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One year after "The Race" was officially declared a draw, the teams that sequenced the human genome are still squabbling about who was the true winner. The controversy centers around the different strategies used and whether the sequence published by [Celera Genomics](#) can really be considered a victory for whole-genome shotgun (WGS) methodology. In the Early Edition of the [Proceedings of the National Academy of Sciences](#), Eugene Meyers and colleagues from Celera [respond](#) to an [attack](#) by the leaders of the public human genome sequencing (HGS) project. They claim that their artificial shredding was performed on 677,708 'bactigs' and not the HGS genome assembly. The data were combined with 27 million mate-paired reads to create greater coverage. They say that the shredded data were insufficient to create a full assembly structure and that simulations based on shredding of the finished chromosome 22 sequence are misleading. Although the two published sequences are of similar length, the Celera scientists claim that theirs was superior because of better long-range contiguity and accuracy. They go as far as to jibe that "having 2.6 Gbp of data is not the same as having it properly assembled". In the same issue of [Proceedings of the National Academy of Sciences](#), Phil Green of the [Howard Hughes Medical Institute](#) and the [University of Washington](#) attempts to dispel some of the 'myths' that surround the sequencing race and laments that the competition may have done more harm than good as it produced "[widespread misinformation, exaggerated claims and a compromised product](#)".

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