Ecography

E6629

Machac, A., Janda, M., Dunn, R. R. and Sanders, N. J. 2010. Elevational gradients in phylogenetic structure of ant communities reveal the interplay of biotic and abiotic constraints on species density. – Ecography 33: xxx–xxx.

Supplementary material

Appendix 1

Geography of the montane systems

The geological system of Great Smoky Mts (2000 km^2) was formed approximately 200–300 mya. The mountains' convenient north-south orientation allowed the species to migrate along their slopes during the times of climate changes (e.g. ice age 10 kya) (King 1968). Therefore, the environment of Smoky Mts remained undisturbed by climate fluctuations for over a million years, hence, providing species a sufficient time for wide diversifications (US Geological Survey 2010). The elevational span of the montane system is 250–2000 m (Fig. S1); we have sampled approximately 90% of the extent of this elevational gradient (Sanders et al. 2007).

Vorarlberg Mts (2600 km^2) consist of several montane systems (Silvretta, Ratikon, Verwall, Arlberg) formed during the Alpine orogeny (65 mya) (Fenninger et al. 1980). Flora and fauna of the region have been largely affected during the ice ages. Nowadays, the temperate climate predominates but, indeed, fluctuates with elevation (350–3000 m) (Austrian Geological Survey 2010) (Fig. S1).

Chiricahua Mts (2200 km^2), composed of Tertiary volcanics, are situated in the deserts of southeastern Arizona, USA (Jenney and Reynolds 1989). Particular biological diversity of the mountain range stems from its position on the interface of four ecological regions (Sonoran desert, Chihuahuan desert, Rocky Mountains, and Sierra Madre) (US Geological Survey 2010). The elevational gradient spans from 1100 to 2900 m (Fig. S1).

