



Perspectives

Collaboration and Sharing: A New Culture of International Genomics Community

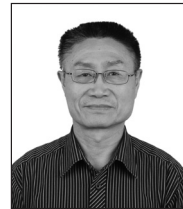
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Besides its unprecedented scientific achievements, the International Human Genome Project (HGP) cultivated a new culture of the genomics community: “owned by all, conducted by all, shared by all” (Muzny *et al.* 2006). It set up a brilliant example for international collaborations.

Thanks to the efforts of the HGP Consortium, as well as its sponsors and supporters, human genome has been generally acknowledged as the common heritage of the mankind (U.N. 1998). When looking backwards, we, the Chinese participants, shall sincerely thank our colleagues from the leading developed countries to have accepted China,



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The authors would like to thank colleagues at BGI for their work at promoting this new culture of international collaboration.

then and now a developing country, to participate in this international endeavour. Involving research partner from developing countries in such a global project literally began to remodel international landscape of scientific collaboration. "Science should be done by all, and big science should be done by vast and inclusive collaboration, including those countries that might be judged to be lagging behind by the usual historic and economic measures" (Yang 2011).

The HGP Consortium developing the *Bermuda Rules* (U.S. Department of Energy, Office of Science, 1996) to release all the scientific data immediately for free use by all, was a milestone in humanity. For the first time in scientific collaboration, regardless of all the input and contributions made by its participants, the achievements had to be freely shared within the public domain. More significantly, contemporary science unprecedentedly unites the developed countries and the developing ones, and allowed the upstream fundamental knowledge to drive the flourishing of downstream biotech, bioindustry and bioeconomy all over the world.

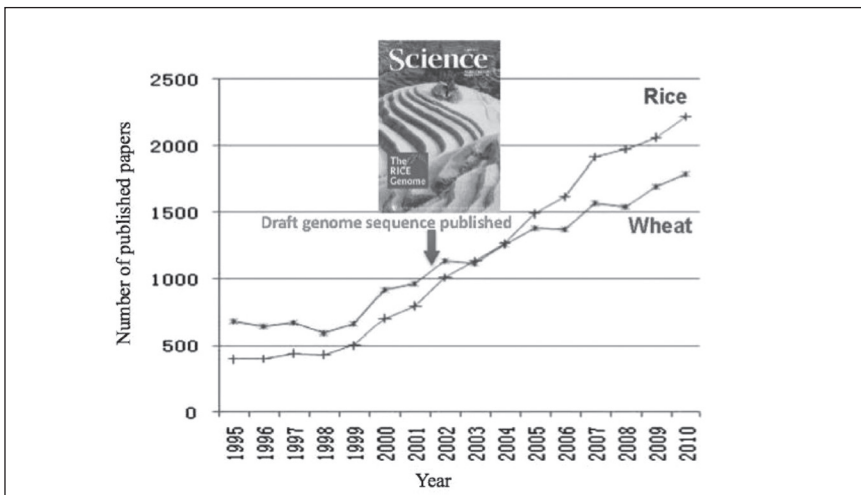
As a late comer, China joined the HGP with the conviction that "we are on your side by joining you!" Actually, BGI (formally known as the Beijing Genomics Institute) was born for and out of the HGP. We have, therefore, changed the history together with colleagues from developed countries. "Protecting the ownership of human genome" was appreciated by other sectors of our societies, and eventually adopted as a core principle by the United Nations General Assembly at the Universal Declaration on the Human Genome and Human Rights in 1998, and by the UNESCO at the International Declaration on Human Genetic Data in 2003 (U.N. 1998; UNESCO 2003).

The debate on gene patenting caught serious attention when in 2005 Jensen *et al.* revealed that "nearly 20 per cent of human genes are explicitly claimed as U.S. IP" (Jensen *et al.* 2005). In 2011, our British colleagues provoked the community to reflect on current framework of intellectual property rights, and presented the *Manchester Manifesto* for comments on *Prometheus* (Rhodes *et al.* 2011). A series of responding papers were published on 2011's third issue of *Prometheus*, whereas we supported the *Manchester Manifesto* and introduced the following case of freely sharing rice genome data (Yang 2011).

Inheriting the HGP spirit, BGI continues promoting international collaboration for the good of all. One illustrative example is our decade's work on the rice genome. The first rice genome sequence was published for

free-sharing in 2002 (Yu *et al.* 2002), and catalyzed revolutionary research on rice. In contrast, fewer studies have been carried out on wheat, another important staple food crop for humans which historically gained more research attentions from plant geneticists (Figure 1). In particular, free access to genomic data inspired colleagues from developing countries to carry out more research on rice (Figure 2). Some may argue that phenomena could be explained by any other reasons, for example, increasing funding by the “emerging nations”. But more clear and convincing evidence is that the number of cloned genes and QTLs skyrocketed the moment the rice genome sequence becoming freely accessible (Figure 3).

