SEQUENCING & GENOMICS

Elevating Science and Healthcare: MGI's DNBSEQ™ Technology Across Diverse Frontiers

About MGI

MGI Tech Co., Ltd. (referred to as MGI) is committed to building core tools and technology to lead life science through intelligent innovation. With a focus on R&D, production and sales of DNA sequencing instruments, reagents, and related products, MGI provides real-time, panoramic, and life course equipment and systems for precision medicine, precision agriculture, precision healthcare and other relevant industries. MGI is a leading producer of clinical high-throughput gene sequencers, and its multi-omics platforms include genetic sequencing, medical imaging, and laboratory automation.

As of September 30, 2023, MGI has more than 2,900 employees, and 36% of whom are R&D personnel. Founded in 2016, MGI operates in more than 100 countries and regions, serving more than 2,600 customers. It has established scientific research and production bases, global training and service network in many countries and regions around the world. MGI is one of the few companies in the world that can independently develop and mass-produce low-, medium- and high-throughput clinical gene sequencers from GB to TB. Providing real-time, comprehensive, life course solutions, its vision is to lead life science innovation.

VISION Leading Life Science Innovation

MISSION To Develop and Promote Advanced Life Science Tools for Future Healthcare

Find Out More ...

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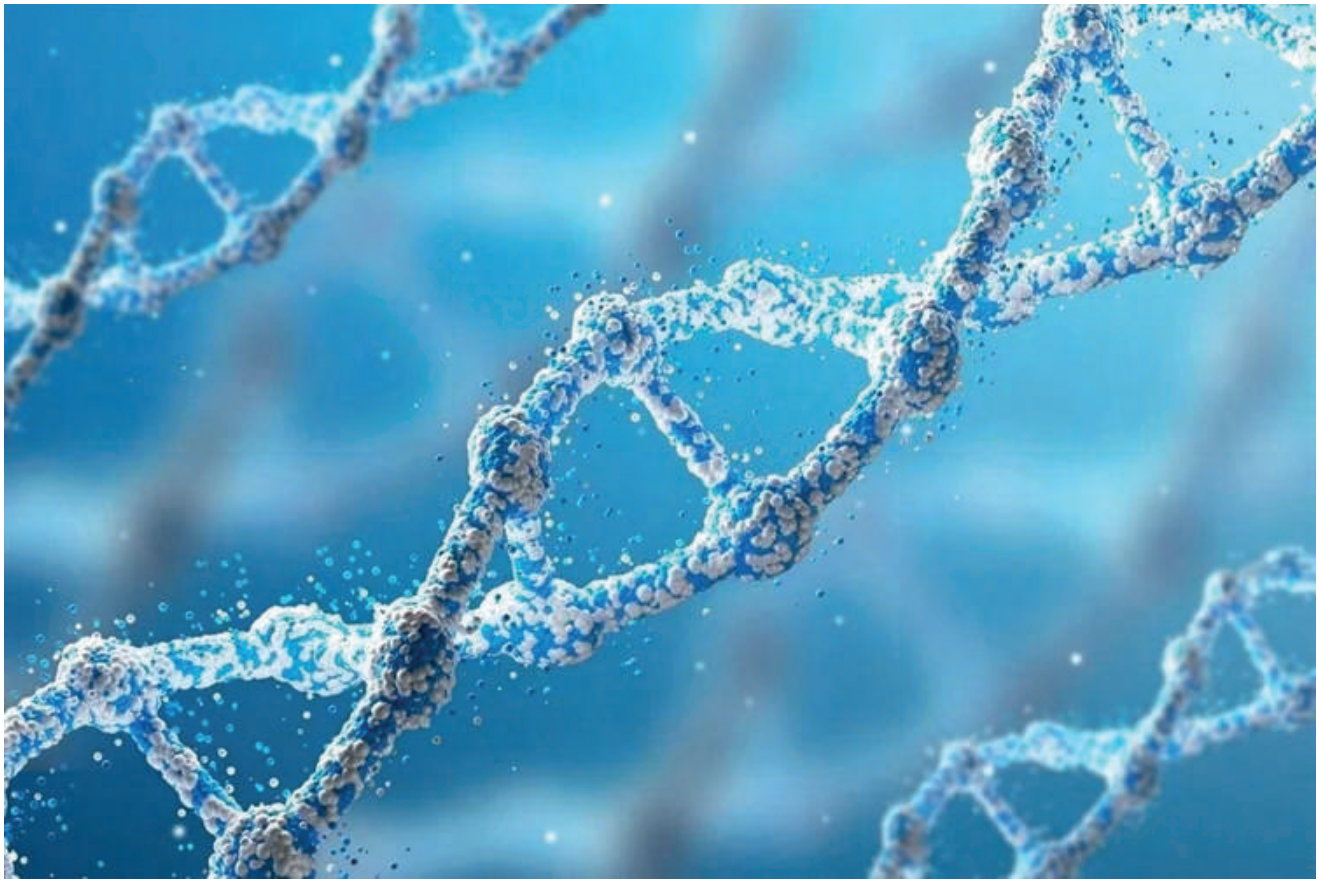
UNIQUE SEQUENCING TECHNOLOGY

Revolutionizing Genomics Research: MGI's DNBSEQ™ Sequencing Solutions Break Barriers and Achieve Research Goals

Next-generation sequencing (NGS) is an evolving field that has revolutionized genomics research in various disciplines and is propelling the use of genomics for the greater good. MGI is one of few companies to offer whole workflow solution with one-stop-shop, real-time, for whatever the genetic sequencing needs. MGI's DNBSEQ™ platforms feature high throughput technology, transforming sequencing projects in all realms of research.



Next-generation sequencing - Achieving all research goals

Since its dawn in the early 2000s, NGS has reformed how researchers read genetic codes, enabling faster and more precise sequencing. NGS advances in various disciplines, including population genomics, biodiversity, agricultural genomics, and clinical genomics. With much higher sensitivity in detecting low-frequency variants, NGS is especially important in the diagnosis and treatment of rare diseases through precision medicine.

MGI launched the first DNBSEQ™ platform in 2015 and through the 8 years' innovation, it now offers an extensive product portfolio of ultra-high-, high- and medium-throughput sequencers, accommodating all sequencing needs with accessibility and affordability. MGI's expertise enables researchers to attain their goals and push their research and development to the next level.

What if cost was not a barrier?

A drawback that has limited accessibility to genetic sequencing has been the financial barrier associated with the required computational power, data storage, and labor time. Reducing these costs is paramount to unlocking the full potential of NGS and allowing more research sectors across the globe to utilize the technologies. MGI is committed to removing the barrier through continuous technology innovation.

The DNBSEQ-T20×2.*

In 2022, MGI broke the $100 genome barrier by launching the ultra-high throughput sequencer DNBSEQ-T20×2*. This single set can produce up to 50,000 whole-genome sequences (WGS) in one year per 30x human genomes, making NGS much more accessible to researchers globally.

Utilizing advanced dip-immersion biochemistry, two imagers, and a rotational, robotic handling arm, one DNBSEQ-T20×2* sequencer can assay six slides simultaneously. This can provide 42 Tb of data per run with PE100 and up to 72 Tb per run with PE150. With DNBSEQ-T20×2*, MGI can now produce the highest throughput per run with high quality sequencing data.

Trade-offs between speed, low cost, and flexibility

MGI also recognizes the trade-offs that arise when reducing costs, such as reduced speed and flexibility. MGI's DNBSEQ-T7* sequencer addresses these trade-offs, providing researchers with great flexibility. The sequencer has various applications in agriculture, multi-omics, precision medicine, metagenomics, biodiversity etc. This sequencer has been supporting customers across the globe in places such as Thailand, Indonesia, and Brazil, aiding in major national genome projects.

The DNBSEQ-T7.*

Partnering with the South Australian Genomics Centre, MGI introduced this ultra-high throughput sequencer for commercial use for the first time in Australia. In Brazil, MGI is supporting Pensabio's large national genomic sequencing project, which aims to sequence the complete genomes of thousands of patients with rare diseases and hereditary cancers. This project will identify genetic markers that can be tracked for important early diagnosis and treatment.

DNBSEQ-T7* is supporting the Genomics Thailand Initiative to increase the country's competitiveness and put them on the map in genomic medical research, improving medicine management standards for its citizens. It is also assisting the Ministry of Health in Indonesia with its National Genome Project, working towards establishing a precise, credible population database of 10,000 genomes for medical research.

With this sequencer, researchers in both developed and developing nations can conduct large-scale genomics studies without encountering trade-offs on performance. MGI can help researchers accomplish a genomics project at any scale.

Right targeted sequencing within 24 hours

When it comes to disease diagnosis and treatment, time is precious, as faster diagnosis means faster treatment. Delivering the correct targeted therapy to patients in a reduced time frame is vital in increasing patient survival rates.

Thanks to one of our most recent sequencers, DNBSEQ-G99*, MGI delivers targeted sequencing results as quickly as 24 hours.

DNBSEQ-G99*, offers mid- to low-throughput assays at an ultra-high speed, perfect for targeting specific gene sequences and for small genome sequencing. With a triangular matrix of single spots on the sequencing flow cell and highly precise temperature control, the DNBSEQ-G99* platform gives a greater data output density in a shorter time with an overall throughput of 8-48 Gb per run.

The DNBSEQ-G99.*

The turnaround time of a PE150 sequencing run is shortened to a groundbreaking 12 hours, meaning the pathology labs could potentially assign the right targeted therapy to a patient by the end of the day.

DNBSEQ-G99* was central to the diagnosis of the first imported case of monkeypox to mainland China in 2022, allowing a quick response to taking the necessary actions to control the disease outbreak.5 Faster diagnosis of diseases like monkeypox allows for quicker development of vaccines to manage the spread of diseases much earlier on.

What if there was a company that understands all your needs when it comes to genomics research?

Although MGI is significantly advanced in its sequencers and focused on continuing to break down the financial barriers associated with them – offering an extensive product portfolio of ultra-high-, high-, and medium-throughput sequencers to accommodate different sequencing needs at a competitive cost – the company realizes that research goes further than sequencing genetic data.

MGI offers a one-stop-shop solution for research that includes lab automation, single-cell platforms, BIT platforms, and a lab information management system and data management system. MGI continues to provide laboratories across the globe with the most cutting-edge genomic techniques with accessibility and affordability.

References and Further Reading

For more information, please visit: http://mgi-whatif.com/

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AGRIGENOMICS

MGI improves agriculture globally with accessible genetic sequencing solutions

With advances in agrigenomics, scientists have successfully improved a large number of crops varieties by using genetic resources and innovative breeding solutions. To accelerate the breeding and improvement of crops globally, MGI has long played a part in providing agricultural scientists and breeders alike with high-quality and accessible genomics tools and solutions to promote genome sequencing and genotyping research and facilitate the construction and improvement of agrigenomics databases.

According to the Food and Agriculture Organization of the United Nations, we will need to produce 50% more food by 2050 to feed an estimated 9 billion people if the planet's population continues to grow at its current speed. At the same time, crop yields have been forecasted to decrease by over 25% as weather patterns become more extreme, further weakening an already-fragile global food system.

Given the changing climate, expanding population, and increasing demands for nutrition, the application of modern genomics tools to agriculture is of fundamental importance. By applying genomics technologies to the breeding and management of crops, researchers can develop more resilient crops and new varieties to improve sustainability. To this end, high throughput sequencing has become indispensable for breeding practices.

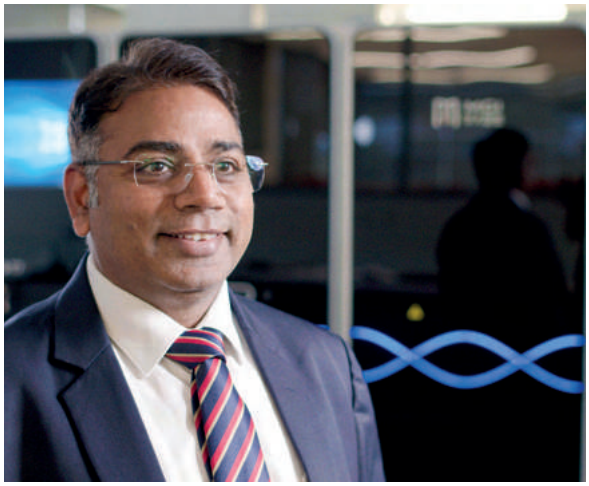
However, there are many challenges that lie ahead in the wider application of agrigenomics. Dealing with agrigenomics data that is extremely large in scale and highly repetitive requires ultra-high accuracy and efficiency, and most importantly, high cost-effectiveness. In developing countries where agriculture is an important way of life for millions of small-scale households, the lack of access to improved seeds and advanced technology can mean lower resilience in face of weather-related disasters, driving many rural families into dire circumstances.

