Scientists discover new method of gene identification

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Scientists studying the genes and proteins of human cells infected with a common cold virus have identified a new gene identification technique that could increase the genetic information we hold on animals by around 70 to 80 per cent. The findings, published in *Nature Methods*, could revolutionise our understanding of animal genetics and disease, and improve our knowledge of dangerous viruses such as SARS that jump the species barrier from animals to humans.

Modern advances in genome sequencing—the process of determining the genetic information and variation controlling everything from our eye colour to our vulnerability to certain diseases—has enabled scientists to uncover the genetic codes of a wide range of animals, plants and insects.

Until now, correctly identifying the genes and proteins hidden inside the genetic material of a newly sequenced species has been a monumental undertaking requiring the careful observation and cataloguing of vast amounts of data about the thousands of individual genes that make up any given animal, plant or insect.

Dr David Matthews, the study's lead author and a Senior Lecturer in Virology at the University of Bristol's School of Cellular and Molecular Medicine, said: "Gene identification is mainly led by computer programmes which search the genome for regions that look like genes already identified in other animals or humans. However, this type of analysis is not always effective."

The Bristol team has now discovered a more effective way of detecting the genetic information present in animals, plants and insects using cutting-edge analysis tools to directly observe the genes and all the proteins they make.

To prove their technique worked, the researchers conducted an experiment to see how good their process was at gene discovery. Human cells were infected with a well-understood common cold bug to mimic a newly discovered virus. These infected cells were then analysed using the technique as if they were cells from a newly sequenced organism infected with a newly discovered virus.

The resulting list of "discovered" genes and proteins, when compared to the genetic information already known about humans and cold virus, proved extremely successful and demonstrated the power of this method.

A similar analysis of hamster cells provided directly observed evidence for the existence of thousands of genes and proteins in hamsters in a single relatively inexpensive experiment. Direct evidence for the existence of almost all of theses genes and proteins in hamsters is not available in the 'official' lists of hamster genes and proteins.

Dr Matthews added: "These findings open up the potential to take powerful analysis tools currently used to study human diseases and apply them to study any animal, insect or even plants – something previously either very challenging or simply not possible. This technique will also make it easier and much more efficient for scientists to study anything from farm animals and their diseases to insect pests that damage crops.

"In recent years, a number of dangerous new viruses have been transmitted from animals to humans including Influenza, SARS, Ebola, Hendra and Nipah viruses. Earlier this year three people became seriously ill and two of them died when they contracted a new SARS-

like virus in the Middle East which is thought to have come directly from bats.

"Why bats harbour these viruses with limited ill effect is a mystery as the genetic make-up of these creatures is poorly understood. We are starting to apply our technique to laboratory grown bat cells to analyse the genetic and protein content of bats to gain more insight into their genetics and to understand how they are able to apparently co-exist with these viruses which all too often prove fatal in humans."

More information: De novo derivation of proteomes from transcriptomes for transcript and protein identification, by Vanessa C Evans et al., *Nature Methods*, dx.doi.org/10.1038/nmeth.2227

Provided by University of Bristol