LOYOLA COLLEGE IN MARYLAND
—1852—

23 July 2004

Dr. Jack Werren
Department of Biology
University of Rochester
Rochester, NY

Re: Nasonia Genome Initiative

Dear Dr. Werren,

I offer my full and enthusiastic support for the Nasonia Genome Initiative. As you have clearly outlined, sequencing the genome of *Nasonia vitripennis* is not only worthwhile based on scientific merit, it also offers to greatly advance efforts to improve global human health and agriculture. Venoms from parasitoids in the family Pteromalidae, including *N. vitripennis*, have been shown to be highly lethal and specific for several species of flies that are of significant medical and veterinary importance. For these venoms to reach their full potential in fly control programs, venom genes encoding insecticidal proteins must be identified, cloned and incorporated into delivery systems that will be used to target vectors of disease and agricultural pests. Sequencing the Nasonia genome is a key step to allow identification of these venom genes. Once identified, the venom gene sequences can then be used to rapidly isolate similar genes in other species of parasitoids that produce potent insecticidal venoms.

Parasitoid venoms target tissues that typically are not exploited by current synthetic insecticides. These venoms also seem to be unique in their mode of action as evidence is accumulating that at least with some venoms, G-protein dependent signal transduction pathways are manipulated to elicit cell death. This establishes a linkage between venom proteins and both apoptotic and oncotic death pathways, and suggests that these venoms may be useful tools for studying various aspects of cell death and signal transduction, and potentially they may be used to treat or block the effects of aging, pathogens, or even fat accumulation associated with obesity. These possibilities can only be realized by having easy access to venom proteins for laboratory and clinical testing. In goes without saying that the Nasonia Genome Initiative will provide

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great strides in identifying and cloning venom genes to be used in the above mentioned investigations.

Below is a brief description of ongoing projects in my laboratory that will be significantly impacted by the Nasonia Genome project. Please let me know if I can assist this effort in anyway.

With Regards,

David Rivers
Associate Professor of Biology

Relevance to Human Health: My lab has shown that venom from *Nasonia vitripennis*, as well as several closely related pteromalids, is highly potent and selective for several dipterans that are vectors of disease of humans, livestock, and poultry. Of particular significance to human health is our recent finding that venom is highly toxic to several mosquitoes that are vectors of such diseases as malaria, encephalitis, yellow fever, and West Nile. Efforts are underway to isolate insecticidal proteins, and to identify and clone venom genes with the hope of constructing biorationale insecticides. It goes without saying that such an undertaking would benefit enormously by the Nasonia genome project.

Genomic and generic resources: In a collaborative project with Dr. Mary Lowe (Physics Department) at Loyola College, we are attempting to develop a robotic PCR detection assay that allows rapid assessment of parasitism rates and species abundance in parasitized stable flies and house flies collected from poultry and dairy facilities. In brief, the method is based on unique ITS sequences of ribosomal DNA found in key indigenous parasitoid species. This work is in its early stages; Dr. Lowe is anticipating generating unique primers for *Nasonia vitripennis* and other pteromalids, and the amplified ITS regions will be sequenced and deposited in GenBank. Currently, sequences have been identified by Sue Ratcliffe's (U. of Illinois) and David Taylor's (USDA-Nebraska) lab for Muscidifurax species that we are using as a template.