Leveraging MGI's cutting-edge technologies, scientists today can have access to highly accurate, accessible and efficient sequencers* to further their research, uncover the full potential of agrigenomics and become one step closer to ending world hunger. Aimed at producing more resilient and sustainable food systems across the continent, the African BioGenome Project (AfricaBP) sets off to sequence 100,000 endemic African species within the next ten years with help from MGI. Utilizing MGI's single-tube long fragment read (stLFR) technology, the project recently saw its first plant species being sequenced and will continue towards building a full genomic database for the benefit of African scientists and breeders.

The African BioGenome Project

Elsewhere in Australia, Professor Rajeev Varshney, Fellow of the Royal Society and Director of Centre for Crop and Food Innovation at Murdoch University (MU) and a strong advocate for MGI, has been using the core DNBSEQ™ technology and its relevant tools for over seven years, citing various advantages including high accuracy, decreased duplicates, and extreme low index hopping rate in a wide range of past innovative agriculture projects that tackled food security issues in the developing world.

In an effort to improve yields of chickpea, one of the most important and low-cost sources of protein, as well as a rich source of many micro-nutrients and fiber, Prof. Varshney sequenced 429 chickpea lines from 45 countries to identify genes for drought tolerance and disease resistance. With these key insights and findings, scientists can improve breeding applications through the crop's genetic diversity, domestication and agronomic traits. Later in 2021, he led the sequencing and mapping of 3,366 chickpea genomes, thereby providing a deeper understanding of the chickpea genome and accelerating relevant crop improvement program.



Professor Rajeev K Varshney FRS, Murdoch University

More recently, Prof. Varshney again joined hands with MGI to sequence 10,225 chickpeas, representing the largest effort of its kind for crops utilizing MGI's sequencing platform. A detailed map of variation developed using sequencing data can help to identify superior variety for improvement-related traits in breeding system. Disease and climate resistance genes are expected to be applied in a wider range to enhance crop productivity.

This year, Prof. Varshney, on behalf of MU, announced the launch of SABC-Advanced Genomics Platform for Australian horticulture, especially focusing on improving the performance of five popular horticultural fruit crops, which either lack basic genomic resources or they are not being used in breeding programs In addition to monetary investment, MGI is supplying the project with its latest sequencing platforms, namely MGISP-960 High-throughput Automated Sample Preparation System, DNBSEQ-T7 Ultra-high Throughput Genetic Sequencer* and ZTRON All-in-one Genetic Data Platform. By adopting MGI's state-of-the-art DNBSEQ™ technology, large scale sequencing data can be generated in a highly accurate, efficient and affordable manner by scientists like Prof. Varshney, allowing breeders to later use this knowledge to produce new and more climate-resilient cultivars.

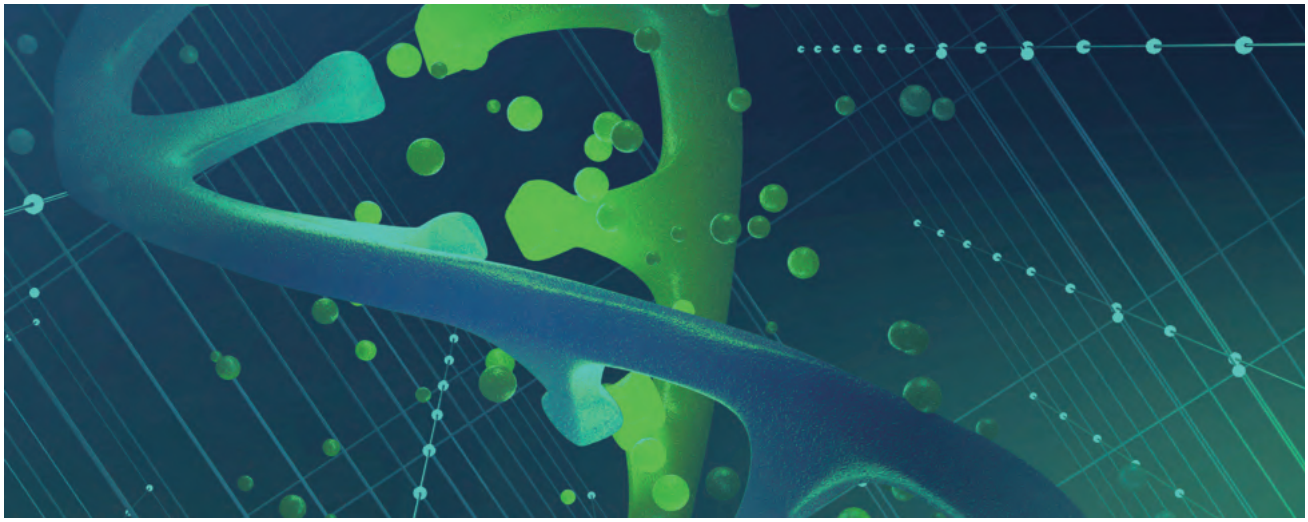
100,000
Endemic species sequenced within 10 years with The African BioGenome Project

10,225
Chickpeas sequenced with MGI's sequencing platform

Meanwhile in Europe, KeyGene, an international research company focused on developing and applying technology innovations for crop improvement, became the first in the Netherlands to acquire, install and adopt MGI's DNBSEQ-G400 gene sequencer* in plant breeding and plant research. Based on DNBSEQ™, there is optimism to addressing some of the pain points in the agrigenomics area. The DNA nanoballs technology is robust and provides highly accurate sequence data, tackling extreme variation in DNA quality among many diverse crops. Moreover, it aids in resolving haplotype- based genotyping navigating through complex highly repetitive heterozygous genomes that often differ in ploidy level, commented by Dick Roelofs, Program Scientist & Team Leader DNA Innovations at KeyGene. This fast and flexible medium-size platform uses a unique type of chemistry based on DNA NanoBalls (DNBs) synthesized through rolling circle which offers innovative possibilities for research projects at KeyGene, including emerging fields like single-cell genomics.

"With the application of MGI's sequencing platform, we anticipate being able to sequence more samples more cost-effectively," said Dick Roelofs. "In addition, G400's flexibility provides us with better control over the turnaround time for data production, while guaranteeing high accuracy sequence output at low cost and allowing us to develop new sequencing and genotyping applications for crop improvement in the future."

From AfricaBP to MU in Australia and KeyGene in the Netherlands, MGI's high-quality, accessible and efficient tools are enabling greater efficiency in agricultural breeding, producing more productive and nutritious crops to feed our burgeoning population. Powered by DNBSEQ™, MGI's end-to-end sequencing solutions, including full range of sequencers, automation platforms, single-cell systems, and bioinformatics products will continue to support scientific research on crop breeding to improve the global food system.



AGRIGENOMICS

How do De novo sequencing, QTL mapping, WGS, and lcWGS empower breakthroughs in agrigenomics

Sequencing technology is playing an increasingly important role in agriculture, including crops, livestock and poultry, aquatic organisms, and more. In recent years, scientists have made great progress in the basic research of animal husbandry and molecular breeding of crops. Based on high-throughput sequencing, a series of key technologies have emerged to empower genome map construction, gene mining, and molecular breeding, thereby improving the overall competitiveness of the agricultural industry.

There are generally several types of sequencing in the agricultural sequencing field:

De novo sequencing

De novo sequencing is a method used to obtain the complete genome sequence information of the species, including different types of DNA libraries construction, sequencing, assembly and annotation with bioinformatics methods.

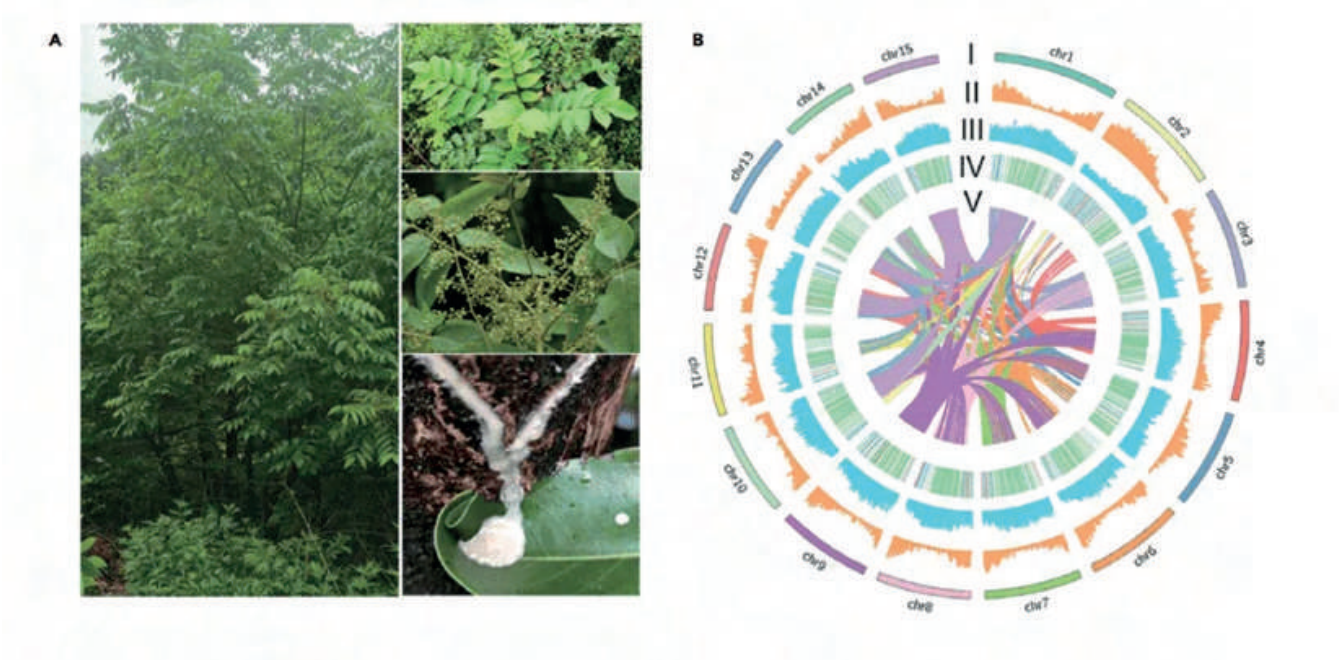
In a recent paper published by iScience titled "The chromosome-level genome for Toxicodendron vernicifluum provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis", researchers from Xi'an Botanical Garden of Shaanxi Province in China successfully provided the first chromosome-level genome for Toxicodendron vernicifluum.

The lacquer tree (Toxicodendron vernicifluum) is an important tree with economic, industrial, and medicinal values. Despite its considerable significance, genetic information of the species remains scarce, which has hindered its study and utilization.

Using genomic, transcriptomic, and metabolomic techniques, researchers thoroughly screened

and discovered the candidate genes responsible for urushiol and lignin production in the lacquer tree. The availability of this genomic data will be helpful in the exploration of urushiol biosynthesis, as well as molecular breeding and engineering of lacquer trees.

During the research, a total of 130.8 Gb of short reads and 106.28 Gb of ONT long reads were obtained based on DNBSEQ™ and Oxford Nanopore platforms, respectively. After quality control and trimming, there were 124.4 Gb of DNBSEQ™ clean reads and 105.28 Gb of ONT high-quality reads.



In their data, researchers found 79 orthologs containing 33 TvPKS genes involved in urushiol biosynthesis according to their co-expression profile and homological structure. Based on this, researchers drew the skeleton of the urushiol biosynthesis pathway and provided more details at the whole genome level.

DNBSEQ-G400*, the sequencing platform based on DNBSEQ™ technology, helped support the assembly of the genome, including generating short reads to correct the error for long reads and producing Hi-C data for chromosome-level assembly and RNA-seq.

