

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). Detailed voucher collection information, 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 which were 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 \(2017\)](#); [Romiguier 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*

We performed non-destructive extraction and preserved same-specimen vouchers for each newly sequenced sample. We re-mounted all vouchers, assigned unique specimen identifiers (Table S1), and deposited them in the ASU Social Insect Biodiversity Repository (contact: Christian Rabeling, [christian.rabeling@asu.edu](mailto:christian.rabeling@asu.edu)). Detailed voucher collection data can be accessed at [10.5281/zenodo.4341310](https://doi.org/10.5281/zenodo.4341310). 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 acceptance for 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\_assemble\_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).

### *Alignment*

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.

### *Partitioning*

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. 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.

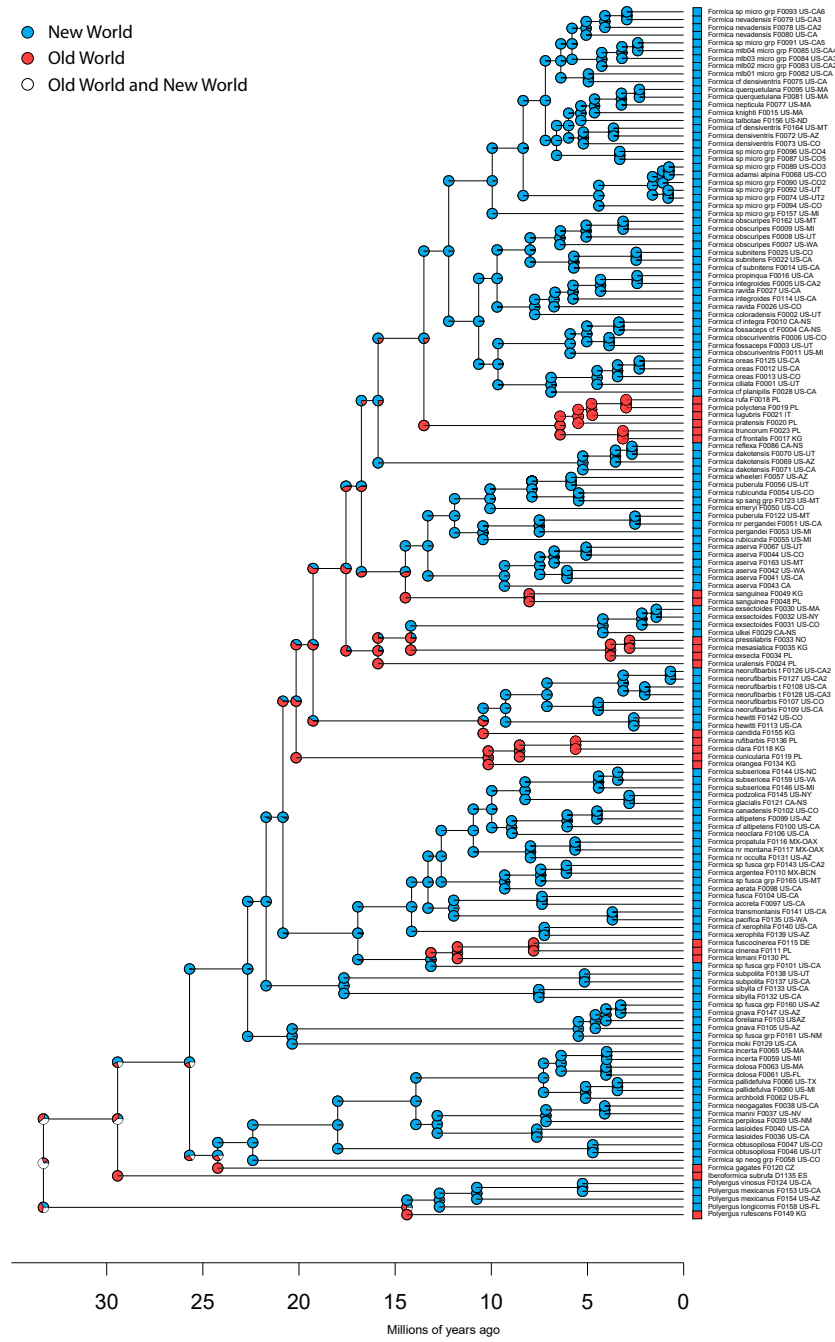
For each species we collected literature and previously unpublished field research data on nest structure, colony structure, and colony foundation mode. We discretized nest structure into three categories: i)

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.

