New insights into the software of life

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A series of discoveries by an international consortium of scientists, including a team from The University of Queensland's Institute for Molecular Bioscience (IMB), will transform our understanding of how our genome works to produce a complex organism like a human being. The findings of the consortium 'FANTOM', led by the Genomic Sciences Center, RIKEN Yokohama Institute and Genome Science Laboratory and RIKEN Wako Institute, will be published today in two papers in the prestigious journal *Science*.

Spokesman for the IMB team Professor David Hume, who has been a member of the FANTOM consortium for the past 5 years, and a senior author on both papers, said the massive data sets produced by the consortium, which were on the same scale as the completion of the human genome sequence, provided the scientific community with the tools to understand the control of protein production, truly the software of life.

"Genes provide the code for making the building blocks of our bodies - the proteins – and the consortium has a made a massive step towards identifying all of those building blocks. But the genome must also contain the code to ensure that protein building blocks are made in the right place at the right time.

"The new data provides several indications of the molecular basis of evolution and why we are so much more complex than the simple worm, despite the fact that we only have a small number of additional conventional genes.

"In simple terms, the data shows that in mammals each individual gene uses multiple different mechanisms to produce different forms of protein. In a sense, each 'gene' is actually multiple different genes," Professor Hume explained.

The second of the papers in Science deals extensively with another area to which the IMB team has made a major contribution; outputs of the genome (RNAs) that do not code for protein.

IMB Director Professor John Mattick, co-author of these papers, has predicted the importance of non-coding RNA in development and evolution in a series of papers published internationally over the past five years, including an article published in this same issue of Science entitled Functional genomics of non-coding RNA.

"I congratulate all IMB staff and students involved in this research collaboration, particularly David Hume who has been pivotal in developing the IMB's partnership with RIKEN over several years."

As part of the collaboration with RIKEN, Professor Hume's group has recently been awarded a grant from RIKEN to continue the translation of this work into the next phase, the Human Genome network project.

Source: Research Australia

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