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Cornell University
Biotechnology Building, Ithaca, NY 14853-2703

July 15, 2004

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

Dear Jack,

I am writing in support of the *Nasonia vitripennis* genome sequencing proposal that you and colleagues are putting forward. You build a strong case for this project, demonstrating that there are well documented inbred lines, that there are excellent genetic resources including maps available, that the community is highly active and would use the sequence to leverage a wealth of interesting science, and that there are compelling reasons to understand the genomics of a parasitoid wasp for purposes of biocontrol. An issue that makes me particularly excited about *Nasonia* is that most parasitoids have mechanisms for inactivating the innate immune system of their host. In many cases, parasitoid wasps use either active polydnavirus, transferred with the egg, to either inactivate or overcome the host immunity. A deeper understanding of the *Nasonia-Musca* interaction would likely lead to approaches for inactivating innate immunity in a wide variety of harmful insects, and could greatly improve the efficacy of microbial biocontrol. Study of host-parasitoid interaction is of great intrinsic interest to evolutionary biologists, and having genome sequences would enable much more rapid progress in this area. The idea of doing shallow coverage of two additional species immediately opens the door to evolutionary analysis that allows genome-wide inference of genes that show patterns of divergence consistent with positive selection. Such analysis could serve to direct efforts to identify functional differences, and those associated with host interaction could be highly informative. In sum, this is a timely and very well motivated study.

Sincerely,

A handwritten signature in black ink that reads "Andrew G. Clark".

Andrew G. Clark
Professor, Molecular Biology & Genetics