QTL mapping

Many agronomic traits of crops, such as quality, yield, and stress resistance, are quantitative traits. With continuous updates and improvements in molecular markers, mapping populations, and statistical analysis methods, quantitative traits locus (QTL) mapping has proved an effective approach for dissecting the genetic mechanisms of complex quantitative traits. In recent years, increasing numbers of candidate genes within QTL intervals for important agronomic traits of crops (tomato, rice, and wheat) have been isolated and cloned.

In a research published in G3: Genes, Genomes, Genetics named "Mapping of a major QTL controlling plant height using a high-density genetic map and QTL-seq methods based on whole-genome sequencing in Brassica napus", researchers from the Oil Crops Research Institute in the Chinese Academy of Agricultural Sciences set out to determine the genetic impact on plant height.

Plant height is a crucial element related to plant architecture that influences the seed yield of oilseed rape.

Traditional QTL mapping typically constructs segregating populations derived from two parental inbred lines, which is laborious, time-consuming, and costly. In recent years, a combination of QTL-seq and traditional QTL mapping has become popular for identifying QTL and involves a mutual QTL verification process in crops. In a previous study on B. napus, a major QTL underlying boron uptake was identified by QTL-seq and then molecular markers were developed based on resequencing data to fine-map the candidate gene.

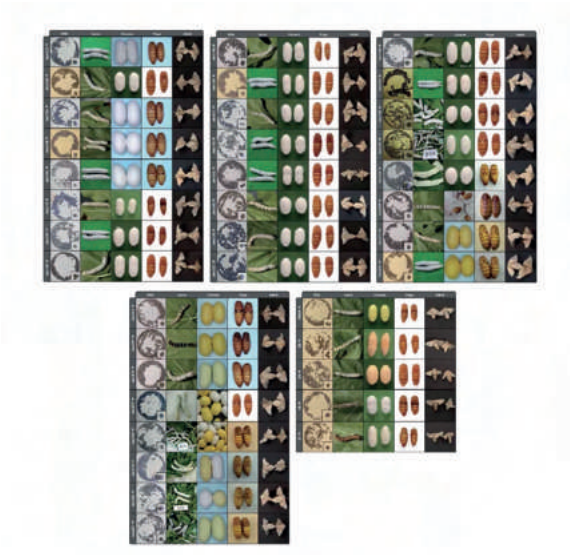
Therefore, a sequencing platform with high data quality and sequencing throughput is a critical tool for agricultural genetic breeding. In this research, MGI's DNBSEQ-G400* sequencing platform was used to analyze QTL and transcriptome sequencing of specific parts of 200 rapeseed F2 isolated populations. In the end, the key QTL locus controlling plant height was identified on chromosome 10 of the rapeseed.

Whole-genome sequencing (WGS)

Whole-genome sequencing (WGS) is a comprehensive method for analyzing entire genomes. It is helpful in quickly discovering genetic variation related to important traits of animals and plants and shortening the experimental cycle of molecular breeding. WGS is now widely used for sequencing of any species, such as agriculturally important livestock, plants, or disease-related microbes.

Researchers from the National Academy of Agricultural Science in Korea shared in "Whole-genome sequences of 37 breeding line Bombyx mori strains and their phenotypes established since 1960s" the whole-genome sequences of 37 breeding line B. mori strains established over the past 60 years, along with a description of phenotypic characteristics and photos. These whole-genome sequences linked to the phenotypic characteristics of the established breeding line could be valuable resources for the understanding of B. mori genome and provide more insights into the molecular background of various phenotypes.

The researchers completed library construction and data generation using MGI's



DNBSEQ-G400* sequencing platform and MGIEasy DNA Library Prep Kit.

Low-coverage whole genome sequencing (lcWGS)

Low-coverage whole genome sequencing (lcWGS) has emerged as a powerful and cost-effective approach for population genomic studies in both model and non-model species.

According to "Accelerated deciphering of the genetic architecture of agricultural economic traits in pigs using a low-coverage whole-genome sequencing strategy", researchers from the China Agricultural University and South China Agricultural University developed a new, highly accurate, cost- and time-efficient lcWGSmethod to obtain high-density single-nucleotide polymorphism (SNP) markers for a large Duroc pig population.

By assessing 21 important agricultural traits in commercial pig herds, they performed genome-wide association and fine-mapping analyses with high resolution and compared the results of the inheritance model in depth. Results show that artificial selection plays a significant role in altering the genetic architecture of agricultural animals, especially for loci that affect economically important traits. The lcWGS strategy had been proven useful for agricultural breeding.

The researchers completed Tn5 Library generation and sequencing on DNBSEQ™ technology-based sequencing platforms DNBSEQ-G400*. DNBSEQ™ significantly improves the accuracy of testing, while its low depth resequencing (Lc-WGS) genotyping is also more accurate than other methods. MGI's automatic database building scheme significantly shortens the experimental period and reduces errors commonly found in manual database building, meeting the aging requirement of molecular breeding.

From developing the economic trait markers of species and other omics research directions, to protecting the health of crops and livestock, and contributing to global agriculture, MGI provides end-to-end products for a diverse range of scenarios.

GENETIC SEQUENCERS

DNBSEQ E series

Portable
Genetic Sequencer

348*312*257
~15kg

DNBSEQ-G99

Rapid and Flexible
Genetic Sequencer

607*680*640
140kg

DNBSEQ-G50

Benchtop
Genetic Sequencer

654*489*545
108kg

DNBSEQ-G400

Comprehensible and Flexible
Genetic Sequencer

1086*756*710
200kg

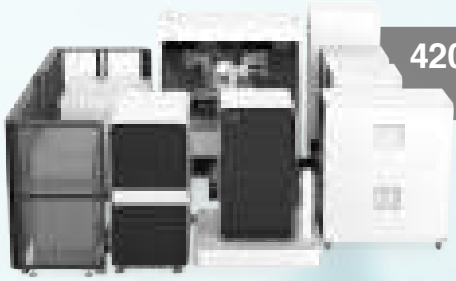
DNBSEQ-T7

Ultra-high-throughput
Sequencer

1656*903*1815
765kg

DNBSEQ-T20x2

Ultra-high-throughput
Sequencer



4200*4800*2000
~10000kg

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POPULATION GENOMICS

MGI breaks down barriers in population genomics with comprehensive end-to-end genomic solutions

With human genetic patterns constantly changing, understanding these dynamic variations helps unlock more possibilities to tackle diseases and genetic disorders and reinvent molecular medicine. For decades, many countries have been making progress towards establishing national genome projects and cohort research, initiating an exciting era for genomics, precision medicine and precision health overall. A global life science leader and innovator, MGI has been making these projects possible worldwide with high-quality, simple and fast genetic testing packages designed for high-throughput requirements.

The discovery of the ABO blood group is often thought to have catapulted the contemporary study of human genetics in the 20th century. Then, at the start of the 21st century, the Human Genome Project set up a new chapter in the assessment of our species' variation. Since then, the cost of sequencing a whole genome has dropped from $3.8 billion to as low as $300, opening new opportunities to build repositories of genomic data.

By the start of 2020, there were 187 genomic initiatives globally of which 50% originated in the U.S. and 19% in Europe. Several countries such as the U.S., U.K., Germany, Japan, and Australia also have existing population-based sequencing programs underway. However, there are still blanks awaiting to be filled in underrepresented countries, races and ethnicities. For instance, while nearly 60% of the global human population is spread across Asia, they have been grossly underrepresented in the genomes created so far.

Dedicated to facilitating innovative life science technology accessible and beneficial to all, MGI has been enabling large-scale human genome projects and cohort research in underrepresented countries by providing a customizable and automated total solution – from library preparation, to sequencing and bioinformatic analysis. Empowered by its core DNBSEQ™ technology, the

ultra-high-throughput DNBSEQ-T20×2 and DNBSEQ-T7 sequencers* have been widely adopted in mapping national genomic landscape. Since DNBSEQ-T20×2* was launched, MGI successfully broke barriers by lowering the cost of whole genome sequencing to under $100 when running 50,000 WGS per year, driving the development and expansion of genomics globally.

Capable of producing up to 50,000 WGS per year, DNBSEQ-T20×2* supports the operation of six slides simultaneously to produce up to 42Tb per run with PE100 or 72Tb per run with PE150. Meanwhile, known for its high-efficiency and productivity, DNBSEQ-T7 *can generate 6Tb of data per day and complete up to 60 whole human genomes per day. Besides their ultra-high throughput, both platforms have achieved big leaps in overall accuracy, as well as the reduction of duplicates and index hopping, making them highly suitable for scientific research, clinical research and disease prevention.

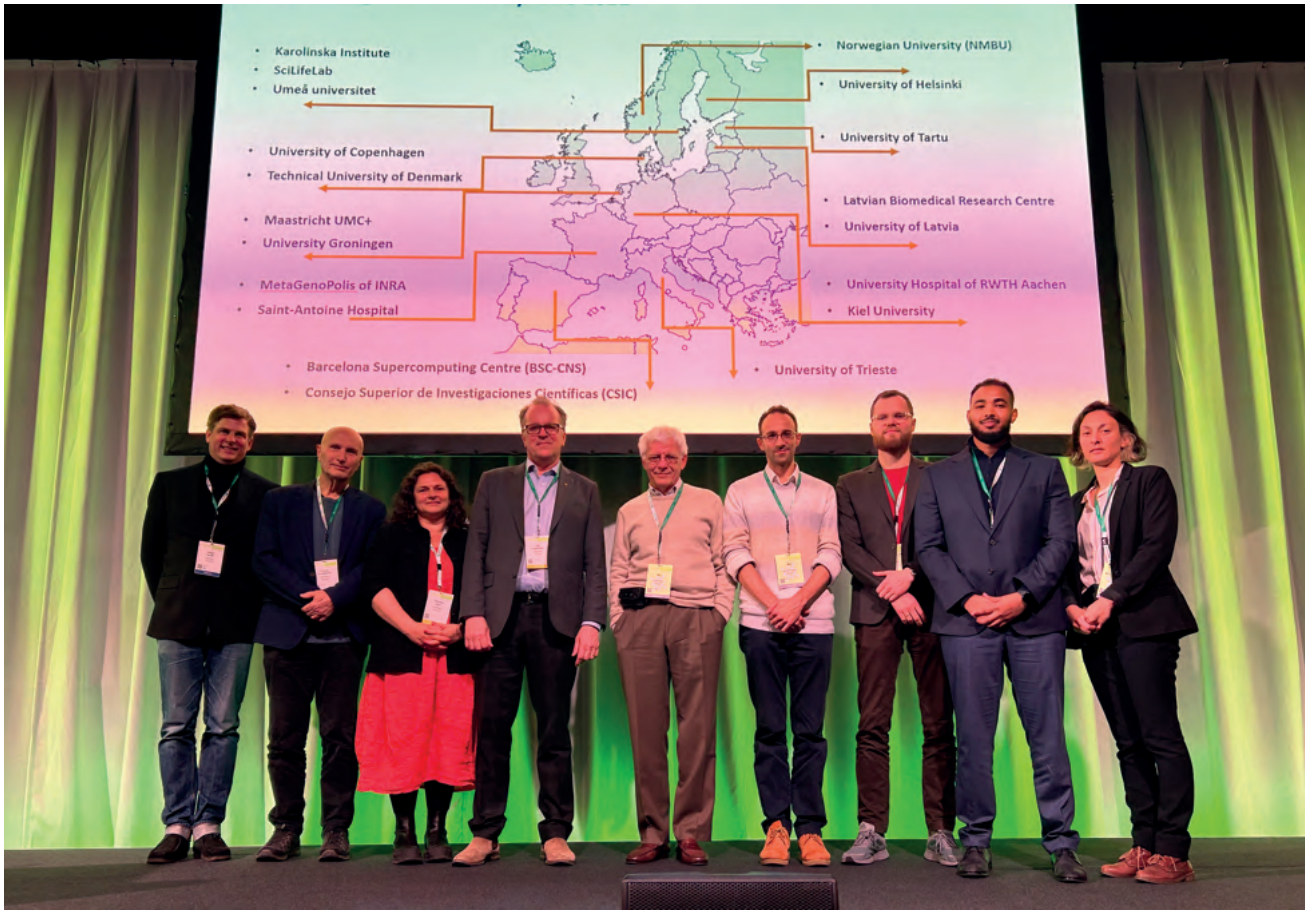
Genomics Thailand Initiative

Offering its strong technological expertise in national genome projects in countries such as Indonesia and Thailand, MGI is empowering life sciences development and future healthcare. The Indonesian Biomedical & Genome Science Initiative and Genomics Thailand Initiative have been making headways in establishing their respective comprehensive genome databases by cataloging thousands of citizens' genomes. In China, MGI is also playing a key role in The China Metabolic Analytics Project, a pivotal large-scale genome project that has set out to build a genomic database with 100,000 deep whole genome sequencing data and 1,000,000 genotyping array data. As of today, the project has achieved breakthrough results and mapped the first human blood virome of the Chinese population.

