

The evolution of social parasitism in *Formica* ants revealed by a
global phylogeny

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Supplementary figures, tables, and references

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Supplementary Methods

Data availability

Trimmed reads generated for this study are available at the NCBI Sequence Read Archive (to be submitted upon publication). Assembled sequences, analyzed matrices, configuration files and output of all analyses, and code used are available on Zenodo (DOI: [10.5281/zenodo.4341310](https://doi.org/10.5281/zenodo.4341310)).

Taxon sampling

For this study we gathered samples collected in the past ~60 years and available as either ethanol-preserved or point-mounted specimens. Taxon sampling comprises 101 newly sequenced ingroup morphospecies from all seven species groups of *Formica* ants [Creighton \(1950\)](#) that were recognized prior to our study and 8 outgroup species. Our sampling was guided by previous taxonomic and phylogenetic work [Creighton \(1950\)](#); [Francoeur \(1973\)](#); [Snelling and Buren \(1985\)](#); [Seifert \(2000, 2002, 2004\)](#); [Goropashnaya et al. \(2004, 2012\)](#); [Trager et al. \(2007\)](#); [Trager \(2013\)](#); [Seifert and Schultz \(2009a,b\)](#); [Muñoz-López et al. \(2012\)](#); [Antonov and Bukin \(2016\)](#); [Chen and Zhou \(2017\)](#); [Romiguiet et al. \(2018\)](#) and included representatives from both the New and the Old World. Collection data associated with sequenced samples can be found in Table S1.

Molecular data collection and sequencing

Briefly, we extracted DNA from all newly sequenced specimens using a DNeasy Blood and Tissue Kit (Qiagen, Valencia, CA, USA) and followed a library preparation protocol that follows was slightly modified from [Blaimer et al. \(2015\)](#). We used a KAPA Hyper Prep Library Kit (Kapa Biosystems, Inc., Wilmington, MA, USA) with magnetic bead cleanup [Fisher et al. \(2011\)](#) and a SPRI substitute [Rohland and Reich \(2012\)](#) as described in [Faircloth et al. \(2014\)](#). We used TruSeq adapters [Faircloth and Glenn \(2012\)](#) for ligation followed by PCR amplification of the library using a mix of HiFi HotStart polymerase reaction mix (Kapa Biosystems), Illumina TruSeq primers, and nuclease-free water.

We enriched each pool with 9,446 custom-designed probes (MYcroarray, Inc.) targeting 2,524 UCE loci in Hymenoptera [Branstetter et al. \(2017\)](#). We followed library enrichment procedures for the MYcroarray MYBaits kit [Blumenstiel et al. \(2010\)](#) except we used a 0.1× of the standard MYBaits concentration and added 0.7 μL of 500 μM custom blocking oligos designed against the custom sequence tags. We ran the hybridization reaction for 24 h at 65 °C, subsequently bound all pools to streptavidin beads (MyOne C1; Life Technologies) and washed bound libraries according to a standard target enrichment protocol [Blumenstiel et al. \(2010\)](#). We used the with-bead approach for PCR recovery of enriched libraries as described in [Faircloth \(2015\)](#).

We submitted pre-pooled libraries to the University of Utah High Throughput Genomics Core Facility for quality control on Agilent Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA) and normalization. The pooled libraries were then sequenced using one full and one partial lane of a HiSeq 125 Cycle Paired-End Sequencing v4 run. Quality-trimmed sequence reads generated as part of this study are available from the NCBI Sequence Read Archive (to be submitted upon publication).

Processing of UCE data

We performed read cleaning, assembly, and matching of assembled contigs to UCE probes using Phyluce bioinformatics pipeline ([Faircloth 2015](#)). We trimmed the FASTQ data using Illumiprocessor, a wrapper around Trimmomatic [Bolger et al. \(2014\)](#), with default settings (LEADING:5, TRAILING:15, SLIDING-WINDOW:4:15, MINLEN:40). Assemblies were done using Trinity v20140717 [Grabherr et al. \(2011\)](#) with the phyluce_assembly_assemblo_trinity wrapper. We then assessed orthology by matching the assembled

contigs to enrichment probe sequences with `phyluce_assembly_match_contigs_to_probes` (`min_coverage=50`, `min_identity=80`).

Processing of UCE data

We used phylogeny-aware UPP workflow [Nguyen et al. \(2015\)](#) to align all UCE sequences. We used AMAS [Borowiec \(2016\)](#) for alignment wrangling and obtaining summary statistics and AliView [Larsson \(2014\)](#) for visualization. Although alignment trimming has been criticized in the past [Tan et al. \(2015\)](#), we decided to trim the alignments because of substantial computational burden associated with analysis of untreated data with high proportion of gaps. We used trimAl [Capella-Gutierrez et al. \(2009\)](#) and its “gappyout” algorithm, which is a relatively relaxed algorithm for removal of gappy sites. Visual inspection of alignments revealed that occasionally sequences were misaligned towards flanks. To automatically identify and discard the misaligned sequences we wrote a custom R script (R Core Team) that leveraged packages `ape` [Paradis et al. \(2004\)](#); `Paradis (2012)`, `seqinr` [Charif and Lobry \(2007\)](#), `doParallel`, and `plyr`. The script first generates a matrix of uncorrected p-distances from a UCE locus alignment and for each taxon it computes average p-distance to all other taxa. Then it creates a distribution of average per-locus p-distances for each taxon and detects outliers defined as sequences that lay above 3 SD from the mean of that distribution. Once identified, the script removes outliers using AMAS. This procedure resulted in removal of 0.97 % of all sequences. For downstream analyses we retained only alignments that had 110 or more taxa (70 % of total), resulting in 2,242 loci on average 667 nt long. The resulting concatenated matrix was 1,497,044 nt long and contained 17.58 % of missing data and gaps.

Processing of UCE data

We used ModelFinder [Kalyaanamoorthy et al. \(2017\)](#) as implemented in IQ-TREE [Nguyen et al. \(2014\)](#). For each UCE we selected the best model under AICc. These models were then used for by-locus partitioned analysis of concatenated data matrix [Chernomor et al. \(2016\)](#). We have also employed the newly proposed strategy of partitioning UCE loci based on a sliding window approach that groups UCE sites with similar entropies [Tagliacollo and Lanfear \(2018\)](#). Unfortunately, many partitions identified using this approach were saturated and caused numerical instability in maximum likelihood analyses using IQ-TREE, resulting in unreasonably long tree lengths. A detailed investigation of optimal strategies for UCE partitioning is beyond the scope of this study and although the concatenated tree had unreasonably long branches, its topology was identical to that obtained with partitioning by locus (data not shown). We therefore proceeded with downstream analyses using per-locus partitioning.

Phylogenetic and concordance analyses using maximum likelihood

We used IQ-TREE [Nguyen et al. \(2014\)](#) for maximum likelihood inference of phylogeny on single-locus alignments and concatenated data matrix. To test the robustness of the partitioned concatenated analysis, we performed unpartitioned analysis under HKY+4G model, which was the most common model identified as best under AICc for single loci. To assess the sensitivity of our results using measures other than bootstrap support we performed a quartet sampling analysis with 500 maximum replicates ([Pease et al., 2018](#)). Results are summarized in Figure S7.

Species tree analyses

In addition to concatenated analyses we performed coalescent-based species tree estimation using ASTRAL-III ([Zhang et al., 2018](#)). Because summary coalescence methods such as ASTRAL have been shown to be

negatively impacted by error in estimated gene trees [Roch and Warnow \(2015\)](#) we used the weighted statistical binning pipeline [Mirarab et al. \(2014\)](#); [Bayzid et al. \(2015\)](#). We collapsed all nodes with ultrafast bootstrap [Minh et al. \(2013\)](#) support below 95 for the binning pipeline, which resulted in identification of 1,733 supergenes containing from one to three UCE loci. We then used IQ-TREE to estimate supergene trees under a fully partitioned model (i.e. with branch lengths unlinked across partitions). Because of recent criticism of the statistical binning pipeline [Adams and Castoe \(2019\)](#) we also performed an analysis where raw trees from individual locus analyses were used. We mapped all terminals to putative species using morphology and the concatenated tree as guidance. Because some of the 101 species we recognized using morphology were non-monophyletic on the concatenated tree, we mapped the terminals onto 113 total monophyletic lineages representing putative species (Figures S4–S6). To test the effect of missing data [Sayyari et al. \(2017\)](#) on the position of *Formica talbotae* we performed additional analysis that used only the 67 loci which contained at least 50 % complete sequence for this taxon (Figure S6).

