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Era of the epigenome - can Oz keep up?

The unveiling of the first human epigenome, published recently in *Nature*[1] is big news for molecular biologists around the world. It is both a feat of data crunching and a much sought after prize as scientists seek to unravel the meaning of the 3 billion bases that make up our DNA sequence. Remarkably, the largely US-lead blockbuster had a good tingle of green and gold: three of the 18 scientists involved were Australian. Even more remarkable is that these three were previously only known for their work on plants. The question you might ask is: has the well entrenched divide between plant and human biology finally been breached by this small troop?


Harvey Millar & Julian Tonti-Filippini

Before we venture to this vexed question let us first explain what we are dealing with and the benefits that may flow from this research.

Defining the sequence of the human genome was hoped by many to be the end of the puzzle of defining what humans are and what causes our diseases. But some years on it is clear that many other factors, such as environment, diet and disease, can affect our genes and how they perform through 'epigenetics'. This field describes modifications of the DNA in our genome other than changes in its sequence. These can be chemical changes to the DNA or differences in how tightly-packed it is. How the DNA in our genome is modified can determine whether a gene is turned on or off or up and down, like a switch or a volume control.

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To fully explore the role that epigenetics plays in the control of human genes, we needed supplementary maps to the genome: maps of the epigenome. A key part of this is a record of the tens of millions of tiny chemical decorations, termed DNA methylation, where they are on DNA, and which genes they can influence. These epigenetic changes are a normal part of human development; however, if they go wrong it can affect health and cause disease.

For example, turning off genes that protect cells or regulate metabolism can lead to cancer. Even conditions as varied as asthma and schizophrenia are influenced by epigenetics, which is predicted to be of greater relevance for human diseases than genetic differences between individuals.


Ryan Lister

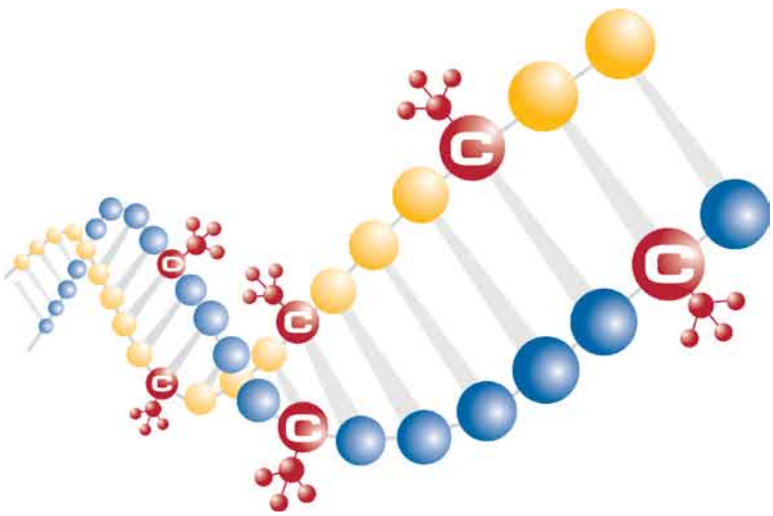
The excitement of those in-the-know is that now, beyond the genes themselves, we have a blueprint of the key controls that drive our genes. And what is even more exciting is we know our epigenomes are dynamic and regularly change.

So what can we do with these maps of the epigenome?

Firstly, they generally provide a first baseline for future studies, just like the human genome now provides a baseline for comparisons of human genomes from all over the world.

Secondly, important medical advances may result from this: The study identified many genes which were previously unknown as being under epigenetic control, and revealed the importance of different kinds of methylation and how they influence genes. Using this template, medical researchers can now embark on the design of tests that screen for epigenetic diseases.

Medical researchers may also be able to influence the methylation pattern that epigenetically controls the expression of disease causing genes, and find new ways to, for example, turn off cancer cells. DNA methylation is a reversible process providing the exciting prospect of new targeted drugs that may help cure epigenetic diseases in the future. However, medical research is still at the very beginning of understanding how small numbers of the tens of millions of marks could be changed through gene-specific DNA modification enzymes.



Finally, these maps will give important new insights, for example into how stem cells can maintain their ability to develop into any type of cell in our bodies. We may also speculate that in the near future, just as you may have your genome sequenced to uncover genetic propensity to disease or highlight special potentials, you could also have your epigenome(s) analysed. This would, for example, let you see how your (or your parent's) environment or diet has effected your genes in tuning them up or down through epigenetic marking in different cells of your body. Indeed, when it comes to your epigenomes you may find that ignorance is not bliss.

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So, why were Australian plant scientists involved in this study?

Last year we were all part of a team that mapped the first epigenome of a model plant, the thale cress Arabidopsis thaliana. That developed the pipeline and the know-how to tackle the much larger human epigenome, along with a series of other collaborators as part of the NIH Roadmap Epigenome Program.

What this shows is that the traditional barriers and artificial divisions, which for so long kept researchers specialising on particular species or taxonomical kingdoms apart, are rapidly breaking down. The new data rich biology is enveloping us and unique research tools from different model systems enable greater understanding of how shared cellular mechanisms operate.

Of course, it is positive that Australian researchers were involved. However, the study also highlights a significant hole in Australian science and in the gumption of our government for science funding: While innovative Australian software (www.annoj.org) and data handling was involved, along with Australian researchers, the human epigenome mapping was conceived, funded and driven in the USA by the NIH and from The Salk Institute for Biological Studies.

If Australia is going to properly join the drive towards large scale post-genomic science and the rich rewards in innovation it offers, we need to act fast and decisively so that home grown researchers can flourish within our own country through greater resources to a savvy but under-funded university sector.

[1]*Lister, R et al. (2009) Human DNA methylomes at base resolution show widespread epigenomic differences. Nature. Oct 14. Advanced-online, doi:10.1038/nature08514*

2009 Prime Minister's Prizes for Science

Prime Minister's Prize for science

Winner of the PM's Science Prize for 2009 is **CSIRO** scientist ***Dr John O'Sullivan***, whose work in the field of radio astronomy eventually led to the invention of wireless LAN technology. By sending information over many different frequencies and then recombining the signal at the receiving end where a computer chip is positioned to process them, O'Sullivan and colleagues were able to overcome the problem of noise caused by echo. CSIRO applied for an Australian patent for the technology in 1992, a US patent in 1996 and in 2009 were finally able to agree on licensing terms with the makers of wireless computers.

2009 Science Minister's Prize for Life Scientist of the Year

Monash University scientist, ***Dr Michael Cowley*** has won the 2009 Science Minister's Prize for Life Scientist of the Year for his work on how the brain controls fat metabolism. Working on monkeys and mice, he identified the specific neurons in the brain that control weight and showed how they are controlled by the weight regulating hormone, leptin.

He is the inventor of 10 families of patent applications, with 85 patents to date. And the company he founded, **Orexigen Therapeutics**, has four potential drugs for obesity under development with two at an advanced stage of trials.

2009 Malcolm McIntosh Prize for Physical Scientist of the Year

The 2009 Malcolm McIntosh Prize for Physical Scientist of the Year was awarded to ***Amanda Barnard***. During a PhD that took just 17 months to complete, Dr Barnard developed a computer model that is able to construct virtual nanoparticles and test how they might behave in different environments. By creating her computer generated nanoparticles in a virtual environment she was able to predict their likely behavior before the real particles are released into the environment. Dr Barnard is currently a research scientist with **CSIRO Materials Science and Engineering**.

▶ **More information: www.scienceinpublic.com/blog/media-releases/pmprizes2009**