Advances in 2006

A Year of Unprecedented Progress

The nation's investments in cancer research returned unprecedented gains in 2006. For example, knowing the sequence of the human genome catapulted our understanding of cancer at the genomic and proteomic level to a new height. Together, this knowledge and recent advances in biomedical technologies and bioinformatics are ushering in a new era of personalized medicine. The paragraphs below highlight examples of the exciting advances made in 2006 in cancer prevention, diagnosis, treatment research, and infrastructure development that will enable us to understand, pre-empt, and manage cancer based on patient-specific disease characteristics.

A New Era of Cancer Prevention, Diagnosis, and Treatment

These featured advances demonstrate the potential to drastically reduce the burden of cancer through a comprehensive understanding of critical steps in cancer development.

Vaccines for Cervical Cancer Prevention. Cervical cancer, claiming more than 200,000 lives worldwide last year, is caused almost exclusively by human papillomavirus (HPV) infection.

This year, the Food and Drug Administration (FDA) approved Gardasil®, a vaccine that is 100 percent protective against the development of cervical cancer and genital warts caused by four subtypes of HPV. A second vaccine is being reviewed by the FDA. These vaccines show how basic discoveries arising from population studies, molecular biology, and immunology can be rapidly translated through public and private research efforts to solve significant public health problems, and in this case, perhaps the elimination of cervical cancer as a threat to women's health.

Advances in Lymphoma Diagnosis. NCI researchers used gene expression arrays, which measure the levels of activity of thousands of genes in cells, to identify three distinct subclasses of diffuse large B-cell lymphoma (DLBCL), each requiring a different approach to therapy. Importantly, the researchers were able to distinguish between DLBCL and Burkitt's lymphoma, which are similar in appearance microscopically but require very different treatments that dramatically affect survival rates. This research also shows clearly that an individual's response to therapy is based both on the tumor's molecular characteristics and inherited genes that control the patient's response to drugs.

Infrastructure to Advance Personalized Medicine

NCI and some of its partners undertook several bold projects to provide new knowledge and integrate diverse components of infrastructure across the cancer research enterprise. This infrastructure will help overcome major barriers to generating, integrating, sharing, and deploying critical cancer information to hasten and support a new era of personalized medicine. Examples include:

The cancer Biomedical Informatics Grid (caBIG™). As investigators increasingly rely on computerized data analysis and bioinformatics, managing and sharing data in real time has emerged as a major challenge. This movement toward "digital biology" is made more daunting by the serious lack of consistent data formats, vocabularies, standards, and tools for bioinformatics

applications. This year, the pilot phase of caBIG™, an open source "plug and play," grid-based computing program, was successfully completed. The 80 participants in this achievement included 40 major Cancer Centers, FDA, and the private sector. caBIG™ will expand partnerships to increasingly provide the connectivity needed to support the advent of personalized medicine.

Cancer Genetic Markers of Susceptibility (CGEMS). Genetic changes called single nucleotide polymorphisms (SNPs) may be associated with increased risk of some cancers. In 2006, NCI initiated CGEMS to scan the entire human genome and identify SNPs associated with either increased or decreased risk for breast and prostate cancer. Data from CGEMS and similar studies will provide the basis for predicting cancer risk and taking appropriate steps to prevent it.

The Cancer Genome Atlas (TCGA). NCI and the National Human Genome Research Institute launched TCGA as a three-year pilot program to take the first step in identifying all important genetic changes in every cancer. TCGA leverages data from thousands of researchers working over several decades. The project also capitalizes on data from the completed human genome project and advances in genome analysis technologies and bioinformatics. The pilot will develop and test the complex science and technology framework needed to systematically identify and characterize the

genomic changes associated with cancer. All data will be publicly available to researchers worldwide through caBIG™.

The Repository for Molecular BRAin Neoplasia DaTa (REMBRANDT). NCI and the National Institute of Neurological Disorders and Stroke created REMBRANDT, a publicly available bioinformatics knowledge base of primary brain tumor data. REMBRANDT integrates extensive clinical and genomic data from brain tumor patients participating in clinical trials. This single resource enables data sharing among many institutions and investigators, helping researchers and clinicians identify and evaluate personalized, molecularly-targeted therapies for patients with brain cancer.

Essential Infrastructure. A new Clinical Proteomics Program is developing the standards needed to characterize patterns of protein markers in human serum for very early detection of cancer. NCI's Integrative Cancer Biology Program in computational and mathematical models began the difficult task of analyzing the accelerating volume of data generated by so many advanced technologies. Finally, the NCI's Nanotechnology Alliance for Cancer began harnessing nanotechnologies for cancer diagnostics, targeted imaging, and drug delivery. These and other efforts will fill critical knowledge gaps and provide the level of understanding needed to realize a new era of molecular-based personalized cancer medicine in the next decade.