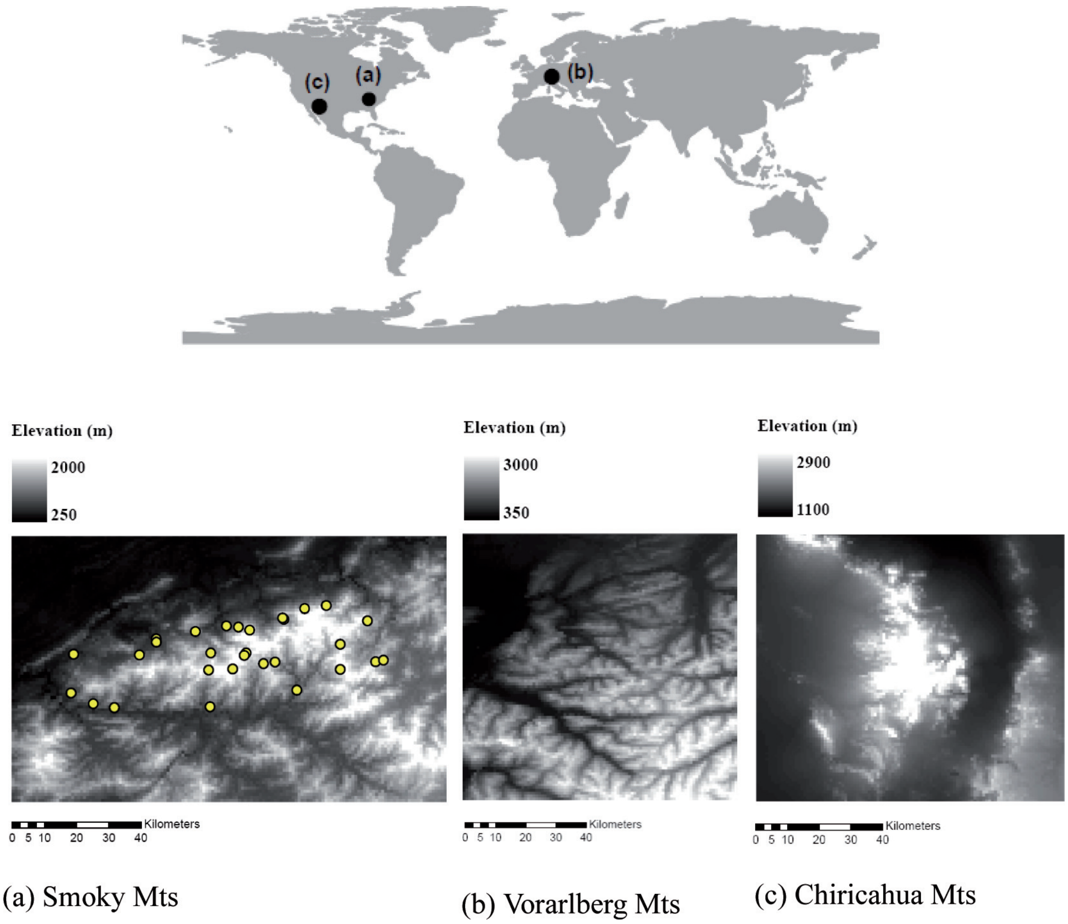


Figure S1. Geography of the three montane systems. A general position as well as topology (beneath) of individual montane systems is given. Sampled sites are depicted as circles. Specific geographic coordinates of sites sampled in Chiricahua Mts and Vorarlberg Mts were not provided within the original studies (Andersen 1997, Glaser 2006).

Appendix 2

Phylogeny reconstruction

Description of the phylogenetic structure of ant communities requires reconstruction of phylogeny for each regional species pool. None of the montane areas used in this study exceeded area of 3000 km^2; therefore, all species occurring within each montane system were considered as the regional species pool for each analysis.

We constructed a phylogeny for the species sampled in each of the montane systems based on published genus-level molecular phylogenies (Brady et al. 2006, Moreau et al. 2006). The molecular data were based on these studies' datasets provided at TreeBase database (<www.treebase.org>). Species found in the elevational gradients considered here, but not included in the above studies were substituted with closely related taxa (Table S1) with relationships as according to Bolton (2003). The molecular dataset was extended using additional sequences (same loci as in the source studies) available for particular species in GenBank in order to incorporate the within-genus variability and to resolve some of the genus-level polytomies. These additional sequences as well as their GenBank codes are listed in Table S2.

The edited sequences were aligned in *MAFFT v6* (Katoh et al. 2002) and used for phylogenetic reconstruction (Smoky Mts: 4510 base pairs; Chiricahua Mts: 4572 bp; Vorarlberg: 6803 bp). The reconstruction was performed in PAUP 4.0 via maximum likelihood procedure with topology constraint (Swofford 1993). The convenient model of sequence substitution was identified uniformly as GTR + I + G for all of the three datasets by Modeltest 3.7 (Posada and Crandall 1998). Trees were randomized using tree bisection-reconnection algorithm (TBR); the best tree was identified by heuristic likelihood search. The tree topology, on which molecular data were forced, corresponded with the genus-level phylogeny in Bolton 2003, Brady et al. 2006, and Moreau et al. 2006. We constrain the topology with respect to these studies because they are conclusive and methodologically precise. Moreover, artifacts (e.g. long-branch repulsion) may arise when the sampling for phylogeny reconstruction is not comprehensive and includes only taxa from the regional community (Siddall and Whiting 1999). Hence, the constrained topology is more suitable than the one we could obtain.

Branch lengths were estimated on basis of substitution rates in the combined dataset of molecular data; the results are depicted in Fig. S2, Fig. S3, and Fig. S4. Additional sequences from GenBank enabled us to resolve some of the generic polytomies; particularly the relationship between *Camponotus* and *Pheidole* species in the Chiricahua Mountains (Fig. S2). Some artifacts in NRI and NTI calculations may arise when the phylogeny is not fully resolved, but this usually applies if the polytomies are situated on the basal branches rather than on terminals (Swenson 2009), which is not our case.