Divergence time inference

For divergence time analyses we used a node dating approach, as implemented in MCMCTree, a part of the PAML package, v4.9e [Yang \(2007\)](#). MCMCTree utilized rapid approximate likelihood computation [dos Reis and Yang \(2011\)](#), which makes it suitable for divergence dating of genome-scale data sets [dos Reis et al. \(2012\)](#). We constrained our root node with soft bounds around a conservative maximum age estimate of 79 Ma, which corresponds to the lower bound of the 95 % highest posterior density interval for that split in [Blaimer et al. \(2015\)](#). Although *Formica* has a rich fossil record, the affinity of these fossils is uncertain because, as this study shows, morphology has thus far been misleading about phylogeny. Because of this, we conservatively constrained the split of *Polyergus* and *Formica*+*Iberoformica* to be at least 34 Ma, or one of the younger estimates for the age of Baltic amber [Aleksandrova and Zaporozhets \(2008a,b\)](#). We ran each analysis unpartitioned, under the HKY+4G model for 20 million generations. We examined each run's statistics in Tracer.

Biogeographic analyses

For biogeographic inference we used BioGeoBEARS v1.1.2 [Matzke \(2013\)](#). We discretized the distribution of *Formica* species into two regions, the New World and Old World. Model selection implemented in BioGeoBEARS suggested DEC+J [Matzke \(2014\)](#) as the best-fitting model and we used it for all downstream analyses. We used 100 replicates of biogeographical stochastic maps [Dupin et al. \(2017\)](#) to estimate the number of times *Formica* dispersed between the Old and New World. We used our time-calibrated tree with taxon duplicates removed such that each species or putative species was represented by only one terminal. Results are summarized in Figure S2.

Ancestral state reconstruction

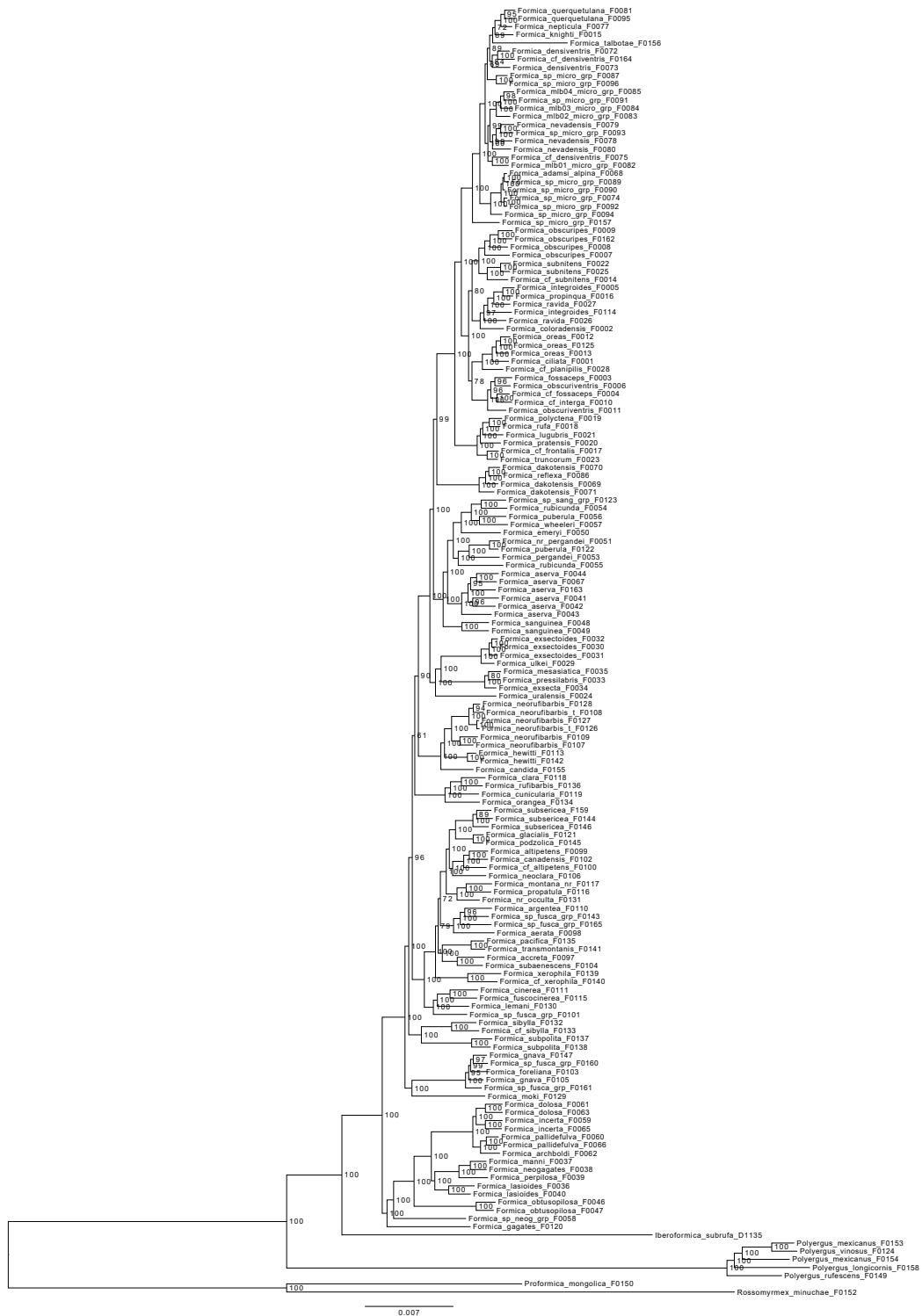
In order to investigate the evolution of natural history traits in *Formica* and *Polyergus* we used stochastic character mapping ([Huelsenbeck et al., 2003](#)). We used the same time-calibrated tree as for biogeographic analyses but with distant (*Rossomyrmex minuchae* and *Proformica mongolica*) outgroups and *Formica* taxa for which we had insufficient life history data (see Table S2) pruned.

For each species we collected literature and previously unpublished field research data on nest structure, colony structure, and colony foundation mode. We discretized nest structure into three categories: i) monodomous, ii) polydomous, and iii) supercolonial. For the analysis we assigned the highest nest structure complexity recorded, meaning that if a species is known to form monodomous, polydomous, or supercolonial nests, we characterized it as supercolonial. We discretized colony structure into i) monogynous or ii) polygynous. We assigned species to the polygynous category if they have been observed to be either monogynous