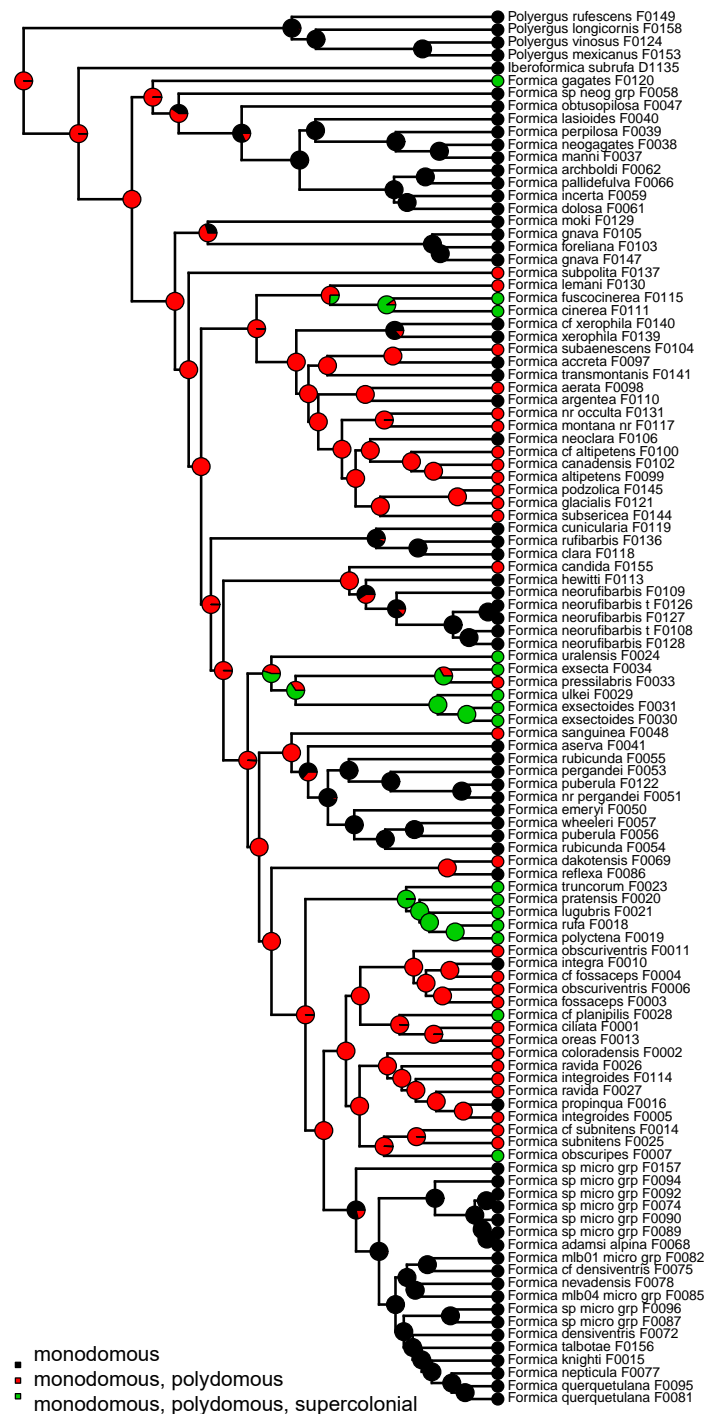
We performed ancestral state reconstruction on each of the three characters (nest structure, colony structure, and colony founding). We first compared three commonly-used variants of the discrete character evolution Mk model (Lewis, 2001): all rates equal (character state change rates are equal for all 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.