Table S1. List of substituted species; convenient substitute species were identified according to Bolton (2003).

Original taxon	Substitution
Ephebomyrmex imberbiculus	*Pogonomyrmex maricopa*
Formicoxenus nitidulus	*Temnothorax* sp.
Harpagoxenus sublaevis	*Leptothorax muscorum*
Myrmecina americana	*Pristomyrmex* sp.
Paratrechina faisonensis	*Prenolepis imparis*
Paratrechina melanderi	*Prenolepis imparis*
Paratrechina parvula	*Prenolepis imparis*
Ponera coarctata	*Hypoponera opacior*
Ponera pennsylvanica	*Hypoponera inexorata*

Table S2. Additional sequences used for phylogeny reconstruction; species are listed with GenBank code of the sequence used.

Chiricahua Mts	
Acanthomyops latipes	DQ353091.1
Acanthomyops latipes	DQ352963.1
Aphaenogaster albisetosa	EF013093.1
Aphaenogaster albisetosa	EF012965.1
Aphaenogaster texana	DQ352956.1
Aphaenogaster texana	DQ353026.1
Camponotus modoc	AF398165.1
Camponotus nearcticus	AY334396.1
Camponotus ocreatus	EU367343.1
Camponotus ocreatus	EU367166.1
Camponotus sansabeanus	AY334382.1
Camponotus sayi	AY334385.1
Camponotus schaefferi	AY334388.1
Camponotus ulcerosus	AY334390.1
Camponotus vicinus	AY325957.1
Dorymyrmex insanus	AF147046.1
Hypoponera opacior	EU155410.1
Lasius alienus	DQ353683.1
Leptothorax rugatulus	AY158899.1
Liometopum apiculatum	EF013004.1
Myrmecina graminicola	EF013015.1
Myrmecina graminicola	EF013723.1
Myrmecina graminicola	EF013143.1
Myrmecocystus depilis	EU142961.1
Myrmecocystus mendax	EU142959.1
Myrmecocystus mexicanus	EU142976.1
Myrmecocystus mimicus	EU142974.1
Myrmecocystus navajo	EU142962.1
Myrmica striolagaster	EF013018.1
Paratrechina hystrix	EF013034.1
Paratrechina hystrix	EF012906.1
Paratrechina hystrix	EF013162.1
Pheidole cerebrosior	EF518326.1
Pheidole desertorum	EF518339.1
Pheidole diversipilosa	EF518341.1
Pheidole hyatti	EF013036.1
Pheidole rugulosa	EF518398.1
Pheidole sciophila	EF518400.1
Pheidole tucsonica	EF518437.1
Pheidole vallicola	EF518440.1
Pogonomyrmex barbatus	AY542362.1
Pogonomyrmex californicus	AY542370.1
Pogonomyrmex maricopa	DQ353571.1
Polyergus breviceps	EF013043.1
Prenolepis imparis	EF013047.1
Pseudomyrmex apache	AY703585.1
Solenopsis xyloni	EF013063.1
Solenopsis xyloni	EF013191.1
Tapinoma sessile	EF013066.1
Tetramorium hispidum	DQ352866.1
Trachymyrmex arizonensis	EF013075.1