In early 2023, MGI joined hands with Brazilian life science company, Pensabio, to facilitate the genome sequencing of thousands of patients with rare diseases and hereditary cancers. The results will serve as foundation for countries to track diseases for early diagnosis and develop corresponding precision medicine for citizens.

Aside from supporting these far-reaching projects, MGI continues to innovate and upgrade its products and technologies specific to population genome projects. Under its global “What if?” campaign first rolled out in Australia, MGI believes sequencing is more than the sequencer. Integrating sample pretreatment, library preparation, high-throughput sequencing, genetic data management and more, MGI provides a total package for population genomics. Each sequencing laboratory can achieve an annual throughput of 50,000 to 1 million WGS, with a fully automated process from sample to report. Amidst a market that is in urgent need of high-quality and comprehensive sequencing solutions, MGI’s one-stop sequencing solution for large-scale population genomics projects will spur further advances in precision medicine and drive progress towards the goal of making sequencing more affordable and accessible to everyone.

The comprehensive workflow starts with the high-throughput MGISP-960 automated workstation which guarantees high speed and easy operation, improving overall project efficiency and productivity. After nucleic acid extraction, library construction and high-throughput sequencing, ZTRON is used for automatic bioinformatics analysis, storage and governance of massive sequencing data. It can speed up analysis by 60 times with a capacity 2 times larger with its high-performance edge computing and storage solution, further contributing to the rapid and easy implementation of large population genome projects.



The Million Microbiome of Humans Project

Beyond supporting national population genome initiatives, MGI has made considerable efforts towards the ambitious goal of building the world's largest database of human microbiome through The Million Microbiome of Humans Project, which aligns with MGI's vision to improve human health through innovative life science. Scientists from China, Sweden, Denmark, France, and Latvia will rely on MGI's DNBSEQ™ microbial genome sequencing technology to sequence and analyze one million microbial samples of different populations, aiming to construct a microbiome map of the human body and laying a solid data foundation for micro-ecological research. Through the project, MGI continues to contribute to scientific breakthroughs which in turn benefit mankind and healthcare worldwide.

MGI's innovative tools have not only redefined the end-to-end, high-throughput "sample to data" process, but more importantly, turned a new page for many countries and races to develop better understanding of their origins, revolutions and to eventually improve human health. In addition, with highly accessible solutions, MGI is lowering the technical and cost-related barriers for countries eager to kickstart their own human genome projects and furthering the global development of precision medicine.

POPULATION GENOMICS

From Sanger Sequencing to the Human Genome Project: The Evolution of DNA Sequencing Technology

The Human Genome Project was an international scientific research project set out to map, identify, and sequence all the genes that make up the human genome, as well as improve the tools for data analysis for the future deciphering of genetic information. The project began in 1990 and was completed in 2003. Since its completion, it has helped to accelerate the field of human biology, providing us with crucial information about the human blueprint. With such a rapidly evolving scientific landscape, the field of genomics has seen tremendous breakthroughs, and new research is utilizing genomics technology to continue to push the boundaries of medical science. One company that is helping to accelerate these discoveries is MGI, a leading producer of advanced high-throughput genome sequencing technology.

With the 7th birthday of MGI on April 2023 coinciding with the 20th anniversary of the Human Genome Project, we look back at where it all started as well as the importance of sequencing technology in advancing the field. In this inspiring interview, we speak to Dr. Radoje Drmanac, co-founder of Complete Genomics and Chief Scientific Officer at MGI, to learn more.

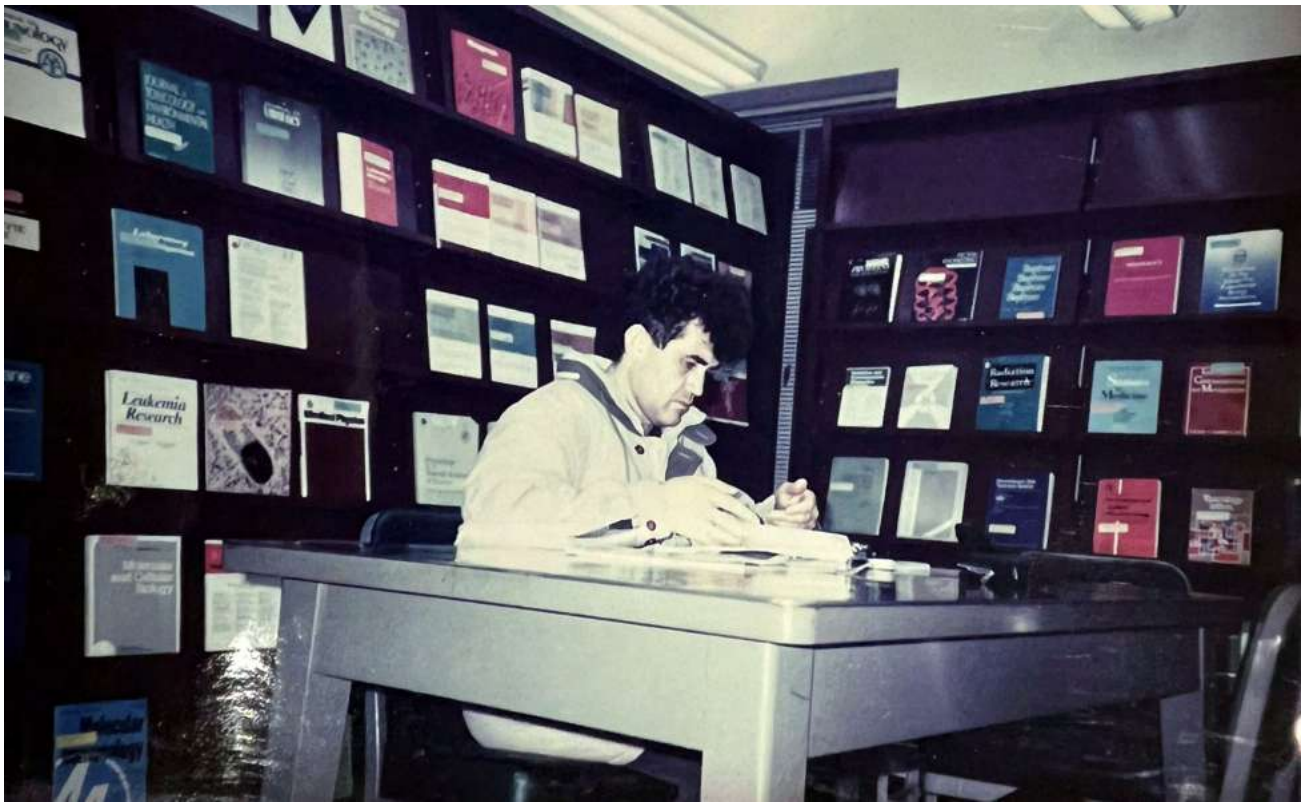
Dr. Radoje Drmanac

Dr. Radoje (Rade) Drmanac is the co-founder and has served as Chief Scientific Officer since June 2005 at Complete Genomics and Chief Scientific Officer since 2013 at MGI Tech. He invented and led development of massively parallel DNA sequencing using DNA nanoarrays, ligation-based DNA sequencing, and haplotyping by co-barcoded sequence reads.

The Human Genome Project (HGP) is celebrating its 20th anniversary this April. As someone involved in this project from the start, how did this project come about, and what was your involvement?

The field of genomics was already around before the Human Genome Project started in the 1980s. Many people like George Church, Hans Lehrach and myself were involved in thinking about how to create chromosome maps or expression sequence tags. Through such thinking, I became involved in genetic engineering at the Institute for Molecular Genetics and Genetic Engineering in Serbia. There I started thinking about how to improve DNA sequencing as sequencing at that time was carried out using the Sanger method. Although I never used this method myself, I watched my colleagues conduct gel sequencing, and it soon became clear how slow and difficult it was.

In 1987, I proposed a new method for more efficient sequencing based on DNA arrays called sequencing by hybridization (SBH). At the same time, the US Department of Energy (DOE), developer of atomic bombs, was studying the impact of radiation in causing genetic mutations. They held a meeting to discuss how to find and identify these mutations, and I believe George Church told them that the best way would be to sequence the whole genome in exposed people. They initiated a first round of grants to improve technologies for genome analysis, including sequencing. I applied for this grant from Serbia in 1987, and to everybody's surprise, including my own, we received a $150,000 grant to develop that sequencing by hybridization method that held so much promise for faster, much higher throughput sequencing.



In 1988, I proposed massively parallel sequencing (MPS) using microarrays, a radically new approach, and the proposal was to use emulsion polymerase chain reaction (PCR) on micro-sized beads to create millions of clonal DNA on such small beads to form these novel DNA microarrays. Before this, picking and arraying clones was the only viable method.

Then, as a postdoc in 1991, through this connection with the DOE, the whole team – all nine of us – moved to Argonne National Laboratory near Chicago in the US to continue to develop sequencing by hybridization technology using the DOE grants.

We also published a couple of papers, the first being in journal Genomics, a paper on genome sequencing by SBH that was very popular. Then in Argonne National Laboratory, together with Lee Hood, we published a paper in the journal Science in 1993 that proved in a blind test that sequencing by hybridization was highly accurate and could be used to sequence DNA using oligo hybridization.

That is how I first became involved in the Human Genome Project.

How did the Human Genome Project help to propel parallel sequencing technologies in the life sciences?

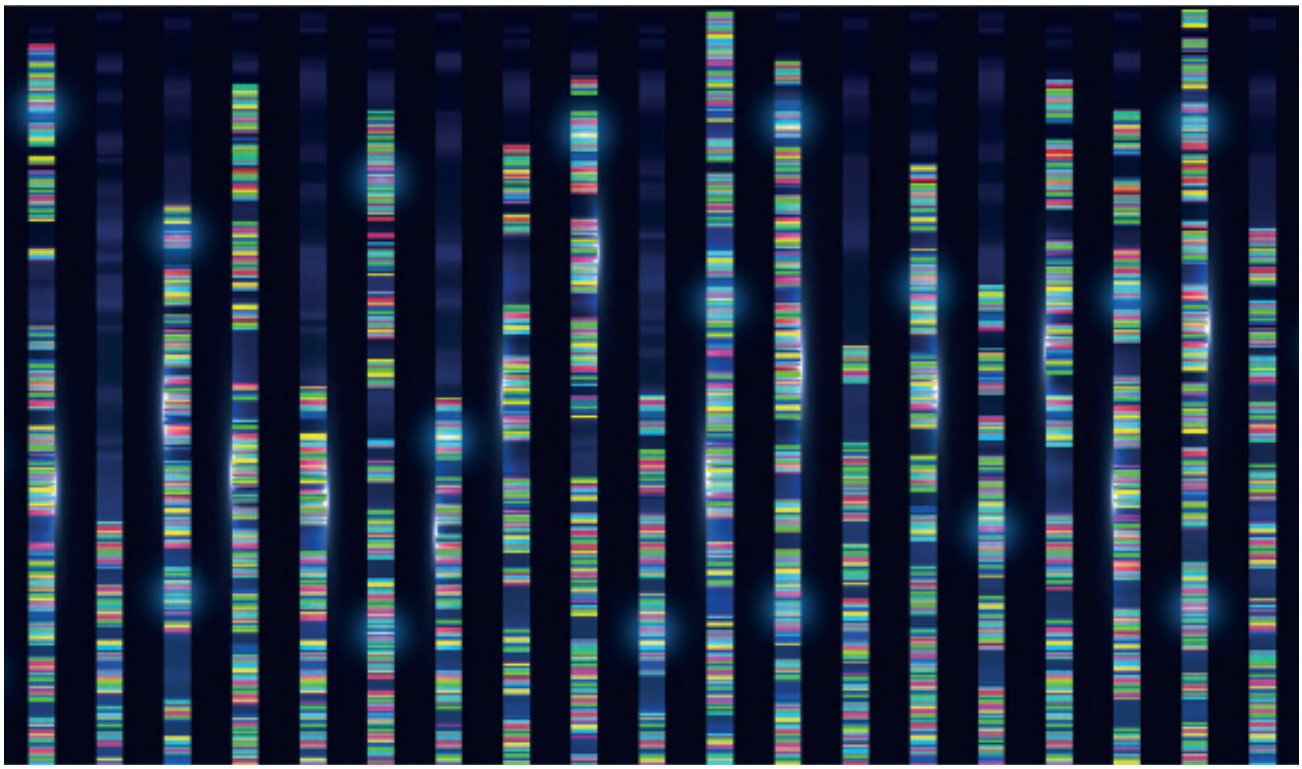
I proposed massively parallel sequencing in 1988, and sequencing by synthesis was also proposed in the 1990s, both long before the genome was sequenced. However, once the genome was sequenced, these two technologies and our sequencing by ligation became possible, allowing for routine, affordable individual genome sequencing.

