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## Contributed Talk Abstract

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### The draft genomes of *Aphaenogaster* species from across a biogeographic gradient

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#### Abstract Text:

#### Background/Question/Methods

Climatic change is altering all ecosystems. Among other ecosystem services, ants disperse seeds, and seed dispersal plays a key role in determining rates of range shifts of many plant species. Recent field and laboratory climate-change experiments have demonstrated that ant communities in eastern North American forests will respond to climatic change and that genetically based traits involved in heat and cold tolerance will contribute to community dynamics. To address the need for detailed genetic information about the ant communities of this region, we sequenced whole genomes of six species of ants in the genus *Aphaenogaster*: *Aphaenogaster ashmeadi*, *A. floridana*, *A. fulva*, *A. miamiana*, *A. picea*, and *A. rudis*. Whole colonies were collected from field sites in eastern North America. Live individuals from each colony were isolated from debris, placed in 50-ml Falcon centrifuge tubes and immediately flash frozen in a -80 C freezer. DNA was extracted from each colony and sequenced on an Illumina HiSeq 2500 at the Broad Institute (Cambridge, Massachusetts, USA). Raw sequences were processed to remove chimeric and contaminant sequences and assembled using ALLPATHS-LG with additional post-assembly processing with Pilon, which reduced coverage gaps by 3.1% on average, yielding reduction of 3.9 Mb of gaps on average.

#### Results/Conclusions

The genomes of all six species were successfully sequenced; both raw sequences and the assembled genomes are stored at Harvard Forest (Petersham, Massachusetts, USA); assemblies and annotations are being processed for submission to NCBI's genome database. All genomes showed high assembly quality (70% fragments mapped). Across all species, average shortest contig length at 50% of the genome (i.e., *N50*) was 18864 bases; average assembly GC content was 38.18%; and average genome size was 471 Mb. Initial regression analyses of *N50*, GC content, and genome size revealed that none of these genomic characters varied significantly with latitude. These results provide a useful resource for examining contributions of genetic variation underlying the response of ant assemblages to climatic factors. Further work investigating variation in genomic content and mapping of target coding regions from previous experimental transcriptomic work on *Aphaenogaster* and other ants and social insects could improve predictions of the response of these ecosystems to climatic change.

#### Topic Selection:

Genetics And Molecular Techniques

#### Title:

The draft genomes of *Aphaenogaster* species from across a biogeographic gradient

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#### Preferred Presentation Format:

Oral

First Presenting Author

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**Would you like to volunteer as a session presider?** No

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