

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

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Dear Jack,

I am writing in support of the proposal to sequence the genome of *Nasonia vitripennis*. I have long believed that *Nasonia* was poised to be an important model system for evolution, development, and behavior. As you know, I work with honey bees and though the genome sequence has been a tremendous asset, we still have fundamental biological problems to overcome that do not exist for *Nasonia*. For instance, *Nasonia* can be easily mated, large populations of reproductives maintained in small vials, take up very little laboratory space, and lines can be put into diapause when not being used. The genome consists of just 5 chromosomes with a good set of visible markers. You can make recombinant inbred lines with *Nasonia*, something that I cannot do with bees. In addition, you have a growing community working on *Nasonia* in the US and Europe. *Nasonia* also have interesting behavior that has been genetically mapped and interspecific crosses can be made to study genetic changes that are associated with speciation. You already have multiple genomic maps and behavioral and morphological QTL.

I think the prospects of a *Nasonia* genome sequence are very exciting. It would nicely complement the honey bee genome sequence by providing an outgroup to compare against. *Nasonia* and honey bees differ in their morphology, evolutionary history, and ecology, but they are both haplodiploid, a great asset for genetic studies. I am 100% in favor of this project. Good Luck!

Sincerely,

Robert E. Page, Jr.  
Professor and Chair