2004 EPA Star Graduate Fellowship Conference

Next Generation Scientists—Next Opportunities



Genetic structure of a world-wide ant invasion

Background

- The little fire ant *Wasmannia auropunctata* is native to the Neotropics but has numerous invasive populations throughout the world, including the US (Hawaii and Florida), many Pacific islands and Central Africa (Cameroon and Gabon).
- By tending plant pests *W. auropunctata* can directly harm agriculture. Its surprisingly painful sting makes work on infested farms nearly impossible.
- *W. auropunctata*'s arrival is usually correlated with decreases in abundance and species richness of ants and other invertebrates. Reports of attacks on vertebrates are also common.

Study goals

Ultimately, I plan to use the multiple introductions of *W. auropunctata* for studying parallel evolution of invasive populations. However, the following questions must be addressed first:

- I. Is 'auropunctata' just one species?
- **II.** Given *W. auropunctata's* large native range, where are the sources of invasive populations?
- **III.** What are the genetic relationships between populations?



W. auropunctata worker scavenging dead bullet ant.

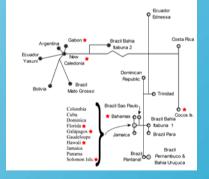
Results



Distribution and sampling of *W. auropunctata*. Native range is outlined in black. The two types of circles represent two different clades (see below).

Methods

- Sequenced COI/COII region of mtDNA, including tRNA leucine and an intergenic spacer
- Genetic relationships determined using traditional phylogenetics (not shown) and a genotype network.
- Relationships used to test McGlynn's (1999) observation that invasive populations are smaller in size then native population using Purvis and Rimbaut's (1995) algorithm.



Median-joining network of *W. auropunctata* populations. Invasive populations are marked by stars. Note that the edge joining the two clades (grey and black-dotted) has been scaled down by a factor of 2.5.

- Two genetically distinct sympatric clades, according to both intraspecific network and traditional phylogenetic models. Both clades are invasive.
- At least three separate source populations:
 - ➤ Caribbean region → Florida & Pacific
 - ➤ South America → Africa & New Caledonia
 - ➤ Central America → Cocos Island
- <u>High genetic relatedness</u> of invasive populations.
 - > Low power for testing relative size of native vs. invasive populations (N=3, Wilcoxon signed rank test P=0.091).

Future directions

- Are the Caribbean populations native?
 - ➤ Fine scale genetic analysis.
- Are there two cryptic species?
 - ➤ Morphological and behavioral studies.

References

McGlynn, T.P. 1999. Am. Nat., 164: 690-9 Purvis A. & Rambaut A. 1995. CABOIS, 11:247-251

