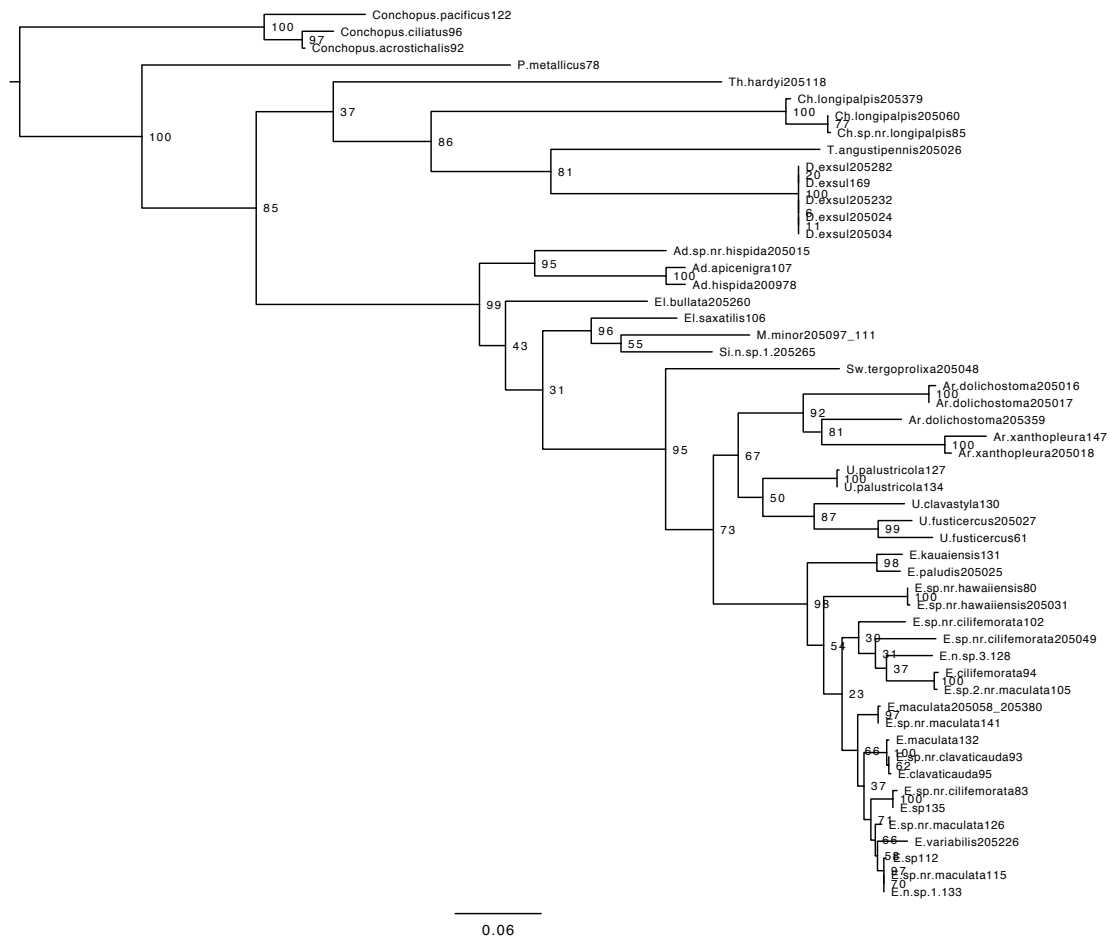


FIGURE S1G. ND2