This motivated me to start Complete Genomics in 2005, acquiring funding and starting operations in 2006. In 2005, we invented DNA nano balls and pattern arrays for massively parallel sequencing. These clonal arrays were critical to implementing efficient massively parallel sequencing, and our DNA nano balls were, and still are, the best approach for this. We were the first to implement pattern arrays, while others used random arrays.

When we started Complete Genomics, within a couple of years of implementation, we achieved a milestone, an event that promoted the genomic revolution. We sequenced and published in the journal Science in 2010, for the first time, a whole human genome for $5,000, a 10-fold improvement, using patterned DNA arrays of DNA nanoballs, a much more efficient, higher-density sequencing platform.

Seven years after the first genome was sequenced for $3 billion, your team published a $5000 genome, almost 1 million fold cheaper. What was this journey like, and were there any particular R&D challenges that you had to overcome?

Many people in the industry, including some of the people we hired, believed that such dense arrays, were unachievable. Despite this initial resistance, we started making the arrays, and the first genome was sequenced with, I believe, 600 nanometers center to center, a sub-one-micron array. We have since continued to push the edge of possibilities. One limitation at the time was that cameras had fewer pixels than they do today. Today, we have cameras with a hundred times more pixels and much faster imaging.



As the industry was still new, we had to offer it as a service initially. As such, we started this service for routine genome sequencing for scientists. They would send us their important samples, and we would sequence them. Nonetheless, there was still a lot of debate regarding the accuracy of whole genome sequencing by short reads and, despite our efforts, we still had some errors, so even though it was quite accurate, it was not yet perfect.

There were also questions surrounding whether we could detect a single mutation that causes a disease. As this had never been carried out before, and as the genome is so big comprising 3 billion chemical letters, there were also uncertainties regarding our ability to identify the single mutation that causes disease.

All things considered, it was really rewarding when, with a long-time friend and colleague, Lee Hood, we decided to sequence the first family. We sequenced a family of four, two parents and their two children who were affected with a disease called Miller Syndrome, to prove that we could identify the cause of Miller Syndrome in the affected children.

We successfully detected the genetic cause of this disease and published our findings that demonstrated our ability to sequence genomes accurately. These results also highlighted the importance of sequencing family genomes and their role in discovering genetic diseases. With that paper and the many others that followed, people soon realized that the genome could be sequenced efficiently, affordably, and quite accurately, and this is what kickstarted the genome revolution.

You have had an incredible career, from being the technology developer for the Human Genome Project to the sub-hundred dollar human genome and CoolMPS technology. Over the past 20 years, how do you feel the genomics industry has evolved?

In one sentence, the genomic revolution was made possible by massively parallel sequencing. Everybody knows that the progress we continue to see would not be possible without this technology. The cost would not have been able to come down from $5,000 to $1,000 or even to the very first $100 and sub $100 genome. Over the last 20 years, many applications have been developed for sequencing because of this ability to carry out efficient sequencing in almost any lab. Today, almost every aspect of omics uses sequencing.

We measure protein levels in the blood by sequencing barcodes. People measure gene activities by sequencing. Sequencing became the single assay to measure the molecular state of our cells. It was not just genome sequencing, but all other omics were enabled by MPS. At the same time, long single-molecule sequencing was also achieved and made available by multiple companies.

The revolution then spilled out into knowledge by sequencing all of these samples, having all these assays, sequencing millions of genomes. We also learned how to barcode single cells, and now, using dens DNA nanoball arrays, we have the best spatial omics to monitor gene expression in tissue sections at the subcellular level. All this is enabled by massively parallel sequencing, and these applications are still growing.

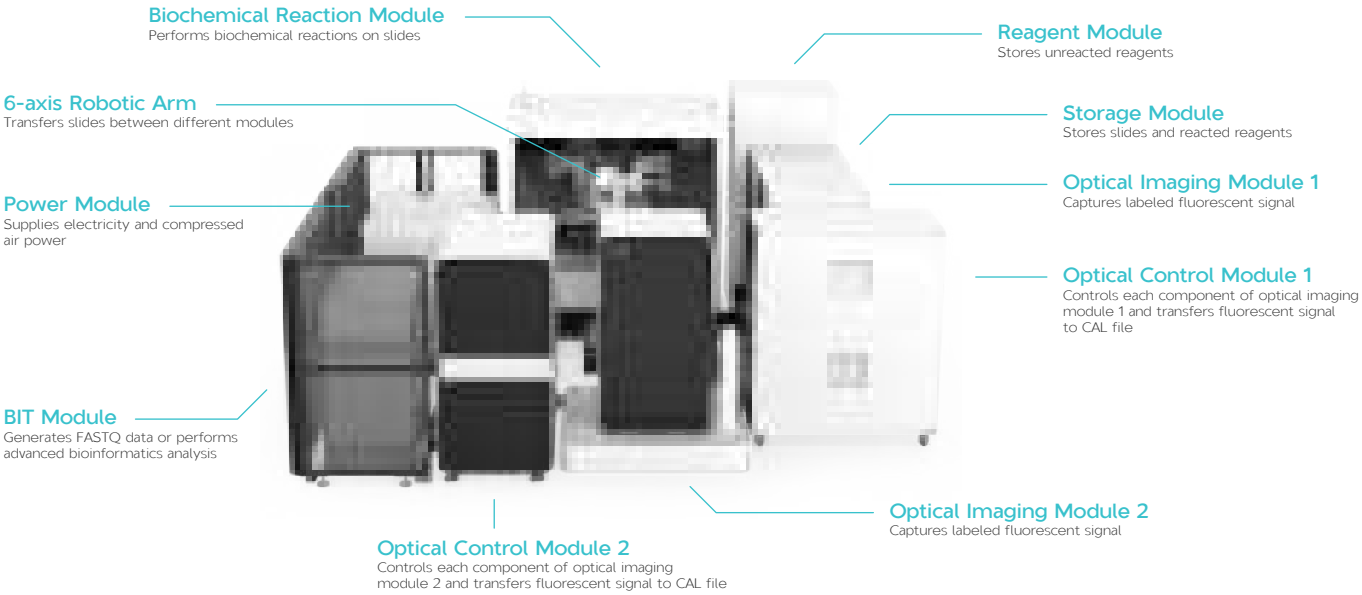
We have seen in recent years that sequencing is the key to accelerating the field of omics. What role have both Complete Genomics and MGI played in this discovery, and what role will they continue to play in its future?

We have always pushed the boundaries, starting with the $5,000 genome, which was so important. In a way, it proved that routine genome sequencing was possible and that there is value in individual genome sequencing. After this, we continued to build on initial studies and develop many different instruments.

Our DNBSEQ-T7* will be remembered as a critical instrument, the first to achieve pair-end 2x150 bases high-throughput genomes in 24 hours. The T7* is an example of the power of DNBSEQ™ when it is properly implemented with really cool engineering.

We have now also announced DNBSEQ-T20×2* providing a sub-hundred-dollar genome. Our DNBSEQ™ provides the highest resolution spatial omics due to the high-density arrays. I believe we will be the first to achieve the $10 genome, as there is no doubt that DNBSEQ™ enables that. We can make four times higher array density than today. The drive for the $10 genome is not just for the inherited genome but because it will allow annual checkups using deep sequencing in the immune system, cell-free DNA, and in the microbiome, enabling us to monitor our health and our aging at the molecular level.

DNBSEQ-T20x2* Product Components:



One technology that is a less expensive and more efficient technology for sequencing is CoolMPS, as it allows much longer reads in massively parallel sequencing. We have already implemented SE400 using standard sequencing technology. With CoolMPS, we are working on getting to 1,000 bases continuous reads, the SE1000 – continuous MPS for 1,000 bases. This is so important because it will bring affordable genome sequencing to an even higher level of completion. There are some types of sequences, like triple repeats, that, when they expand, cause a disease like fragile X. With these longer reads, we will be able to measure how long these repeats are, which will tell us if expansion is causing disease or if it is still tolerable.

Combining the efficient sequencing with our single tube LFR technology for haplotype phasing, solving blind spots by resolving the pseudogenes, separating pseudogenes from the real genes, and using these longer reads all redefines massively parallel sequencing and brings it to the level that will enable faster understanding of our genetic program. With this understanding, our omics tests will be so efficient that we can bring health monitoring omics to all.

We will have such a deep understanding that when we obtain the state-of-the-art measures of our tissues at the molecular level, we will know what this means and how to prevent disease and slow aging. We already have a level of understanding that our tissues are primarily aging because of epigenetics. In a way, epigenetics is controlled by a genome program that uses methylation and other marks to differentiate cells. In the beginning, there is only one cell, and then we have hundreds of tissues in the developed organism. Every tissue is locked into its state

by these methylation and other marks called epigenetic modifications. These marks are lost or changed during life, i.e., modified, leading to a loss of young and healthy tissues. We can reverse this process using transcription factors that promote the re-establishment of young tissue epigenetic marks. However, it is important that we do not just live longer but that we have longer healthy and more productive lives.

Everything in biosciences is growing exponentially thanks to these technologies. Our understanding is exponential, and our technology's ability to measure things is exponential. We will definitely have a $10 genome within this decade, and 1,000 base MPS reads, so that, in a decade or two, after deep understanding of our molecular nature maybe we will be in control of aging.

With the 20th anniversary of the Human Genome Project and the 7th birthday of MGI both this April, how do you personally feel about how far the field of genomics has come? Where do you feel that this sector is heading?

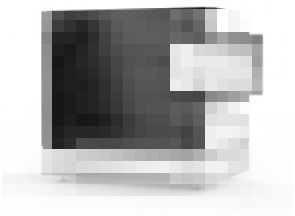
I am really happy with how things have panned out. If we had not merged with MGI, the field would be in a totally different place than it is today. Yet, from the beginning, we have always had this feeling or hope that we could do this almost unlimited level of sequencing. There are so many genomes and other omics to sequence, and we are unlikely to stop improving even at $10 genome.

The whole field is unstoppable, and we will continue to do wonders, and I am certain that the true importance of massively paralleled sequencing or any large-scale, efficient sequencing is still underestimated.

The green energy revolution and electric vehicles are critical. But efficient sequencing, I think, will be recognized as one of the most important human technologies because it concerns our health. Our genome touches all aspects of our lives, including genetic needs for personalize parenting or personalized learning. The whole of medicine will be changed. Imagine having the ability to deeply, efficiently, and accurately measure your molecular health at an affordable price. When you combine that enormous data set with artificial intelligence, suddenly, we have predictions or preventions of disease and aging that are affordable to everybody.

