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July 19. 2004

Dear Jack,

I am extremely excited about the Nasonia genome project. Let me explain. The sequenced and annotated Drosophila genome has had a tremendous impact on basic and applied research on basic and applied research. Three quarters of the human disease genes have a structural homolog in humans and it appears most of these are functionally conserved as well. Drosophila is proving a excellent model organism for addressing outstanding issues in cancer and a wide array of other human diseases including neurological, immune, endrocrine, and behavioral. In addition, Drosophila and other insects possess potent anti-microbial peptides and these are likely to prove to be an excellent source of novel antibiotics.

Given the extensive evolutionary distance between Nasonia (Hymenoptera) and Drosophila (Diptera), it is likely that Nasonia will possess homologs to those human disease genes not present in Drosophila. In addition comparative genomics between genes conserved in all three organisms (Nasonia, Drosophila, Human) will provide insights into evolutionary conserved domains within these genes. Sequencing Nasonia also will likely yield additional distinct anti-microbial peptides. An advantage of Nasonia over other Hymenoptera, is that well developed genetic approaches are available for functional analysis of identified genes. As Nasonia is a haplo-diploid, powerful saturation F1 genetic screens for recessive mutations are readily accomplished.

On a final note, Nasonia provides the best opportunity for understanding the molecular and cellular events controlling parthenogenesis. This is the only parthenogenetic organism in which genetic and cellular approaches are well developed. A fully sequenced genome would facilitate identification of the genes involved in this process. Although parthenogenesis is widespread and has independently evolved multiple times, little is known about this process. Elucidating the underlying mechanisms has important practical implications because a central feature of parthenogenesis is regulating centrosome number. Unregulated centrosome number is a common phenotype of all cancers. These studies also may eventually lead to a means of inducing parthenogenesis in organisms that do not naturally undergo parthenogenesis. Inducing development without contributions from the male has a number of advantages including the generation of large numbers of isogenic progeny.

Sincerely,

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