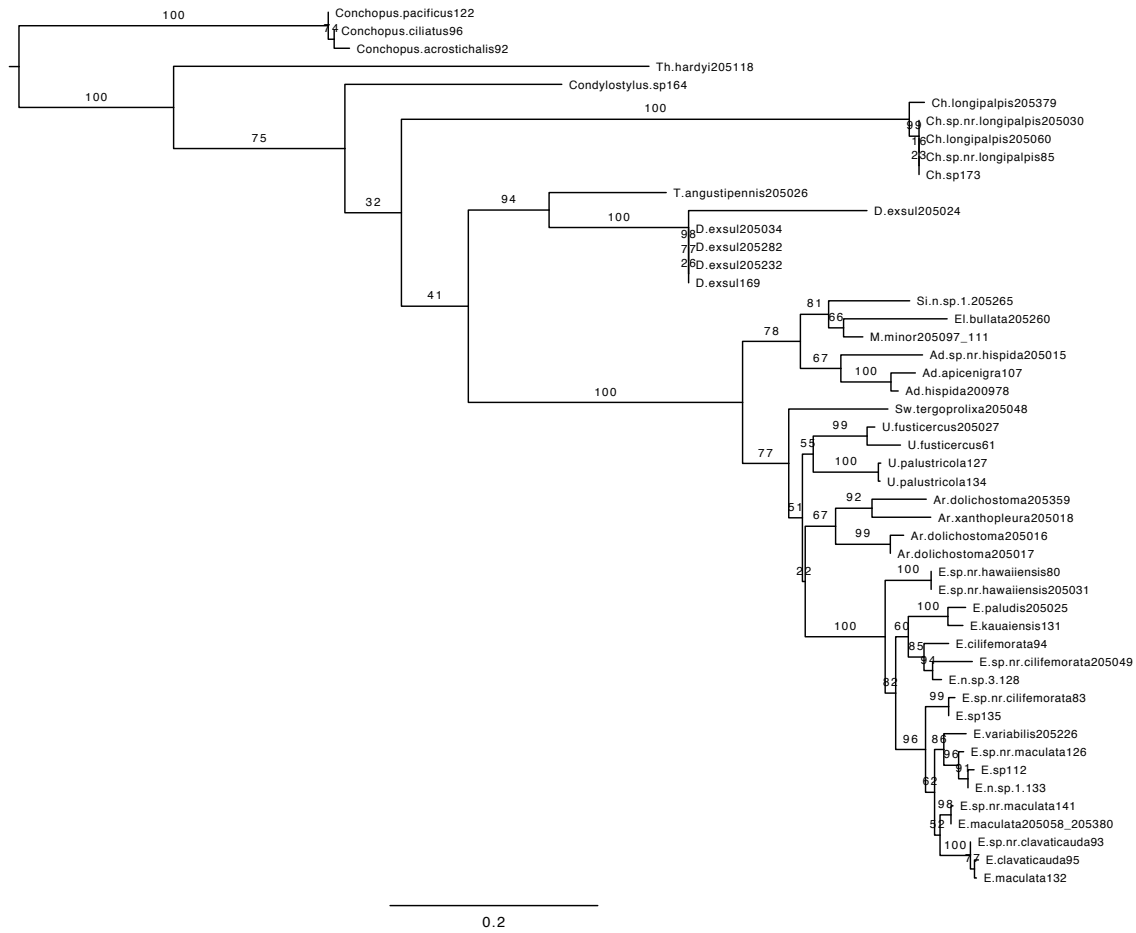


FIGURE S1H. 12S

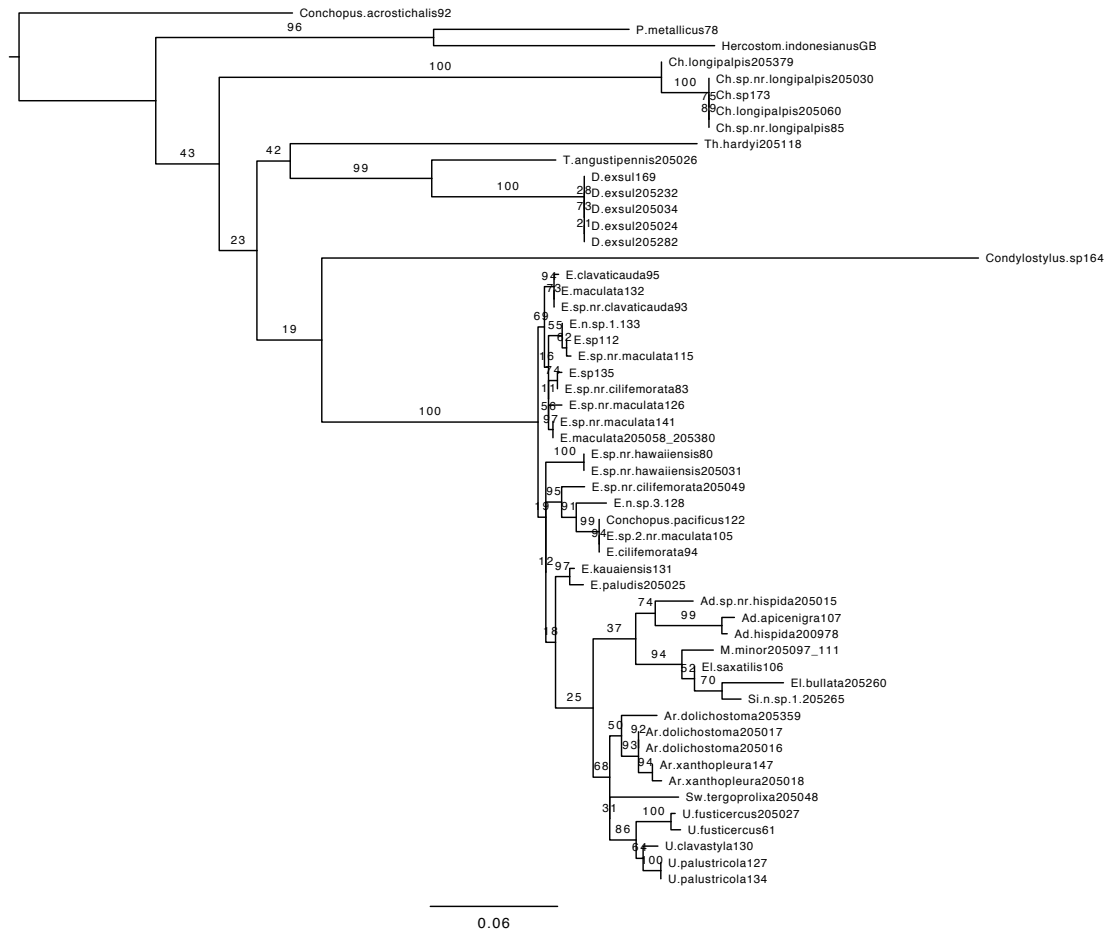


