PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Mouse control

ArticleInfo		
ArticleID	:	4081
ArticleDOI	:	10.1186/gb-spotlight-20010510-03
ArticleCitationID	:	spotlight-20010510-03
ArticleSequenceNumber	:	152
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2001–05–10 OnlineDate : 2001–05–10
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

Pete Moore
Email: pete.moore@dial.pipex.com

With scientists and publicists still trying to make out that there is no competition, the race between Celera and the publicly funded sequencing effort completes another lap. This time the finishing line was the announcement of a draft sequence of the mouse genome.

This round of the competition had a staggered start, with Celera announcing that it had begun sequencing in April 2000, and the publicly funded Mouse Sequencing Consortium being initiated in October 2000. Unlike the sequencing of the human genome, when Celera and the HGP held hands to cross the finishing line together and publish their data simultaneously, Celera took this one alone.

On 27 April, Celera took first place, stating that its whole genome shotgun process had provided the company with a 6X coverage of the mouse genome, derived from three strains of mouse (129X1/SvJ, DBA/2J and A/J). Celera claims that its sequence covers more than 99% of the genome, with 95% in segments of at least 100,000 base-pairs and 80% in segments of at least one million base-pairs.

On 8 May, the Mouse Sequencing Consortium sent out a press release stating that its £40 million ($58 million) project has now got 3X coverage of the sequence from one strain of mouse (C57BL/6J - commonly called Black 6). Its sequence covers 94% of the mouse genome.

The senior co-ordinators were quick to pour praise on their own work:

"This is another validation of Celera's whole genome shotgun sequencing and assembly strategy," said Celera's president and chief scientific officer Craig Venter.

"This represents a landmark on a journey that will allow researchers all over the world to create new models of disease and to test potential therapies. Congratulations to the scientists at the Wellcome Trust Sanger Centre" said Director of the Wellcome Trust Mike Dexter.

"This is a great day for finding genes in the human," joined in Francis Collins, director of the National Human Genome Research Institute. The expectation is that comparing mouse and human sequences will allow researchers to identify previously unrecognised genes and regions that control their activity. "This is essentially using evolution's 'lab notebook' to understand how the genome works," explained Collins.

The same questions hang in the air as arose when the human genome was announced. Which sequence is better? But in this context, what is 'better'? The Wellcome Trust has at any rate already decided that the public data are all its researchers will need, and has told its grant holders that they cannot use Wellcome funds to pay for access to Celera data.

In the meantime researchers anticipate the next round of competition to culminate in the announcement of an annotated version of the mouse genome. Will Celera or the Mouse Sequencing Consortium squeak first?

References

1. Celera, [http://www.celera.com]

2. The Human Genome Project, [http://www.sanger.ac.uk/HGP/]

3. 'Craig Venter is 'Scientist of the Year' *BioMedCentral* 18 December 2000, [http://www.the-scientist.com/news/20001218/02]

4. Sanger Centre, [http://www.sanger.ac.uk]

5. The Wellcome Trust, [http://www.wellcome.ac.uk/en/1/hme.html]

6. National Human Genome Research Institute, [http://www.nhgri.nih.gov/]

7. Mouse genome page at the Sanger Centre, [http://www.sanger.ac.uk/Projects/M_musculus]

This PDF file was created after publication.