



complete description to date of the gene activity which takes place as human cells divide.

Researchers have managed to gather data which details the behaviour of protein molecules encoded by over 6000 genes in cancer cells, as they move through the cell cycle. The team has used advances in technology and data analysis to study how genes work over time in cancer cells, as opposed to capturing a 'snapshot' of activity – a leap forward they describe as akin to 'jumping from still photography to video'.

The new results from the Dundee team - carried out in collaboration with the Wellcome Trust Sanger Institute in Cambridge and the University of North Carolina - have been published in the prestigious international journal *eLIFE*.

Cells are extremely complex environments: at any one time, thousands of different genes are active as molecular templates to produce messenger RNA (mRNA) molecules, which themselves are templates used to produce proteins. However, not all genes are active at all times inside all cells. As cells grow and divide as part of the cell division cycle, genes are switched on and off on a regular basis. Similarly, the patterns of mRNA and protein production are different in, for example, immune system and skin cells.

"What we have been able to produce is a detailed analysis of protein activity in human cancer cells that exceeds what was previously possible," said the project leader Professor Angus Lamond, of the College of Life Sciences at Dundee. "It is essential to study how [gene activity](#) varies over time if we are to understand the complex processes in [cancer cells](#), as the dynamic is changing all the time.

"Previously it has been possible to capture a time-averaged snapshot of this activity, but what we can now do is give a much fuller picture."

Dr Tony Ly, the lead researcher on the project in Professor Lamond's team, said, "This work provides a better understanding of the complex relationship between the levels of an mRNA and its corresponding protein product. It also demonstrates how it may be possible to detect subtle but important differences between cell types and disease states, including different types of cancer."

The work of the Dundee team providing this new high-resolution mapping of gene expression at the protein level offers great promise also for the future development of safer new drugs. Almost all drugs directly or indirectly affect proteins.

Proteomics – the comprehensive detailed analysis of cell proteins – is rapidly emerging as the next major phase beyond genome analysis, with great potential to improve our understanding of human disease and help the development of new treatments.

The proteomics research team in Dundee led by Professor Lamond has established a major international role in this new field that is set to soon increase further with the imminent opening of the new Centre for Translational and Interdisciplinary Research (CTIR) building at the University of Dundee.

The CTIR building, due to open this summer, will provide space for a major expansion in proteomics equipment combined with new computing resources for advanced data analysis. This will cement the leading role Dundee has established in advanced protein analysis within the UK.

Provided by University of Dundee

Citation: Researchers capture 'most complete' picture of gene expression in cancer cell cycle

(2014, March 6) retrieved 10 April 2024 from <https://medicalxpress.com/news/2014-03-capture-picture-gene-cancer-cell.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.