FIGURE S1i. 16S

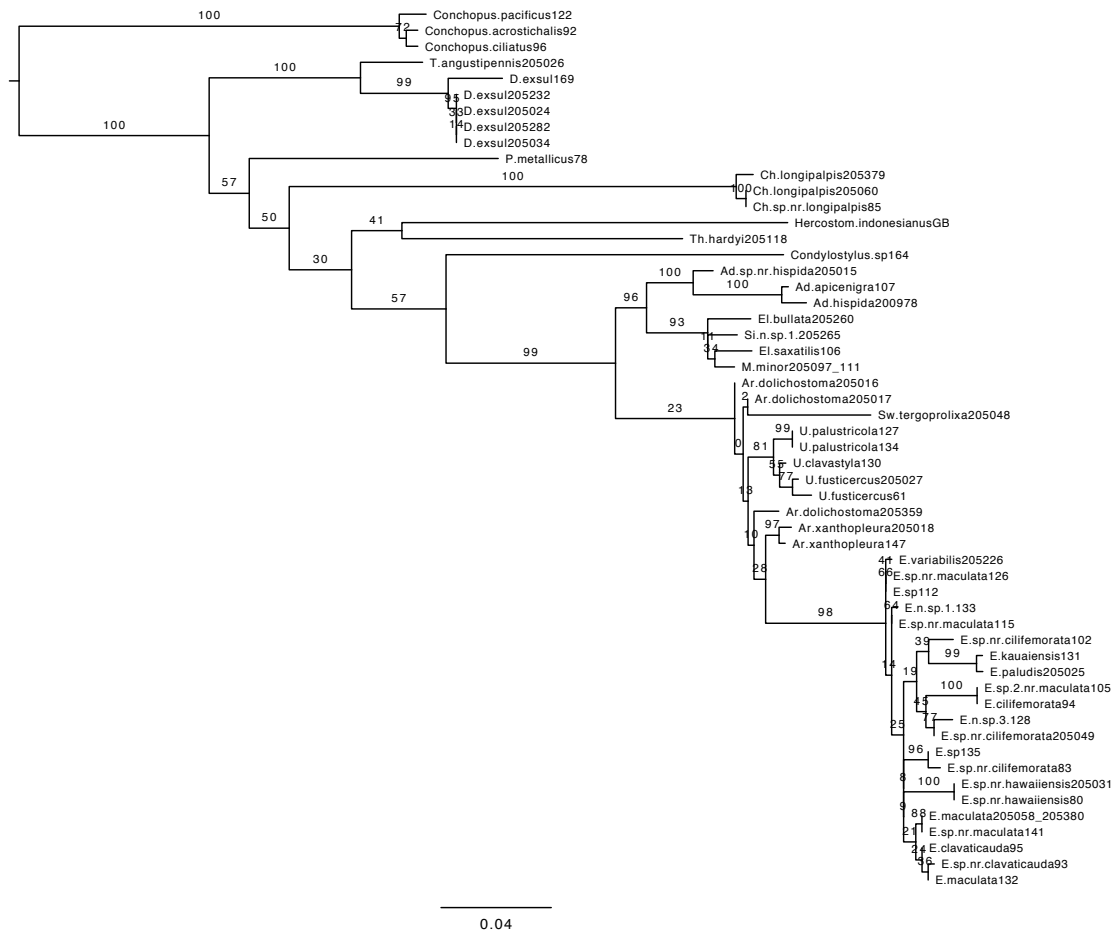


