

LORD LLOYD OF KILGERRAN AWARD 2004 LECTURE

Dr Richard Durbin FRS

Held at The Royal Society on Tuesday 26th October 2004

In the Chair: The Rt Hon the Lord Jenkin of Roding

LORD JENKIN said that the prize was awarded to a person who had applied science and technology for the benefit of society. Dr. Durbin's work in developing software which allowed global access to genome sequence was of outstanding benefit. Without it the use of the sequence would have been limited to specialized areas.

DR. DURBIN said that the realizing the value of the sequence meant converting its inherent value into applications, which could be used for medical or other use. He explained the nature of the genome project, which had permanently changed biological science. It was pure information, finite and complete and an accurate reference resource. It enabled the transfer of knowledge between related genes and species. The ENSEMBL genome browser provided convenient and efficient access to the information. The value in access to the sequence lay in the quicker development of knowledge, in particular of genetic abnormalities. Studies in genetic structure across organisms required access to the gene sequence; value lay in the collaboration, which followed from the feedback from users. Open access and transparency was essential. The ability for others to use the information was more important than verification; it enabled publication of work, which was the essential mechanism for research. Research advanced knowledge; in short, the open use of data was a proven way to achieve public good. It enabled layered annotation of material (an analogy could be drawn with the development of Ordnance Survey maps) to take place, as

results of research flowed back into the system. Any hypothetical disadvantage in the free transfer of reference information was outweighed by the knowledge that returned through annotation.

In response to a short discussion, which followed, Dr. Durbin emphasised the substantial work that still needed to be done. We were at the start, not the end of the use of genome research. We did not yet have sufficient knowledge to trace evolution of living matter, although there was knowledge of human evolution. More work could be done on environmental and third world problems; but the Sanger Institute was a health institute, and that governed priorities. But third world work had been done, such as the malaria project. Many diseases had genetic components, but often many genes were involved and it would take considerable further work to use genetic information in individual cases. Although the information growth was outrunning computer capability, computing power was not a limiting factor.

Sir Geoffrey Chipperfield KCB

The presentation will be available on our web site www.foundation.org.uk