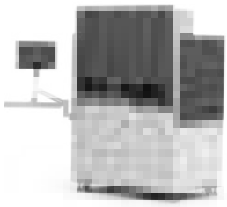
LAB AUTOMATION SYSTEMS

MGISTP-3000



1100*680*1050
~200kg

MGISTP-7000



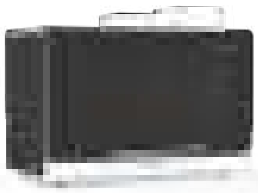
1470*960*2100
~500kg

Sample Preparation

MGISP-NE32

430*395*435
32.5kg

MGISP-NEX



1410*799*970
~232kg

Nucleic Acid Extraction

MGISP-NE384

1220*742*960
268kg

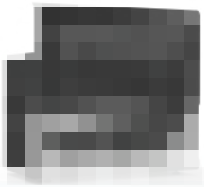
Nucleic Acid Extraction

DNBelab D Series

356*315*275.5
15kg

Digital Microfluidics

MGISP-Smart 8



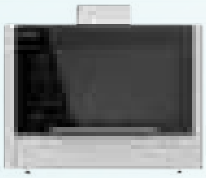
1410*799*970
~220kg

MGISP-100

780*725*777
130kg

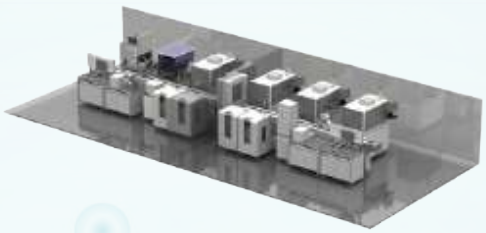
Automated Liquid Handling Workstation

MGISP-960



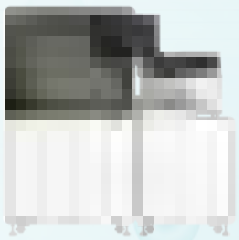
1240*740*1110
250kg

MGIGlab-L



Automated Liquid Handling Workstation

MGIFLP-L50



851*1840*1821
558kg

All-in-one Library Preparation & Sequencing Workstation

Request a Quote

PRECISION ONCOLOGY

Partnering with Gene+ to Provide Accessible, High-Quality Oncology Solutions

The rise of genomics has changed the face of cancer medicine in terms of prevention, screening, diagnosis, and treatment. Since 2018, MGI has been working with Beijing GenePlus Technology Co., Ltd ("Gene+"), a leading supplier for oncology and precision medicine in China, to provide intelligent and comprehensive high-throughput sequencing technology for solid tumors, lymphoma, pathogenic microorganisms, early detection of cancer, immunization, and other areas.

Utilizing its core DNBSEQ™ sequencing platforms, MGI empowers the Gene+ all-in-one high-throughput sequencing solution for customers and users in more than 70 key hospitals and companies in fields such as oncology and analysis of pathogens. Moreover, MGI is the original equipment manufacturer of the Gene+Seq-2000 genetic sequencer, which was based on MGI's day-to-day, medium throughput benchtop sequencer DNBSEQ-G400* and has been certified by the Chinese National Medical Products Administration (NMPA).

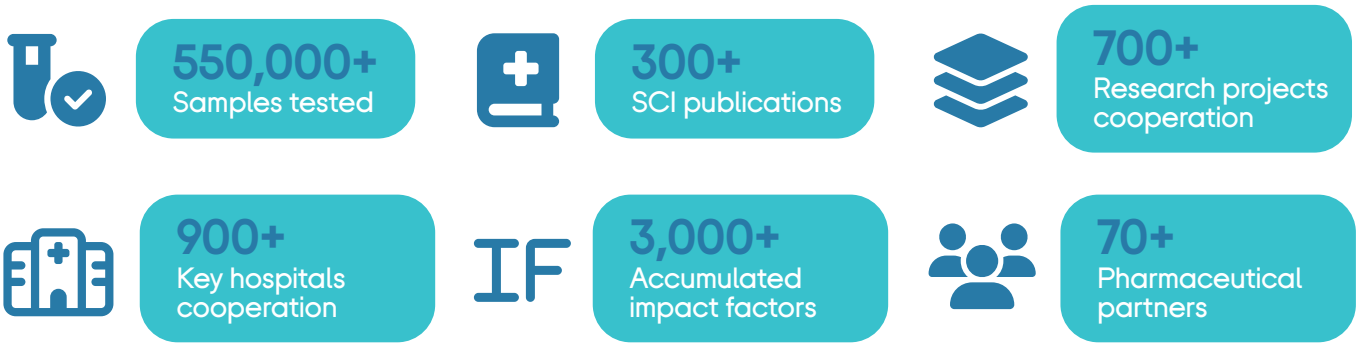
The key to precision oncology is developing targeted therapy by exploring different biomarkers of tumors and finding their origin. However, this is never easy given the inherent complexity and heterogeneity of cancer, as well as its risks of genetic mutation. To this end, supported by MGI's DNBSEQ™ technology, Gene+ has been contributing to clinical trials and research to help clinicians determine the safest and most effective cancer treatment by combining clinical features and individualized tumor genetic profile. Based on this powerful technology, Gene+ has furnished a complete tumor detection product matrix with great clinical application results.

Specifically, MGI's DNBSEQ™ technology's significant advantages of low duplication rate and high data utilization rate make it especially valuable for high-depth sequencing and analysis of low-concentration oncology samples or those of high complexity, such as peripheral blood and circulating tumor DNA. DNBSEQ-G400*, with a detection limit between 0.1-0.2%, has enabled the Gene+ lung cancer MRD product, OncoMRD Lung, to achieve a low-frequency mutation detection rate of 0.02%, which plays a critical role in improving the overall product performance and thereby diagnostic accuracy. Backed by these significant advantages, DNBSEQ™ enabled the first study, published on **Cancer Discovery**, to ever define the potentially cured population in localized non-small cell lung cancer by way of longitudinal undetectable MRD.

Together with MGI, Gene+ has achieved:

GenePlus achievement

Beijing GenePlus Technology CO., Ltd., with genetic technology as its core, focuses on the exploration of precision oncology and is committed to becoming the most trusted cancer prevention and treatment service platform.



Statistical data as of 2023.06

Equipped with the versatile and flexible DNBSEQ-G400*, the Gene+ all-in-one solution enables clinicians and researchers to conduct clinical diagnosis and research, which have accurately and effectively informed precision cancer medicine in terms of selecting the optimal treatment for a patient based on the specific genetic makeup of their tumor.

In addition to facilitating high-quality, high-efficiency cancer sequencing, the partnership between MGI and Gene+ is rooted in a shared vision for promoting the growth of precision oncology and making it more accessible to all. Augmented by a strong interdisciplinary collaboration among experts and stakeholders with medical, clinical, biological, translational, and technical expertise, MGI and Gene+ maintain ongoing technical communications on reagent optimization, product design, and technological update to improve the performance and accuracy of applied products.

Gene+, Beijing

As early as in 2018, MGI and Gene+ announced the "100T" project aimed at evaluating the performance of domestic sequencers, bringing the Gene+Seq-200/2000 sequencing platform and relevant tumor high-throughput sequencing solutions into clinical application and public awareness. It laid the foundation for accelerating the application and accessibility of domestic sequencing instruments, as well as generating new clinical research results and evidence to help improve cancer survival. In 2022 alone, Gene+ published more than 75 articles and achieved remarkable results in large-scale clinical studies such as TRACELib002, TNBC, and CTONG2201.

While cancer precision medicine is gaining momentum, many advances in the field have yet to reach the masses due to high costs and insufficient clinical trial design and data. The competitive pricing and low running cost of DNBSEQ-G400* have significantly increased the cost-effectiveness of cancer sequencing with Gene+, removing another barrier in making it part of routine medical care, while making precision oncology ever more of an accessible option for patients and medical personnel.

To date, the Gene+ all-in-one high-throughput sequencing solution, as empowered by MGI's high-quality, high-accuracy, and cost-effective sequencing technology, has benefited over 300,000 patients in need of accurate tumor diagnosis and treatment. Besides informing treatment, it can also identify mechanisms of drug resistance and relapse, which has helped to slow the progression of the disease. Precision oncology brings with it a full cycle of management characterized by treatment that is directed to the root cause of the disease. Instead of longer treatment with a high risk of failure, targeted therapy is improving cancer patients' chances of recovery, allowing them to get back on their feet far more quickly, with significantly fewer negative side effects, and at a much lower cost.

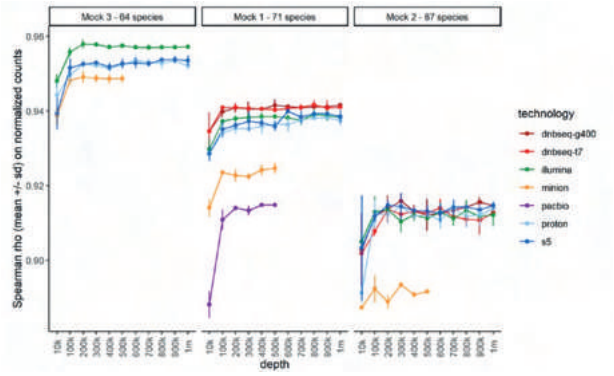
Looking ahead, MGI and Gene+ have plans to collaborate on more of MGI's innovative sequencers, including DNBSEQ-G99* which features ultra-fast applications, DNBSEQ-E25* which boasts portability, and DNBSEQ-T7* with ultra-high throughput. Furthermore, they will work closely on multi-dimensional development projects such as laboratory automation, methylation technology development, and single-cell product application promotion to further advance clinical and scientific research in precision oncology.

METAGENOMIC RESEARCH

MGI's DNBSEQ-T7* facilitates ultra-deep sequencing of high-complexity metagenomic samples

PEER-REVIEWED PUBLICATION - SCIENTIFIC DATA

Thanks to high-throughput sequencing technologies, shotgun metagenomic methods were made possible and had effectively transformed microbiology. Today, advances in both short- and long-read technologies are overcoming many of the previous challenges affecting metagenomic profiling, especially of highly complex samples and environment.



Overall comparison between observed and excepted mock compositions for each platform.
Credit: Victoria Meslier, Benoit Quinquis, Etc.

Researchers from France's National Research Institute for Agriculture, Food, and Environment (INRAE) examined the performance of seven short- and long-read sequencing platforms in analyzing high-complexity metagenomic samples. The study, published in the Nature Portfolio journal Scientific Data, ran mock samples between 2018 and 2019 on various mainstream sequencers at the time, including MGI's DNBSEQ-T7* and DNBSEQ-G400*.

Within this wide range of sequencing technologies tested, DNBSEQ-T7* was recognized for its ultra-high throughput and excellent accuracy. "We were surprised by the T7's performance*," said senior author Mathieu Almeida, a research fellow at INRAE. "It provides ultra-deep sequencing in a single run with similar low error rate compared to the other platforms, making it at the time of our study one of the most affordable technologies for metagenomic sequencing."

In the study, three uneven synthetic microbial communities were constructed, consisting of up to 87 genomic microbial strains DNAs each and spanning 29 bacterial and archaeal phyla. They represented some of the most complex and diverse communities used for sequencing technology comparisons. The mock1 (71 strains) was sequenced using all platforms, mock2 (64 strains) was additionally sequenced to estimate the impact of various microbial richness, while MGI's platforms were not performed on mock3.

To assess the impact of sequencing depth, the team ran a subsampling analysis and compared observed and theoretical genome abundances across samples at multiple depth from 10,000 to 1 million reads. Overall, Spearman rank correlations for all platforms were high at above 0.9 when mapping at least 100,000 reads. Among them, the correlations of T7* and G400* were the best in mock1 and remained excellent in mock2.

In addition, differential analysis between observed and excepted species abundances was performed in mock1. Results showed that over or under abundance estimation for most genomes had little to do with the sequencing platform, read length, taxonomy, GC-content, genome size and genome completeness, even at a low depth of 500,000 reads. In fact, most genomes were accurately estimated on all sequencers, with the observed normalized abundances generated by T7* charting very close to the excepted values.

