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2010 : March 2010 - New Hot Papers : Jian Wang & Jun Wang Discuss Moving Towards a Personal Genome Era

**new hot papers - 2010**

March 2010



**Jian Wang & Jun Wang talks with *ScienceWatch.com* and answer a few questions about this month's New Hot Papers in the field of Molecular Biology & Genetics.**



Left to right:  
Jian Wang & Jun Wang

**Article Title: The diploid genome sequence of an Asian individual**

Authors: **Wang, J, et al.**

Journal: NATURE, Volume: 456, Issue: 7218, Page: 60-U1, Year: NOV 6 2008

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(addresses have been truncated.)

**SW: Why do you think your paper is highly cited?**

This paper is one of the representative papers which first demonstrated the application of next-generation sequencing technology to decipher a human genome. In addition, the paper studied an Asian genome, which is of interest for the community and also greatly expands the scope of the field of personal genomics.

**SW: Does it describe a new discovery, methodology, or synthesis of knowledge?**

Our paper provided a detailed description of the first Asian genome. As new sequencing technology was used, some analytical tools were also developed, including read alignment, genetic variations identification, as well as other bioinformatics methodologies.

**SW: Would you summarize the significance of your paper in layman's terms?**

We have deciphered the DNA sequence of an Asian individual.

In addition to mapping this genetic knowledge about one of the largest ethnic groups in the world, it also brings forward the possibility of providing genomes at a cost which is orders of magnitude lower than that found in the **Human Genome Project**

*"We think this paper is one of the symbols that indicate we are moving towards a personal genome era, where an individual's healthcare is personalized and one could*

(HGP).

It suggests that, in the near future, everyone could have an affordable personal genome and enjoy the benefits of personalized healthcare.

*have an early prediction, precaution, and prevention of diseases... "*

**SW: How did you become involved in this research, and were there any problems along the way?**

It has always been a goal of the Beijing Genome Institute (BGI) to finish the genome sequence of an Asian individual. When the technology became feasible for us to achieve it, we developed new bioinformatics methodologies, and thus began the sequencing.

There have been many problems throughout the entire process, including experimental difficulties in getting the new platform handled smoothly, getting a sense of the characteristics of the new types of data, and the development of a high-throughput bioinformatics analysis pipeline to deal with the gathering of data which lie far beyond what conventional tools could handle.

**SW: Where do you see your research leading in the future?**

We think it may serve as a demo case and protocol for genome re-sequencing studies using new-type sequencing data. It also enables researchers to study more human genomes and to characterize complete genomic patterns of information about the human population.

**SW: Do you foresee any social or political implications for your research?**

We think this paper is one of the symbols that indicate we are moving towards a personal genome era, where an individual's healthcare is personalized and one could have an early prediction, precaution, and prevention of diseases due to the availability of knowledge about one's own genome and genetic information.

It has helped change the current mainstream style of medical care from a focus on the curation of diseases to a concentration on keeping people healthy. We believe that the length and quality of individual lives will benefit greatly from further research and development in this field.

**Jian Wang, Ph.D.**

**Director**

**Beijing Genome Institute (BGI)**

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KEYWORDS: STRUCTURAL VARIATION; REVEALS; DISEASE; DNA.

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