

Myrmecological News	25	Digital supplementary material
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Digital supplementary material to

PIERCE, M.P., BRANSTETTER, M.G. & LONGINO, J.T. 2017: Integrative taxonomy reveals multiple cryptic species within Central American *Hylomyrma* FOREL, 1912 (Hymenoptera: Formicidae). – Myrmecological News 25: 131-143.

Tab. S1: *Hylomyrma* specimens morphologically measured and morphometric data. See separately uploaded xls file.

Tab. S2: A selection of statistics summarizing the results of illumina sequencing, read assembly, and UCE capture for all specimens included in this study.

Taxon Name in Tree	Tot. Raw Reads	Tot. Contigs	Tot. Contigs Coverage (x)	Tot. Contigs Mean Length	Tot. UCE Contigs	UCE Contigs Mean Length	UCE Contigs Coverage (x)	UCE Contigs Reads on Target	UCE Contigs Unique Reads Aligned
<i>Hylomyrma_blandiens</i> _EX1598	4,868,234	57,077	6.4	391.6	2,306	880.4	42.4	47.7%	36.6%
<i>Hylomyrma_cf_dentiloba</i> _sp1_EX824	3,237,012	28294	6.3	450.5	2,251	1,030.5	25.9	56.5%	32.9%
<i>Hylomyrma_immanis</i> _EX1599	3,748,188	29,202	6.7	436.1	2,266	978.6	30.8	53.3%	33.9%
<i>Hylomyrma_montana</i> _EX1593	3,342,334	27,627	7.1	461.4	2,263	1,022.4	31.8	60.4%	36.2%
<i>Hylomyrma_montana</i> _EX1604	3,647,322	33,107	6.9	412.4	2,251	755.2	28.7	44.1%	31.2%
<i>Hylomyrma_plumosa</i> _EX1594	5,319,632	62,279	6.2	396.8	2,327	969.6	42.2	48.7%	36.8%
<i>Hylomyrma_reginae</i> _EX1600	2,976,564	24,276	7.5	466.5	2,239	910.1	29.8	59.8%	34.3%
<i>Hylomyrma_versuta</i> _EX1595	3,960,908	35,809	7.4	445.8	2,278	909.1	34.5	52.1%	34.5%
<i>Hylomyrma_versuta</i> _EX1596	5,213,394	61,366	6.8	365.9	2,352	744.0	47.8	45.1%	35.5%
<i>Hylomyrma_versuta</i> _EX1597	3,337,228	29,645	7.3	439.2	2,274	848.2	31.3	53.3%	33.9%
<i>Manica_hunteri</i> _EX809	8,764,240	137620	5.2	354.4	2,322	1,148.9	46.2	32.4%	41.0%
<i>Myrmica_incompleta</i> _EX808	2,891,086	21876	7.8	488.2	2,216	816.5	18.6	39.3%	28.9%
<i>Patagonomyrmex_angustus</i> _EX1645	9,517,342	168,201	5.2	373.2	2,305	1,185.8	60.1	38.9%	45.1%
<i>Pogonomyrmex_occidentalis</i> _EX810	3,420,086	39589	5.7	363.7	2,305	1,015.4	35.7	60.5%	37.9%
mean	4,588,826	53,998	6.6	417.6	2,283	943.9	36.1	49.4%	35.6%
min	2,891,086	21,876	5.2	354.4	2,216	744.0	18.6	32.4%	28.9%
max	9,517,342	168,201	7.8	488.2	2,352	1,185.8	60.1	60.5%	45.1%
95 CI ±	1,092,124.7	23,254.9	0.4	22.8	20.0	69.5	5.6	4.6%	2.1%

Tab. S3: A selection of statistics summarizing the UCE and COI data sets analyzed in this study.

