MedicalXpress

'Treatments waiting to be discovered' inside new database

August 5 2014

Your genes are blueprints for proteins, and molecules called microRNA can help to determine how often these genetic blueprints are manufactured into proteins. Researchers often ask what microRNA regulates a gene related to disease. Or what gene is regulated by a microRNA found in sick patients? The answers to these questions could help doctors and researchers manipulate protein levels in the body that cause disease, especially cancer. A University of Colorado Cancer Center study recently published in the top-ranked journal *Nucleic Acids Research* (NAR) describes a database named multiMiR, the most comprehensive database collecting information about microRNAs and their targets.

"You can't imagine the tangled web of data that describes the cause and effect relationships of microRNAs and genes. This multiMiR database will let researchers search efficiently through these relationships for pairings relevant to the diseases they study," says Katerina Kechris, PhD, associate professor of Biostatistics and Informatics at the University of Colorado Denver, and one of the study's senior authors.

In addition to assisting researchers search for relationships between microRNAs and their genetic targets, the database includes drugs known to affect these microRNAs and also lists diseases associated with microRNAs.

"Right now, within this database, investigators can find clues to potential new treatments for various diseases including cancer," says Dan

Theodorescu, MD, PhD, professor of Surgery and Pharmacology at the CU School of Medicine, director of the University of Colorado Cancer Center and one of the study's senior authors.

The project includes nearly 50 million records representing the combination of 14 previously existing microRNA data repositories. The multiMiR database also links to previous research results relevant to these microRNAs. multiMiR combines this functionality within the leading open-source statistical software, R, allowing for increased flexibility for analysis and accessibility by data analysts everywhere.

Basically, researchers can input names of microRNAs, genes, drugs, diseases or any combination thereof. Then the researcher can ask the database for validated or predicted genetic targets of microRNAs, or for validated/predicted microRNAs that regulate specific genes. Similar is true of diseases and drugs – informatics tools show which diseases are associated with microRNAs and which (if any) drugs have been linked to a specific miRNA queried.

Case studies described in the article show how microRNAs may affect voluntary alcohol consumption in mice, candidate genes within signaling pathways associated with chronic obstructive pulmonary disease, and the microRNA:gene interactions that influence bladder cancer.

"We need data and then we need clever ways to look at it otherwise we drown in the wealth of information," Theodorescu says. "This new tool will allow us to ask new questions of more data with greater precision and get better, more insightful results that will ultimately help develop new approaches for patient treatment."

Provided by University of Colorado Denver