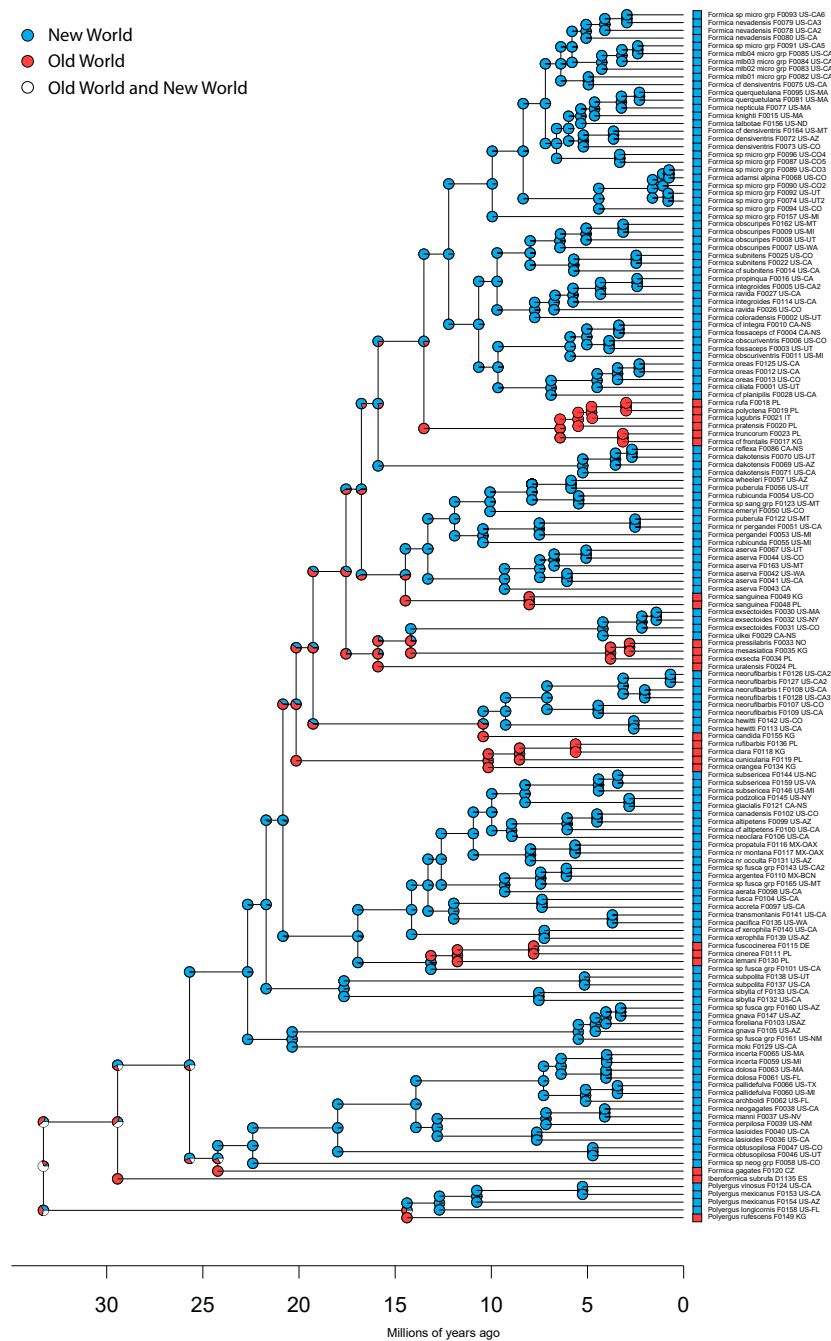
or polygynous. We discretized colony founding mode into five categories: i) independent colony foundation via haplometrosis or pleometrosis, queen readoption occurs, budding absent or at low frequency, ii) facultative temporary social parasitism with budding at low frequency, iii) facultative temporary social parasitism with budding at high frequency, iv) obligate temporary social parasitism and dulosis without budding, v) permanent social parasitism. The coding of character states for each species and references to original research articles are available in Table S2.

We performed ancestral state reconstruction on each of the three characters (nest structure, colony structure, and colony founding). We first compared three commonly-used variants of the discrete character evolution Mk model (Lewis, 2001): all rates equal (character state change rates are equal for all states), symmetric transition rates (character state change rates are different for each pair of states), and all rates different (character state change rates are different for each transition). We also fit the meristic model (assuming characters change in step-wise fashion). We fit these four models using "fit" functions the R package GEIGER v2.0.6 (Harmon et al., 2007) to all three characters. We used Akaike Information Criterion corrected for sample size (AICc) weights as computed by the "aic.w" function in Phytools v0.6-44 (Revell, 2011) to see which model fit best. This approach identified the all rates different model to be the best fit for nest and colony structure and the symmetric model was found best-fitting for colony founding.

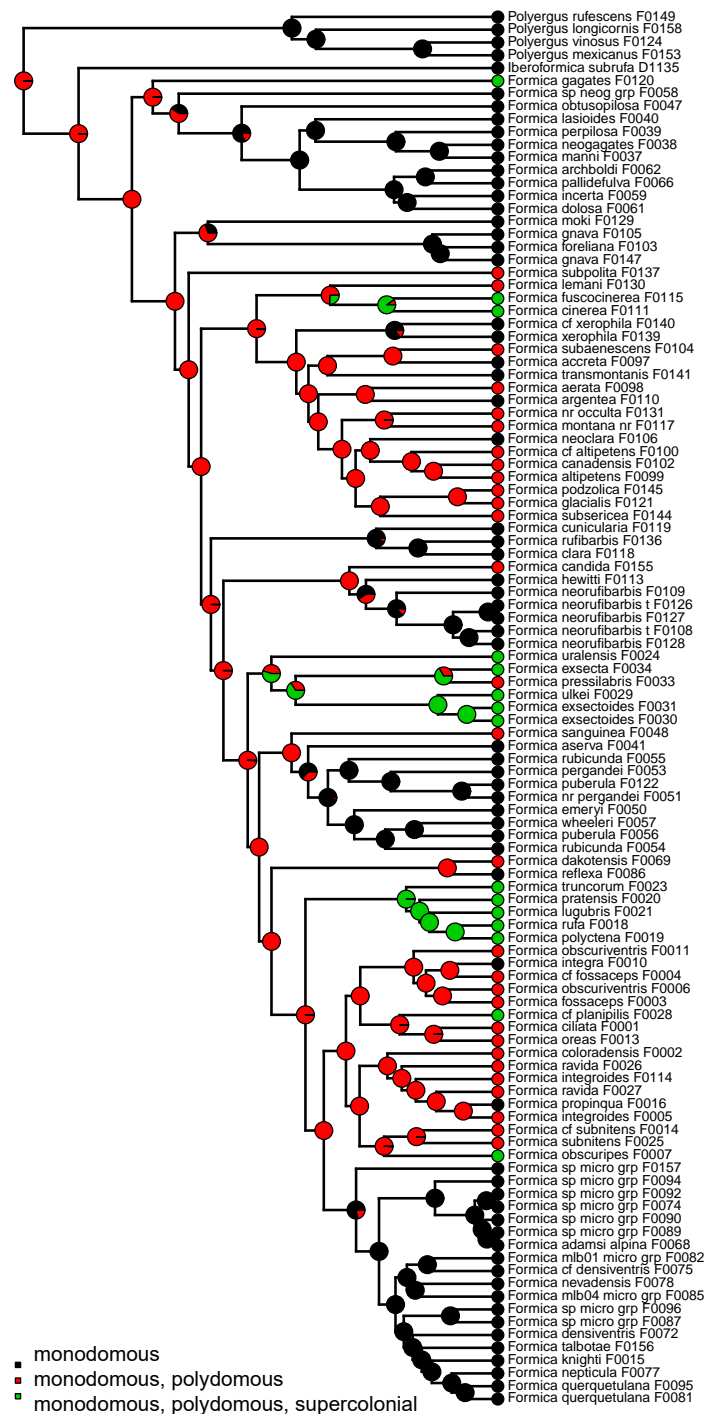
Ancestral reconstruction results are found in Figures S3-S5.



