New method for studying gene activity developed

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(PhysOrg.com) -- Researchers from UQ's Institute for Molecular Bioscience (IMB), Harvard University and RocheNimblegen Inc. have developed a new method for examining genetic information that reveals clues to understanding gene structure and activity in the body.

The method, published today in the prestigious journal *Nature Biotechnology*, allows researchers to delver further than ever before into the human genome.

It involves combining existing gene capture techniques with state-of-the-art 'deep sequencing' technology. Deep sequencing enables millions of different DNA molecules to be read in parallel.

The team, including Dr Tim Mercer, Dr Marcel Dinger, Ms Jo Crawford and Professor John Mattick from the IMB, used the new method to examine the human transcriptome – the set of RNAs that are expressed in different cells at any particular point in time.

“Every cell in the body has a copy of the entire genome, but different cells use different genetic information,” said Dr Mercer, who led the study.

“The transcriptome represents the collection of those genes that are being expressed in response to various developmental and environmental conditions.

“Understanding the transcriptome is important in understanding development and disease. For example, cancer researchers can examine the particular forms of the genes that are active in the lead-up to tumour development and understand how cancers form.”

The analysis showed the human transcriptome was even more complex than previously thought, and opened the door to further studies that can identify the differences in gene expression that cause variation between cells.

It also identified many new transcribed versions of important cancer-causing and developmental genes, as well as many novel RNAs that do not encode proteins, showing that our understanding of human gene expression is far from complete.

“This method, known as RNA CaptureSeq, can survey the entire genome at far greater resolution than previously possible to identify areas associated with complex diseases, and is also less expensive than traditional genetic analyses,” Professor Mattick said.

“Given these advantages, and the challenge of understanding the full range of gene products, we foresee RNA CaptureSeq as an important approach with a wide range of research and clinical applications,” he said.

More information: The paper can be accessed at: www.nature.com/nbt/journal/vao … nt/abs/nbt.2024.html

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