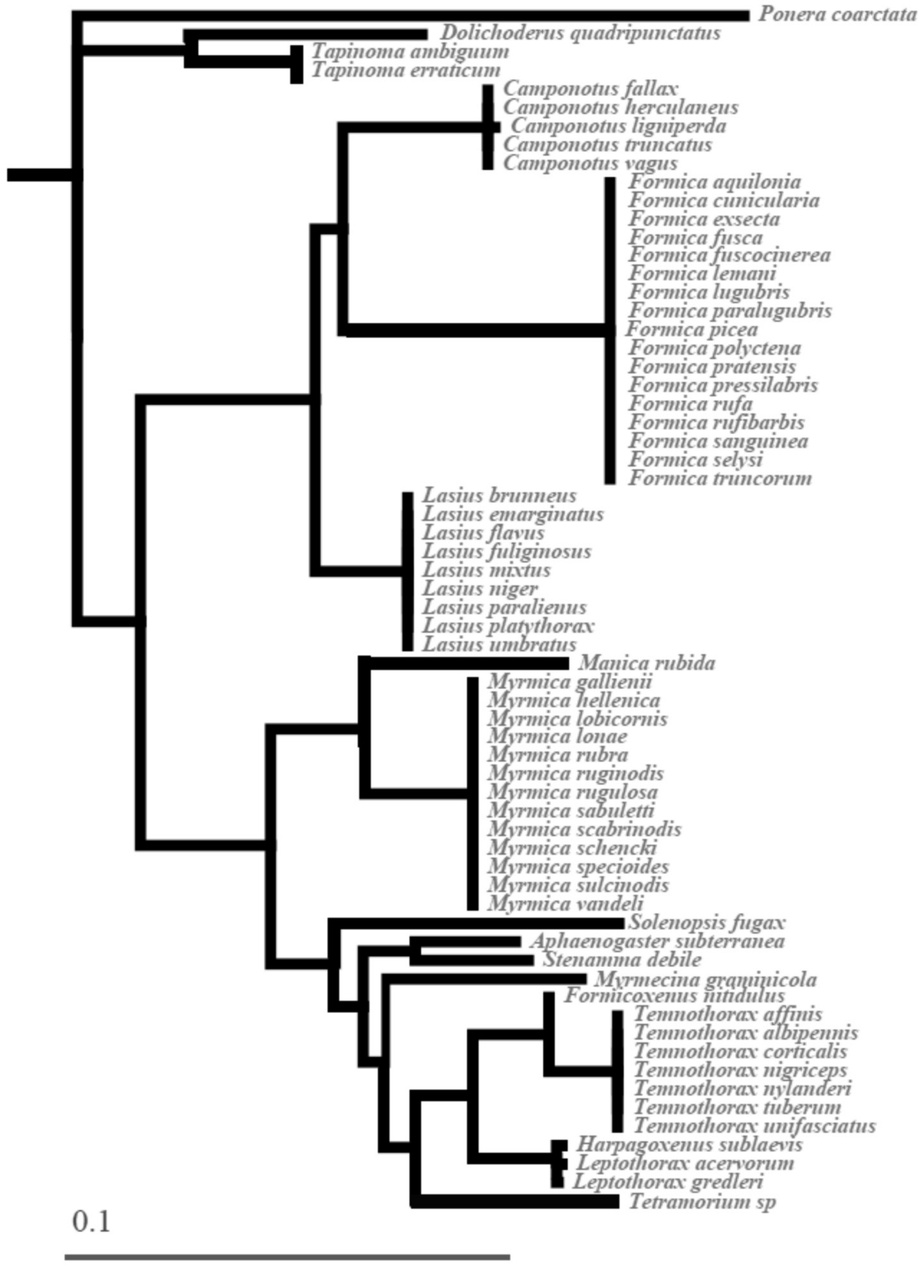
Vorarlberg Mts	
Camponotus ligniperda	X73270.1
Camponotus vagus	AY185224.1
Formica selysi	AY185226.1
Formicoxenus provancheri	DQ353412.1
Formicoxenus provancheri	DQ353587.1
Formicoxenus provancheri	DQ353011.1
Harpagoxenus sublaevis	X73272.1
Lasius niger	EU143223.1
Lasius niger	EU143083.1
Lasius niger	EU142964.1
Leptothorax acervorum	X73275.1
Manica rubida	AY185237.1
Myrmecina graminicola	EF013015.1
Myrmica rubra	AF332515.2
Myrmica rubra	AH010525.1
Ponera coarctata	AY185253.1
Tapinoma erraticum	AY185217.1

