



THE VICTOR CHANG  
CARDIAC RESEARCH INSTITUTE

## MEDIA RELEASE

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### **Introducing: Computers That Catch The Right Diseases**

While viruses and computers tend to go hand-in-hand, a new program developed by researchers at the Victor Chang Cardiac Research Institute could find computers being used in the fight to narrow down the number of possible disease-causing genes.

Called "Gentrepid", the computer program developed at the VCCRI, highlights suspect genes in regions of DNA identified by gene researchers. This greatly reduces the number of genes that need to be considered and therefore saves thousands of dollars in additional experiments.

The program was developed in collaboration with VCCRI colleagues who were trying to determine the cause of inherited heart diseases, such as atrial fibrillation and dilated cardiomyopathy. Dr Richard George of the VCCRI is working to make the system available to genetics researchers worldwide.

"The identification of genes responsible for human disease is critical to gaining an understanding of disease mechanisms and is essential for the development of new diagnostics and therapeutics," Dr George said in his paper published in this month's Nucleic Acids Research Journal. "Determining which genes cause a particular disease is a difficult task."

Experimental analysis of the DNA of individuals in a family afflicted with an inherited disease can successfully locate a region of DNA harbouring a disease gene. However these regions are often very large, containing hundreds of genes. This means that further experiments are needed to identify the disease gene, and these are time consuming and costly.

Genes are the blueprints for proteins and the new program works by looking at the actual proteins and how they work in our bodies. Gentrepid analyses proteins using two complementary but different methods: Common Pathway Scanning (CPS) and Common Module Profiling (CMP) to determine if they are involved with a disease.

CPS looks at social networks of proteins. If one protein has been implicated with a disease it is likely that its buddies, the other proteins it interacts with, are also involved. CMP looks at the structure of the proteins. Over the last twenty years, researchers have found that proteins are made from a limited repertoire of building blocks. Around 1000 of these protein "Lego" blocks have been discovered. CMP looks for Lego blocks in proteins that have already been implicated in the disease in question.

In order to test the efficiency of Gentrepid, a set of known disease genes was run through the program and Gentrepid successfully predicted disease genes from diseases such as Alzheimers, breast cancer, type II diabetes and familial hypertrophic cardiomyopathy. Successful predictions were made for more than half of the diseases.

The combined approach of using the two complementary programs – CPS and CMP, means Gentrepid is a powerful tool for predicting disease genes, which will help accelerate the process of disease gene discovery.

Dr George is presenting the system to the Bioinformatics Australia 2006 conference at the Sydney Convention Centre today, Wednesday, 22<sup>nd</sup> November.

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