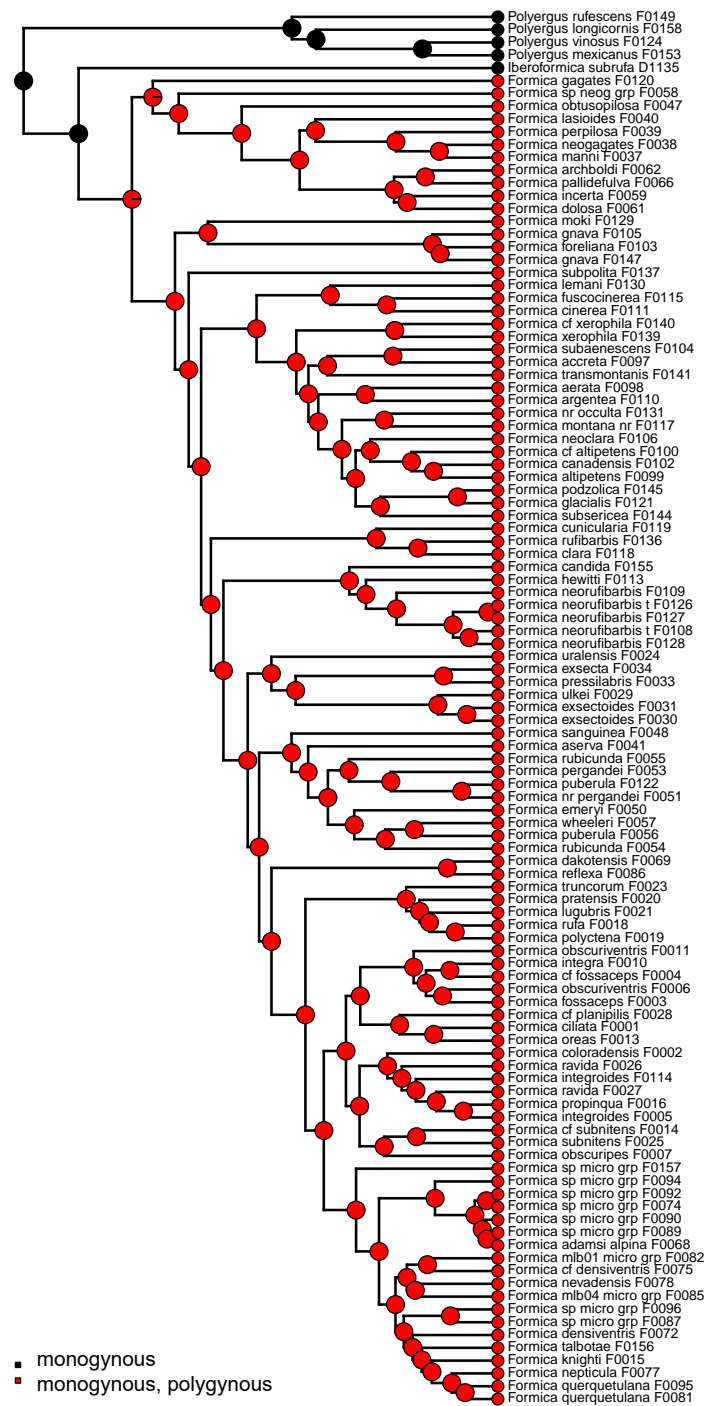


Supplementary Figure S2: Biogeographic history of *Formica*, *Iberoformica* and *Polyergus*. Pie charts depict relative likelihoods of range estimations from BioGeoBEARS under DEC+J. Pie charts at nodes correspond to ancestral state estimations and charts on the corners correspond to ranges immediately 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.

