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## **GENEGO IS AWARDED DOD GRANT FOR SYSTEMS BIOLOGY PROTEOMICS PLATFORM**

**St. Joseph, Michigan, June 27th, 2005** – GeneGo, Inc., a leading provider of databases, software and services in systems biology, announced today they have been awarded a SBIR grant from Department of Defense (DARPA) for the development of a systems biology suite of tools for visualization and analysis of proteomics data. In Phase I, GeneGo will adapt its data-mining platform MetaCore for handling a broad range of proteomics data types; connectivity of these data with other OMICs datasets; and will develop new algorithms for reconstruction of protein-state specific biological networks and pathways.

“Proteomics enables experimental analysis of protein complexes and protein-protein interactions, which carry out most cellular processes. Therefore, proteomics data is destined to play a central role among OMICs datasets characteristic for a condition,” said Dr. Tatiana Nikolskaya, Chief Scientific Officer and President of GeneGo. “However, proteomics data is more complex and ambiguous than, for instance, microarray gene expression or DNA sequences. We know how to work with processed proteomics datasets, but it is the details such as fold, post-translational modification, sequence variation, local abundance in compartments, which define the cellular state in normal and disease. In our proposal, we emphasized these specifics as well as systemic approach to the understanding of proteomics and other OMICs datasets.”

In the scope of the grant, GeneGo will work in collaboration with Associate Professor Austin Yang’s group from the University of Southern California.

“Because of rapid advance of proteomic technologies and improved of mass spectrometry user interface, most laboratories can generate a very large amount of data in a rather short period of time. Thus, one of the major issues facing most proteomics laboratories now is how to establish a proper bioinformatics workflow and how to adequately validate and interpret their proteomic results. Unfortunately, like most “omics” analyses, because hundreds or thousands of proteins are examined in a single experiment, it is very difficult to evaluate the biological significance or resolution of any given proteomics analysis. Two years ago, we decided to incorporate Metacore into our proteomics data analysis

workflow. By integrating the conventional proteomic analysis with a well-annotated network or pathway analysis program such as Metacore, we are able to quickly and objectively evaluate our proteomic results with high confidence. Recently, we have used this combination of bioinformatics and mass spectrometric approaches to address the roles of amyloid in altering synaptic signaling pathways in Alzheimer's disease," said Professor Yang.

### **About GeneGo**

GeneGo is a Michigan-based company developing systems biology technology for life science research. The Company's original computational platform allows an integration and analysis of different kinds of experimental data (mRNA expression, proteomics, metabolites, phenotypic data etc.) and relevant active chemistry (metabolites, drugs, other xenobiotics) within the framework of biological pathways and networks. GeneGo's first product, MetaCore™, assists scientists in the areas of target selection and validation, identification of biomarkers for disease states and toxicology. GeneGo's second product, MetaDrug™, is designed for medicinal chemists and enables prediction of metabolites and their likely toxicity in humans.

For more information, please visit the company's Web site at [www.genego.com](http://www.genego.com) .

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