Variability in the molecules of life

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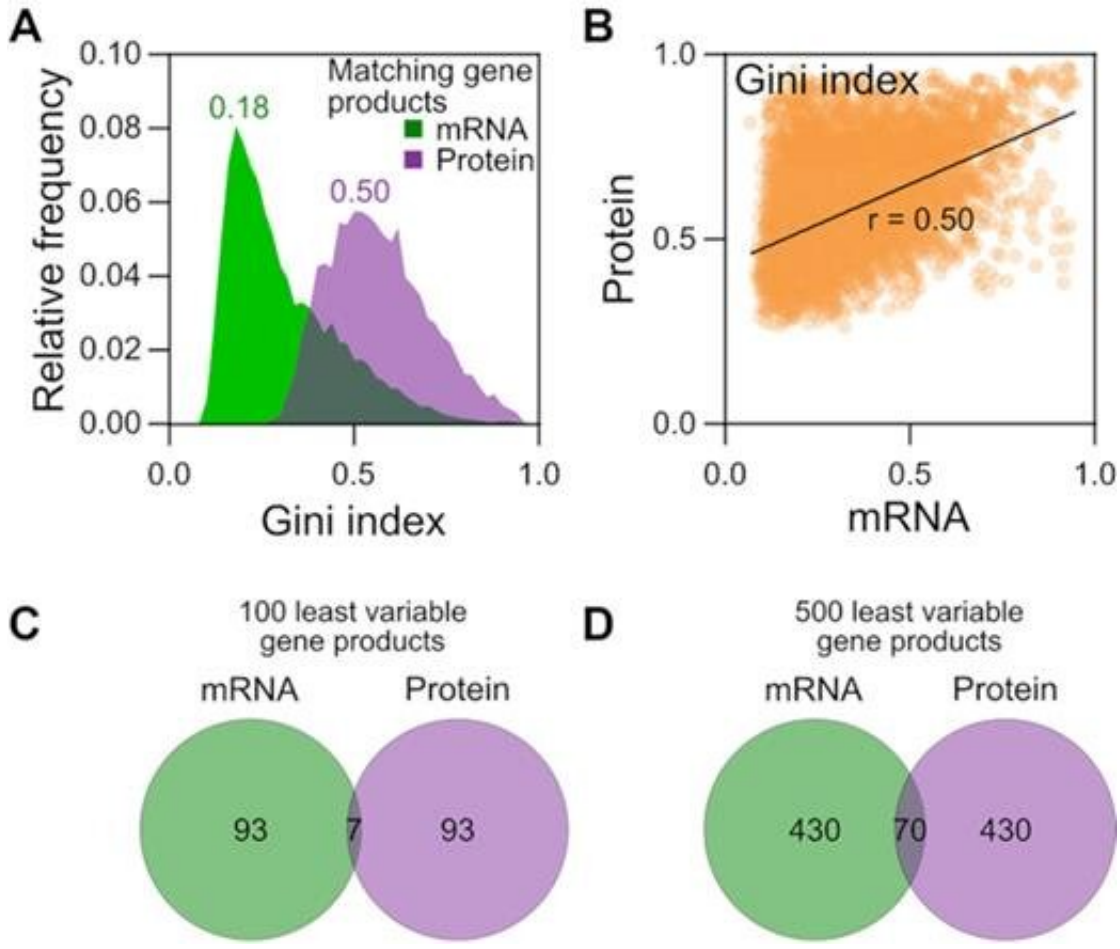

Variability in mRNA and protein concentration levels across different tissue types. (A) Concentration variability distributions of matching mRNAs and proteins (n = 8828) across 29 paired human tissue types, based on previously published transcriptomics and proteomics data (7). Numbers in figure denote mode (bin width: 0.02). (B) Correlation of mRNA and protein concentration variability (n = 8828), using transcriptomics and proteomics data from the 29 tissue types (7). (C) Overlap of the 100 least variable mRNAs and proteins across tissues (7). (D) Overlap of the 500 least variable mRNAs and proteins

across tissues (7); r = Pearson's correlation coefficient. Credit: *NAR Genomics and Bioinformatics*

How variable are gene transcripts and proteins, the molecules of life, across the tissues and organs of the human body? Furthermore, how variable are they within the same tissue type from different people? Understanding this variability will be key for the realization of personalized medicine. These questions are the focus of a new study led by researchers from Uppsala University, which is published in *NAR Genomics and Bioinformatics*.

"We noticed that the variability in abundance in different tissue types was higher on the protein level than on the transcript level, which indicates that data from both the transcript and protein levels is necessary to understand a biological system," says Christine Wegler, researcher in the Drug Delivery Group headed by Professor Per Artursson at the Department of Pharmacy, Uppsala University, and SciLifeLab, Sweden.

In the flow of biological information, the genes in our DNA are first read and replicated as transcripts, also known as messenger RNAs (mRNAs). These transcripts are then translated into proteins, which carry out the intended biological function. The abundances of these important molecules throughout the human body have been well characterized, but direct comparisons of variability patterns at the transcript and protein levels have been less comprehensive. Any discrepancies in variability between the transcript and protein levels could have implications for the regulation of information flow from gene to protein. In addition, a closer look at the variability within the same tissue type from multiple donors could provide essential information for personalized treatment in certain disease states.

Professor Per Artursson's research group has combined publicly available transcriptomics and proteomics data with a new in-house dataset of protein concentrations in the liver and small intestine (jejunum) from 38 human donors. They found that transcript variability across tissue types was not well reflected at the protein level, and that protein abundances vary more across different tissues than transcript abundances.

An in-depth analysis of protein abundance variability in the liver and small intestine showed that some proteins were present at similar levels in the respective tissues across all donors, while other proteins varied widely also within the same tissue type.

"We found that proteins that are essential for cell survival had similar abundances across the different donors, showing that cells need to maintain consistent levels of these proteins. In contrast, many of the most variable proteins within tissues were related to disease, leading us to suggest that variability analysis could be a simple tool in the early stages of biomarker discovery. Our study thus not only provides insight on basic biology, but can also contribute to advancing the field of personalized medicine by highlighting protein abundance differences within the same tissue type from different people," says Christine Wegler.

More information: Christine Wegler et al. Global variability analysis of mRNA and protein concentrations across and within human tissues, *NAR Genomics and Bioinformatics* (2019). DOI: 10.1093/nargab/lqz010

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https://phys.org/news/2019-11-variability-molecules-life.html