ABSTRACT (ESA 2017): The draft genome of *Aphaenogaster* species from across a biogeographic gradient

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**Background/Question/Methods**

Climate change rates are currently on track with the worst case scenarios, resulting in both terrestrial and aquatic ecosystem responses. Ants play important roles in ecosystems, including seed dispersal, which is a known factor in determining the rates of shifts in the range of many plant species. Recent field and laboratory climate experiments have demonstrated that ant communities in Eastern Forest ecosystems are likely to respond to climate change and that genetically based traits involved in heat and cold tolerance are likely to contribute to community dynamics. To address the need for detailed genetic information about the ant communities of this region, we conducted whole genome sequencing of six species of ants from the genus *Aphaenogaster*: including, *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, MA). Raw sequences were processed to remove chimeric and contaminant sequences and assembled using ALLPATHS-LG with an additional post-assembly processing using Pilon, which reduced the gaps in coverage by 3.1% on average for an average reduction of 3.9 Mb of gaps.

**Results/Conclusion**

The genomes of all six species were successfully sequenced; and both raw sequences and the assembled genomes are currently stored at Harvard Forest (Petersham, MA). Assemblies and annotation are currently 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 analyses using linear regression 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 the contribution of genetic variation underlying the response of these communities to climatic factors. Further work investigating the variation in genomic content (e.g. gene ontology or GO terms) and mapping of target coding regions from from previous experimental transcriptomic work on *Aphaenogaster* and other ants and social insects could improve predictions of the response of these ecosystems to climate change.