## Comment

## **Fly's time** Gregory A Petsko

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Genome sequences are coming so thick and fast these days that it's easy to forget when any new one guaranteed a cover article in *Nature* or *Science* - and occasionally, as in the case of the human genome, in both. I used to do a column about each new eukaryotic sequence as soon as it came out; I haven't felt the need to do that in quite a while. Soon there will be hundreds of bacterial genomes sequenced and dozens of eukaryotes, so I guess a certain jaded attitude is understandable. Still, it wasn't that long ago that any new one, especially from an important model organism, was considered so important that sometimes there were races between competing scientific teams to produce them.

Of all these races, those between teams from the public and private sector were the fiercest, involved the most colorful characters, and raised the most compelling issues. We remember the epic contest between Francis Collins' government-funded group and the rival band from Craig Venter's Celera Corporation to sequence the human genome, which led to a brokered announcement of a "tie", heralded by pictures of the team leaders posing uneasily with one another and President Clinton. We tend to forget, however, that these same battle-lines were drawn earlier, and not over the genome of *Homo sapiens* or any other mammal. They were drawn over the humble fruit fly, *Drosophila melanogaster*.

It is this struggle between, well, if not exactly God and mammon, then at least public mammon and private mammon, to sequence the fly genome, that is the subject of Michael Ashburner's new book, Won for All: How the Drosophila Genome Was Sequenced (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 2006, ISBN 0-87969-802-0). Mike (we aren't on a first-name basis, but you'll see in a minute why I call him that; as a matter of disclosure, I do know many of the participants in the story very well) is a well-known fly geneticist who has spent much of the past decade making significant advances in bioinformatics. He's one of the people responsible for the Gene Ontology (GO) database, which attempts to link the known functions or

attributes of genes and their protein products to well-defined pathways and processes in the cell. Because he moves easily between the worlds of genetics and computational biology, he was at the center of much of the action that took place between the summer of 1998, when Venter announced that he was going to sequence the fly genome as a warm-up for his whole-genome shotgun sequencing of the human genome, and November of 1999, when the *Drosophila* sequence, produced in record time by combining the results from Celera's shotgun data with the partial sequence information from the publicly-funded effort that had been going on for a number of years, was annotated in a frenetic two-week 'jamboree'.

The book isn't meant to be a detailed history of that period; rather, it's a very personal account of Mike's perceptions of, and interactions with, the other principals. We meet Gerry Rubin, the brilliant geneticist who had put together the public effort, which involved labs in both the U.S. (chiefly at Berkeley) and Europe (chiefly at the Sanger Center). Essential to the very idea of a publicly funded sequencing program was the immediate release of data to the whole community without restriction. We meet Gerry's private sector counterpart, the equally brilliant Craig Venter. Driven out of the National Institutes of Health by their refusal to back his program for sequencing expressed sequence tags (ESTs), Craig had founded first The Institute for Genome Research (TIGR), which had done the first genome sequence (Haemophilus influenzae) in 1995 by the same shotgun sequencing method, and then Celera, whose mission - totally antithetical to that of the public effort - was to make money by selling sequence information. We meet Suzi, Phil, Jim and a host of other characters. We frequently have no idea who they are when we meet them, because Mike nearly always calls them only by their first names, even when they are introduced into the story for the first time. To be fair, he does add their family names and a bit of bare-bones background information in footnotes. He loves footnotes. Oh god, does he love footnotes. I thought Oliver Sacks loved footnotes more than any writer I had ever encountered, but Mike puts him to shame. Won for All is 74 pages long. It has 161 footnotes. On many pages, the word count in footnotes is greater than that of the text. It really breaks the flow of the narrative to have to keep referring to them, but if you don't, you often have no idea what is going on. I wish Mike had just integrated most of that information into the story; lots of good writers manage to do that without losing the casualness of the style.

And this style is about as casual and breezy as you could ask for. Mike says he wrote this piece a number of years ago as a kind of therapy (only deciding to publish it now), and it does have something of the same stream-of-consciousness air as might come from an analyst's couch. Although this makes the book confusing at times, it doesn't make it uninteresting. One gets to know quite a lot about Mike as a person: he hates the airlines (who doesn't?), has a similar attitude toward Marriott hotels (again, makes sense to me), believes absolutely in openness in science, and in general seems the kind of chap it would be fun to hang out with. We learn how Gerry Rubin (the hero of the story, in many ways) immediately realized that the sensible thing to do in order to get the job done was to join forces with Craig Venter rather than to compete with him - I wonder how many people who had as much invested in their own program could have subordinated their own egos to the good of the cause so readily. We learn about the negotiations that went on between the fly genetics community and the corporation, which led to the sequence being available without restrictions as soon as it was complete. We learn about the skepticism in the sequencing community about the possibility of using the whole-genome shotgun approach on so large a genome; Craig was right about its power, as he was about ESTs and a number of other things. For me, the anxiety about the partnership with private enterprise seemed a bit silly at the time, and certainly does now; there was never a possibility that the fly sequence could have made the kind of money that Celera was ultimately looking for, so there was no incentive for them to try to keep it to themselves. The part of the book that I like the best is the description of the annotation jamboree. I always wondered what it was like in the heady few days when these first really important genome sequences were completed, and Mike really makes you feel like you were there.

Won for All concludes with two very good appendages: an Epliogue, by Scott Howley, and an Afterward, by Ethan Bier. The Epilogue is the best concise history of fly genetics I have ever read, and the Afterward is an excellent summary of what having a genome sequence can do for a field. Both of these short essays should be widely read. I hope Cold Spring Harbor Laboratory Press allows some organ with a large circulation to reprint them.

It's been my experience that nearly every nonfiction book I have ever read is at least twice as long as it need be. These days, authors seem to equate density, either of style or of

pages or both, with profundity and erudition. The result is usually neither, but rather tedious repetition. Frequently, one only needs to read the first and last chapters to have a very good idea of the entire argument. My little complaints about style notwithstanding, Michael Ashburner's book does not suffer from this problem. Won for All tells an engaging, historically important story in a generally entertaining fashion. By showing the results of open access to the Drosophila genome sequence, he makes, without preaching, the strongest case I have ever read for unfettered sharing of scientific results. I was rather sorry when it ended; I sort of wish it had been twice as long. I read it in one sitting, and it went very fast. But then, when you have a well-told tale with a happy ending, I guess time flies.