Omics future on personalized medicine, computer breeding and open platform

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As one of the most influential and fruitful annual conference in "Omics", the 8th International Conference on Genomics (ICG-8) was successfully concluded on November 1st with numerous updates provided on on-going research applying today's accurate and affordable technologies to advancing human health and agricultural breeding. The three-day conference, co-organized by BGI and *GigaScience Journal*, also provided an excellent platform for deeply discussing the challenges and opportunities brought by the continuing explosion of big data.

Professor Huanming Yang, Chairman of BGI, opened the conference with his warm welcome remarks to over 400 worldwide participants, including an elite class of world-class researchers and industry decision makers. The prestigious speakers brought their excellent presentations covering various topics on emerging technologies and tools, human diseases, crop improvement, and science's advocacy.

Having a DNA Dream and Celebrating the Milestones of Life Science

Luther King's famous "I Have a Dream" speech in 1963 has caused such a sensation and is still widely circulated today. In his opening speech, Professor Yang elaborated his dream, a DNA dream: To sequence everything on the planet for satisfying the demand of green development; to sequence everybody in the world for a healthy future.

In recent years, BGI has grown very fast with the persistence of their DNA dreams. Their contribution has accounted for ~50% of the genomics community's sequencing capacity in the whole world since 1999, and today they can sequence 100 human genomes per day. The robust technology platforms and capacity put them on the accelerated path to fulfilling their dreams.

Genomics is the first most globalized field in life science. The 'Strong-Strong' and 'Win-Win' collaboration can further accelerate the realization of DNA dream. Dr. Jun Wang, Director of BGI, introduced the Million Genomes Project in BGI and called for more like-minded researchers to join such grand project. He also shared many existing cooperative projects, such as the 1,000 Genomes, and a metagenomic study in type 2 diabetes (T2D).

The year 2013 is very special, which marks many anniversaries of the milestones in life science, such as the SARS Virus at Ten, the 30th anniversary of PCR, the 30th anniversary of Plant BioTech, the 50th anniversary of Discovery of RNA double helix, the 50th anniversary of mass newborn screening, the 50th anniversary of the 1st community mental health act, and the 80th anniversary of "Gene Is Real". Especially noteworthy is that this year marks the 60th anniversary of the historic discovery of DNA's double helix structures. Since then, DNA has launched a scientific revolution and forever changed human understanding of life.

The history is the memory of the past experience, but the future is unknown and challenging. While tracing the development of life science in the past, Yang also looks into its splendid future as well. He emphasized that next year marks the 15th birthday anniversary of BGI, and the 60th anniversary of genetic code.

Exploring Disease Mysteries, From Bench to Bedside

Every year, millions of people die of top deadly diseases such as lung cancer, malaria, tuberculosis, diarrheal diseases, HIV/AIDS, cerebrovascular disease, and others. Even worse, for many of these diseases there is no treatment, cure or vaccine, or the possibility of effective prevention or control. The emerging of clinical trans-omics is promoting a revolutionary shift, which enables clinicians to pursue the Omics direction for eliminating the disease threats. In this conference, researchers shared many wonderful cases of the applications of cutting edge sequencing technologies to explore the disease mysteries.

Dr. Jonathan Flint from Wellcome Trust Centre for Human Genetics, UK discussed their genetic studies of major depression in 10,000 Chinese women. Many people with a depressive illness never seek treatment. In fact, depression is the most common psychiatric disorder. In Dr. Flint's study, they attempted to find the DNA variants associated with depression. The results indicated that major depression might have multiple dimensions of genetic liability.

Prostate cancer is the most common malignancy and its incidence is increasing rapidly in China. Dr. Colin Collins from Vancouver Prostate Centre, Canada, shared his insights into the application of genomics in prostate cancer research, and introduced their developed novel tools that may help to establish a system for drug target discovery and personalized oncology.

Dr. Hidewaki Nakagawa from RIKEN Center for Genomic Medicine, Japan, shared their study on liver cancer, one of the most common and deadly cancers worldwide. He mentioned that the comparison among whole genomic pictures of heterogeneous liver cancers could clarify the underlying liver carcinogenesis and achieve molecular sub-classification of liver cancer, which facilitates its biomarkers discovery and genome-based personalized medicine for liver cancer.