Matrix	Taxa	Taxon Occupancy	Loci	Length (bp)	Mean Length (bp)	95 CI ±	Locus Min (bp)	Locus Max (bp)	Informative Sites	% Missing
UCE Matrix	14	95%	1,374	1,267,360	922.39	11.71	224	1,880	167,340	8.8%
COI Matrix	37	na	1	657	na	na	na	na	241	3.41%

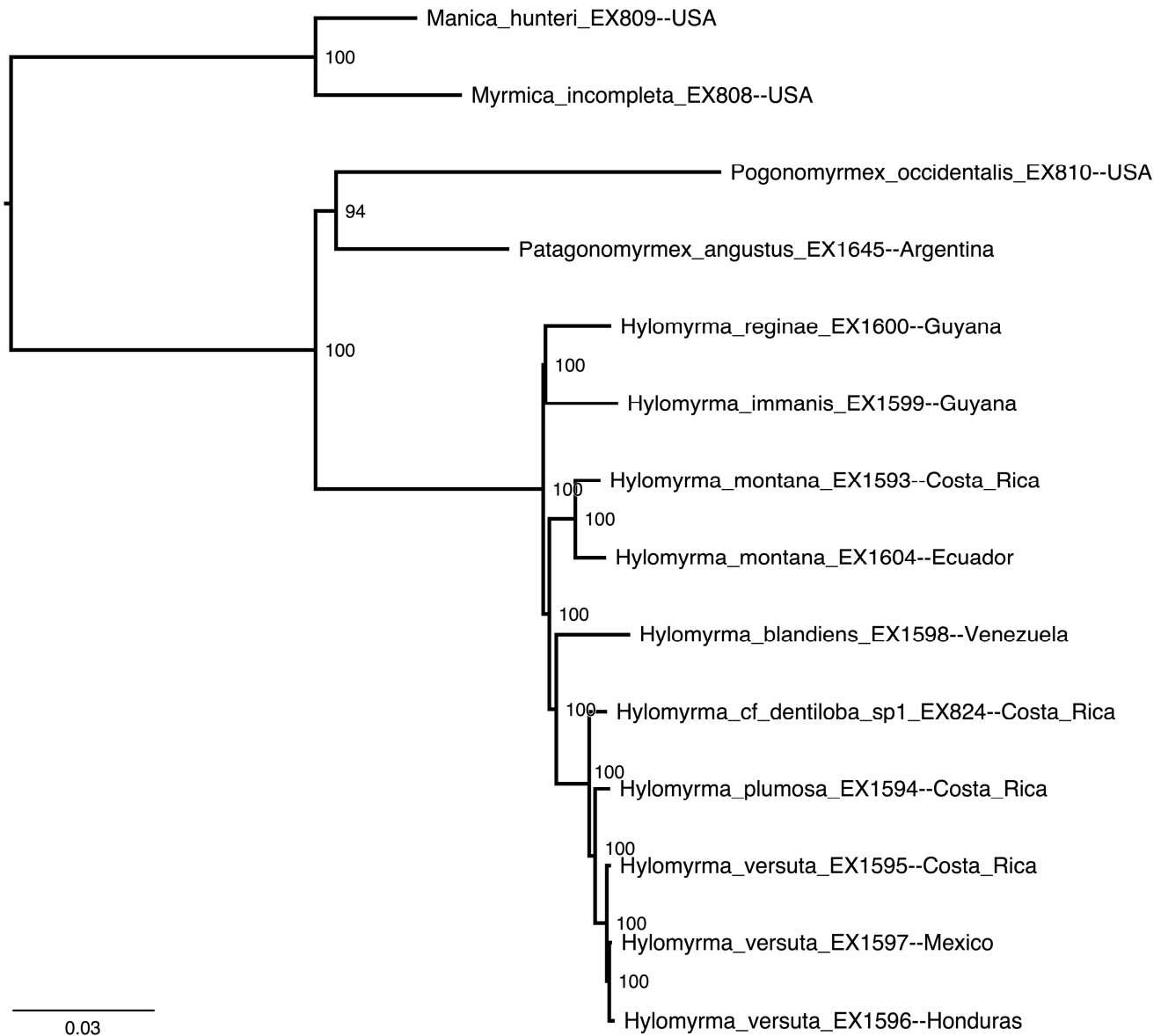


Fig. S1: Phylogenetic tree of *Hylomyrma* based on 1371 UCE loci. Tree inferred with RAxML by performing a best tree plus rapid bootstrap search on the concatenated UCE data set. Matrix partitioned using the hcluster algorithm in PartitionFinder (data pre-partitioned by locus). Partitioning by locus and unpartitioned analyses produced the same result, except with slightly lower support for *Pogonomyrmex* + *Patagonomyrmex* (92% and 89%, respectively). Node labels indicate support values from 100 bootstrap replicates.

