The University of Cambridge and the Structure of DNA

Nicole Noronha

One fateful day in 1953, in a momentous culmination of Pauling's work on hydrogen bonding, Chargaff's on nitrogenous base pair ratios, and Rosalind Franklin's on X-ray crystallography; Francis Crick and James Watson published their model of the structure of DNA at Cambridge University.

Knowledge of DNA structure not only laid the framework for Crick's central dogma, that information cannot flow from a protein back to a nucleic acid, a tenet of modern molecular biology; but also unlocked the possibility of a plethora of applications from insulin producing bacteria and genetically modified organisms to the linkage of diseases to specific DNA mutations.

However, despite the beautiful simplicity of the DNA double-helix structure, we now know that DNA is much more complex than it first appears. Researchers have recently found variations in DNA structure from Watson and Crick's double-helix model which may play roles in gene regulation and disease. For example, Z-DNA, which has a left handed helix so the DNA is coiled backwards in comparison to the normal structure, has been implicated in the editing of genes [1] and in leukemia development due to its instability [2].

Thus, fifty-five years later, the science of DNA structure is still a developing field after its initial elucidation, which is undoubtedly one of the most famous events in Cambridge's scientific history. ■

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References:
[1] Wang, A. H. J. et al. Nature 1979 282:680–686
[2] Wang, G. et al Proc Natl Acad Sci USA 2006 103(8):2677–2682

Sanger Sequencing

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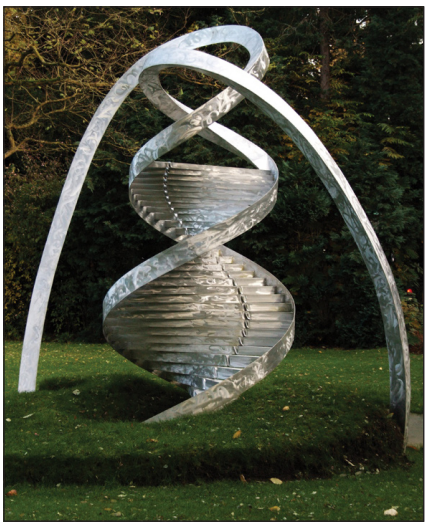
Genetics is a rapidly advancing field of science, and many of the greatest discoveries in genetics are owed to DNA sequencing. Sanger sequencing forms the basis for most of the DNA sequencing methods used today.

Frederick Sanger's chain-termination DNA sequencing relies on copying the DNA sequence, but it stops copying every time it hits a particular DNA 'letter' (either A, C, G or T). By measuring the length of the incomplete copies, scientists can determine where that letter occurs in the DNA.



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Sanger sequencing was one of the first and most popular methods of rapid DNA sequencing. The method provided scientists with a convenient way to sequence genes and entire genomes, thus paving the way for modern-day genomics and genome-sequencing projects such as the Human Genome Project. The advancement of

> **"Sanger sequencing was one of the first and most popular methods"**

DNA sequencing has revolutionised molecular biology, medicine, forensic science, agriculture and evolutionary biology. For example, scientists have discovered that many medical conditions arise from genetic mutations, and doctors may soon be able to treat patients with personalized medicine and gene therapy. Moreover, genetically modified foods have a significant share of the market, and genetically modified organisms such as mosquitoes may be used to prevent malaria and other diseases. ■

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