



COLLEGE OF NATURAL AND  
AGRICULTURAL SCIENCES  
DEPARTMENT OF ENTOMOLOGY - 041  
FAX: (909) 787-3086

RIVERSIDE, CALIFORNIA 92521-0314

Dr. J.H. Werren  
Department of Biology  
University of Rochester  
Rochester, NY 14627  
USA

Riverside, July 14, 2004

Dear Jack

I am very excited to hear about the possible sequencing of the *Nasonia vitripennis* genome. *Nasonia* has long been the model system for genetics in Hymenoptera, and having its genome sequenced will allow us to go beyond just the phenotypic studies that have been done on this wasp. Many important aspects of hymenopteran genetics such as the sex determination and factors like dosage compensation because of its haplo-diploidy will now become topics that can be studied. The sex determination genes will be particularly interesting because the recent findings of the genes involved in the sex determination of the honey bee. It is well known that the sex determination system in *Nasonia* differs from that of the honeybee, it is assumed to be more derived. The transition of the "honeybee" system to the "nasonia" system can be studied at the gene level once the *Nasonia* genome has been sequenced.

In the FIBR-NSF program the *Wolbachia* found in *Nasonia* will be sequenced. The interactions between the *Nasonia* genes and those of the *Wolbachia* will now be open to study through the use of gene chips and large strides can be made in understanding the interactions between these two organisms. This will be particularly useful in comparative work with the *Drosophila-Wolbachia* system where both the host and the *Wolbachia* have already been sequenced.

*Nasonia* belongs to the Chalcidoidea, the group of parasitoids used most frequently in biological control programs of pest insects. It would be extremely beneficial to have available the complete genome of a Chalcidoid to start to unravel the genetics of such behaviors as host searching and host specificity. Understanding the genetic basis of these behaviors is very important particularly in the light of the recent concerns about potential host switching by introduced parasitoids.



Therefore in conclusion both from the fundamental perspective and from the applied perspective, the choice of sequencing the genome of *Nasonia vitripennis* is excellent. No other member of the Hymenoptera could be a better choice to sequence in addition to the already sequenced Honey bee. I hope that the *Nasonia* genome will receive a high priority.

With Regards,

A handwritten signature in dark ink, reading "R. Stouthamer". The signature is written in a cursive style and is underlined with a single horizontal line.

Richard Stouthamer  
Associate Professor of Entomology & Associate Entomologist  
Department of Entomology  
University of California  
Riverside, California 92521