

Letter from the editor

“We wish to suggest a structure for the salt of deoxyribonucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.....”

J.D. Watson
F.H.C. Crick

We may remember these simple opening lines from this seminal paper published in Nature half a century ago. Not only has the double helical structure of DNA proved to be of considerable biological interest, it has been the basis of several disciplines such as recombinant DNA technology and genomics. It is therefore fitting that after 50 years, we now have the completion of a high quality comprehensive sequences of the genomes of bacteria such as *E.coli K12*, *Mycobacterium tuberculosis*, *Pseudomonas aeruginosa*, *Vibrio cholerae*, plants such as *Arabidopsis thaliana*, *Oryza sativa*, fungi such as *Saccharomyces cerevisiae*, and of course human, *Homo sapiens*, among many other organisms.

Indeed, I have attempted to summarize a most interesting and comprehensive feature by Francis Collins and his colleagues (Nature 422, 24 April 2003) that the genomic era is now a reality.

The completion of the human genome project has ushered in a revolution of biological research. Continual influx of ever larger and more complex genome data sets in the public databases, have transformed the study of virtually all life processes. At no other time, has the genomic approach so permeated biotechnology and biomedical research. The identification of human disease genes, each one previously considered a formidable task in terms of personnel and years of hard work previously, can now be routinely accomplished by one or two researchers with access to DNA, associated phenotypes, a thermal cycler, a sequencer and a line to the world wide web. The gene by gene investigation has been virtually overtaken by the availability of microarray platform technologies in which one can scan for tens of thousands of genes in a day. Funds that would have otherwise have gone into employment over several years are now being invested into more sophisticated and faster technologies. Given this mind boggling pace, how do developing countries ever hope to catch up with the action or even be a part of the scenario? We will do well to remember that despite the impressive technological advances have been made, one will still have to go back eventually to the phenotypes. These can only come from populations, the majority of whom reside in developing countries. This is also true of biological diversity and unique ecosystems. The workable way to go would be in mutual collaboration among individuals and institutions.

There has been a move in some developing countries in the South East Asian region to invest largely in infrastructural development in terms laboratory building and the acquisition

of the latest equipment. These efforts are laudible, but seem to ignore the fact that the important things include asking what are the major scientific questions, and what are the main programmes to be put in place given the advantages of that particular country. In terms of resources, there is a paucity of national disease databases, despite healthcare and other systems that have been in existence for the past 30-40 years. Internal communications could also be improved.

Collins *et al* have put together a vision for the future of genomics research in any field which may be used as a guideline. The genome projects must be the foundations of the relevant platforms of Genomics to Biology, Genomics to Health and eventually Genomics to Society.

In terms of Genomics to Biology, there are several challenges. Firstly, the endeavor must be to comprehensively identify the structural and functional components encoded in the human and other genomes. Then efforts must be made to elucidate the organization of genetic networks and protein pathways and establish how they contribute to cellular and organismal genotypes. Next would be the development of a detailed understanding of the heritable variation followed by the understanding of evolutionary variation across species and mechanisms underlying it. Policy options that facilitate widespread use of genome information in research, clinical and other relevant settings must be developed.

Where Genomics and Health is concerned, the challenges are to develop robust strategies for identifying genetic contributions to disease and drug response. Strategies must be developed to identify gene variants that contribute to good health and resistance to disease. The utilization of genome based approaches to prediction of disease susceptibility and drug response, early detection of illness and molecular taxonomy of disease states should be promoted. Understanding of genes and pathways must be utilized to develop powerful new therapeutic approaches to disease treatment and management. Investigations of how genetic risk information is conveyed, how it influences health strategies and behaviors and how these collectively affect health outcomes and costs, should be undertaken. Effort must also be directed toward genome based tools that improve the health of all.

In terms of Genomics to Society platform, there are four challenges which include development of policy options for the uses of genomics in medical and non-medical settings, understanding the relationships between genomics, race and

ethnicity and the consequences of uncovering these relationships, understanding the consequences of uncovering the genomic contributions to human traits and behaviors and finally to access how to define ethical boundaries for uses of genomics.

In order to make these challenges realities, there are six crosscutting elements that will have to be in place. They include Resources, Technology Development, Computational Biology, Training, Ethical Legal and Social Implications (ELSI) and last but not least Education.

Resources would include genome sequences, comprehensive reference sets of coding sequences, collections of transgenic and knock-out organisms, reference sets of proteins, databases, cohort population and large molecular libraries.

Technology development would include sequencing and genotyping technologies, *in vivo* real time monitoring of gene expression and localization, large scale mutagenesis approaches, improved imaging methods, lab based phenotyping and proteomics, linking of molecular profiles to biology.

Computational biology will enable the generation of hypotheses and stimulate experimental approaches to test them. We will need new approaches solving problems, reusable software modules for interoperability, programmes to elucidate effects of non-genetic factors and gene-environmental interactions, new ontologies for new data types and improved knowledge management systems.

Scientific, medical and social/ethical training must be improved to equip scientists, clinicians and scholars to face the challenges now facing genomics. Imperative to the training would be the computational skills, interdisciplinary skills, and the sharing of different perspectives.

In terms of education, healthcare professionals must have sufficient knowledge of genomics to use the outcomes of the research effectively. The public must be knowledgeable to make informed decisions about participation in research and to incorporate findings into their own health care. Genomics should be introduced into high school systems as the students will be both the users of genomic information and also researchers of the future.

Society must formulate policies to address many of the questions raised by genomics. Focused ELSI research that directly informs policy and practices, would provide knowledge for direct use by researchers, policy makers and the public.

Of course, not every nation will be able to fulfill all aspects of the vision on its own but collectively, it would be possible. Enough for now, back to the bench.

Who knows what will be achieved on the centenary of the double helix ?

Maude E. Phipps
Chief Editor