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NIH funds new virus database at UT Southwestern

DALLAS – Oct. 13, 2009 – The National Institutes of Health has awarded a \$15.7 million contract to UT Southwestern Medical Center and Northrop Grumman Corp. to develop an open-access national online database and analysis resource center that will help scientists study and combat viruses such as those that cause hepatitis, encephalitis, smallpox, acute respiratory distress and dengue fever, as well as newly emerging pathogenic viruses.

The National Institute of Allergy and Infectious Diseases (NIAID), part of the NIH, awarded the contract and designated approximately \$2.7 million of the total for UT Southwestern, which will act as a subcontractor on the project.

Previous work at UT Southwestern headed by Dr. Richard Scheuermann, professor of pathology, clinical sciences and in the Cancer Immunobiology Center, led to the development of an open-access database sponsored by the NIH for influenza, including the pandemic H1N1 virus, commonly referred to as swine flu.

“When the first gene sequences for swine flu were being released, researchers had a lot of questions about this newly emerging disease,” said Dr. Scheuermann, chief of biomedical informatics at UT Southwestern. “They wanted to know everything from where the virus was coming from to what could be predicted in terms of whether the disease was something humans would have protective immunity against.”

The database supported by the new contract will be developed using the influenza model at UT Southwestern. The new Virus Pathogen Database and Analysis Resource (ViPR) will enable researchers to develop an online bioinformatics center that will contain data and analysis tools for a wide range of viral pathogens. The viruses that will be part of the database include *Herpesviridae*, the causative agents of herpes and chicken pox; the *Flaviviridae* family, which includes the hepatitis C and West Nile viruses; and *Poxviridae*, which causes smallpox.

“The ViPR resource will support gene sequence data, information about the immune response to viral infection, and information about the protein structure of viruses,” said Dr. Scheuermann, principal investigator on the local portion of the new contract. “This database will bring all that information together in one place.”

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In investigating H1N1, Dr. Scheuermann said his team plugged the virus' genetic sequences into the NIH-sponsored Influenza Research Database he oversees and found that the genetic coding of the H1N1 virus is nothing like the normal circulating seasonal influenza virus. ViPR, which will have the same kind of functionality as the influenza database, will help researchers answer similar questions about other human pathogenic viruses. The ultimate goal is to develop better diagnostic tools, therapeutics and vaccines, he said. The ViPR database is scheduled to be available in December at <http://www.viprbrc.org>.

In addition to providing gene-sequence information on numerous viruses, ViPR will offer tools enabling the analysis and visualization of host-pathogen interactions. The resource also will support the integration of data such as collection methods and geographic coordinates from surveillance and epidemiological studies, as well as data from clinical trials.

Dr. Scheuermann said sharing scientific data in open-access portals like ViPR is increasingly important as the volume and diversity of life-science information continues to accumulate.

“While the consistency of data sharing and the protection of that data must be periodically evaluated, collaboration between investigators is generally required in order to compile enough data to make meaningful conclusions,” he said. “This bioinformatics resource center is one example of how the NIAID, aided by research centers like UT Southwestern, is leading the effort and developing the infrastructure to support data sharing.”

The ViPR collaborators from UT Southwestern include Jyothi Noronha and Burke Squires, database analysts in pathology; Elizabeth McClellan, graduate research assistant; and Victoria Hunt, research study coordinator in pathology. Others on the project include Vecna Technologies and researchers at the University of Washington, University of Rochester and the Cold Spring Harbor Laboratory in New York.

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