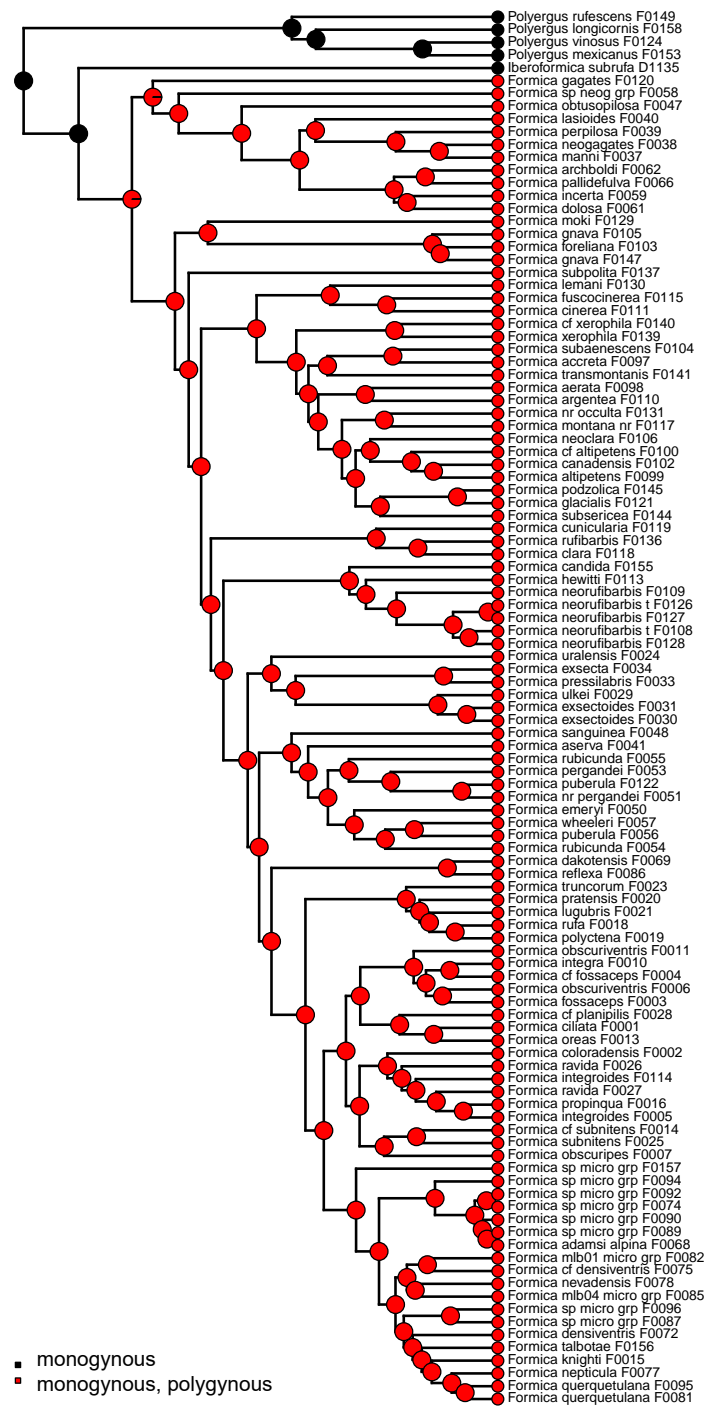
Supplementary Figure S1: Phylogram of *Formica* and outgroups from concatenated alignment inferred under maximum likelihood using IQ-TREE. Support in ultrafast bootstrap (values above 95 indicate strong support). Scale in substitutions per site.



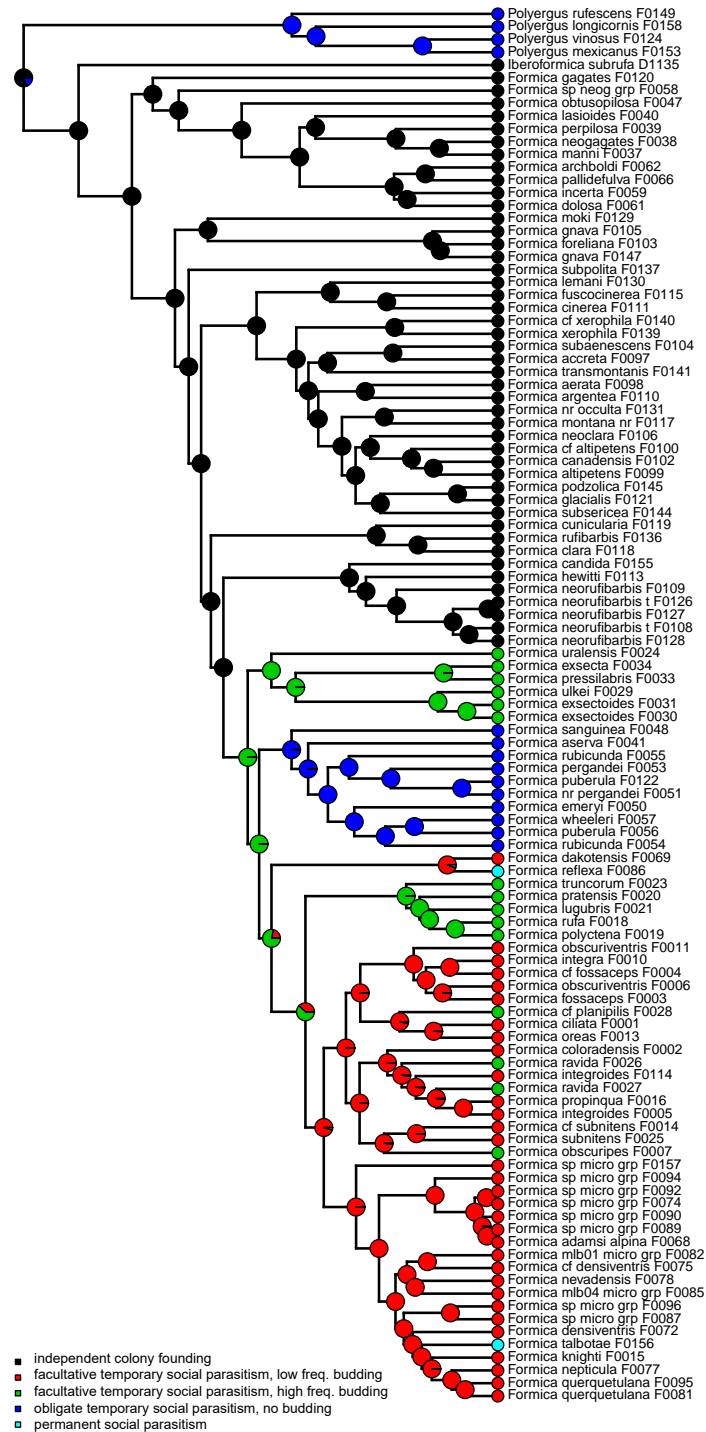
Supplementary Figure S2: Biogeographic history of *Formica*, *Iberoformica* and *Polyergus*. Pie charts depict relative likelihoods of range estimations from BioGeoBEARS under DEC+J. Pie charts at nodes correspond to ancestral state estimations and charts on the corners correspond to ranges immediately following speciation. Numbers preceded by the letter F indicate extraction code and correspond to identifiers in Table S1. Country and state/province codes as in main text Figure 1.



