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Celera defends human sequence

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The publication this week (February 17) of an assessment of the quality, accuracy, and completeness of the human genome sequence produced by Celerain 2001 could reignite the controversy over the validity and independence of the data.

The article in the February 17 Proceedings of the National Academy of Sciences by Sorin Istrail and colleagues at Applied Biosystems in Rockville, Md., is in response to twopapers published by members of the Human Genome Project (HGP) - the publicly funded collaboration that simultaneously sequenced the genome (*Proc Natl Acad Sci USA* 2004, **101:**1916-1921).

"We hope it puts to rest, once and for all, all this whining that's been going on that the genome could not be assembled without the public data," J. Craig Venter, founder of Celera Genomics and coauthor of the paper, told us. "It's stopped in recent months, fortunately, but I think there's a lot of leftover upset because we came in and sequenced the genome so quickly. I think people are now starting to move on other issues. Fortunately."

He said that this publication was to set the scientific record straight and to put the information out where anybody can access it independently. The assembly now released to GenBank is the one described in the *Science* paper of 2001. "Nobody's ever happy to have their data attacked, and I'm quite pleased with it, actually; it's a good paper and it's a historic paper," he said. "[Senior GenBank Computational Biology Branch Investigator] David Lipman was very excited to have the data in GenBank, so I think it's a nice and a first all the way around."

Bob Waterston, professor and head of the Department of Genetics at the Genome Sequencing Center, Washington University in St. Louis School of Medicine, one of the leading critics of the Celera data, was not impressed. "I don't think there is anybody really interested in revisiting [the controversy], I mean it would have been good to have had this information 3 years ago," he told us. "I'm not sure what point he is making. If you look at the data, it still has lots of holes in it and it's not the finished sequence."

Waterston, a member of the HGP consortium, described the differences between the two approaches to sequencing the human genome as being like shredding up Sunday newspapers and trying to reassemble them from the shredded bits. Celera simply shredded the whole thing, but the public HGP cut the newspaper into sections before shredding it.

Celera argues that their approach is the more cost effective one, as it cuts out the intermediate step, but Waterston does not agree. "They've not completed the experiment," he said. "In *Drosophila,* Celera did a whole genome shotgun and then Gerry Rubin's lab spent 2 or 3 years on the process of trying to finish it, and they're still trying to do it... They didn't finish directly from the whole genome shotgun data, so was that more cost effective? It's an assertion, and it may be right, but I don't think it's really been tested."

"I think if there is sufficient quality information available, and now that it's really independent... it'll be interesting to compare the differences; and I presume most of them should be polymorphisms,"

Waterston said. "Some of them may be errors in one sequence or another, but it'll be interesting to have another human sequence to compare to the reference."

"I think that it's good to be going forward, I would see that as the major benefit," he said. "We only have one human sequence, and there are six billion out there, so it will be good to have two."

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