Gene expression patterns may help determine time of death

- **International team of scientists led by Roderic Guigó at the Centre for Genomic Regulation (CRG) in Barcelona shows that changes in gene expression in different tissues can be used to predict the time of death of individuals.**

- **Their results, which are published in *Nature Communications* this week, may have implications for forensic analyses.**

International team of scientists led by Roderic Guigó at the Centre for Genomic Regulation in Barcelona showed that changes in gene expression in different tissues triggered by death can be used to predict the time of death of an individual. As reported in a paper published in *Nature Communications* this week, researchers suggest that by analysing a few readily available tissues (for example lung or skin tissue), the post-mortem interval (time elapsed since death) can be determined with considerable accuracy and may have implications for forensic analyses.

It all started with the GTEx project, which aimed at creating a reference database and tissue bank for scientists to study how genomic variants affect gene activity and disease susceptibility. GTEx was designed to sample as many tissues as possible from a large number of individuals in order to understand the causal effects of genes and variants, and which tissues contribute to predisposition to disease. *"GTEx data allow us to ask questions about genetic variation and its effects on gene expression both in one tissue and across many tissues. Since the samples we are using all come from deceased donors, we need to find out if there were changes in gene expression related to the death or the time of death, so we could better model our predictions of variation between tissues or in disease,"* explains Roderic Guigó, lead author of this study and coordinator of the Bioinformatics and Genomics Programme at the CRG.

To understand the tissue-specific changes to gene expression following the death of a person, Roderic Guigó and his colleagues studied RNA-sequencing data of over 7,000 samples from 36 different tissues obtained from 540 donor within the GTEx project. They show that the time since death has an effect on gene expression and that this effect varies from tissue to tissue. The authors developed models for the prediction of the post-mortem interval based on these tissue-specific gene expression changes using high-throughput sequencing of the cell.

"*We found that many genes change expression over relatively short post-mortem intervals, in a largely tissue specific manner. This information helps us to better understand variation and also it allows us to identify the transcriptional events triggered by death in an organism,*" adds Pedro G. Ferreira, CRG Alumnus currently at the Institute of Molecular Pathology and Immunology, University of Porto in Portugal.

Researchers have studied the effect of different covariates on biological analysis. The model could be further improved to make it applicable to a forensics scenario and to devise a protocol for the potential implementation in forensic pathology.

Reference: Ferreira G. Pedro, et al. "The effects of death and post-mortem cold ischemia on human tissue transcriptomes" Nature Communications (2018) 9:490. DOI: 10.1038/s41467-017-02772-x

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