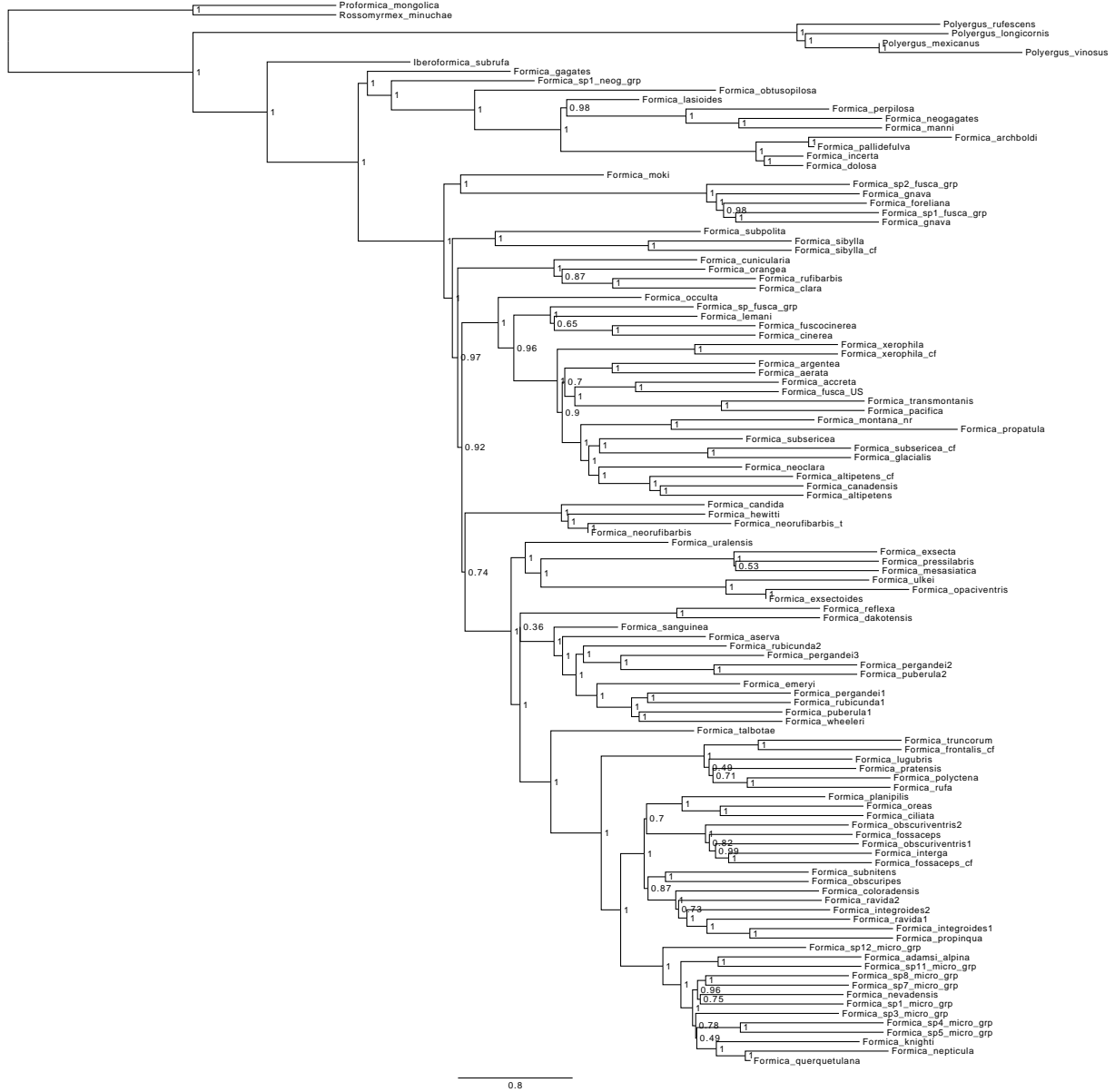
Supplementary Figure S3: Ancestral state reconstruction of nest structure using stochastic character mapping in Phytools of *Formica* nest structure under all rates different model. Pie charts at nodes correspond to ancestral state estimations and circles at tips correspond to states extant species. Numbers preceded by the letter F indicate extraction code and correspond to identifiers in Tables S1 and S2.



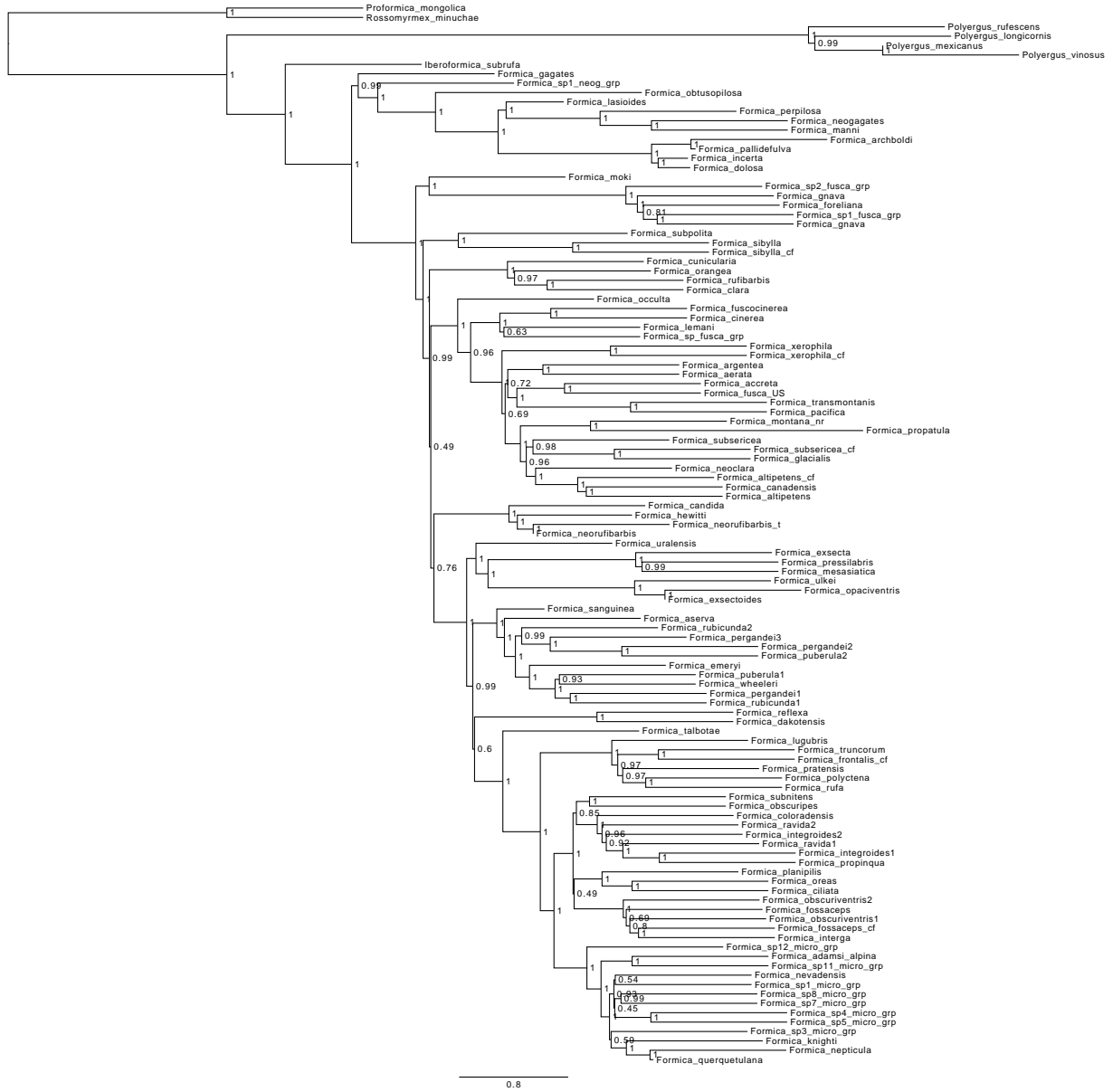
Supplementary Figure S4: Ancestral state reconstruction of colony structure using stochastic character mapping in Phytools of *Formica* colony structure under all rates different model. Pie charts at nodes correspond to ancestral state estimations and circles at tips correspond to states extant species. Numbers preceded by the letter F indicate extraction code and correspond to identifiers in Tables S1 and S2.



