File S1: Biogeography of genus *Sericomyrmex*.

We conduct ancestral biogeographic range reconstruction, based on a previously published genomic data set. The results of our biogeographic analysis confirm a South American origin of the genus, with the ancestral ranges of two main clades, *amabilis* and *scrobifer*, estimated as the Amazon region and Chaco-Brazilian region, respectively. However, statistical support of the nodes is rather low, which is why we chose to include it only in supplemental material of this paper. We hope our study will encourage further investigation of *Sericomyrmex* ancestral range reconstruction.

Methods

We used a dated phylogeny of *Sericomyrmex*, generated in a previous study (JEŠOVNIK & al. 2017), to estimate the historical ranges of *Sericomyrmex* species. The phylogeny was the product of a BEASTv2.4.1 (BOUCKAERT & al. 2014, DRUMMOND & BOUCKAERT 2015) analysis of a genomic data set consisting of a 88,157-base-pair alignment of 100 ultraconserved-element (UCE) loci and 11 taxa, including 10 *Sericomyrmex* samples (JEŠOVNIK & al. 2017). The data included one representative of each *Sericomyrmex* species, sampled based on a larger phylogenomic analysis that included 88 samples. For the paraphyletic species *S. amabilis,* one representative from each of two populations was included, one from the main *S. amabilis* population, which is the sister of *S. saussurei,* and one from the *S. amabilis VE* population, which is the sister of the clade consisting of the combined main population of *S. amabilis* and *S. saussurei*. The phylogeny lacked two species, *S. lutzi* and *S. radioheadi,* for which we unfortunately did not have genomic data (JEŠOVNIK & al. 2017). For our biogeographical

analyses we excluded all outgroups except the sister species of *Sericomyrmex*, *M. explicatus* (KEMPF, 1968). We defined our biogeographic areas based on MORRONE (2006) and RIVAS-MARTINEZ & al. (2011): Mesoamerican region (A), Northwest South America (B), Amazon region (C) and Chaco-Brazilian region (D), as shown in Figure 1. We used the R package BioGeoBEARS, which allows running the analyses with the different models of geographic range evolution and compares their likelihood by estimating the probability of the data under each model. The models included are likelihood versions of DIVA (RONQUIST 1997), DEC (REE & SMITH 2008), and BayArea (LANDIS & al. 2013), each of them with and without "+J", which accounts for founder-event speciation (MATZKE 2014). We set the dispersal constraints between adjacent regions to 1.0, and between non-adjacent regions to 0.5 (A-C) and 0.01 (A-D). The maximum number of areas allowed was set to three.

Results

Analyses using different models produced comparable, but not identical, estimates of ancestral area (Figure S1). The model comparison with AICc, a second-order Akaike information criterion, which takes into account sample size (BURNHAM & ANDERSON 2002), didn't strongly favor one model over the others (Table 2). Interestingly, the model with highest likelihood for our data is BAYAREALIKE (AICc=59.18), which recovers the ancestral area for almost all nodes to be BCD, corresponding to the entire South American *Sericomyrmex* distribution range (Figure S1). Considering that BAYAREALIKE model was developed for data sets with large numbers of areas (unlike ours, which has only four) (LANDIS & al. 2013), we consider it

biologically less realistic than the next, only slightly worse-fitting model (AICc=60.04, Table S1d), DEC. Also, simulations under DEC produce geographic patterns of species that are often widespread and sympatric (MATZKE 2013), which in *Sericomyrmex* we actually observe for the majority of sampled species (for *S. mayri*, *S. saussurei*, *S. parvulus* and *S. bondari*, and for *S. amabilis* and *S. opacus*). Results of the analysis under the DEC model (Figure 1) indicate that the range of the most recent common ancestor of *Sericomyrmex* and its sister species *M. explicatus* most likely lived in seasonally dry Chaco-Brazilian region, although this result has very low support (16%). The ancestral range for the ancestor of all *Sericomyrmex* species is recovered as BCD, with mediocre support (55.3%), the entire South American range of today's *Sericomyrmex*. At that historical point, approximately 4–5 million years ago, *Sericomyrmex* split into two main clades, the *amabilis* and *scrobifer* clades. The ancestral ranges for the two main clades are estimated to be the Amazon, for the *amabilis* clade (with support of 27.6%), and the Chaco-Brazilian region, for the *scrobifer* clade (with 42%). Further lineage splitting into species within each clade most likely occurred in the same regions: in the Chaco-Brazilian region for the *S. scrobifer* clade and the Amazon region for the *amabilis* clade for all species except the most recent common ancestor of the paraphyletic *S. amabilis* and *S. saussurei*, which is estimated as BC (Amazon + Chaco-Brazilian region). In general, the support values for ancestral-area estimates are low (Table 1). The highest support, in addition to 55% for the ancestor of all *Sericomyrmex*, is recovered for the ancestral area of *S. scrobifer* and *S. maravalhas*, Chaco-Brazilian region, 88.5%.
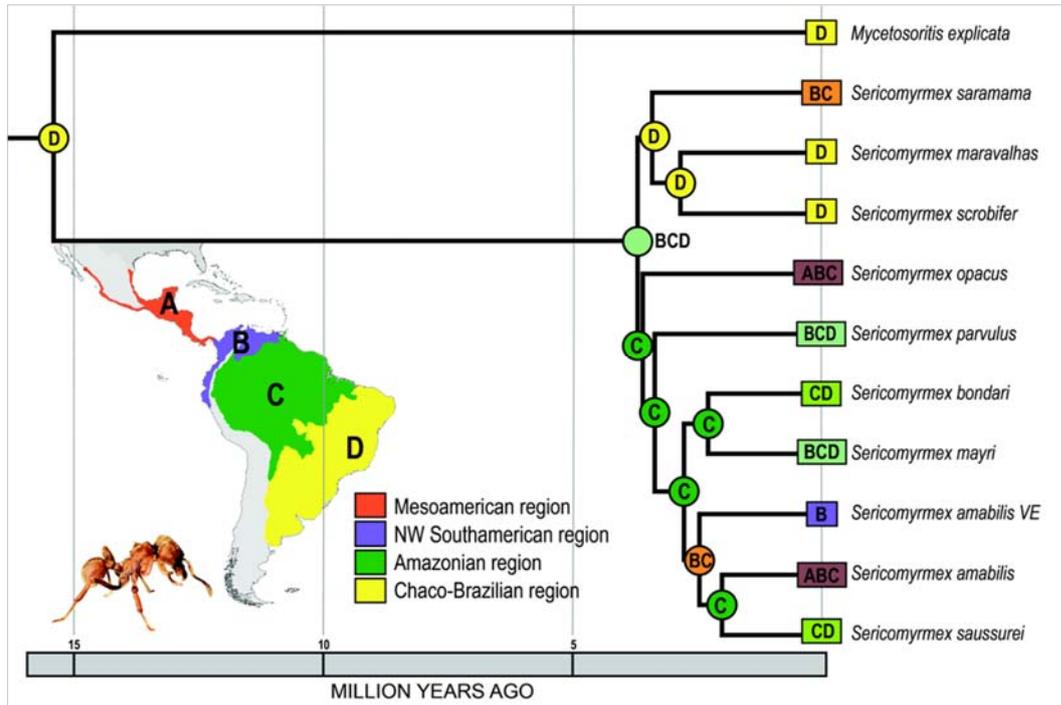
Fig. 1: Ancestral range reconstruction. The dated phylogeny of *Sericomyrmex* with the most likely ranges indicated at nodes as estimated with BioGeoBEARS (model DEC). The geographic ranges of extant species are indicated at the branch tips.

