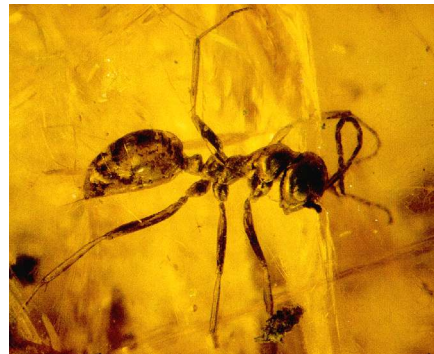
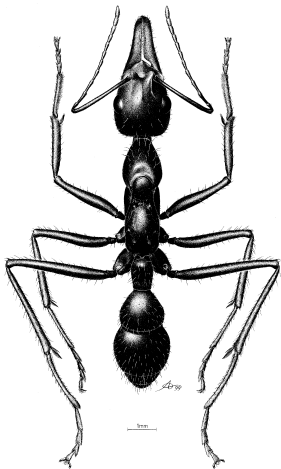


AToL: Collaborative research on ant phylogeny: a comprehensive evolutionary tree for the world's premier social organisms

NSF EF-0431330; 10/01/2004 – 09/30/2009

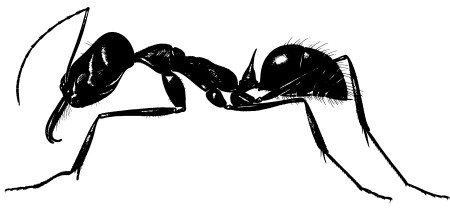
P.S.Ward¹, Seán Brady², Brian Fisher³ & Ted Schultz²



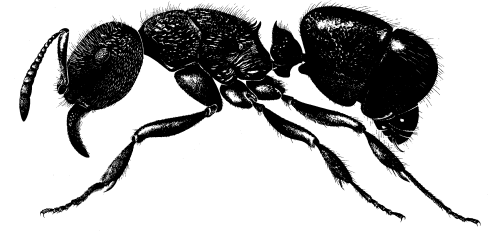
¹University of California, Davis, CA, USA

²Smithsonian Institution, Washington, DC, USA

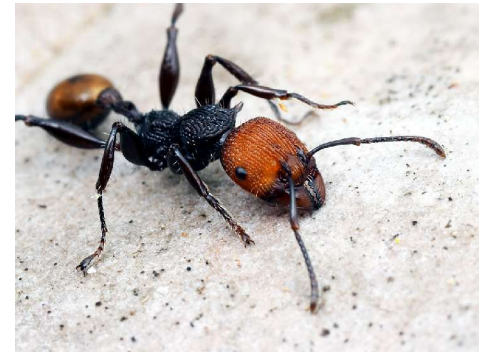
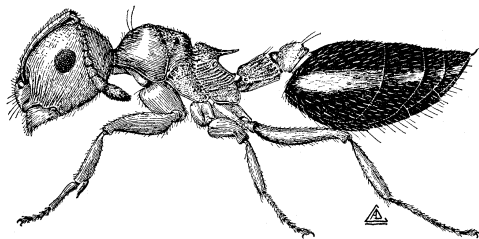
³California Academy of Sciences, San Francisco, CA, USA



Why ants?

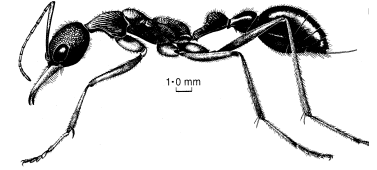


- world's most successful group of eusocial insects
- ~12,000 described species (and perhaps as many undescribed species)
- ants occupy most terrestrial ecosystems, and assume key roles as predators, scavengers and herbivores
- symbiotic relationships with other organisms (fungi, plants, hemipterans, etc.) are common
- ant live in complex societies, with multiple castes and a diverse array of social behaviors





