

Using Simple Genome, Researchers Move Personalized Medicine Closer to Reality

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(PhysOrg.com) -- Researchers at Columbia University have developed a statistical method that accurately predicts how an organism will respond to dozens of commonly used drugs. This clinical and conceptual advance moves medical science a step closer to an era of personalized medicine -- one where doctors could prescribe treatments based on an individual patient's genome.

“Our study shows proof of concept and suggests how we should go about developing personalized medicine,” said Dana Pe’er, an assistant professor in the department of biological sciences and head of Columbia’s Computational Systems Biology Lab. “The hope is that one day you’ll go to the doctor, and for every disease you might have, they’ll say, ‘Here’s the medicine for you and the dose for you, and you won’t have side effects.’”

Pe’er and her co-authors, including doctoral student Bo-Juen Chen, worked with yeast as a [model system](#). Their findings appear in the current issue of *Molecular Systems Biology*.

Unlike many other genomic-medicine studies that focus solely on [DNA](#), Pe’er’s study relied on a combination of DNA and RNA data to predict drug resistance in yeast and identify the genes that cause it. RNA, which is synthesized from DNA, reflects which genes in a cell are turned off and on—information known as gene expression.

“RNA gives us a much more sophisticated measure than DNA of what’s

going on in the cell,” said Pe’er.

She and Chen started with a set of data containing information on how well or how poorly 104 strains of yeast grew in the presence of 94 chemicals, or drugs. Each strain came with a genomic sequence and a gene expression profile. After identifying the genes responsible for variation among the strains, the team designed a computer function to determine, for each drug, which genetic features correlated with resistance. Pe’er and her coworkers then took previously untested strains of yeast and asked the computer to predict their level of resistance based on genomic and [RNA](#) data.

Their program, called Camelot, accurately predicted how well or how poorly the yeast grew in the presence of 87 out of 94 drugs. To test these results, they went back into the lab and genetically modified the yeast, deleting the genes they had identified as causing drug resistance. When they retested the modified yeast, exposing them to the drugs once more, they saw that the strains were no longer resistant, just as their model had predicted.

“To our knowledge, our approach is the first to systematically predict [drug resistance](#) and identify the genes that cause it,” said Pe’er.

Provided by The Earth Institute at Columbia University ([news](#) : [web](#))

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