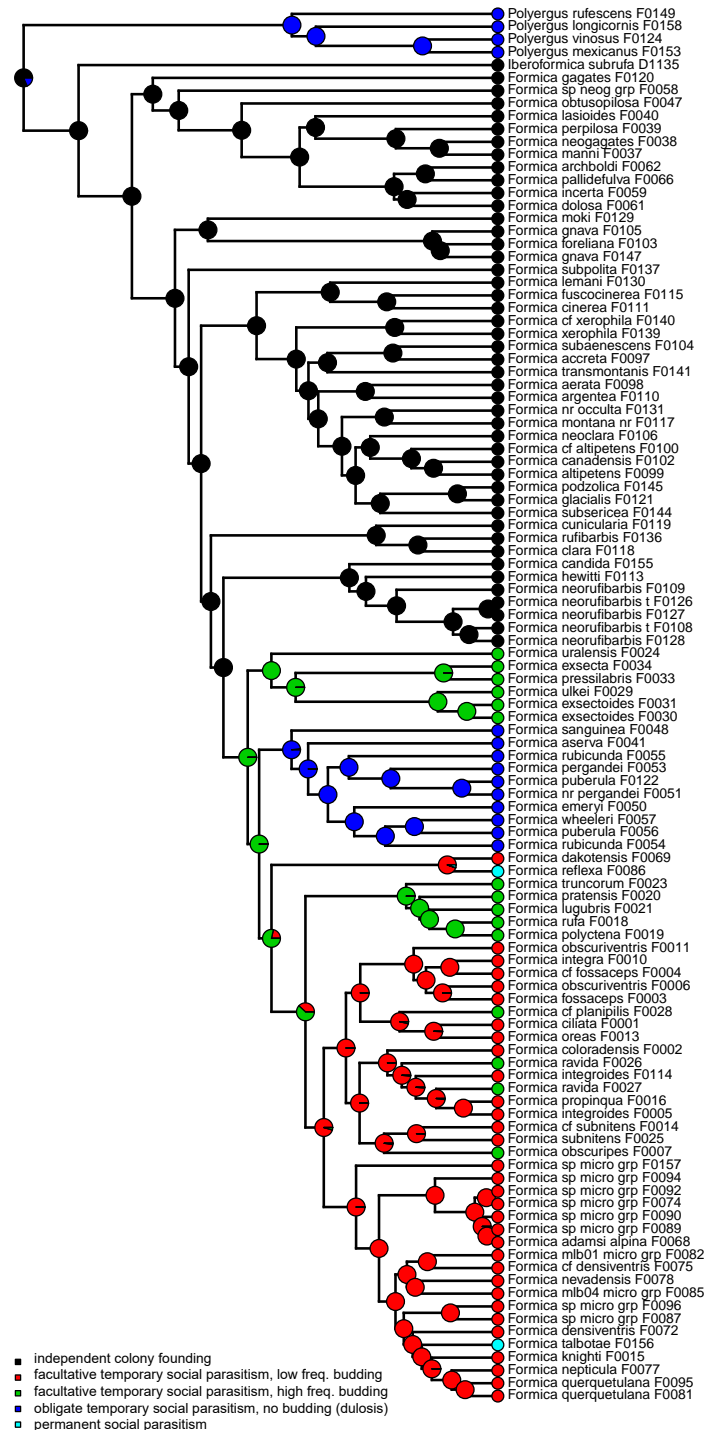


Supplementary Figure S3: Ancestral state reconstruction of nest structure using stochastic character mapping in Phytools of *Formica* nest structure under all rates different model. Pie charts at nodes correspond to ancestral state estimations and circles at tips correspond to states extant species.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





