New markers for allergic disorders thanks to analysis of medical databases

January 11 2011

Researchers at the University of Gothenburg, Sweden, have developed new methods for analysing medical databases that can be used to identify diagnostic markers more quickly and to personalise medication for allergic disorders. They could also reduce the need for animal trials in clinical studies.

Published in the journal PLoS Computational Biology, the study builds on data analyses of freely available medical databases representing studies of countless numbers of patients in the

PubMed database, and microarray data in another major database. The use of microarrays is a method that allows scientists to study all 20,000 human genes at the same time for various disorders.

Groups of researchers in Gothenburg, Oslo and Rome have developed computational methods to simulate how a change in the interaction between several different genes in the lymphocytes (a kind of white blood cell) controls the immune system. They identified the genes by reviewing abstracts of all 18 million articles included in PubMed, and then constructed a network model of how these genes interact.

"The model can be compared to a printed circuit card in the lymphocyte which the cell uses to make decisions about whether to activate or suppress the immune system," says Mikael Benson, a researcher at the Sahlgrenska Academy's Unit for Clinical Systems Biology and consultant at the Queen Silvia Children's Hospital. "These decisions are made

constantly as the lymphocytes are constantly exposed to different particles, just through breathing for example. Some of the particles could be dangerous and need to trigger a decision to mobilise the immune system. However, sometimes wrong decisions are made, which can lead to various disorders such as allergy or diabetes."

The researchers then carried out data simulations of how the network model reacted to repeated exposure to particles, which resulted in four reaction patterns, one of which was to suppress the immune system, while the other three were to trigger it in various ways.

"We found that the genes in the model reacted in lymphocytes from patients with various immunological disorders. We'll be using the model to identify diagnostic markers so that we can personalise medication that we're testing in clinical studies of allergy patients."

Benson believes that these methods will become increasingly important in the future, as the huge amount of information in medical databases is growing all the time. This information could serve as an important resource for researchers in their endeavours to investigate and verify medical hypotheses.

"These methods could reduce the need for animal trials and lead to major savings in both time and money," says Benson. "They could also mean quicker and better-designed experiments and their results could generate new knowledge about diagnostic markers or new medicines."

More information: Combining network modeling and gene expression microarray analysis to explore the dynamics of Th1 and Th2 cell regulation, *PLoS Computational Biology*.