



# International Teams Publish Three New Ant Genome Studies

February 01, 2011

## International Teams Publish Three New Ant Genome Studies

By [a GenomeWeb staff reporter](#)

NEW YORK (GenomeWeb News) – In a trio of papers appearing online last night in the *Proceedings of the National Academy of Sciences*, international research teams reported that they have sequenced three new ant genomes: those of the Argentine ant, red harvester ant, and fire ant.

By comparing the newly sequenced genomes with those of other ant and insect species sequenced previously, those involved in the studies are gaining insights into the genetic and epigenetic mechanisms underlying everything from ant evolution and social structure to chemical communication strategies and insecticide resistance.

For instance, the studies suggest that — as in bees — DNA methylation may contribute to the process by which ants sharing the same genetic sequence become specialized into phenotypically and behaviorally different castes.

"Our analysis suggests that ants may utilize the same genetic system as honeybees to create their social structures, although we have yet to understand whether the process works in exactly the same way across species," San Francisco State University biologist Christopher Smith, who was an author on the Argentine and red harvester ant genome papers, said in a statement.

In the first of these studies, an international team led by investigators at San Francisco State University and the University of California at Berkeley used Roche 454 and Illumina sequencing to tackle the genome and transcriptome of the Argentine ant, *Linepithema humile* — an invasive pest that often attacks native ant populations.

Along with clues about how Argentine ants have spread to new parts of the world, the genome sequence is expected to offer insights into some of the genetic adaptations that help the ants resist insecticides and other control efforts.

"When the Argentine ants invade, they devastate the native insect communities while promoting the population growth of agricultural pests," University of California at Berkeley environmental science researcher Neil Tsutsui, who is co-corresponding author on the Argentine ant genome paper and a co-author on the red harvester ant study, said in a statement.

"This genome map will provide a huge resource for people interested in finding effective, targeted ways of controlling the Argentine ant," he added.

Using the Roche 454 GS FLX Titanium and Illumina Genome Analyzer, the researchers generated sequence representing 215.6 million bases, or about 86 percent of the 250.8 million base Argentine ant genome, to about 23 times coverage.

The team also got transcriptome data for ants from different age groups, castes, and locations by sequencing complementary DNA with the Roche 454 GS FLX. DNA from the study came from a California ant colony.

Their subsequent analyses of the genome turned up 16,123 protein-coding genes coding for 16,177 transcripts. Among the gene families that seem to have been expanded in the ant compared to the honeybee, *Drosophila melanogaster*, or the parasitoid wasp *Nasonia vitripennis* were cytochrome P450 genes as well as genes coding for odor and taste receptors.

"Ants are ground-dwellers, walking along trails, and for many, living most of their lives in the dark, so it makes sense that they would have developed keen senses of smell and taste," Tsutsui noted.

Meanwhile, an international research group led by investigators at the University of Lausanne found an abundance of detoxification, odor receptors, and lipid processing-related genes when they used Roche and Illumina platforms to sequence 352.7 million of the roughly 484 million bases that make up the genome of another pest species: the fire ant, *Solenopsis invicta*.

Along with DNA methylation-related genes hinting at epigenetic mechanisms in the genome, the researchers found

other functional clues based on the ant's gene repertoire. For example, their analyses suggest the *S. invicta* genome houses as many as 400 odor receptor genes, including 297 that seem to code for full-length proteins.

"Comparison with other genomes shows that the fire ant genome has many unique properties probably associated with the complex social life of this species," corresponding author Yannick Wurm, an ecology and evolution researcher affiliated with the University of Lausanne and the Swiss Institute for Bioinformatics, and his co-authors concluded.

"[T]he sequencing of the fire ant genome provides the foundation for future evolutionary, biomedical, sociogenetic, and pest-management studies of this important pest species and facilitates comparisons with other social species," they added.

For their part, an Arizona State University-led team used Roche 454 sequencing to sequence the genome and transcriptome of the red harvester ant, *Pogonomyrmex barbatus*.

Again, researchers detected genes expected to contribute to DNA methylation, as well as an abundance of genes coding for proteins related to detoxification, odor receptors, and chemical detection.

A fourth paper describing efforts to sequence and characterize the leaf cutter ant genome is reportedly set to appear later this month in *PLoS Genetics*.

## Related Stories

- [Eurofins MWG Operon to Offer Sequencing Services on Roche's GS Junior](#)  
September 28, 2010 / [In Sequence](#)
- [CIRAD, Penn State-Led Team Reports on Chocolate Genome Sequencing Effort](#)  
December 27, 2010 / [GenomeWeb Daily News](#)
- [Researchers Sequence Woodland Strawberry Genome](#)  
December 27, 2010 / [GenomeWeb Daily News](#)
- [Combination of Sequencing Techniques IDs Potential Tumor Suppressor Genes](#)  
December 7, 2010 / [In Sequence](#)
- [New Products](#)  
October 5, 2010 / [In Sequence](#)