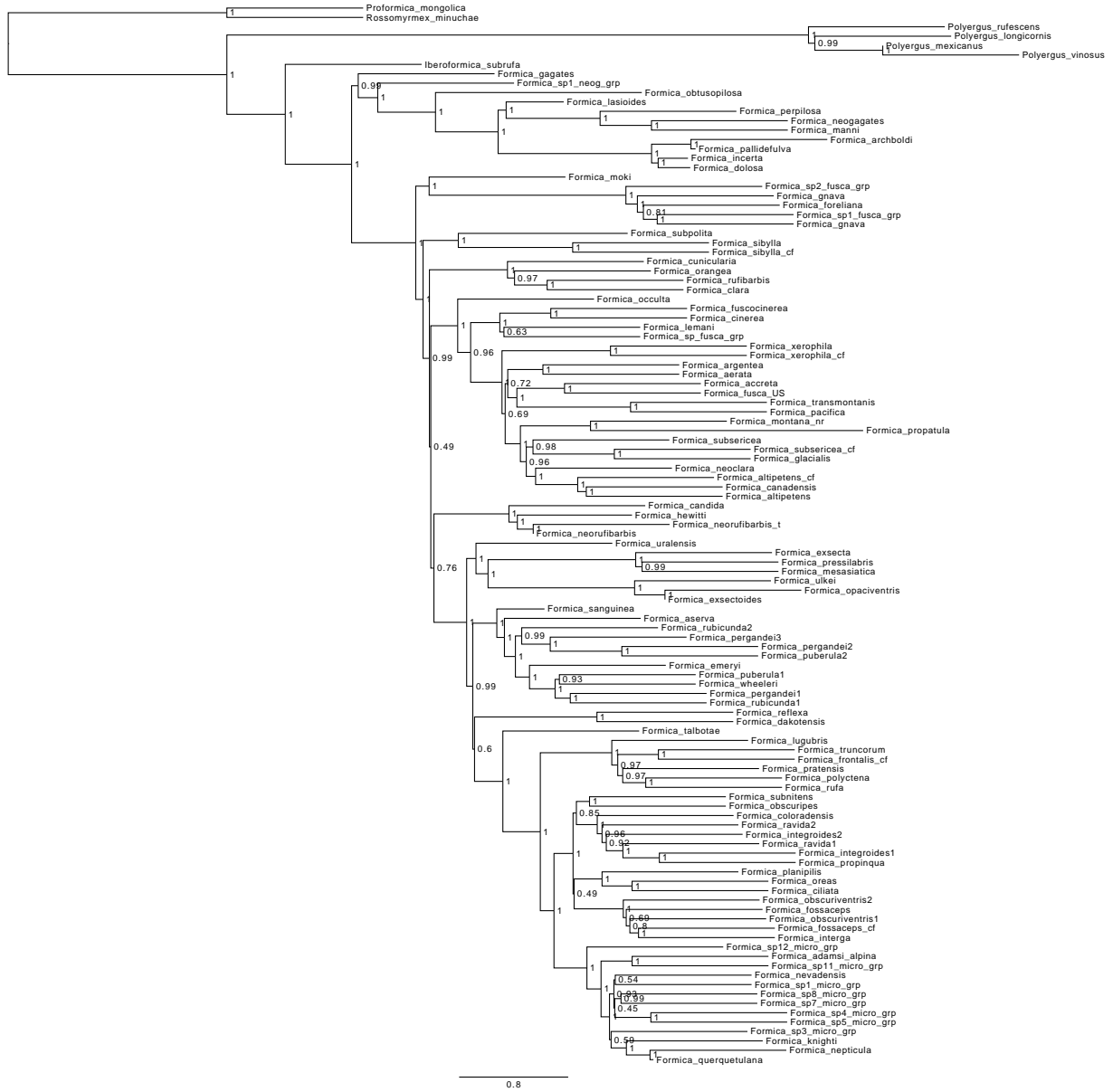
Supplementary Figure S4: Ancestral state reconstruction of colony structure using stochastic character mapping in Phytools of *Formica* colony structure under all rates different model. Pie charts at nodes correspond to ancestral state estimations and circles at tips correspond to states extant species. 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.



