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January 24, 2008

Small Organisms, Giant Questions: *D. Melanaogaster's* use in the Public Interest

Surrounded by large themes of national prominence, fruit fly research ironically became an issue during the 2008 Presidential Campaign, in which John McCain and his running mate Sarah Palin criticized research funding on the small organisms.<sup>1</sup>

Regardless of politics, their comments pose an important question: is there a sound public policy reason why sequencing the DNA of fruit flies should be funded? Thirteen species of fruit fly have had their genomes sequenced according to the National Human Genome Research Institute's database.<sup>2</sup> This level of data leads to two important questions. First, is there a value in sequencing the most common fruit fly – *drosophila melanogaster* – and second, is there a value of sequencing 12 other related organisms? The answer in both cases is yes, but for different reasons. Scientists often use “model organisms” – species that are simpler than humans yet retain important components of our biochemistry or anatomy – to investigate research questions without the logistical issues of human experiments. This concept underpins the answer to the first question – fruit flies are a model organism for human genetics and development. Answering the second question involves the concept of “comparative genomics” – the study of multiple genomes and the ways in which they are interrelated. Sequencing

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<sup>1</sup> <http://www.insidehighered.com/news/2008/10/28/palin>

<sup>2</sup> <http://www.genome.gov/10002154>

twelve other species can provide a rich set of data by which to compare fruit fly physiology and chemistry, and by extension, that of humans. In both cases, sequencing these genomes has valid public benefits.

By using the common fruit fly *D. melanogaster* as a model organism, scientists can create experiments to investigate key questions of genetics and development. *D. melanogaster* is the most common model organism for humans and it also has one of the longest experimental histories of any model organism in biology.<sup>3</sup> The length of this history makes it convenient to continue studying it, since the amount of data available on the species is prodigious. In a mid-January PubMed search, titles of more than 12,000 articles mention the species, and almost 32,000 reference the species in the body of their arguments. Due to the quantity of data, scientists can focus on very specific questions in their experiments, instead of “reinventing the wheel” by studying other organisms. In economic terms, using fewer species is more efficient than studying many, since the underlying biological processes in many cases has varied little over evolutionary history.

Due to its underlying similarities to humans, *D. melanogaster* provides important insights into critical biological processes in humans. A survey of some of the recent connections shows just how diverse the benefits can be. According to a recent release in Science Daily, scientists studying the fruit fly’s brain have been able to isolate areas of memory. Understanding the mechanism of memory in the fruit fly may lead to understanding of human memory, with applications to neurological disorders like

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<sup>3</sup> [http://genome.wellcome.ac.uk/doc\\_wtd020807.html](http://genome.wellcome.ac.uk/doc_wtd020807.html)

Parkinson's.<sup>4</sup> An historical article from Science in the mid-1980s indicates that scientists may soon fully know the genetics behind early development (for example, how cellular tissues differentiate between a liver cell and a neuron). As the final paragraph of the article states, understanding this gene in *D. melanogaster* may lead to an understanding of human development, an area of intense study.<sup>5</sup> In fact, about a decade after this article, the Nobel Prize in Medicine was awarded to several scientists for their work on *D. melanogaster* and early development. As the press release from the committee notes, the genes they studied have direct counterparts in the human genome.<sup>6</sup> As these examples indicate, the sequencing of the fruit fly genome has and will continue to have great benefits for understanding human genetics and development.

The benefits of sequencing one species in the Drosophila family may seem obvious considering the broad research done on *D. melanogaster*, but the benefit of sequencing twelve other species of the same family may not be as readily obvious. However, not only are these closely related sequences beneficial, they open up a completely new area of scientific research with enormous implications for human health. Scientists use the concept of “comparative genomics” to detect the similarities and differences between diverse genomes to detect the evolutionary pressures on a species and the functions of individual genes. *D. melanogaster* and its related species provide a natural extension of the model organism concept – in this case, the creation of a model system of several species to detect phylogenetic differences between different species. This new research area is already moving at a fast pace. In a recent news

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<sup>4</sup> <http://www.sciencedaily.com/releases/2008/03/080324173545.htm>

<sup>5</sup> <http://www.sciencemag.org/cgi/reprint/224/4654/1223.pdf>

<sup>6</sup> [http://nobelprize.org/nobel\\_prizes/medicine/laureates/1995/press.html](http://nobelprize.org/nobel_prizes/medicine/laureates/1995/press.html)

article in *Science*, sequencing the twelve species of *Drosophila* led scientists to publish more than 40 papers on a variety of subjects. They noticed two major discoveries. First, some amino acid coding sequences did not always end at a stop codon – a result different from that taught in most biology courses. Second, they discovered the basics of how genes create a regulation network within a biological system. Such knowledge could help scientists explore the nature of human diseases.<sup>7</sup> A specific example of this technique may be worthwhile. In a research paper by B Hoopengardner, scientists wanted to understand the process by which cells recode certain RNA strands, changing adenosine bases to inosine. They used comparative genomics of a channel protein to detect this process. Understanding how this recoding takes place may open possible avenues to explore human neurological diseases.<sup>8</sup>

*D. melanogaster* and its related species provide scientists a strong framework to explore genetics and development with direct benefits to human health. *D. melanogaster* is used by scientists as a model organism that includes many of the same genes as humans. Work on the species has even led to a Nobel Prize. Sequencing other phylogenetically similar species gives scientists the option of using the modern technique of comparative genomics to explore questions of gene function and evolutionary pressure. Such techniques are at the heart of current genetic and development research. As this paper has demonstrated, there is a clear public interest in sequencing these species for the purpose of biological research.

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<sup>7</sup> “Fruit Fly Blitz Shows the Power of Comparative Genomics” DOI: 10.1126/science.318.5852.903

<sup>8</sup> Nervous System Targets of RNA Editing Identified by Comparative Genomics  
Barry Hoopengardner, Tarun Bhalla, Cynthia Staber, and Robert Reenan (8 August 2003)  
*Science* 301 (5634), 832. [DOI: 10.1126/science.1086763]