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SANTA BARBARA • SANTA CRUZ

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

RIVERSIDE, CALIFORNIA 92521-0314

Telephone (909) 787-6351
E-mail john.heraty@ucr.edu

June 28, 2004

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

Dear Jack,

I wanted to let you know that I wholeheartedly support *Nasonia vitripennis* (Walker, 1836) as a candidate for the genome project. This is a very important taxon, both in terms of its biological background and its phylogenetic position within the Hymenoptera. Recently, the genome of *Apis mellifera* L. was sequenced. This is also a member of the Hymenoptera, but it occupies a very distinctly different branch of the wasp phylogenetic tree. In terms of comparative genomics, there is no better choice than a parasitoid wasp within the superfamily Chalcidoidea. Because they are largely parasites, Chalcidoidea are ecologically and economically one of the most important groups of insects in controlling both natural and agricultural insect populations. More than 22,000 species of Chalcidoidea are described, and more than 400,000 species are estimated to exist. For biological control, species of Chalcidoidea are responsible for the greatest number of successes for importations against introduced agricultural pests. Biologically, *Nasonia* is probably one of the most studied groups of wasps, with at least 278 published references over the last 40 years in all areas of their biology. In contrast to the pollen-feeding, eusocial *Apis mellifera*, *Nasonia* is a parasitoid of other insects, it is reproductively controlled by the bacterial genus *Wolbachia*, and it tolerates high levels of inbreeding that are atypical of most insects.

Phylogenetically, *Nasonia* are very distant from *Apis mellifera*. There are 19 superfamilies of Hymenoptera, with approximately 113,000 species described. *Apis* and *Nasonia* both belong to the suborder Apocrita or thread-waisted wasps. Apocrita is further divided into the Aculeata, which includes all of ants and generally larger wasps and bees, and the Parasitica, an informal grouping of all of the primarily parasitic wasps. *Apis* is a derived lineage within the Apoidea in the Aculeata, whereas *Nasonia* (Pteromalidae: Pteromalinae) is a derived member of the Chalcidoidea. Except for the inclusion of one of the sawfly groups, no two taxa could be chosen to better represent the most divergent lineages within Hymenoptera. The prospect of having the complete genome sequenced for both of these taxa is exciting. This would allow for comparisons

of change across a phylogenetically old divergence (about 100-160 million years). This comparative information would be critical in assessing changes in sequence, function, amino acid change, gene duplication, gene order and other important aspects.

Currently, the National Science Foundation is supporting a Tree-of-Life grant for the Hymenoptera. The focus of this research is on the phylogenetic relationships of all Hymenoptera using a broad survey of both morphology and molecular data. *Nasonia vitripennis* has been chosen as one of 99 'core' species of Hymenoptera that will require an intensive survey of both character systems. With the results of this study, we hope to be able to determine both the relative placement of taxa, and their estimated time of divergence. A genome project on *N. vitripennis* would only enhance the amount of information available from both studies.

Again, I strongly support using *Nasonia vitripennis* for the genome project.

If you need any further information, please contact me.

Sincerely,

A handwritten signature in black ink, appearing to read "John Heraty". The signature is fluid and cursive, with the first name "John" and last name "Heraty" clearly distinguishable.

John Heraty
Associate Professor

new phone as of 07/04: (951) 827-6351