# Research team maps cell interactions

October 29 2008

(PhysOrg.com) -- Proteins make up the machinery of the cell. Their interaction with each other is responsible for how the cell functions within a living organism. Intrigued by what these interactions may look like, scientists have been working to map networks of physical DNA-, RNA-, and protein-protein interactions.

Northeastern University physicist Albert-László Barabási, in collaboration with a research team lead by Marc Vidal from Dana Farber Cancer Institute, carried out a comparative quality assessment of binary interactions using the yeast S. cerevisiae as a model system.

In order to better understand interactome network structure and functions, Barabási and his collaborators developed advanced methodology to analyze currently available maps by comparing the quality of existing high-throughput binary and co-complex data sets to information obtained from curating low-throughput experiments.

In the paper discussing the study, the authors talk about extensive quality assessments, during which they found that protein connectivity within cells significantly influences the phenotype of the cells. In identifying several hundreds of interactions between high-quality binary proteins and testing and re-testing those to filter out false positives, the group developed an empirically controlled mapping framework to produce a second-generation high-quality, high-throughput Y2H data set covering 20% of all yeast binary interactions.

While relying on confirmed protein-protein interactions beyond those

seen in previous studies, this study confirmed that the more connected proteins are, the more consequential their actions will be for the behavior and the phenotype of the entire cell. The high-quality interaction map and the research team created as a result of this collaboration will take understanding of the interactome network's global and local properties and its relationship with multicellular functions to a new level.

"We found that only a few percent of the newly identified interactions are false-positives, which is much lower than previous quality assessments of large-scale yeast two-hybrid experiments suggested," said Barabási, Distinguished Professor of Physics and Director of the Center for Complex Network Research at Northeastern University. "We can conclude that protein connectivity correlates with genetic pleiotropy, i.e. the more connected is a protein, the larger the consequences of its removal."

The study, conducted in collaboration with Boston's Dana Farber Cancer Institute and Harvard Medical School, appeared in the latest issue of *Science* magazine.

Provided by Northeastern University