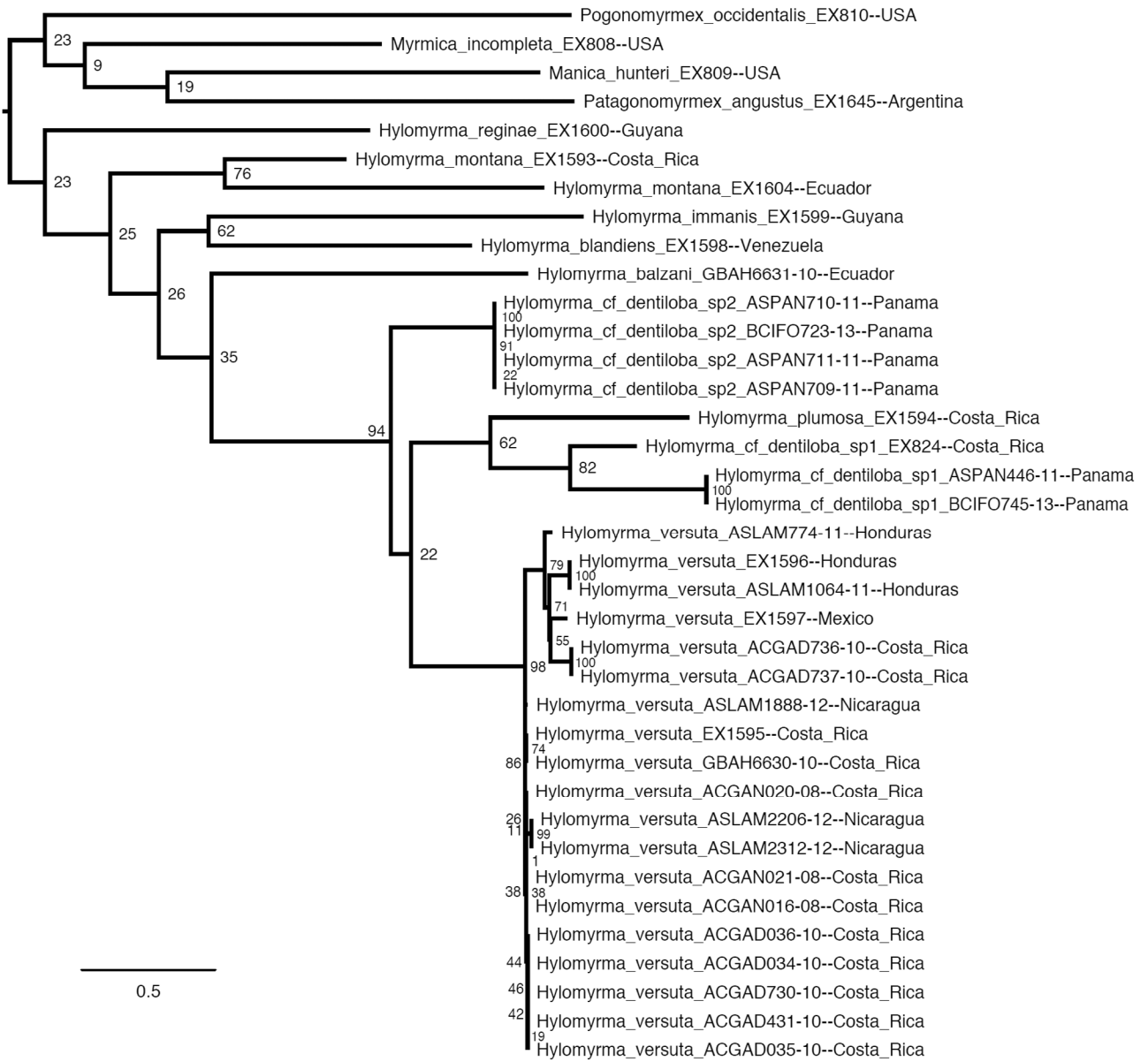


Fig. S2: Phylogenetic tree of *Hylomyrma* based on 657 bp of the barcoding gene COI. Tree inferred using RAXML with the data partitioned by codon position. Node labels indicate bootstrap support values from 100 replicates.