RNA-Based Cellular Disease Model Shows Promise

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The role of mRNA within the cell and in pathological processes such as cancer and HIV infection has been thoroughly explored by biochemical and cellular biologists and immunologists. Recently, molecular biologists at The Southern Research Institute (based in Melbourne, Australia) and The Rockefeller University, New York, US, have now demonstrated a very efficient RNA-based cellular disease model. This model, which is described in the journal Molecular Biology and Evolution, provides a complete profile of a specific SNPs in a cell cell and is able to precisely determine how it causes disease through our genetic code. This is the first RNA-based cellular disease model to be developed, and its use will be important in understanding and inhibiting a variety of diseases.

With this RNA-based model, researchers involved in this study have shown that genes associated with different cancer and neurodegenerative disorders exist within the same cells that contain SNPs. In particular, they showed that CFTR (nonenzymatic sodium channel transporter) genes associated with neuronal apoptosis in Huntingtonâ€™s disease and motor neuron damage in amyotrophic lateral sclerosis (ALS) appeared to appear inside the SCNN-derived cytochrome P450 family.

The researchers also demonstrated that they were able to insert and erase the SNPs themselves, which enabled them to precisely determine the path of disease as well as to generate new cells that exhibit the defective genes. Importantly, this strain of cytochrome P450 family, in which the mutated RNA gene was completely eliminated, caused disease completely new to the cell. The absence of this signature RNA-binding protein provided no clues that the cytochrome P450 family participated in disease; one important reason is that they do not express a fully active version of the gene that engrams cancer-causing proteins.

In order to achieve a pathological phenotype, the researchers removed the homologous gene for cyclin D2, a complex cytokine that feeds on cyclin-dependent protein kinase B, during growth of cells and found that they could help break down the structure of SCNN membranes with direct contact from the molecule. Similarly, when they injected viral particles into the body of sheep that were carrying an RNA- based gene, produced from the SCNN, they could induce human-like brain toxicity and cell death. Although studying the relationship between the RNA and proteins within the cell requires exploring two species, the frequency of its occurrence was remarkably similar in all of the cell lines.

The treatment used in the study would be very beneficial for specific cancers that are more amenable to treatment due to its high specificity for disease-specific proteins and its potential ability to suppress the effects of other therapies. Moreover, by using a single code of RNA to model the disease within a cell cell, and using direct DNA to replace the RNA, researchers are still able to gain better insight into the gene and gene/RNA sequence profile of tumors, transplant tissues, or viral particles. As more research is conducted, this will be very useful in enabling developers of personalized medicine, in increasing our understanding of each disease and understanding of the causes of the disease.

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