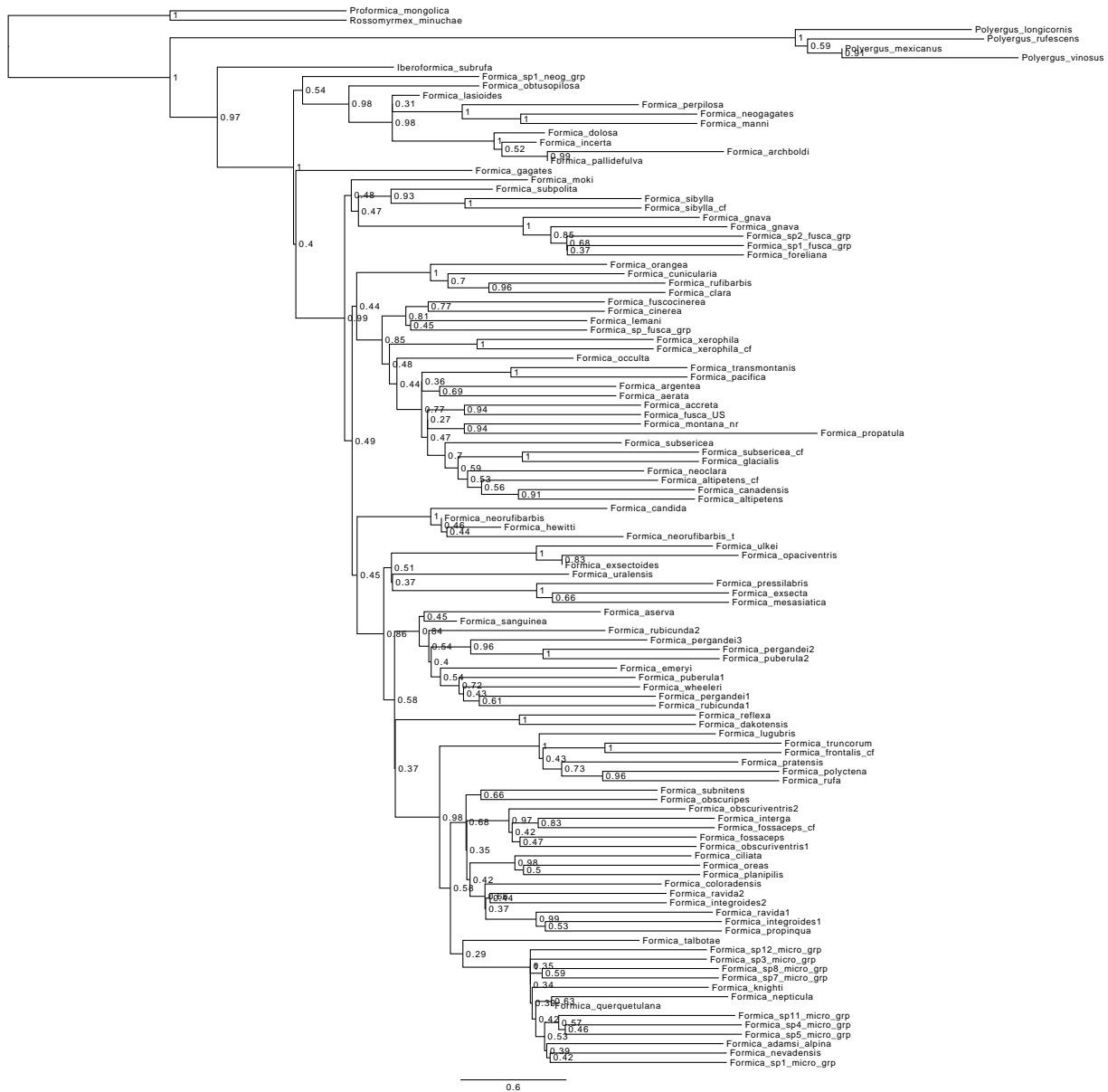
Supplementary Figure S5: Ancestral state reconstruction of colony founding mode using stochastic character mapping in Phytol of *Formica* colony founding under symmetrical rates model. Pie charts at the nodes correspond to ancestral state estimations and circles at tips correspond to states extant species. Numbers preceded by the letter F indicate extraction code and correspond to identifiers in Table S1 and S2.



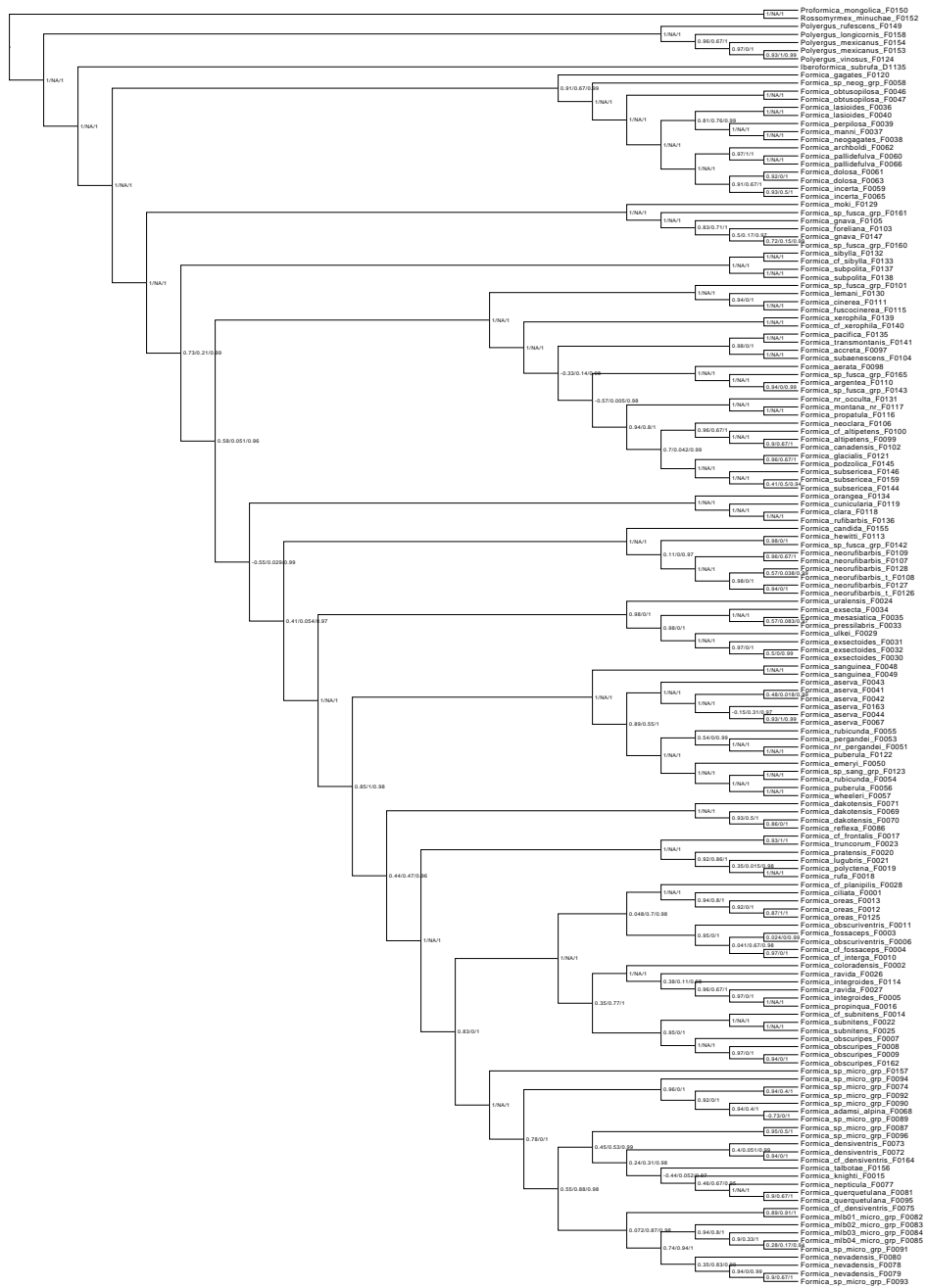
Supplementary Figure S6: Species tree inferred under coalescent using ASTRAL-III and 1,733 weighted supergene trees identified using statistical binning pipeline. Support is expressed in local posterior probability and branch lengths are in coalescent units.



Supplementary Figure S7: Species tree inferred under coalescent using ASTRAL-III and all 2,242 individual UCE locus trees. Support is expressed in local posterior probability and branch lengths are in coalescent units.



Supplementary Figure S8: Species tree inferred under coalescent using ASTRAL-III and 67 individual UCE locus trees for which at least 50 % of sequence length was available for *Formica talbotae*. Support is expressed in local posterior probability and branch lengths are in coalescent units.



Supplementary Figure S9: Support from quartet sampling analyses. The values are: quartet concordance score (QC) / quartet differential score (QD) / quartet informativeness score (QI). Briefly, QC measures how often the concordant quartet topologies are inferred over discordant quartets in different replicates, with a value equal 1 when all replicates result in concordant topology, QD measures whether frequencies of two discordant topologies are equal (=1) or skewed (<1), and QI measures what proportion of replicates were informative. Contrast values for colony dependent clade or monophyly of *difficilis* group (1/NA/1), meaning that all replicates were informative and resulted in the same topology with support for placement of clade of Palearctic species related to *Formica rufibarbis* (-0.55/0.029/0.99) indicating that discordant topologies were inferred more often than those concordant with the input tree, that quartet topologies were highly skewed, but most replicates were informative. The former indicates maximal support, while the latter shows that the position of this clade within the "fusca grade" is highly uncertain, perhaps due to incomplete lineage sorting.

