EXHIBIT AB

Progress in science depends on new techniques, new discoveries and new ideas, probably in that order

Sydney Brenner (Nobel Prize in Medicine, 2002).

There has never been such a profound period of change in biomedical science as has occurred in the first two decades of the 21st century as the result of new genetic technologies. Our understanding of the genetic basis of disease is increasing exponentially as a result – and is continuing to revolutionise the way we discover, diagnose and treat genetic disorders.

Timeline of Change

In May 2003 there were around 1,700 known disease-causing genes. At that time the Prince of Wales Hospital laboratory was typical of many genetics laboratories and provided complete diagnosis for three major disease genes, at costs in the range of $700-1700 each with turn-around times for a result of about 3-6 months. Today, as the result of genomics there are approximately 5,000 known disease genes – and they can all be sequenced in parallel within a few days at a cost of approximately $1,000.

There have been several enablers of this revolution:

i) The human genome sequence was completed in its entirety in April 2003. It took 13 years to establish the organizational, collaborative and technological expertise to generate the human genome sequence, at an estimated cost of US$5 billion. The online open access availability of the annotated human reference genome has been one of the fundamental building blocks of genetics.

ii) In 2004, researchers identified that segments of the human genome could be present in different number of copies in different people. Usually most human genes come in pairs, one on the chromosome that a person inherits in her mother's egg cell and one on the chromosome inherited from her father's sperm cell. When the sperm and the egg fuse to form an embryo, that cell has 2 copies of most genes. In 2004, Lafrate *et al.*, 2004; Sebat *et al.*, 2004 showed that large-scale variations in copy number (i.e. instead of 2 copies there may be 1 copy = a deletion of a gene on one chromosome, or 3 or more copies = a duplication/triplication of one gene) were common findings in the genome. These copy number variants occurred in hundreds of places in the genome, and in some instances the loss or gain of genes caused disease. The full extent of copy number loss and gain had not been previously appreciated. We now know that 5-15% of childhood onset disorders can be due to loss or gain in gene copy number.

iii) In 2009 a suite of new sequencing technologies, the selection of targeted regions in the genome followed by massively parallel sequencing, was first applied to human disease. Genomic Sequencing has revolutionized genetic diagnosis – the availability of this technology now means that the complex task of producing sequencing data from patient genomes can be accomplished in a few days at a cost of approximately $1,000. Since the introduction of genomics, the pace at which the genes underlying genetic disorders are discovered per year has increased, and the proportion of discoveries made by genomic approaches (blue bars in Figure 1 below) as to compared with conventional approaches (red bars) has steadily increased. Since 2013, two major genomics technologies have become mainstream. Whole Exome Sequencing (WES) sequences just that small part of the genome (~1-2% of the whole) that codes for proteins, whereas whole genome sequencing (WGS) sequences all of the genome that is accessible. Combined, WES and WGS have had major impacts on diagnosis and research genetics and discovered nearly three times as many genes as conventional sequencing approaches that were available in the 1990s (Figure 1).

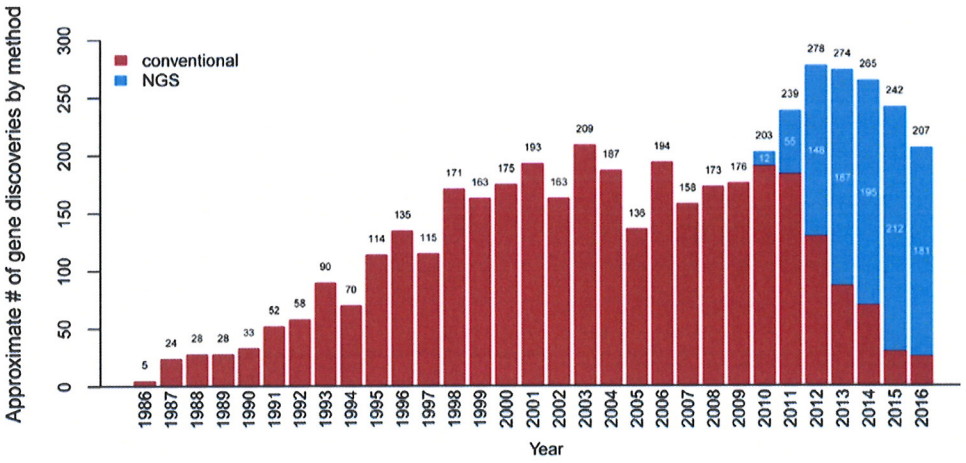

Figure 1. Approximate Number of Gene Discoveries Made by WES and WGS versus Conventional Approaches since 2010 according to OMIM Data

iv, v) Genomic sequencing produces very large amounts of data – an example of this is that in the first week of operation of the genomics facility at Prince of Wales Hospital the sequencing laboratory produced more computer data than the entire activity of the pathology service had produced in the previous 10 years. It would be impossible to transform these raw sequencing data calls into information, and then for practitioners to interpret the medical significance of the variants that are present in the data contains without sophisticated computer algorithms that can rapidly parse the data and compare it to reference datasets of variants in many different human populations. A key enabler has been the aggregation of progressively larger normal population datasets to support this activity (2011 NHLBI Exome Sequencing Project - 6500 samples; 2014 ExAC database - 60,706 samples; 2016 – gnomAD database of 141,456 samples).

vi, vii) The final enablers of this revolution have been international efforts to systematize the evidentiary basis for determining whether a genetic variant is likely to cause disease and the definition of typical categories of admissible evidence that can be used to interpret DNA sequence variants, together with relative weightings of the significance of those difference pieces of information. This international effort has established statistical likelihoods for commonly used terms such as 'likely pathogenic' (90% certainty) and 'pathogenic' (99% certainty) and has resulted in a three tier system of categorization of the pathogenicity of variants, these are: variants that are benign or likely benign (together representing 10% of variants); variants of uncertain significance (80% of variants); and likely pathogenic or pathogenic variants (together 10% of variants). This has been paired with the establishment of a regulatory framework to ensure that laboratory practice offers acceptable levels of patient safety, clinical utility and cost effectiveness (NPAAC Requirements for Human Medical Genome Testing Utilising Massively Parallel Sequencing Technologies - First Edition 2017).

Opinion

There are compelling reasons to consider that considerable progress has been made in genetic diagnostics since the date of Kathleen Folbigg's conviction and that the use of these technologies may offer possibility of generating new information that was not available in 2003.

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