Ant AToL Project: Objectives



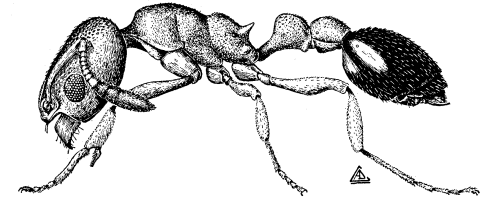
- Infer the phylogeny of all major lineages of ants, using DNA sequence data and morphology
- Estimate divergence times for the origin of ants and major events in ant evolution by incorporating fossil information with molecular dating methods
- Use the inferred phylogeny as a framework for reconstructing the evolutionary histories of key biological features of ants.
- Develop the AntTree interface to AntWeb (www.antweb.org), to provide internet-accessible resources on the phylogeny and diversity of ants
- Provide training in ant systematics to students and other researchers, through graduate student education and the annual Ant Course (www.calacademy.org/research/entomology/ant_course/)

Ant AToL Project: Methods

Taxa

Exemplar approach: ~340 ant species, representing all 21 extant subfamilies, all 63 tribes and most genera

Outgroups: ~10 vespoid wasp taxa



Character sets

Molecular data: ~10 kb of DNA sequence data from 10 nuclear genes plus 1 mitochondrial gene

Morphology: ~300 characters, drawn from external and internal anatomy of adult workers, males, and queens, and from ant larvae

Analysis

Data will be analyzed using a variety of criteria (parsimony, maximum likelihood, Bayesian inference) and strategies geared toward large data sets (e.g., MCMC, genetic algorithms, parallel processing).

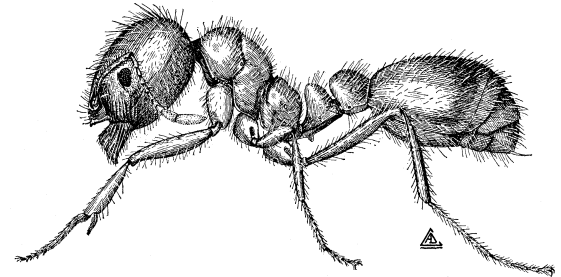
Ant AToL Project: Management

Responsibilities

P. S. Ward (University of California, Davis): overall coordination of the project; development of an integrated morphological data matrix; some DNA sequencing

T. R. Schultz and S. G. Brady (Smithsonian Institution): most molecular systematic work; computationally intensive phylogenetic analyses

