

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

Shotgun strategies

ArticleInfo		
ArticleID	:	4417
ArticleDOI	:	10.1186/gb-spotlight-20020307-01
ArticleCitationID	:	spotlight-20020307-01
ArticleSequenceNumber	:	83
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2002-3-7 OnlineDate : 2002-3-7
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

The two groups that published the draft sequence of the human genome last year used different experimental strategies. The public [Human Genome Project](#) used a hierarchical shotgun (HS) approach, whereas [Celera Genomics](#) chose a whole-genome shotgun (WGS) strategy. In the Early Edition of the [Proceedings of the National Academy of Sciences](#), three leaders of the Human Genome Project question the validity of Celera's claim to have generated their draft sequence by WGS (*Proc Natl Acad Sci USA* 2002, 10.1073/pnas.042692499). Celera assembled the draft sequence using experimental, random shotgun data and sequences from the HGP database that had been artificially 'shredded' into short fragments. Robert Waterston, Eric Lander and John Sulston suggest that this shredding exercise generated a 'perfect tiling path' with few gaps, which is far superior to that generated from random sequences of equivalent or greater coverage. It is therefore difficult to assess the contribution of the HGP data to the Celera assembly. They also raise concerns about how the WGS contigs were anchored to the genome. They conclude that the jury is still out on whether WGS alone could generate a complete sequence for a complex genome. The two sequencing groups also differed in their policy regarding the release of data to the scientific community. Waterston *et al.* end by stating - in what is perhaps a reference to Celera's corporate motto - that "when speed truly matters, openness is the answer."

References

1. The Human Genome Consortium paper: sequencing by collaborative mapping, [<http://www.genomebiology.com/spotlights/articles/SpotlightCompiler.asp?xml=20010213-2.xml&Status=Archive>]
2. The Celera paper: sequencing by random shotgun cloning, [<http://www.genomebiology.com/spotlights/articles/SpotlightCompiler.asp?xml=20010213-1.xml&Status=Archive>]
3. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]