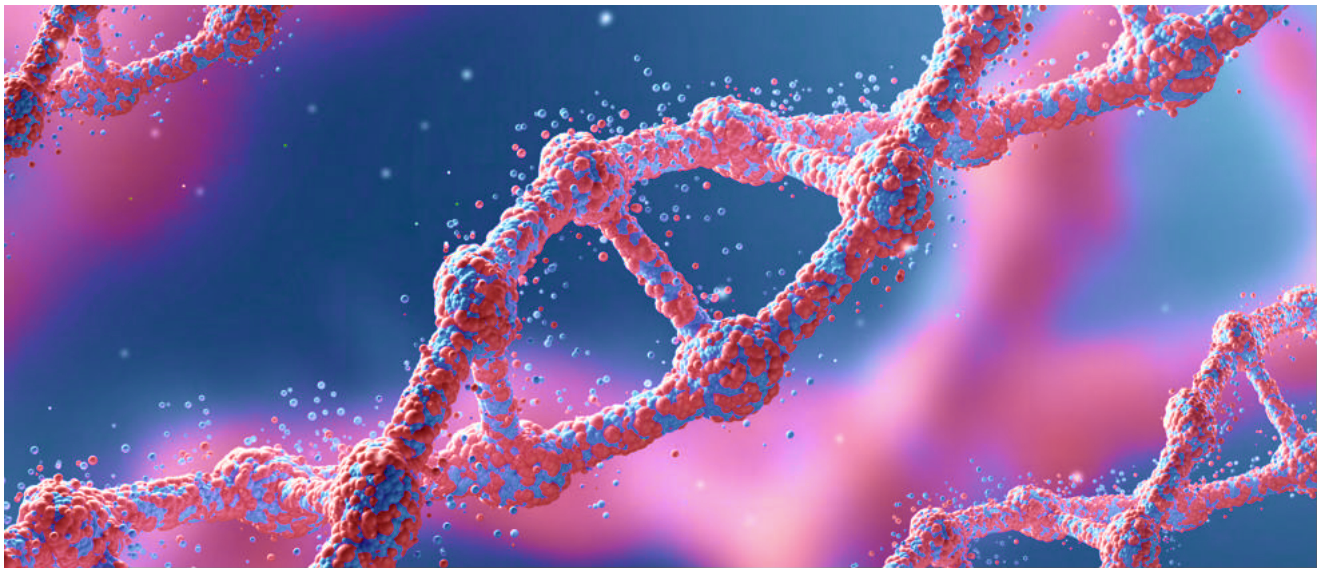
Based on performance analyses of the different sequencers, the study formed a microbial metagenomic sequencing benchmarking database, providing researchers and scientists a comprehensive and authentic reference for sequencing platform selection. In particular, the findings demonstrated the promising value of MGI's DNBSEQ-T7* in metagenomic sequencing.

Boasting high stability and accuracy as shown in the data, combined with outstanding throughput, T7* makes a strong platform for the identification of species and functional genes in highly complex microbial communities. Its upgraded biochemical, fluidics, and optical systems are not only making sequencing more efficient and productive, but also continuing to support research into the structure and diversity of microbial communities.

PANDEMIC RESPONSE

MGI demonstrates comprehensive initiatives in infectious disease monitoring and control

Recent progresses in genomics and bioinformatics have shone a light on their importance as public health tools against infectious disease threats like COVID-19, influenza, monkeypox, and tuberculosis. Powered by cutting-edge high-throughput sequencing and lab automation technologies, MGI has been actively facilitating rapid and accurate analysis of pathogenic DNA for the detection of new threats and epidemic outbreaks, fueling more effective interventions to monitor and prevent the spread of diseases.



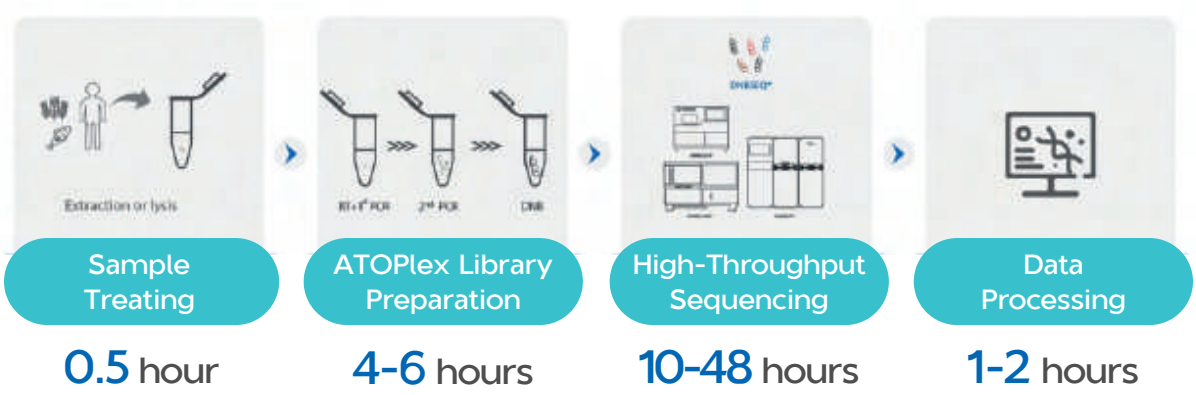
High-throughput sequencing can accurately identify pathogens and provide in-depth information, such as traceability analysis of pathogenic microorganisms, drug resistance genes, and virulence factor analysis. It is gradually becoming one of the most important technical means for the prevention and control of infectious diseases. Virus genome sequencing, enabled by MGI's various types of high-throughput genetic sequencers*, has notably assisted in painting a fuller and better picture of SARS-CoV-2 through COVID-19 diagnosis, study on its epidemiology and virology, and the tracing of geographical origin and source transmission chain of different strains.

In fact, it was gene sequencing that allowed researchers and healthcare professionals to first monitor the spread of the Omicron variant, one of the dominant strains of the virus circulating the world.

MGI's high-efficiency and innovative instruments were utilized in the detection and tracing of the Omicron variant to safeguard local communities in more than 70 countries to date, including South Africa, Serbia, Saudi Arabia, United Arab Emirates, Canada, Australia, and China. Its proprietary ATOPlex technology, an affordable and fast two-step multiplex PCR method, contributed to the discovery of the first case of the Omicron variant in Sweden and Saudi Arabia. Equipped with its multiplex PCR technology, the core platform provided effective whole-genome sequencing and monitoring of the new variant. It also enabled continuous mutation detection and analysis for enhanced detection performance, further contributing to global pandemic control efforts.

Workflow

Fast and Comprehensive

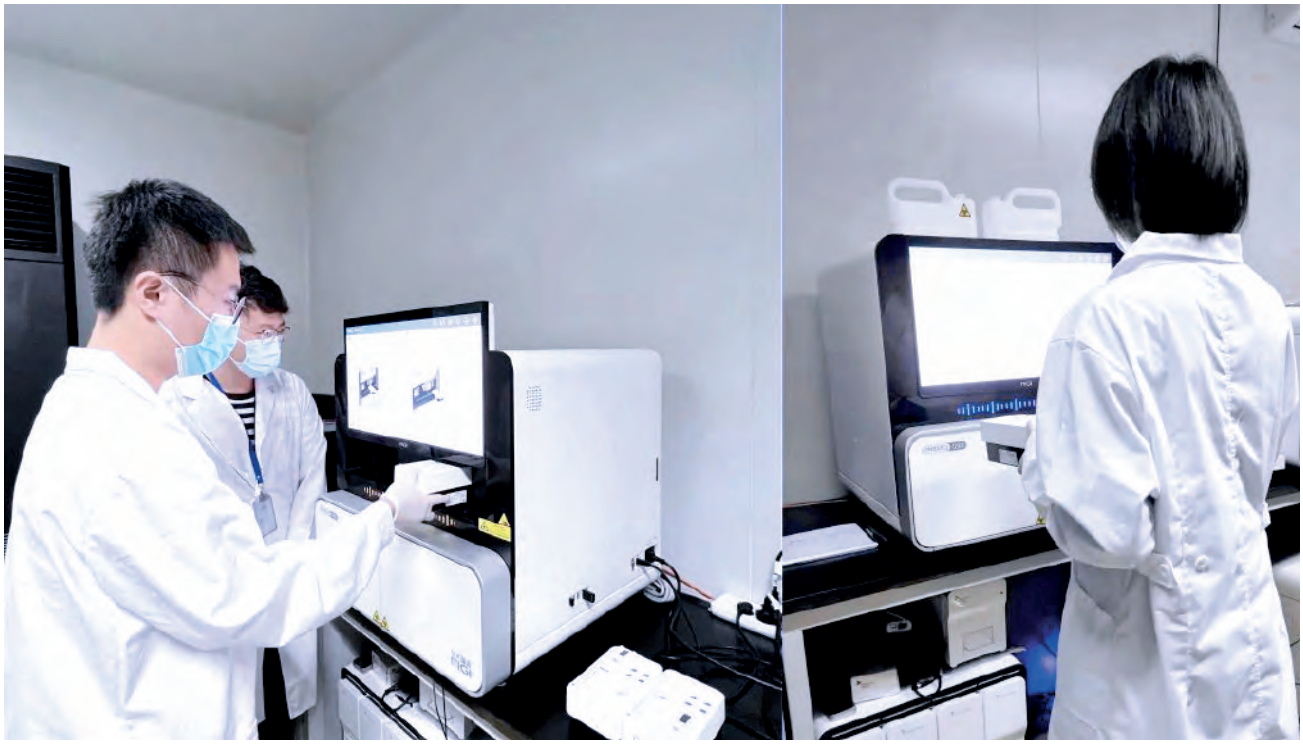


Using ATOPlex, MGI has empowered numerous water monitoring initiatives worldwide to contribute to water quality and food safety improvement. In fact, ATOPlex, along with MGI's DNBSEQ-G50* genetic sequencer and MGISP-100 automated system, were credited for helping scientists from the South African Medical Research Council (SAMRC) in first detecting fragments of the Omicron variant in wastewater samples collected across Cape Town, which informed a timely public health response amidst a surge in local cases during that time. Recently, MGI announced support for a graduate research project at Australia's University of Queensland on wastewater monitoring of antimicrobial resistance in the water environment with ATOPlex. The company also added to its portfolio environmental DNA (eDNA) sequencing products to help detect any potential disease outbreaks in water sources.

Besides SARS-CoV-2, whole genome sequencing and metagenomic sequencing have played an important role in the identification, molecular typing, drug resistance monitoring, and

traceability analysis of other disease agents. To address the continuous need for rapid identification and traceability of new unknown pathogens, MGI provides a high-throughput sequencing platform* integrated with a pathogen detection system, covering the whole process from sample to report output. The system is compatible with DNBSEQ-G99*, DNBSEQ-E25*, DNBSEQ-G400* and DNBSEQ-G50* genetic sequencers, with supporting hardware and compatible reagent kits to enable an extensive range of pathogen testing.

MGI's DNBSEQ™ platform has accumulated a strong, practical foundation in the detection and research of pathogenic microorganisms. At present, it is assisting scientific research units in universities and local disease control institutions in the discovery, genome sequencing and traceability of various pathogenic microorganisms, including Mycobacterium tuberculosis, Chlamydia psittaci, the monkeypox virus, SARS-CoV-2, and influenza viruses. This has in turn enabled early detection of outbreaks, etiological monitoring and early warning, and risk assessment.



First Imported Case of Monkeypox, Chongqing, China.

Notably, the discovery of the first imported case of monkeypox in Chongqing, China was facilitated by the ultra-high-speed DNBSEQ-G99* within 11.5 to 16 hours from sample library preparation, to sequencing and bioinformatic analysis of the virus. In addition, v technology* was used in metagenomic sequencing to successfully identify the main pathogen from the body fluid samples of a patient with severe psittacosis.

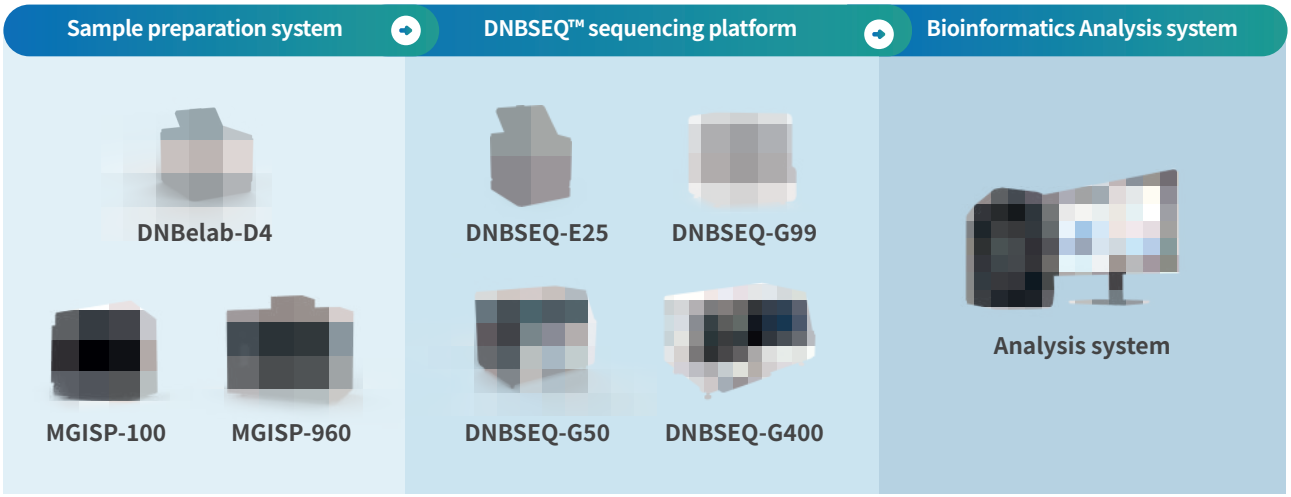
Microorganism fast identification Sequencing Product Portfolio

mNGS solution

Single/mixed infection pathogen identification
Pathogen genome assembly
Drug resistant and virulent gene prediction

tNGS solution

Pathogen genome assembly
Variant surveillance
Genotyping and tracing



The proprietary technology also enabled assembly of the pathogen genome, demonstrating strong data validity, great sequencing coverage and depth, as well as higher detection sensitivity.