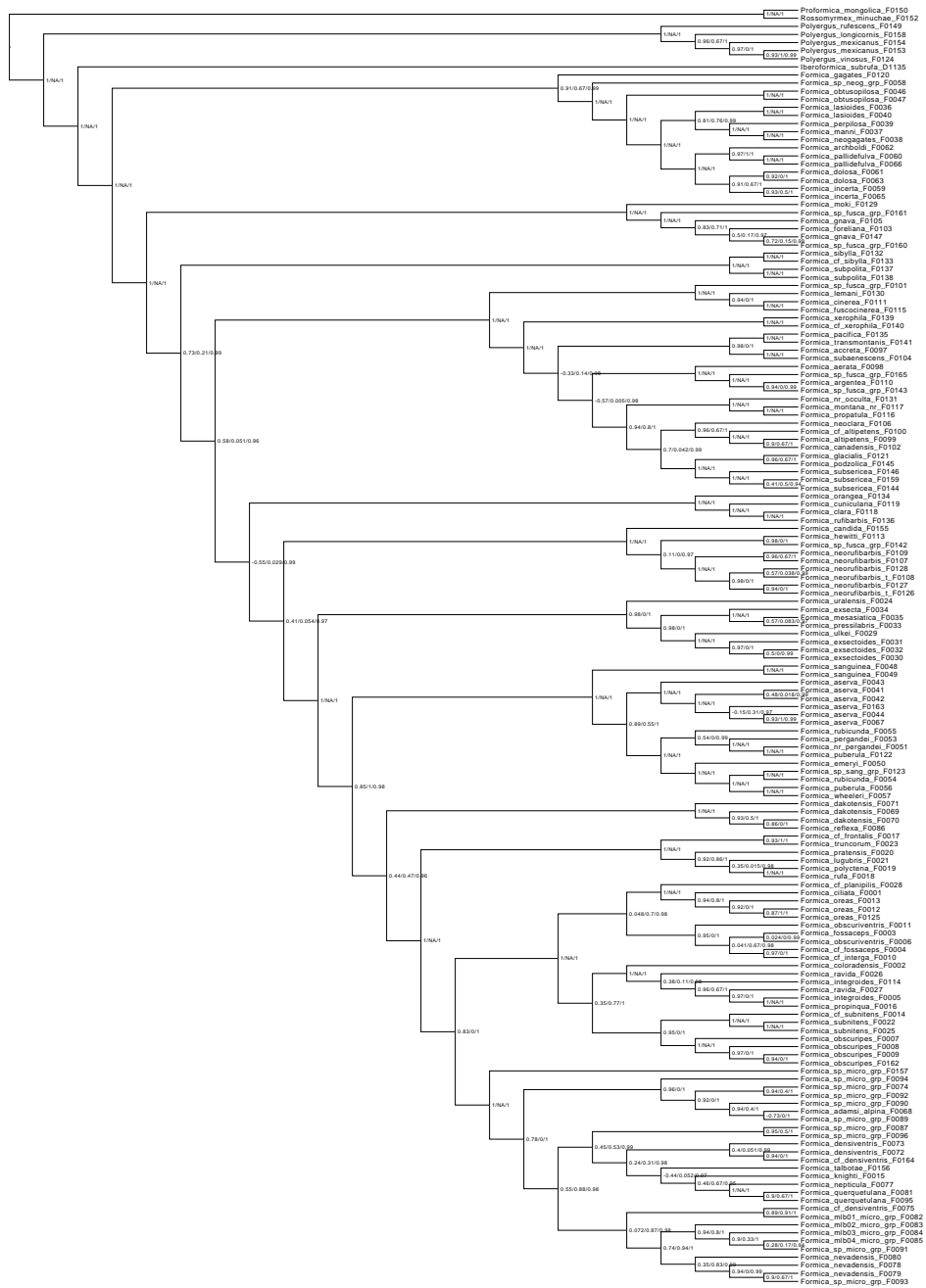
Supplementary Figure S6: Species tree inferred under coalescent using ASTRAL-III and 1,733 weighted supergene trees identified using statistical binning pipeline. Support is expressed in local posterior probability and branch lengths are in coalescent units.



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. Detailed collection data can be accessed at Zenodo (DOI: [10.5281/zenodo.4341310](https://doi.org/10.5281/zenodo.4341310)).

| 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 polycytena     | 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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