FIGURE S1J. CAD

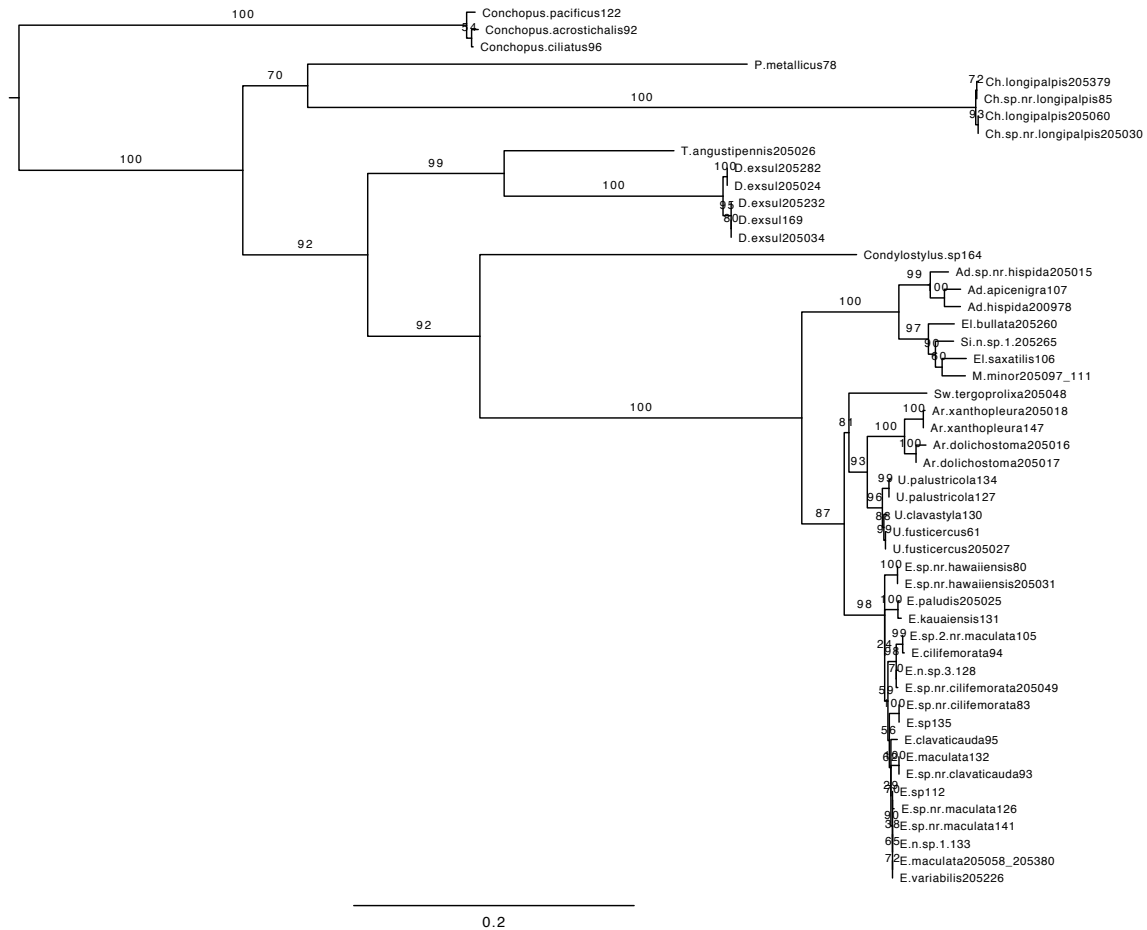