"We need to sequence at least 1 billion human genomes for supporting personalized medicine." said, Dr. Radoje Drmanac, Co-founder and Chief Scientific Officer (CSO) at Complete Genomics, Inc. (CGI). In the conference, he introduced their accurate LFR technology and the applications in reproductive and genomic health. He added, "We are moving into a new era when everybody has their own genomes just like ID cards, securely stored in computer-readable memory and used, in combination with other Omics tests, for their entire life for personalized health management (Genomic Healthcare), primarily in disease prevention."

Dr. Vince Gao, Vice President of BGI Health, introduced the mission of BGI health and presented the milestones achieved during the advancement of their clinical applications and collaborations, and the innovative scientific approaches to meet the future challenges. He said, "Linking through omics disciplines we provide genetic tests targeting on different age stages of the life cycle. We are striving for providing technology leadership and 'trans-omics' expertise to serve the medical and healthcare community."

Breeding in the Computer before in the field

Shrinking levels of surplus food supplies are signaling that the future of food may not be as secure as most think. According to the World Health Organization, about one third of the world's population is well fed, one third underfed, and one third is starving.

In Dr. Jun Wang's presentation, he said, "Breeding in the computer, then in the field", that is to say, breeding plant varieties using computers will allow scientists to test out millions of genetic variations without having to breed them. This will greatly enhance the opportunity for excellent varieties selection and expedite the process of breeding for resistance, and help extricate people out of poverty and hunger.

Rice is one of the three major global crops, together with maize and wheat, which supports human and our domesticated animals. In the conference, Dr. Takeshi Itoh from National Institute of Agrobiological Sciences, Japan, illustrated how to use transcriptomics to give a vivid view of a living organism such as rice at molecular level, and all the results are now available on their website. Dr. Itoh also emphasized that RNA-seq was so versatile that interactions of multiple organisms can be investigated simultaneously.

Dr. Yong Pyo Lim from Chungnam National University shared his view on Brassica genome for applied breeding. Brassica species can adapt to various environment, which are highly regarded for their nutritional value. In Dr. Lim's speech, he mainly focused on the sequencing and molecular breeding system of Chinese cabbage (Brassica rapa). His team has found some key genes associated with biosynthesis pathway in B. Rapa genome.

In addition to the crops, animal genetic breeding can improve the fertility, production and performance of economic animals. Dr. Wen Wang from Kunming Institute of Zoology, Chinese Academy of Sciences, delivered a presentation on mining important agronomic trait genes by evolutionary genomics. Dr. Wang concluded that domesticated species can obtain human-preferred traits rapidly under artificial selection, but the genetic mechanism underlying the rapid evolution of phenotypic traits of domestic plants and animals remain to be an ancient but open questions.

Turning Open-access and Big Data Challenges into Opportunities

One of the major changes occurring today is the open access to scientific research. Open Access could contribute to good scientific practice through the data dissemination, which could be of increasing relevance in the natural and life sciences in view of a spate of scientific fraud cases in recent years. It is only in the most recent two years that there is an over 400,000% increase in daily sequencing data. The handling, storing and sharing of these tremendous volumes of data has become a significant research bottleneck. In the conference, a panel of experts from the fields of science and publishing discussed the opportunities and challenges of the open-access, and shared their open-source genomic research.

Dr. Dan Maclean from the Sainsbury Laboratory is currently engaged in producing software infrastructure specifically for crowdsourcing from genomics communities, involving adapting existing Open Source software. In the conference, he mentioned that the structure of science inhibited collaboration and sharing, which leaded to the slow respond of science in emergencies. One promising way out of embarrassment may be crowdsourced analysis and open access.

Dr. Jacob Shiach from Brightwork CoResearch introduced OpenPCR, Open Source Spectrometers, and Cell printer in his presentation. Among them, OpenPCR is a low-cost, open source Personal PCR machine, helping DIY biologists and professional labs alike. The cell printer is a bioprinter that can magically print 3D living cells. Its open source helps to quicken the development steps and bringing down cost. At the end of the speech, he pointed out that the age of indie science was coming, which was featured by open source and more global collaborations rather than competitions.

The ICG, since its inauguration 8 years ago, has proved itself as a platform to share experiences and expertise, and more importantly, to share visions and foresight of the whole field of "omics" and the life sciences. In the future, BGI will continue to increase the domestic and international scientific cooperation and bring more advancement to the research of "omics" and industry applications.

Provided by BGI Shenzhen

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