B. L. Fisher (California Academy of Sciences): specimen procurement and processing; bioinformatics

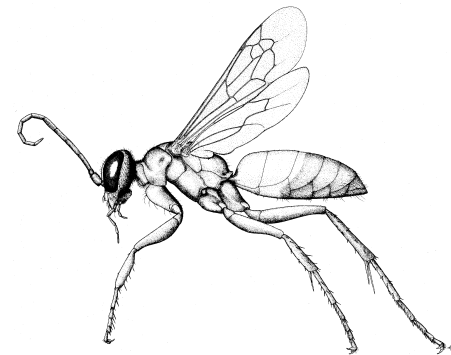


Ant AToL Project: Management

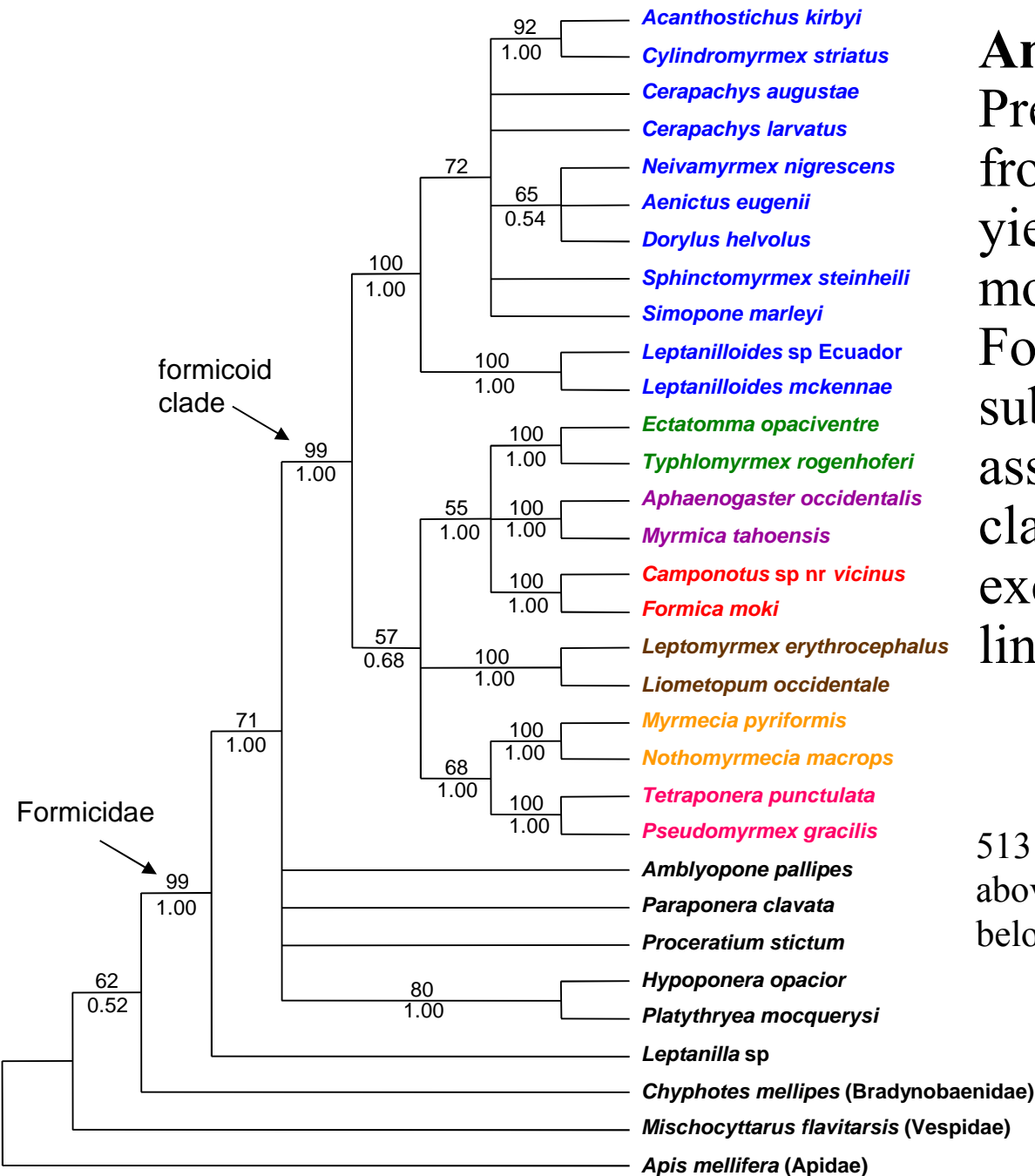
Coordination of research activities among the PIs is enhanced by the *eusocial* nature of ants: specimens of terminal taxa will be drawn from the *same colony series* and shared among the three collaborating institutions.

Thus, there will be **division of labor by research method** (sequencing, morphological analysis, specimen processing and imaging) rather than by taxon.

Collaboration with the **Hymenoptera Tree of Life Project**: sharing of protocols and findings.



Ant AToL Project
 Preliminary results (5.1 kb from five nuclear genes) yield strong support for monophyly of (1) family Formicidae, (2) most extant subfamilies, and (3) an assemblage, the “formicoid clade”, containing all ants except a few older (“basal”) lineages.



5131 bp (950 parsimony-informative)
 above branches: parsimony bootstraps (>50)
 below branches: Bayesian posteriors (>0.50)

Ant AToL Project

The current data suggest that ants arose about 120-140 mya; that there was an early diversification of poneromorph-like taxa; and that this was followed by a second, more exuberant, radiation of ants, beginning about 100 mya.

