A Medical Renaissance?

WITH THE COMPLETION OF SEQUENCING OF THE HUMAN GENOME IN 2001, MANY researchers immediately set their sights on using this information to better understand the genetics and, more recently, epigenetic effects identified during the initiation, development, and progression of cancer. Moving from the pre-genome-era identification of single gene variants associated with hereditary cancers, advances in sequencing technology have enabled the use of a whole-genome approach to examine the differences between the genomes, and epigenetic regulation, of tumor and patient DNA. This issue of Science examines how these advances are shaping our current understanding of cancer at the genomic level.

Unfortunately, there is no magic bullet, as no single genetic variant or epigenetic effect has been identified as a target in the fight against all cancers. In a comprehensive Review, Vogelstein et al. (p. 1546) distill information derived from more than 100 cancer genome sequencing projects into a series of clear principles about tumor biology and then discuss the projected clinical impact of cancer genome analysis on early detection and treatment of the disease. Kilpivaara and Aaltonen (p. 1559) call for standards for cases in which whole-genome sequencing reveals clinically relevant mutations in individual patients to bridge differences between the laboratory and the clinic. McLeod (p. 1563) reviews how best to apply pharmacogenomic information in identifying and tailoring drugs to target cancers. Finally, Suvà, Riggi, and Bernstein (p. 1567) examine how cell fates are controlled by epigenetic regulation and identify parallels between cancer and cellular differentiation.

In addition, Science Signaling presents related content on 26 March and 6 April, highlighting how cancer-associated alterations in the genome or proteome can result in altered signaling that contributes to tumorigenesis, metastasis, and drug resistance. Our Science News department profiles Elaine Mardis (p. 1540), whose expertise in developing DNA sequencing technology led her to become a pioneer in cancer genomic research, and explores how the heterogeneity of individual tumors, revealed by sequencing studies, poses treatment problems. Science Careers profiles Fátima Al-Shahrour, a bioinformaticist who works on interpreting the genome to help select more effective drugs for cancer patients.

Technological breakthroughs, coupled with the greatly reduced costs of sequencing, suggest that in our not-too-distant future, routine cancer treatment will not focus on the organ of origin but rather on the genomic profile of the cancer. This fundamental goal, to be able to read the complex code embedded in our bodies to identify the best therapies for each individual over the course of their treatment, portends a medical enlightenment.

— LAURA M. ZAHN AND JOHN TRAVIS
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Laura M. Zahn and John Travis (March 28, 2013)

Editor's Summary