Environmental Genome Project Develops a New Bioinformatics Tool

The NIEHS Environmental Genome Project is founded on the sound scientific concept that an individual's genetic makeup is a major factor in human disease resulting from exposure to environmental agents. The project is a long-term effort to characterize specific genetic variations, or polymorphisms, that contribute to either resistance or susceptibility to environmentally induced diseases.

The NIEHS has, through the Environmental Genome Project, funded the development of a new bioinformatics tool created by the University of Utah Genome Center. This Web resource, known as GeneSNPs (short for "single nucleotide polymorphisms") integrates gene, sequence, and polymorphism data for nearly 500 human genes implicated in cellular responses to exposures to environmental toxicants. The list of human genes included in this resource is not exhaustive; new environmentally responsive genes will be added to GeneSNPs as information on their roles in vulnerability to environmental exposures becomes available.

GeneSNPs is both a process and a tool for integrating up-to-date public gene resources for single nucleotide polymorphism discovery and analysis. It provides current, integrated, sequence-based views of genes using cDNA sequence, genomic sequence, and SNPs. Current gene categories include cell division, cell signaling, cell structure, gene expression, homeostasis, and metabolism.

Visit the Environmental Genome Project home page at **http://www.niehs.nih.gov/envgenom/home.htm**.