Smoky Mts	
Amblyopone pallipes	AY703688.1
Brachymyrmex depilis	EF013100.1
Camponotus americanus	AY334395.1
Camponotus chromaiodes	AY334392.1
Camponotus pennsylvanicus	AY334391.1
Crematogaster minutissima	AY443981.1
Lasius alienus	DQ353096.1
Lasius umbratus	AB370989.1
Prenolepis imparis	EF013175.1
Solenopsis molesta	EF013190.1
Tapinoma sessile	FJ161757.1
Temnothorax curvispinosus	AY909569.1

Figure S2

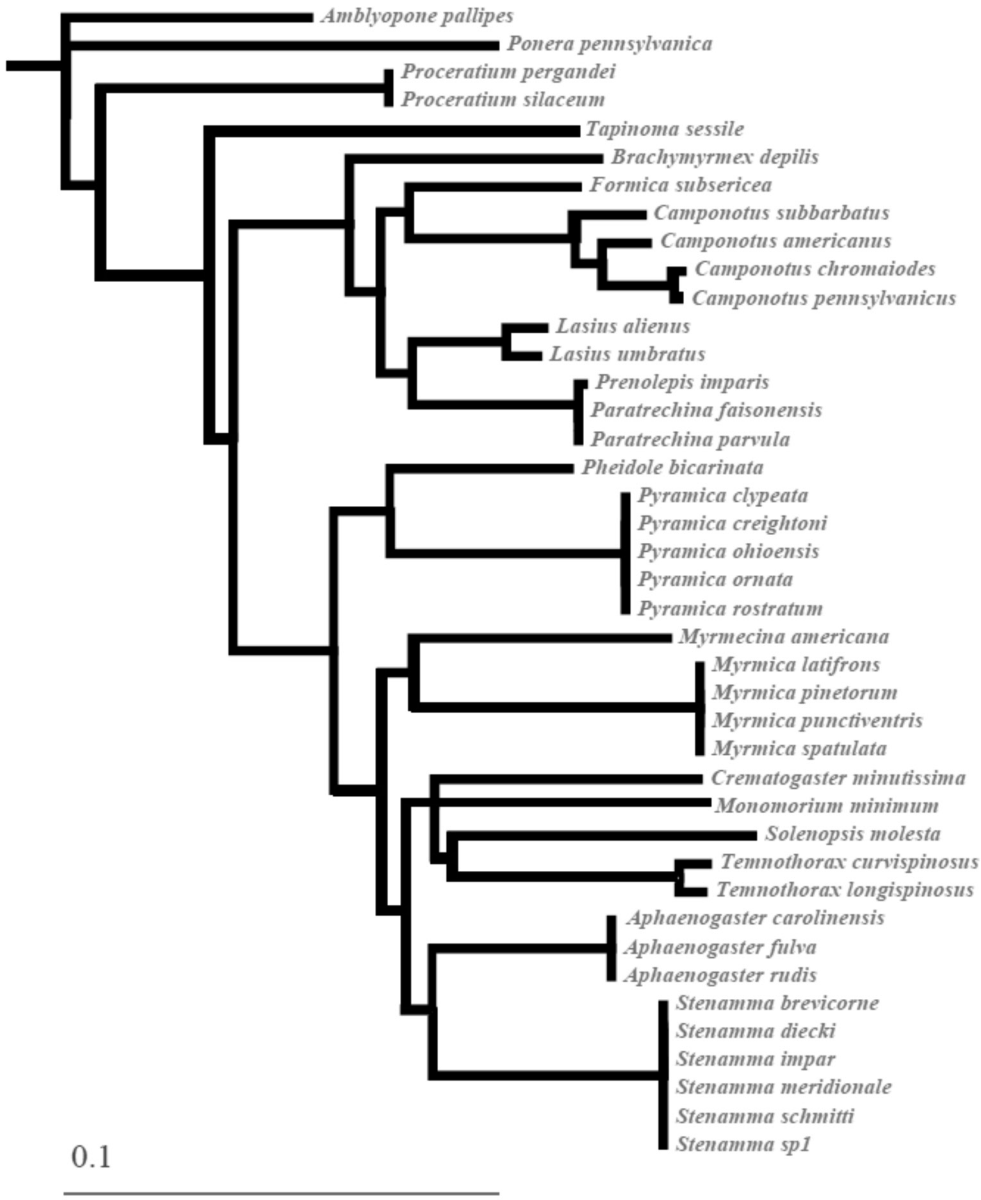
Chiricahua Mts, Arizona

Figure S3



Vorarlberg, Austria

Figure S4



Smoky Mts, Tenn./N. Carolina

Appendix 3

Elevational preferences

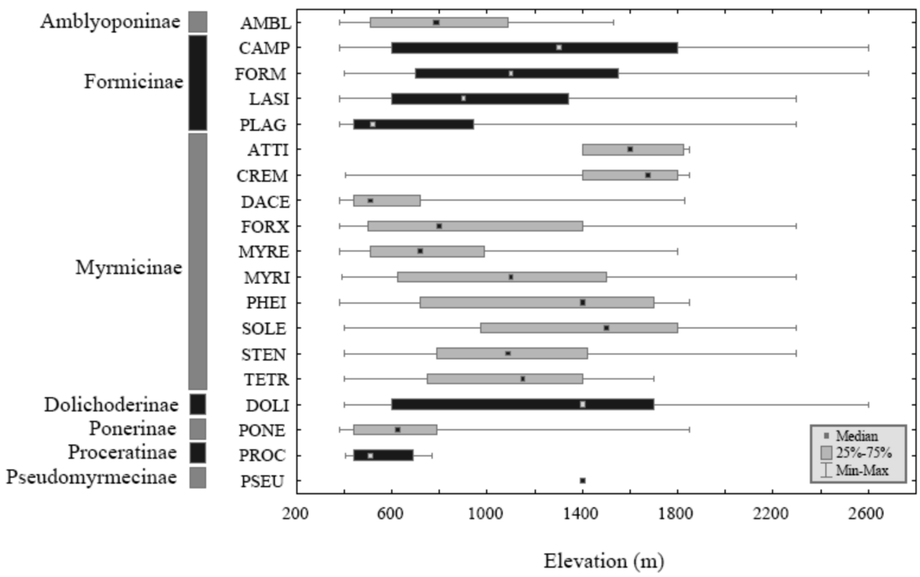
The preference of taxa for particular elevations was inferred by non-parametric Kruskal-Wallis test. The test was performed both at the level of subfamilies and tribes (species of individual tribes are listed in Table S4). The results show a significant difference in preferred elevations (subfamilies: $H (6, n = 800) = 22.342$, $p = 0.001$; tribes: $H (18, n = 800) = 92.998$, $p < 0.001$) among subfamilies as well as among tribes. Multiple comparisons of mean ranks (Table S3) combined with boxplots (Fig. S5) revealed that Ponerinae prefer significantly lower elevations than do Formicinae, Myrmicinae, and Dolichoderinae. No significant differences among the other subfamilies were detected.

Most of the ant tribes, particularly those with specialist diets such as Ponerini, Dacetini (feeds on collembolans), Amblyoponini (feeds on centipedes) and Myrmecinini (feeds on mites) had elevational distributions centered on low elevations. Some generalist lineages are indifferent with respect to elevation, and occupy wide elevational span (Camponotini, Formicini, Tetramorini etc). The relatively few species that occurred at the highest altitudes, tended to come from altitudinally widespread tribes such as Formicini, Stenamini and Camponitini that include one or a few species that appear more tolerant of cold, high elevation conditions (Fig. S5).

The elevational preferences of Attini, Proceratiini and Pseudomyrmecini are most likely biased due to unrepresentative sampling (e.g. Attini were represented by a single genus, *Trachymyrmex*); hence, should be interpreted with caution.

