

SHAPING THE FUTURE OF OMICS FOR ALL

BGI GENOMICS provides high-quality and affordable **WHOLE GENOME SEQUENCING SERVICES FOR RESEARCHERS.**

Powered by self-developed technological platforms and laboratories worldwide,

BGI, a genome sequencing organization headquartered in Shenzhen, China, has been rapidly expanding since 1999 to support milestone projects ranging from human, rice, silkworm to genetic diversity in the world's deepest ocean trench.

In 2021, Jian Wang, BGI co-founder and chairman, was part of an expedition to the western Pacific Ocean, helping to sample organisms living 10 km below the surface. "Our team is keen to support international collaborations, such as the Mariana Trench Environment and Ecology Research Project," says Wang. "We hope that the digitized genetic materials will shed light on questions about the origin of life, biodiversity, and extreme environmental adaptation."

BGI's sequencing capabilities have contributed to more than 50% of the world's genetic sequencing projects, including input to the Human Genome Project (HGP), according to George Church, a geneticist and professor at Harvard Medical

School. Results from the international research effort to determine the DNA sequence of the entire human genome were released in 2003.

BGI was set up in 1999 to participate and contribute to the HGP. Wang and his team completed the sequencing, assembly and analysis on the tip of the short arm of *chromosome 3*, which was then estimated to account for about 1% of the HGP.

The HGP was an important chapter for China, and the work contributed to BGI's development of technologies for new studies including the the first diploid genome sequence of an Asian individual, the International Giant Panda Genome Project, SARS, as well as surveys on Asian rice. Since April 2000, BGI team has enabled new understanding of the evolution and relationship between rice species, paving the way for improved quality, resilience and yield. The HGP broadens the scope for exploration and understanding of other organism genomes. The rice gene map was described in the April 2002 cover story of *Science*.

Jointly initiated by BGI, the Chinese Academy of Agricultural Sciences and the International Rice Research Institute, the '3,000 Rice Genomes Project', published in *Nature* in 2018, analysed the genetic variation, population structure and diversity among 3,010 diverse Asian cultivated rice, covering 92% of rice genes, and obtained 32 million high-quality single nucleotide polymorphisms (SNP) and insertion and deletion of nucleotides into genomic DNA (Indels), allowing researchers to divide Asian cultivated rice into subgroups more accurately.

Sequencing the genomes of Asian cultivated rice, *O. sativa Xian* Group (籼) and *O. sativa Geng* Group (粳), marks a milestone in agricultural research. Previously the groups were incorrectly named *Indica* and *Japonica*, which do not fully represent their relationship and evolution.

Shuaishuai Tai, a BGI Genomics researcher specializing in agriculture genetics, explains that through SNP analysis, and the comparative analysis of the genomes of structural variation

(SV), their work supports the multiple origin hypothesis of different rice lineages.

There are a large number of SVs in Asian cultivated rice, with an average of about 12,000 SVs per genome, which may be the genetic cause of *Xian/Indica* and *Geng/Japonica* hybrid sterility, as well as hybrid decline.

"One of the biggest challenges we overcame 10 years ago was the very low sequencing throughput, and scarce resources. In order to complete the sequencing of the rice genomes, BGI Genomics had to use all the sequencing capacity in Shenzhen and Hong Kong. But after years of innovation, sequencing power is now more than 100 times faster than in the early 2010s," says Tai.

"Around 2019, when we performed the Silkworm Pan-genome Project (sequenced more than 1,000 silkworm genomes) cooperating with Southwest University in Chongqing, China. The DNBSEQ-T7 sequencer, developed by MGI, could produce 6T of data in one day," adds Tai.



Chong Tang, deputy director of research and development department at BGI Tech.



Shuaishuai Tai, an agriculture geneticist in front of a Chinese character representing the rice species, *O. sativa Geng* Group (粳).



The '3,000 Rice Genomes Project', published in *Nature* in 2018, analysed genetic variation, population structure and diversity among Asian cultivated rice strains.

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BRING LIFE SCIENCES TO LIFE

Chong Tang, deputy director of research and development department at BGI Tech, has also led his team through a web-based system called Dr. Tom Data Visualization Solution (Dr. Tom), which promotes flexibility and innovations through convenient analysis, visualization, and interpretation of RNA data types.

Dr. Tom aims to enable researchers from different fields, as well as collaborators with little or no bench lab experience, to share their data and findings more easily. It has become one of the mainstream cloud RNA analysis platforms in China,

with more than 15,000 users scientists and researchers from more than 20 countries. "Our visualization feature is meant to be interactive for idea exchange, encouraging communications and collaborations," says Tang.

Ensuring a large amount of data runs smoothly across the network is another design priority for Tang. "Since the development of next-generation sequencing, processing the data produced is simply not possible for most computers," says Tang. "We are still improving our design, but what used to take a day to quantify genetic data mining now only needs one to two hours."

Affordable sequencing at a faster speed allows health professionals to apply genetic data and clinical practices in diagnosis and treatment. Since 2019, BGI has provided a rapid Whole Genome Sequencing (rWGS) service, executed with BGI's proprietary DNBSEQ™ technology platform, to accelerate large sequencing data. Designed for researchers working on time-sensitive experiments, and available for different branches of science, especially in health care, BGI can provide rWGS results within 10 business days, significantly accelerating the sequencing process.

In 2021, BGI Genomics teamed up with the West China Hospital of Sichuan University to complete the sequencing of 100,000 people with rare diseases within five years.

Using the world-leading sequencer to complete genome analysis and mutation information, the project aims to bring hope for an estimated 20 million people in China with rare diseases, while enhancing diagnosis and treatment standards. ■

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