The genome's 3D structure shapes how genes are expressed

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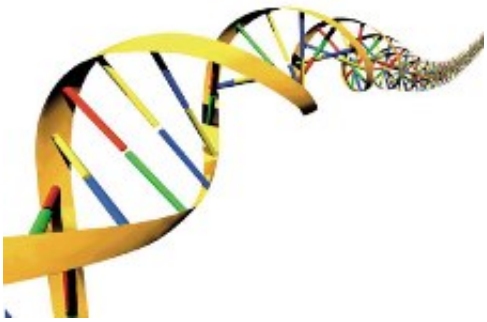

Scientists from Australia and the United States bring new insights to our understanding of the three-dimensional structure of the genome, one of the biggest challenges currently facing the fields of genomics and genetics. Their findings are published in *Nature Genetics*, online today.

Roughly 3 metres of DNA is tightly folded into the nucleus of every cell in our body. This folding allows some genes to be 'expressed', or activated, while excluding others.

Dr Tim Mercer and Professor John Mattick from Sydney's Garvan Institute of Medical Research and Professor John Stamatoyannopoulos from Seattle's University of Washington analysed the genome's 3D structure, at high resolution.

Genes are made up of 'exons' and 'introns' – the former being the sequences that code for protein and are expressed, and the latter being stretches of noncoding DNA in-between. As the genes are copied, or 'transcribed', from DNA into RNA, the intron sequences are cut or 'spliced' out and the remaining exons are strung together to form a sequence that encodes a protein. Depending on which exons are strung together, the same gene can generate different proteins.

Using vast amounts of data from the ENCODE project, Dr Tim Mercer and colleagues have inferred the folding of the genome, finding that even within a gene, selected exons are easily exposed.

"Imagine a long and immensely convoluted grape vine, its twisted branches presenting some grapes to be plucked easily, while concealing others beyond reach," said Dr Mercer. "At the same time, imagine a lazy fruit picker only picking the grapes within easy reach.

"The same principle applies in the genome. Specific genes and even specific exons, are placed within easy reach by folding."

"Over the last few years, we've been starting to appreciate just how the folding of the genome helps determine how it's expressed and regulated,"

"This study provides the first indication that the three-dimensional structure of the genome can influence the splicing of genes."

"We can infer that the genome is folded in such a way that the promoter region—the sequence that initiates transcription of a gene—is located alongside exons, and they are all presented to transcription machinery."

"This supports a new way of looking at things, one that the genome is folded around transcription machinery, rather than the other way around.

Those genes that come in contact with the transcription machinery get transcribed, while those parts which loop away are ignored."

More information: DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements, DOI: 10.1038/ng.2677

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