Table S3. Multiple comparisons of mean ranks for subfamily elevational preferences. Numbers refer to significance level. Significant differences were revealed between the Ponerinae and three other subfamilies (Formicinae, Myrmicinae, Dolichoderinae), with species of the Ponerinae preferring significantly lower elevations than species of those three other subfamilies.

	Ambl	Form	Myrm	Doli	Pone	Proc	Pseu
Amblyoponinae		1.000	1.000	1.000	1.000	1.000	1.000
Formicinae	1.000		1.000	1.000	**0.026**	0.143	1.000
Myrmicinae	1.000	1.000		1.000	**0.021**	0.130	1.000
Dolichoderinae	1.000	1.000	1.000		**0.042**	0.100	1.000
Ponerinae	1.000	**0.026**	**0.021**	**0.042**		1.000	1.000
Proceratinae	1.000	0.143	0.130	0.100	1.000		1.000
Pseudomyrmecinae	1.000	1.000	1.000	1.000	1.000	1.000	



Tribe	n
AMBLYOPONINI	17
CAMPONOTINI	55
FORMICINI	132
LASIINI	94
PLAGIOLEPIDINI	27
ATTINI	4
CREMATOGASTRINI	10
DACETINI	23
FORMICOXENINI	66
MYRMECININI	29
MYRMICINI	131
PHEIDOLINI	65
SOLENOPSIDINI	16
STENAMMINI	62
TETRAMORIINI	16
DOLICHODERINI	26
PONERINI	19
PROCERATIINI	7
PSEUDOMYRMECINI	1

Figure S5. Boxplots show the elevational spans of each ant tribe; tribes are grouped by subfamilies. The table to the right shows full names of tribes and their sample size.

Table S4. List of individual species along with their tribal identity.