Supplementary Table S1: Voucher specimens used in this study.

Extraction ID	Taxon	Specimen ID	Country	Latitude	Longitude
D1135	Iberoformica subrufa	ASU-SIBR2148	ES	37.185	-3.485
F0001	Formica ciliata	ASU-SIBR2001	US	38.26117	-112.51433
F0002	Formica coloradensis	ASU-SIBR2002	US	38.42233	-109.18017
F0003	Formica fossiceps	ASU-SIBR2003	US	38.39467	-109.165
F0004	Formica cf fossiceps	ASU-SIBR2004	CA	44.53050	-64.31912
F0005	Formica integroides	ASU-SIBR2005	US	38.67525	-119.99428
F0006	Formica obscuriventris	ASU-SIBR2006	US	39.12017	-107.44767
F0007	Formica obscuripes	ASU-SIBR2007	US	48.1728	-122.6714
F0008	Formica obscuripes	ASU-SIBR2008	US	38.23367	-112.44917
F0009	Formica obscuripes	ASU-SIBR2009	US	42.44788	-84.01688
F0010	Formica cf interga	ASU-SIBR2010	CA	44.68839	-63.66808
F0011	Formica obscuriventris	ASU-SIBR2011	US	42.45103	-84.01878
F0012	Formica oreas	ASU-SIBR2012	US	38.67577	-119.99431
F0013	Formica oreas	ASU-SIBR2013	US	38.84233	-106.53817
F0014	Formica cf subnitens	ASU-SIBR2014	US	38.67757	-119.98343
F0015	Formica knighti	ASU-SIBR2015	US	41.8652	-70.64777
F0016	Formica propinqua	ASU-SIBR2016	US	39.44008	-120.32349
F0017	Formica cf frontalis	ASU-SIBR2017	KG	42.8	77.47
F0018	Formica rufa	ASU-SIBR2018	PL	51.155	16.985
F0019	Formica polycтена	ASU-SIBR2019	PL	51.39	17.5
F0020	Formica pratensis	ASU-SIBR2020	PL	51.3867	16.805
F0021	Formica lugubris	ASU-SIBR2021	IT	46.586	12.105
F0022	Formica subnitens	ASU-SIBR2022	US	39.82308	-120.13748
F0023	Formica truncorum	ASU-SIBR2023	PL	50.33	16.55
F0024	Formica uralensis	ASU-SIBR2024	PL	51.38	23.55
F0025	Formica subnitens	ASU-SIBR2025	US	39.591	-108.818
F0026	Formica ravida	ASU-SIBR2026	US	39.1695	-107.94817
F0027	Formica ravida	ASU-SIBR2027	US	39.43221	-120.24265
F0028	Formica cf planipilis	ASU-SIBR2028	US	40.72538	-120.20708
F0029	Formica ulkei	ASU-SIBR2029	CA	44.49808	-63.92692
F0030	Formica exsectoides	ASU-SIBR2030	US	41.87383	-70.65183
F0031	Formica exsectoides	ASU-SIBR2031	US	38.73367	-104.896
F0032	Formica exsectoides	ASU-SIBR2032	US	43.01548	-77.57365
F0033	Formica pressilabris	ASU-SIBR2033	SE	68.3381	18.7639
F0034	Formica exsecta	ASU-SIBR2034	PL	50.577	22.984
F0035	Formica mesasiatica	ASU-SIBR2035	KG	42.33	78.24
F0036	Formica lasioides	ASU-SIBR2036	US	33.18522	-116.28849
F0037	Formica manni	ASU-SIBR2037	US	41.63632	-119.84183
F0038	Formica neogagates	ASU-SIBR2038	US	39.42998	-120.24087
F0039	Formica perpilosa	ASU-SIBR2039	US	31.83945	-109.03615
F0040	Formica lasioides	ASU-SIBR2040	US	39.43163	-120.24059
F0041	Formica aserva	ASU-SIBR2041	US	37.68319	-119.17078
F0042	Formica aserva	ASU-SIBR2042	US	48.66648	-122.96887
F0043	Formica aserva	ASU-SIBR2043	CA	44.46380	-63.58094
F0044	Formica aserva	ASU-SIBR2044	US	38.81400	-106.28217
F0046	Formica obtusopilosa	ASU-SIBR2046	US	38.71217	-111.94833
F0047	Formica obtusopilosa	ASU-SIBR2047	US	39.50633	-108.76217
F0048	Formica sanguinea	ASU-SIBR2048	PL	50.448	19.995
F0049	Formica sanguinea	ASU-SIBR2049	KG	42.67	77.18
F0050	Formica emeryi	ASU-SIBR2050	US	39.03167	-104.79633
F0051	Formica nr pergandei	ASU-SIBR2051	US	39.21529	-121.04322
F0053	Formica pergandei	ASU-SIBR2053	US	42.45278	-84.01939
F0054	Formica rubicunda	ASU-SIBR2054	US	39.03033	-105.44217
F0055	Formica rubicunda	ASU-SIBR2055	US	42.45919	-84.01429
F0056	Formica puberula	ASU-SIBR2056	US	37.88800	-109.45433
F0057	Formica wheeleri	ASU-SIBR2057	US	31.91433	-109.271
F0058	Formica sp neog grp	ASU-SIBR2058	US	37.84367	-109.36967
F0059	Formica incerta	ASU-SIBR2059	US	42.45151	-84.01901
F0060	Formica pallidefulva	ASU-SIBR2060	US	42.45948	-84.0256
F0061	Formica dolosa	ASU-SIBR2061	US	30.35995	-84.41848
F0062	Formica archboldi	ASU-SIBR2062	US	30.35995	-84.41848
F0063	Formica dolosa	ASU-SIBR2063	US	41.81444	-70.66315
F0065	Formica incerta	ASU-SIBR2065	US	41.8652	-70.64777

Supplementary Table S1: Voucher specimens used in this study, continued.