Figure 1: The Impact of Free Sharing of the Rice Genome Sequence Data on Global Rice Research

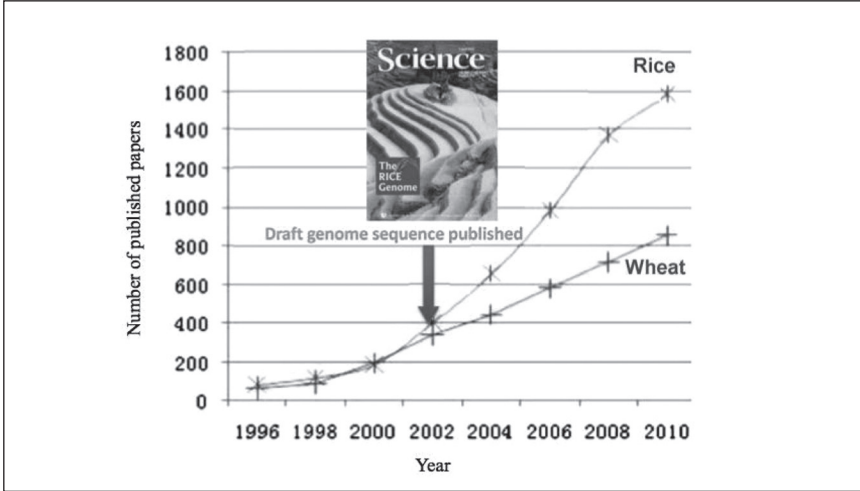


Source: Yang, 2011.

Embracing this new culture of international collaboration, the genomics community unleashed the 21st century’s life-science revolution. Equipped with next-generation-sequencing technologies, our community created a miracle year in 2007 (Silver 2007). Substantial attentions has been given to analyse human genomes, and effective strategies like genome-wide association study have been developed. International research efforts have also been put into tackling genotype-phenotype relations, especially on health and diseases. As illustrated in 2008 by our colleagues Dr. Eric Topol, the director of the Scripps Translational Science Institute, “the study of the human genome and its variations has advanced to the point where

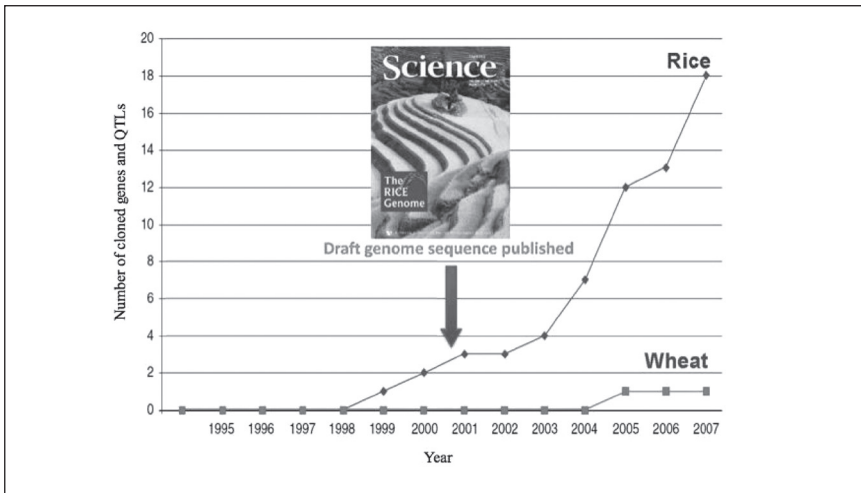
there were more breakthroughs last year than in several of the past decades combined” (Somers 2008).

Figure 2: The Impact of Free Sharing of the Rice Genome Sequence Data on Rice Research In Developing Countries



Source: Yang, 2011.

Figure 3: The Scientific Basis of Impact of Free Sharing of Rice Genome Sequence Data on Rice Research



Source: Yang, 2011.

Recent pandemics like SARS, H1N5 flu and the outbreak of ‘cucumber’ flu in Germany last year, nonetheless, challenged the community’s resolution to solve problems in a hand-in-hand and timely manner. Last year in Germany the highly contagious disease infected over 2000 people in less than a month, and caused death of at least 23 people by early June. Collaborating with colleagues at the University Medical Center Hamburg-Eppendorf, researchers at BGI unmasked the nature of the lethal pathogen over the weekend of the sample’s arrival. On the sixth day, we completed the sequence, and immediately released preliminary analysis together with all the original data (Li *et al.* and the Escherichia coli O104: H4 TY-2482 Isolate Genome Sequencing Consortium 2011). Subsequently, combining international resources, the scientific community processed further research at an exceptional speed and scale. According to Dr. Marina Manrique, “In less than 24 hours we got the reads, the assembly, and the annotation. A good case study” (Kupferschmidt 2011). This singular exercise reinforced the principles of “open-source analysis” and “timely sharing of data” among life-science community, and reminded us of humanitarian responsibility shouldered on us life-scientists.

Alongside this process, our institute, BGI has grown into one of the largest sequencing centres in the world. We set our research mission to ‘sequence every (living) thing on Earth and everybody in the world’. We co-initiated large-scale research projects, including the International 1000 Genomes Project, the International Cancer Genome Consortium, the 1000 Mendelian Disorders Project, the Microbial Genome Project, the Social Insects Research and the Genome 10K Project, not only with our long-time partnering research entities like the National Institute of Health in the U.S. and the Wellcome Trust Sanger Institute in the U.K., but also with new friends from many other countries like India, Saudi Arabia and the People’s Republic of Bangladesh. To fully unlock the mysteries of life, genomics cannot be done alone. Instead, the very nature of sequencing and bioinformatics as revolutionary tools of studying life connotes the need for interdisciplinary and even trans-disciplinary collaborations. Our genuine goal, originated from the HGP, is to promote widespread vast international collaborations for the benefits of mankind, our future generations and coexisting environment.

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