THE HUMAN PROTEIN ATLAS

Important link between genomics and proteomics

Stockholm October 26, 2016

Several previous reports have concluded that RNA levels cannot be used to predict protein levels. However, in a new study from KTH Royal Institute of Technology published in the journal Molecular Systems Biology, scientists show that protein levels can be predicted from RNA levels if a gene-specific RNA-to-protein factor is used.

The human genome consists of DNA, a molecule that contains the instructions needed to build and maintain cells. For the instructions to be carried out, DNA must be "read" and transcribed into RNA transcripts that can be used to produce protein. The transcriptome is a collection of all the transcripts present in a cell. An important issue for molecular biology is to establish if transcript levels of a given gene can be used as proxies for the corresponding protein levels.

In the present study[1], the researchers have developed a mass spectrometry-based method that is sensitive and reproducible in order to measure, at steady-state conditions, absolute protein copy numbers across human tissues and cell lines and compared these levels with the corresponding mRNA levels using transcriptomics.

"We show that the transcript and protein levels do not correlate well unless a gene-specific RNA-to-protein (RTP) conversion factor independent of the cell or tissue-type is introduced, thus significantly enhancing the predictability of protein copy numbers from RNA levels", says the study´s first author Fredrik Edfors. "The RTP-ratio varies several orders of magnitude between different genes, from a few hundred to several hundred thousands and is seemingly conserved across different cell types and tissues."

These new data suggest that transcriptome analysis can be used as a tool to predict the protein copy numbers per cell. Mathias Uhlen, the study leader and professor at KTH, says "There are many efforts around the world to systematically determine the transcript levels in cells, tissues and organs, involving new technologies such as single cell genomics and spatial transcriptomics". He continues "Our data suggest that the knowledge-based transcriptomics resources created as part of these efforts will be valuable also for protein studies, thus forming an attractive link between the field of genomics and proteomics." A comment[2] on the study was published in the same journal in "News and Viewes".

Read the whole paper here: http://msb.embopress.org/content/12/10/883

Reference list

[1] Edfors et al "Gene-specific correlation of RNA and protein levels in human cells and tissues" Molecular Systems Biology (October 26, 2017) accessed on-line at: http://msb.embopress.org/content/12/10/883

[2] Silva et al "Quantifying gene expression: the importance of being subtle" Molecular Systems Biology (October, 2016) accessed on-line at: http://msb.embopress.org/content/12/10/885

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About

Human Protein Atlas

The Human Protein Atlas (HPA) is a Swedish-based program started in 2003 with the aim to map of all the human proteins in cells, tissues and organs using integration of various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology. All the data in the knowledge resource is open access to allow scientists both in academia and industry to freely access the data for exploration of the human proteome. The version 17 (launched August 17, 2017) consists of three separate parts, each focusing on a particular aspect of the genome-wide analysis of the human proteins; the Tissue Atlas showing the distribution of the proteins across all major tissues and organs in the human body, the Cell Atlas showing the subcellular localization of proteins in single cells, and finally the new Pathology Atlas showing the impact of protein levels for survival of patients with cancer. The Human Protein Atlas program has already contributed to several thousands of publications in the field of human biology and disease and it was recently (July 25, 2017) selected by the organization ELIXIR (www.elixir-europe.org) as a European core resource due to its fundamental importance for a wider life science community. The HPA consortium is funded by the Knut and Alice Wallenberg Foundation. For more information, see: www.proteinatlas.org.

The Cancer Genome Atlas

The Cancer Genome Atlas (TCGA) is a collaboration between the National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI). The program has generated comprehensive, multi-dimensional maps of the key genomic changes in large number of cancers. The TCGA dataset consists of 2.5 petabytes of data describing tumor tissue and matched normal tissues from more than 11,000 patients. The data is publically available and has contributed to more than a thousand studies of cancer by independent researchers. For more information, see: https://cancergenome.nih.gov.

Science for Life Laboratory

Science for Life Laboratory (SciLifeLab) is a national center for molecular biosciences in Sweden with state-of-the-art infrastructures for life science with focus on health and environmental research. Technical platforms within the center include genomics, proteomics, metabolomics, bioimaging, structural biology, bioinformatics, systems biology and drug development. There are approximately 1200 persons affiliated with the center divided between two nodes in Stockholm and Uppsala. The center is a collaboration between four universities: Karolinska Institute, KTH Royal Institute of Technology, Stockholm University and Uppsala University. For more information, see: www.scilifelab.se.

Knut and Alice Wallenberg Foundation

The Knut and Alice Wallenberg Foundation is the largest private financier of research in Sweden and also one of Europe’s largest. The Foundation’s aim is to benefit Sweden by supporting basic research and education, mainly in medicine, technology, and the natural sciences. The Foundation can also initiate grants to strategic projects and scholarship programs. For more information, see: https://kaw.wallenberg.org/en.