

UNIVERSITY OF ILLINOIS
AT URBANA-CHAMPAIGN

G. William Arends Professor of Integrative Biology
Department of Entomology
505 S. Goodwin Avenue
Urbana, IL 61801-3799



23 June 2004

Prof. John Werren
Department of Biology
University of Rochester
Rochester, NY 14627

Dear Jack:

I am pleased to write in support of your proposal for a *Nasonia* genome project. I led the successful effort to place the honey bee in the high priority category for sequencing at NHGRI, so I know something about the large effort you are engaged in.

There are great reasons to sequence a *Nasonia* genome that have to do with various aspects of *Nasonia* biology, which you and others have developed so nicely over the years. I am sure you'll be covering this in depth so I will confine my letter to the compelling reasons relating to comparative genomics.

The honey bee (*Apis mellifera*) is the first social insect and the first member of the Hymenoptera to have its genome sequenced. *Nasonia* would be the second member of the Hymenoptera, but it is not a social insect. Rather, it is part of the suborder (Symphyta), which does not contain any of the social insects (all hymenopteran social insects –ants, bees, wasps-- are in the second suborder, Aculeata). But as a hymenopteran, *Nasonia*, like the honey bee, has the haplodiploid mode of genetic determination. As such it is perfectly positioned for comparative genomic analyses that probe whether certain features to be discovered in the bee genome are related either to the sociality or haplodiploidy. Sequence divergences between honey bee and the other insects with sequenced genomes (flies and one beetle) can be much better interpreted with another hymenopteran insect. Both haplodiploidy and the evolution of eusociality are major phenomena, and with creative use of *Nasonia* and *Apis* genomes, we would be well positioned to begin to look for their signatures on genome organization and function, opening up important new lines of study.

Another benefit of having a *Nasonia* genome sequence will be to help identify genes of behavioral significance. The honey bee community is finding it quite fruitful to use genes identified in *Drosophila* as candidate genes for social behavior, and in the process getting insights into how molecular pathways involved in solitary behavior can evolve to serve social contexts. Because *Nasonia* displays several interesting behaviors (courtship, mating, aggression) that have been well studied, we can extend this approach, again taking advantage of the fact that *Nasonia* is in the same order as the honey bee but is not social.

My lab is gearing up for a large-scale analysis of gene regulation, first looking for conserved *cis*-regulating factors. We seek to understand the mechanisms of social regulation of gene expression, using the honey bee model. We believe this line of study has the potential to generate insights of broad general interest, with implications for the understanding of some forms of mental illness. Having the *Nasonia* genome will be of great benefit to our efforts, again because of its phylogenetic position vis a vis the honey bee.

In summary, comparative genomics would greatly benefit from having a second hymenopteran genome sequence, especially one that holds as much promise as *Nasonia*, and the bee community is extremely supportive of your efforts.

Best of luck.

Sincerely yours,

Gene E. Robinson

Gene E. Robinson
G. William Arends Professor of Integrative Biology
Professor of Entomology, Cell & Structural Biology, and Animal Biology
Director, Neuroscience Program
Director, Bee Research Facility