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Dr. John Werren
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RE: Full genome sequencing of *Nasonia vitripennis*

Dear Dr. Werren,

I am writing in support of your proposal to fund the genome sequencing of the chalcidoid wasp *Nasonia vitripennis*. This is a good candidate for genome sequencing for the following reasons.

***Nasonia vitripennis* is a member of a species rich, biologically diverse, economically important group of insects, the Chalcidoidea. Many aspects of the biology of this group are still somewhat mysterious.**

- *N. vitripennis* would be the first species sequenced from the superfamily Chalcidoidea. This is a very diverse superfamily of insects, with >25,000 species described, and many species remain undescribed. Most chalcidoids are parasitoids, insect parasites that kill their host during development. Chalcidoid parasitoids play a critical role in regulating insect populations in nature, as well as in agricultural systems, where they are used for the biological control of economically important pests.
- Chalcidoids have an extraordinary diversity of life histories and developmental pathways. Some chalcidoids develop inside their still living and growing hosts, while others kill or paralyze their host or develop externally. In some species, females develop only on one type of host and males develop only on another type (sometimes females of their own species). In some chalcidoid species, early mitotic divisions are syncytial, like *Drosophila*, and others in which holoblastic

cleavage takes place, more like a mammal. Some of these radical differences in development and life history occur among related species. Systematic analyses of the Chalcidoidea suggest this group radiated extremely rapidly, yet little is known about the basis of this adaptive radiation. A completed chalcidoid genome holds the promise of identifying the genetic basis of some of these diverse life history traits.

- *Nasonia vitripennis* is a species with a long history of genetic studies dating from the 1940s, when *Nasonia* vied with *Drosophila* as a model genetic system. Many stocks with different mutant phenotypes have been kept since this time and could be explored in more detail once the genome sequence was completed. Despite this promising early history, until recently few molecular genetics have been done on this creature, or indeed on other chalcidoids.
- *Nasonia vitripennis* can be easily handled and cultured, allowing experimental manipulation. Single females can be easily isolated in tubes with fly pupae as hosts. The hosts can be purchased from commercial insectaries. The eggs are laid on the outside of the fly pupa so can be manipulated. Finally, and perhaps most importantly, diapause can be induced in *Nasonia*, so that stocks can be held without any maintenance in an incubator for 1-2 years. To my knowledge, *Nasonia* is the only chalcidoid for which the diapause induction technique has been mastered. Diapause induction allows a large number of stocks to be maintained while simultaneously reducing the risk of contamination.
- Several aspects of chalcidoid biology are unknown, and research would be greatly aided by a sequenced genome. A few examples follow: a) The mechanisms of sex determination in chalcidoids is still unknown. It is clearly different from the single locus sex determination system of aculeates (e.g. ants, bees and social wasps) but none of several models explain all of the evidence. A combination of both comparative genomics and gene expression studies will be required to identify the underlying mechanism. b) Many chalcidoids show dramatic differences in behavior after mating, yet little is known about the role of male seminal proteins in causing these behavior changes. In contrast, the seminal proteins of *Drosophila* are becoming well characterized and these gene sequences could be studied for homology with *Nasonia*. c) Lastly, in a superfamily of parasitoids more closely related to aculeate Hymenoptera, the ichneumonoids, it has been found that wasps carry virus-like particles encoded by nuclear DNA that play an important role in parasitoids overcoming host immunity. There is not yet any understanding of how host immunity is overcome in chalcidoids, however, and what sets the physiological limits to host range. A completed genome would allow gene expression and deletion studies that would likely identify some candidate genes mediating host immunity in chalcidoids.

To conclude, a completed *Nasonia vitripennis* genome would offer 1) the opportunity to do comparative studies with other completed genomes of insects including *Drosophila* and the honey bee, *Apis mellifera*, as well as 2) greater access to genome wide profiling

tools and knockout capacity through techniques like RNAi. These expanded approaches offer potential insight into the most unique aspects of *Nasonia* and chalcidoid biology as well as fundamental life history strategies it shares with a wide range of insects.

Sincerely,

Martha S. Hunter

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Section

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