



The University of Georgia

The Center for Tropical and Emerging Global Diseases

March 30, 2004

Dr. Jack Werren
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Dear Jack:

This letter confirms my enthusiastic support for your proposal to sequence the *Nasonia vitripennis* genome. As you know, fully sequenced insect genomes currently include *Drosophila melanogaster*, the mosquito *Anopheles gambiae* and the honey bee *Apis mellifera*. Projects on another mosquito, *Aedes aegypti*, the moth *Bombyx mori*, and the beetle *Tribolium castaneum* are in progress or are soon to be initiated.

My enthusiasm for adding *Nasonia* to this list stems from two main considerations. First, a sequenced genome would greatly facilitate future studies in development and genetics that directly focus on *Nasonia* itself. This species has long been considered a model insect for genetic analysis due to the pioneering studies conducted by researchers beginning almost a century ago. Several genetic resources exist from this early work including linkage maps and numerous characterized mutations. *Nasonia* continues to be the main study organism for several research groups investigating topics ranging from population level questions about speciation processes, as you work on, to developmental genetics. Future research on this model species would clearly expand further if its genome was available.

Of equal importance for sequencing *Nasonia* would be to have a second hymenopteran genome to complement that of the honey bee. As you well know, the order Hymenoptera is an incredibly species rich group (>200,000 species) with arguably the greatest diversity in life history of any animal taxon. *Nasonia* belongs to the superfamily Chalcidoidea which is phylogenetically quite distant from the honey bee. Moreover, most chalcidoids, unlike the honey bee, are parasites of other arthropods. Many of these chalcidoids are of significant economic importance as biological control agents of agriculturally and biomedically important arthropod pests. Having the *Nasonia* genome as a resource could potentially improve biological control by facilitating identification of genes in related species that could be used to enhance their performance as biological control agents. In terms of more fundamental science, *Nasonia* and other related chalcidoids exhibit pronounced differences in early development, sex determination and associations with symbiotic/pathogenic microorganisms relative to the honey bee and other insects. Many of these alterations have likely arisen as a consequence of having a parasitic lifestyle.

Understanding the function and evolution of these complex traits at the molecular level, however, would be hugely helped by having the *Nasonia* genome as a comparative resource.

In summary, sequencing of the *Nasonia* genome should be a high priority because of the critical mass of researchers working on this species and near relatives, the prominent group of insects to which *Nasonia* belongs, and the importance of these organisms economically.

Sincerely,

A handwritten signature in cursive script that reads "Mike".

Michael Strand
Professor