Species	Tribus	Species	Tribus	Species	Tribus
Aphaenogaster subterranea	Pheidolini	*Temnothorax nigriceps*	Formicoxenini	*Pheidole vallicola*	Pheidolini
Camponotus fallax	Camponotini	*Temnothorax nylanderi*	Formicoxenini	*Pogonomyrmex apache*	Myrmicini
Camponotus herculaneus	Camponotini	*Temnothorax tuberum*	Formicoxenini	*Pogonomyrmex barbatus*	Myrmicini
Camponotus ligniperda	Camponotini	*Temnothorax unifasciatus*	Formicoxenini	*Pogonomyrmex californicus*	Myrmicini
Camponotus truncatus	Camponotini	*Tetramorium sp*	Tetramoriini	*Pogonomyrmex maricopa*	Myrmicini
Camponotus vagus	Camponotini	*Acanthomypos arizonicus*	Lasiini	*Polyergus breviceps*	Formicini
Dolichoderus quadripunctatus	Dolichoderini	*Acanthomypos latipes*	Lasiini	*Pseudomyrmex apache*	Pseudomyrmecini
Formica aquilonia	Formicini	*Aphaenogaster albisetosus*	Pheidolini	*Solenopsis aurea*	Solenopsidini
Formica cunicularia	Formicini	*Aphaenogaster texana*	Pheidolini	*Solenopsis sp*	Solenopsidini
Formica exsecta	Formicini	*Camponotus bruesi*	Camponotini	*Solenopsis truncorum*	Solenopsidini
Formica fusca	Formicini	*Camponotus modoc*	Camponotini	*Solenopsis xyloni*	Solenopsidini
Formica fuscocinerea	Formicini	*Camponotus nearcticus*	Camponotini	*Stenamma huachucanum*	Stenammini
Formica lemani	Formicini	*Camponotus ocreatus*	Camponotini	*Stenamma chiricahua*	Stenammini
Formica lugubris	Formicini	*Camponotus sansabeanus*	Camponotini	*Tetramorium hispidum*	Tetramoriini
Formica paralugubris	Formicini	*Camponotus sayi*	Camponotini	*Trachymyrmex arizonensis*	Attini
Formica picea	Formicini	*Camponotus schaefferi*	Camponotini	*Amblyopone pallipes*	Amblyoponini
Formica polyctena	Formicini	*Camponotus sp*	Camponotini	*Aphaenogaster carolinensis*	Pheidolini
Formica pratensis	Formicini	*Camponotus ulcerosus*	Camponotini	*Aphaenogaster fulva*	Pheidolini
Formica pressilabris	Formicini	*Camponotus vicinus*	Camponotini	*Aphaenogaster rudis*	Pheidolini
Formica rufa	Formicini	*Crematogaster colei*	Crematogastrini	*Brachymyrmex depilis*	Plagiolepidini
Formica rufibarbis	Formicini	*Crematogaster depilis*	Crematogastrini	*Camponotus americanus*	Camponotini
Formica sanguinea	Formicini	*Crematogaster isolata*	Crematogastrini	*Camponotus chromaiodes*	Camponotini
Formica selysi	Formicini	*Crematogaster smithi*	Crematogastrini	*Camponotus pennsylvanicus*	Camponotini
Formica truncorum	Formicini	*Cyphomyrmex wheeleri*	Attini	*Camponotus subbarbatus*	Camponotini
Formicoxenus nitidulus	Formicoxenini	*Dorymyrmex insanus*	Dolichoderini	*Crematogaster minutissima*	Crematogastrini
Harpagoxenus sublaevis	Formicoxenini	*Dorymyrmex sp*	Dolichoderini	*Formica subsericea*	Formicini
Lasius brunneus	Lasiini	*Ephebomyrmex imberbiculus*	Myrmicini	*Lasius alienus*	Lasiini
Lasius emarginatus	Lasiini	*Forelius analis*	Dolichoderini	*Monomorium minimum*	Solenopsidini
Lasius flavus	Lasiini	*Forelius maccooki*	Dolichoderini	*Myrmecina americana*	Myrmecinini
Lasius fuliginosus	Lasiini	*Formica gnava*	Formicini	*Myrmica latifrons*	Myrmicini
Lasius mixtus	Lasiini	*Formica occulta*	Formicini	*Myrmica pinetorum*	Myrmicini
Lasius niger	Lasiini	*Formica perpilosa*	Formicini	*Myrmica punctiventris*	Myrmicini
Lasius paralienus	Lasiini	*Hypoponera opacior*	Ponerini	*Myrmica spatulata*	Myrmicini
Lasius platythorax	Lasiini	*Leptothorax carinatus*	Formicoxenini	*Paratrechina faisonensis*	Plagiolepidini
Lasius umbratus	Lasiini	*Leptothorax neomexicanus*	Formicoxenini	*Paratrechina parvula*	Plagiolepidini
Leptothorax acervorum	Formicoxenini	*Leptothorax rugatulus*	Formicoxenini	*Pheidole bicarinata*	Pheidolini
Leptothorax gredleri	Formicoxenini	*Leptothorax sp*	Formicoxenini	*Ponera pennsylvanica*	Ponerini
Manica rubida	Myrmicini	*Liometopum apiculatum*	Dolichoderini	*Prenolepis imparis*	Plagiolepidini
Myrmecina graminicola	Myrmecinini	*Liometopum sp*	Dolichoderini	*Proceratium pergandei*	Proceratiini
Myrmica gallienii	Myrmicini	*Monomorium peninsulatum*	Solenopsidini	*Proceratium silaceum*	Proceratiini
Myrmica hellenica	Myrmicini	*Myrmecocystus depilis*	Lasiini	*Pyramica clypeata*	Dacetini
Myrmica lobicornis	Myrmicini	*Myrmecocystus mendax*	Lasiini	*Pyramica creightoni*	Dacetini
Myrmica lonae	Myrmicini	*Myrmecocystus mexicanus*	Lasiini	*Pyramica ohioensis*	Dacetini
Myrmica rubra	Myrmicini	*Myrmecocystus mimicus*	Lasiini	*Pyramica ornata*	Dacetini

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