Extraction ID	Taxon	Specimen ID	Country	Latitude	Longitude
F0066	<i>Formica pallidefulva</i>	ASU-SIBR2066	US	30.2275	-98.1788
F0067	<i>Formica aserva</i>	ASU-SIBR2067	US	38.66283	-111.94117
F0068	<i>Formica adamsi alpina</i>	ASU-SIBR2068	US	38.39317	-107.19683
F0069	<i>Formica dakotensis</i>	ASU-SIBR2069	US	34.02867	-109.1855
F0070	<i>Formica dakotensis</i>	ASU-SIBR2070	US	38.63500	-111.94817
F0071	<i>Formica dakotensis</i>	ASU-SIBR2071	US	39.41344	-120.32162
F0072	<i>Formica densiventris</i>	ASU-SIBR2072	US	32.65729	-109.85841
F0073	<i>Formica densiventris</i>	ASU-SIBR2073	US	39.75867	-108.78783
F0074	<i>Formica sp micro grp</i>	ASU-SIBR2074	US	38.64883	-111.94983
F0075	<i>Formica cf densiventris</i>	ASU-SIBR2075	US	38.21541	-119.74609
F0077	<i>Formica nepticala</i>	ASU-SIBR2077	US	41.87367	-70.65233
F0078	<i>Formica nevadensis</i>	ASU-SIBR2078	US	39.35788	-122.74716
F0079	<i>Formica nevadensis</i>	ASU-SIBR2079	US	41.56204	-123.21177
F0080	<i>Formica nevadensis</i>	ASU-SIBR2080	US	39.41318	-120.32038
F0081	<i>Formica querquetulana</i>	ASU-SIBR2081	US	41.87383	-70.65183
F0082	<i>Formica mlb01 micro grp</i>	ASU-SIBR2082	US	37.21317	-118.64671
F0083	<i>Formica mlb02 micro grp</i>	ASU-SIBR2083	US	40.94628	-123.0427
F0084	<i>Formica mlb03 micro grp</i>	ASU-SIBR2084	US	39.29111	-120.67918
F0085	<i>Formica mlb04 micro grp</i>	ASU-SIBR2085	US	39.40022	-120.55818
F0086	<i>Formica reflexa</i>	ASU-SIBR2086	CA	44.53050	-64.31912
F0087	<i>Formica sp micro grp</i>	ASU-SIBR2087	US	38.42033	-107.62783
F0089	<i>Formica sp micro grp</i>	ASU-SIBR2089	US	38.18833	-107.62067
F0090	<i>Formica sp micro grp</i>	ASU-SIBR2090	US	38.83800	-106.56167
F0091	<i>Formica sp micro grp</i>	ASU-SIBR2091	US	38.83800	-106.56167
F0092	<i>Formica sp micro grp</i>	ASU-SIBR2092	US	38.64983	-111.95083
F0093	<i>Formica sp micro grp</i>	ASU-SIBR2093	US	41.56204	-123.21177
F0094	<i>Formica sp micro grp</i>	ASU-SIBR2094	US	38.838	-106.56167
F0095	<i>Formica querquetulana</i>	ASU-SIBR2095	US	41.87167	-70.651
F0096	<i>Formica sp micro grp</i>	ASU-SIBR2096	US	39.04167	-104.6615
F0097	<i>Formica accreta</i>	ASU-SIBR2097	US	39.30805	-120.66831
F0098	<i>Formica aerata</i>	ASU-SIBR2098	US	37.80145	-118.5299
F0099	<i>Formica altipetens</i>	ASU-SIBR2099	US	33.90683	-109.1245
F0100	<i>Formica cf altipetens</i>	ASU-SIBR2100	US	38.6739	-119.99411
F0101	<i>Formica sp fusca grp</i>	ASU-SIBR2101	US	37.38932	-118.76612
F0102	<i>Formica canadensis</i>	ASU-SIBR2102	US	39.12017	-107.44
F0103	<i>Formica foreliana</i>	ASU-SIBR2103	US	31.43100	-111.16967
F0104	<i>Formica subaenescens</i>	ASU-SIBR2104	US	37.92051	-122.57471
F0105	<i>Formica gnava</i>	ASU-SIBR2105	US	32.64983	-109.81717
F0106	<i>Formica neoclara</i>	ASU-SIBR2106	US	39.50332	-120.24157
F0107	<i>Formica neurufibarbis</i>	ASU-SIBR2107	US	38.71467	-106.223
F0108	<i>Formica neurufibarbis t</i>	ASU-SIBR2108	US	36.67239	-118.34463
F0109	<i>Formica neurufibarbis</i>	ASU-SIBR2109	US	39.42505	-120.24285
F0110	<i>Formica argentea</i>	ASU-SIBR2110	MX	31.00261	-115.5497
F0111	<i>Formica cinerea</i>	ASU-SIBR2111	PL	51.39	17.5
F0113	<i>Formica hewitti</i>	ASU-SIBR2113	US	38.67984	-119.98373
F0114	<i>Formica integroides</i>	ASU-SIBR2114	US	40.11490	-120.32086
F0115	<i>Formica fuscocinerea</i>	ASU-SIBR2115	DE	48.16452	11.50075
F0116	<i>Formica proapatula</i>	ASU-SIBR2116	MX	17.1873	-96.62085
F0117	<i>Formica montana nr</i>	ASU-SIBR2117	MX	17.61752	-96.36799
F0118	<i>Formica clara</i>	ASU-SIBR2118	KG	42.66	77.47
F0119	<i>Formica cunicularia</i>	ASU-SIBR2119	PL	51.175	17.068
F0120	<i>Formica gagates</i>	ASU-SIBR2120	CZ	48.869	16.652
F0121	<i>Formica glacialis</i>	ASU-SIBR2121	CA	44.98735	-64.06002
F0122	<i>Formica puberula</i>	ASU-SIBR2122	US	45.0446	-110.68078
F0123	<i>Formica sp sang grp</i>	ASU-SIBR2123	US	45.13217	-111.06283
F0124	<i>Polyergus vinosus</i>	ASU-SIBR2124	US	32.85323	-116.43738
F0125	<i>Formica oreas</i>	ASU-SIBR2125	US	38.05273	-119.32138
F0126	<i>Formica neurufibarbis t</i>	ASU-SIBR2126	US	38.06165	-119.34966
F0127	<i>Formica neurufibarbis</i>	ASU-SIBR2127	US	38.06207	-119.34888
F0128	<i>Formica neurufibarbis</i>	ASU-SIBR2128	US	38.04167	-119.29781
F0129	<i>Formica moki</i>	ASU-SIBR2129	US	38.9	-121.02
F0130	<i>Formica lemani</i>	ASU-SIBR2130	PL	50.33	16.55

Supplementary Table S1: Voucher specimens used in this study, continued.

Extraction ID	Taxon	Specimen ID	Country	Latitude	Longitude
F0131	<i>Formica nr occulta</i>	ASU-SIBR2131	US	31.91375	-109.26757
F0132	<i>Formica sibylla</i>	ASU-SIBR2132	US	39.43221	-120.24258
F0133	<i>Formica cf sibylla</i>	ASU-SIBR2133	US	39.431	-120.331
F0134	<i>Formica orangea</i>	ASU-SIBR2134	KG	42.6	75.85
F0135	<i>Formica pacifica</i>	ASU-SIBR2135	US	48.1728	-122.6714
F0136	<i>Formica rufibarbis</i>	ASU-SIBR2136	PL	52.76917	14.30778
F0137	<i>Formica subpolita</i>	ASU-SIBR2137	US	39.50444	-120.23817
F0138	<i>Formica subpolita</i>	ASU-SIBR2138	US	38.72450	-112.20717
F0139	<i>Formica xerophila</i>	ASU-SIBR2139	US	35.80350	-112.11767
F0140	<i>Formica cf xerophila</i>	ASU-SIBR2140	US	38.85876	-122.41834
F0141	<i>Formica transmontanis</i>	ASU-SIBR2141	US	39.188	-123.757
F0142	<i>Formica sp fusca grp</i>	ASU-SIBR2142	US	38.83767	-106.55933
F0143	<i>Formica sp fusca grp</i>	ASU-SIBR2143	US	39.21533	-121.04019
F0144	<i>Formica subsericea</i>	ASU-SIBR2144	US	35.695	-78.69688
F0145	<i>Formica podzolica</i>	ASU-SIBR2145	US	43.01616	-77.57632
F0146	<i>Formica subsericea</i>	ASU-SIBR2146	US	42.45103	-84.01885
F0147	<i>Formica gnava</i>	ASU-SIBR2147	US	31.93200	-109.17783
F0149	<i>Polyergus rufescens</i>	ASU-SIBR2150	KG	42.67	77.18
F0150	<i>Proformica mongolica</i>	ASU-SIBR2151	KG	42.77	74.66
F0152	<i>Rossomyrmex minuchae</i>	ASU-SIBR2153	ES	36.89	-2.78
F0153	<i>Polyergus mexicanus</i>	ASU-SIBR2154	US	39.41591	-120.31704
F0154	<i>Polyergus mexicanus</i>	ASU-SIBR2155	US	31.90882	-109.25211
F0155	<i>Formica candida</i>	ASU-SIBR2156	KG	42.08	76.73
F0156	<i>Formica talbotae</i>	ASU-SIBR2157	US	43.38	-95.185
F0157	<i>Formica sp micro grp</i>	ASU-SIBR2158	US	42.45947	-84.02559
F0158	<i>Polyergus longicornis</i>	ASU-SIBR2159	US	30.35995	-84.41848
F0159	<i>Formica subsericea</i>	ASU-SIBR2160	US	38.9879	-77.2495
F0160	<i>Formica sp fusca grp</i>	ASU-SIBR2161	US	31.8729	-109.23504
F0161	<i>Formica sp fusca grp</i>	ASU-SIBR2162	US	32.59105	-107.97398
F0162	<i>Formica obscuripes</i>	ASU-SIBR2163	US	48.03381	-110.22798
F0163	<i>Formica aserva</i>	ASU-SIBR2164	US	46.7059	-114.53617
F0164	<i>Formica cf densiventris</i>	ASU-SIBR2165	US	38.10233	-111.33653
F0165	<i>Formica sp fusca grp</i>	ASU-SIBR2166	US	48.52302	-113.3808

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