FIGURE S1k. EF1AA

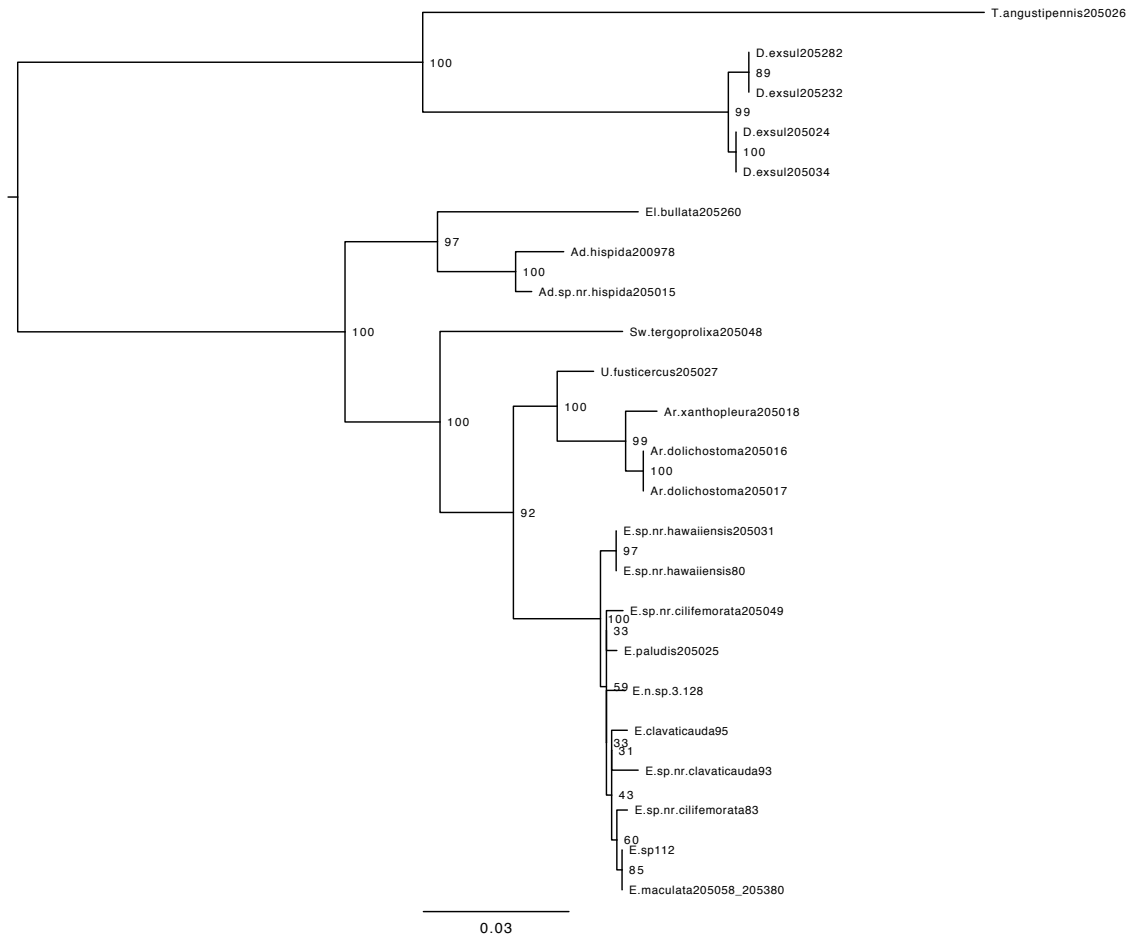


FIGURE S1L. EF1AB