Node	Ancestral Area (AA)	Probability	2nd most likely AA	Probability
M. explicata crown	D	16%	CD	13.8%
Sericomyrmex root	BCD	55.3%	CD	16.1%
amabilis group root	C	27.6%	BC	17.8%
parvulus crown	C	30%	BCD	20.4%
amabilis + mayri	C	32.12%	BC	24.4%
amabilis VE crown	BC	40.1%	C	23.8%
amabilis crown	C	42.1%	BC	26.4%
mayri crown	C	37.5%	CD	26.1%
saramama crown	D	42%	CD	18.2%
scrobifer crown	D	88.5%	CD	7.4%

Table 1. The biogeographic analysis results: probabilities for most likely and second most likely ancestral area at each node.

Discussion

It has long been assumed that the attine ants originated in a tropical rainforest in South America (MEHDIABADI & SCHULTZ 2010), as confirmed recently for the common ancestor of all attine ants (BRANSTETTER & al. 2017). However, the majority of higher-attine ant lineages, including *Sericomyrmex, Trachymyrmex,* and the ecologically dominant leaf-cutter ants, most likely originated in the seasonally dry regions of South America (BRANSTETTER & al. 2017). Our biogeographic analysis reconstructs the range of the most recent common ancestor of *Sericomyrmex* and its sister species, *M. explicatus*, as the seasonally dry Chaco-Brazilian region, albeit with low support (Figure 1, Table 1). However, the range of the most recent common ancestor of the genus *Sericomyrmex*, one of the best-supported nodes in our analyses, is reconstructed as a combination of areas BCD, which includes the majority of the South America: the Northwest South America region (B), the Amazon region (C), and Chaco-Brazilian region (D) (Figure 1). The genus is split into two main lineages, the *scrobifer* and *amabilis* species groups, which are reconstructed as having evolved in different regions: the *amabilis* group in the Amazon region and the *scrobifer* group in the Chaco-Brazilian region. Species from both clades have dispersed to other regions. *Sericomyrmex saramama* (*scrobifer* clade) dispersed to the Amazon and northwest South America, and two of the *amabilis* clade species, *S. opacus* and *S. amabilis*, have dispersed into Mesoamerica. The remaining extant species have overlapping, broad, South American distributions.

The origin of the genus *Sericomyrmex* in the dry Chaco-Brazilian region, followed by the dispersal of one clade into the Amazon region and by further diversification in both

clades, is the most likely sequence of events based on our results, but without robust support. It would be interesting to investigate this further because evolution in seasonally dry areas has important implications for ant-fungus symbiotic evolution (BRANSTETTER & al. 2017). Including the two *Sericomyrmex* species missing from our analyses in future phylogenetic analyses might improve our ability to reconstruct biogeographic history. However, both species have narrow distributions within the Amazon region and, based on the morphological data, we believe they are members of the *amabilis* clade, with *S. lutzi* a close relative of *S. mayri* and *S. radioheadi* a close relative of *S. bondari*. This suggests that an analysis including those species might result in stronger support for the current range estimates for nodes within the *amabilis* clade but would not necessarily contribute to a better-supported range estimate for the *Sericomyrmex* root. Our sampling of nest series in the *scrobifer* clade species is less comprehensive than our sampling of the *amabilis*-clade species. All three species in the *scrobifer* group are rarely collected, so our distribution data is probably incomplete. Full resolving of the biogeographic history of *Sericomyrmex* will require a better understanding of *scrobifer* clade species distributions, especially of *S. saramama* distribution, and the inclusion of the two missing species *S. lutzi* and *S. radioheadi* in future phylogenetic analyses.

Model	AICc
DEC	60,04
DEC+J	62,45
DIVALIKE	61,31
DIVALIKE+J	63,18
BAYAREALIKE	59,18
BAYAREALIKE+J	61,48

Table 2. Model comparison with AICc - results of BioGeoBEARS analysis

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