With a commitment to building core tools and technology to lead life science through intelligent innovation, MGI will continue to empower researchers and healthcare professionals with its full suite of genetic sequencers*, laboratory automation, laboratory management systems and more in monitoring infectious disease threats and providing insights into how and where infections are being passed on to inform public health and policy and mitigate the next pandemic.

CUTTING-EDGE MEDICAL PLATFORM

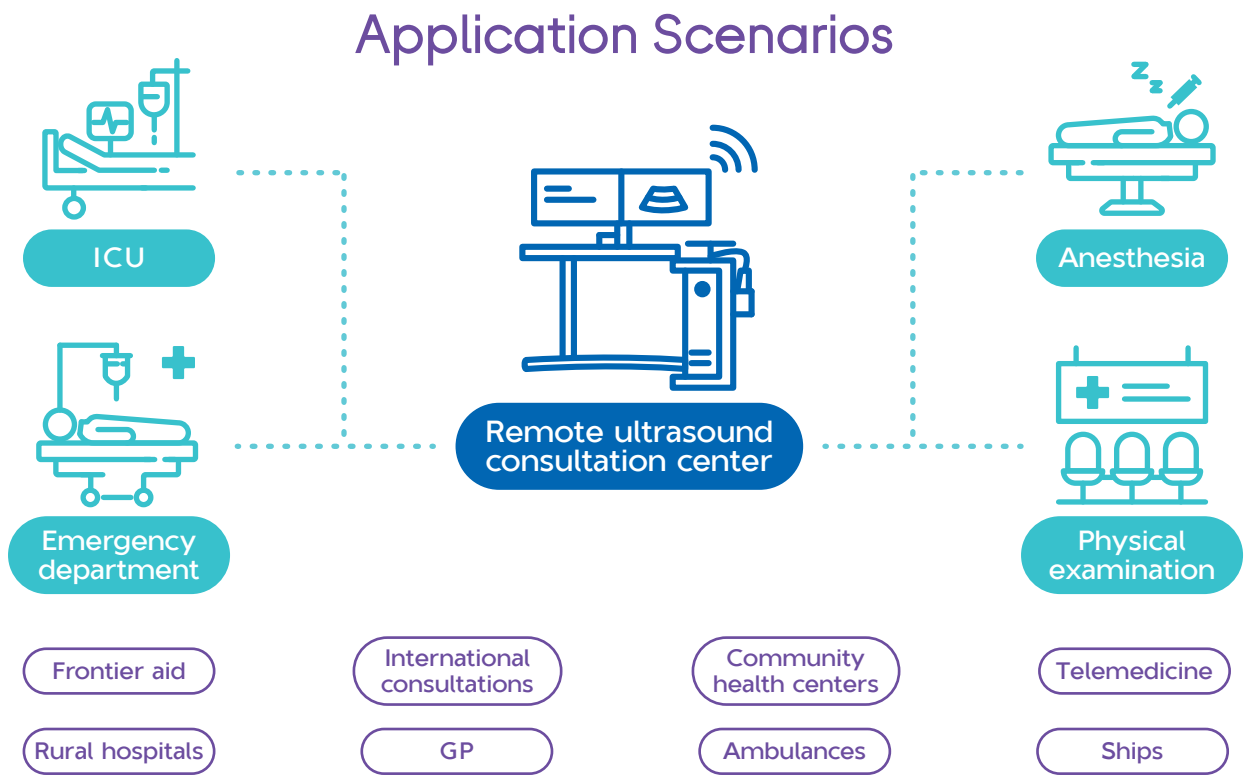
Enhancing medical access in rural areas with pioneering remote robotic ultrasound technology

Today, up to 3.5 billion people – almost half of world's population – lack access to essential health services. Countries are facing insurmountable healthcare challenges, from an increase in patients with multiple chronic diseases amidst an ageing population to massive shortages in doctors and nurses. In rural communities, in particular, infrastructure limitations such as no or poor power supply, hard to reach locations and security issues pose as further hindrances, leading to a greater divide in healthcare access and outcomes in some groups.

Guided by a vision of enabling affordable and effective healthcare for all, MGI, widely known as a leading provider of innovative high-throughput genetic sequencing solutions, has expanded its R&D expertise and know-how to develop new and innovative healthcare tools that are also cost-effective. Leveraging the digital transformation of healthcare that is rooted in the power of new technologies, 4.5G/5G, data, AI and more, MGI introduced its cutting-edge medical platform MGIUS-R3, the first remote robotic ultrasound system in China that can achieve "remote real-time diagnosis".

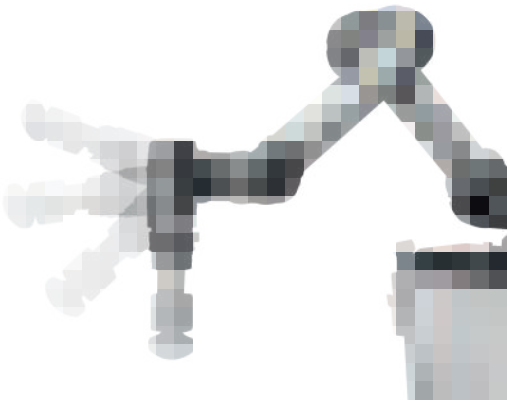
Combining robotic technology, remote real-time control system and high-resolution ultrasound imaging, MGIUS-R3 overcomes the distance limitations of traditional ultrasound diagnosis and treatment methods without the need for a physician to be at the same location as the patient. The device holds great promise for improving health outcomes, lowering the cost of care, promoting access to high-quality precision medical services, and improving the human care experience for all.

“Everyone has the right to access healthcare, and the adoption of digital healthcare tools and services is a vital step towards upgrading the quality and consistency of healthcare services worldwide,” said Dr. Jiang Hui, Chief Operating Officer of MGI. “MGIUS-R3 solves the problem of shortage of ultrasound doctors in remote and rural settings and reduces heavy workload for current doctors. It eliminates geographical limitations and improves healthcare system efficiency by enabling remote patients to access advanced healthcare resources and get diagnosed immediately.”



R3 integrates tele-robotic ultrasound technology and 4.5G/5G networks to provide signal and data connections for remote ultrasound robots to help doctors control patient-end ultrasound probes for diagnosis, while maintaining the high levels of synchronization required between surgeons’ hand movements, image transmission and force feedback. It is equipped with multiple sensitive ultrasound probes on its robotic arm, which can be operated by a doctor through a control system. Its flexible manipulator system can also simulate manual operation throughout the process to perfectly reproduce expert techniques.

After detection, the scan results can be transmitted to the patient through real-time network, while the doctor can conduct real-time communication with the patient through an interactive screen during the whole screening process. Blending robotics, teleoperation and ultrasound imaging technology, MGIUS-R3 is widely used in diverse fields, including healthcare aid in rural areas or island, internal hospital telemedicine, massive body check, breast cancer screening, interventional surgical assistance and more.



Standing at the forefront of digital health, MGI aims to even out the distribution of medical resources and makes ultrasound diagnosis more accessible.

In China, Shenzhen's Luohu Hospital Group began trialing MGIUS-R3 in as early as 2017. During the pandemic, when there was an extreme shortage of doctors and nurses, the device was deployed in local fever clinics, isolation wards and mobile hospitals. At Shenzhen Luohu People's Hospital, MGIUS-R3 was responsible for providing medical testing and ultrasonic diagnosis for nearly 2,000 patients. It not only helped to save lives and ease the shortages in medical resources, but also reduced the risk of transmission of COVID-19 to medical staff.

On International Women's Day in 2022, MGIUS-R3, the world's first tele-robotic ultrasound system that can detect cancer remotely, played a pivotal role in providing a three-day voluntary early breast cancer detection and diagnosis service for nearly 100 female employees at Roche in Shanghai. More recently, MGI entered an exciting partnership with Siemens Healthineers to adopt MGIUS-R3 for liver disease detection for patients in rural areas.

Outside of China, MGI helped establish remote ultrasound diagnosis services and training for the primary care center in Vall d' Herbon Barcelona Hospital with the advanced MGIUS-R3. Despite being over 10,000 kilometers away, a physician from Shenzhen Luohu People's Hospital in China was able to finish a sample scanning of obstetric ultrasound remotely by utilizing MGIUS-R3 for a patient in Vall d'Hebron in Spain. The installment of the device is expected to address the prevalent shortage of doctors in Spain, while facilitating more frequent exchanges of experience and knowledge among doctors and research experts for the benefit of local patients and the healthcare system.

In addition, MGI supported the Department of Internal Medicine at the University of Pisa in Italy to provide remote consultation in community clinics in Pisa, as well as regular consultation

Dr. Andrew Antolana, Radiologist, Vall d'Hebron

services from experts in university hospitals. The application of MGIUS-R3 include Abdomen, Vascular, Small Part, Urology, Gynecology and MSK, with flexible ultrasound image parameters that can be adjusted without any latency, supporting rapid, real-time diagnosis. "Robotic Ultrasound System has consistently demonstrated excellent B-Mode image quality, indicating that the ultrasound equipment itself is of very good quality," said Dr. Mario Meola, Associate Professor of Clinical Nephrology at the University of Pisa.

Over the years, the innovative MGIUS-R3 has garnered numerous honors and awards, notably iF Design Award for its innovative function and exquisite design, as well as first prize in the Blooming Cup 5G Application Competition, Outstanding Product Award in Global 5G Application Competition, and first prize in the China Medical Device Innovation and Entrepreneurship Competition. The device is now in use in over 32 provinces and regions in China, in addition to Latvia, Italy and Spain, proudly contributing to the improvement of local medical ultrasound services and relieving tension in medical resources.

From genomics platforms to automation tools and novel products, MGI never ceases to lower the barriers to access cutting-edge yet affordable technologies. With growing clinical applications worldwide, MGIUS-R3 has the potential to address many of the obstacles brought forth by a fragmented and uneven healthcare system, making sure that no one is left behind.

**Products are provided for Research Use Only. Not for use in diagnostic procedures (except as specifically noted)*

NOVEL PRODUCTS

Remote Robotic Ultrasound System

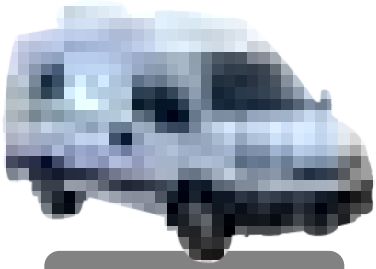
1100*680*1050
120kg

Patient

1200*1000*1500
70kg

Doctor

Robotic Ultrasound Vehicle



5999*2011*2754
4495kg

Wireless Handheld Ultrasound H1 Series

50*32*160

DNBelab C4 Pocket Single-Cell Lab

230*57*42
180g

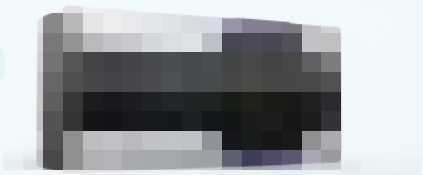
DNBelab C-Tai M4

290*210*230
5kg

BIT Products

MGICLab-LT

Automated
Ultra-low-temperature
Biobank



MGICLab-LN

Automated Liquid
Nitrogen Storage System

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