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5:00 p.m.

Room 1408, Genetics/Biotechnology Center, 425 Henry Mall

Fine-Scale Genomic Structure and Variation in the MCF-7 Breast Cancer Cell Line

Abstract:

Chromosomal abnormalities are found in all types of cancer, and these irreversible genomic mutations influence the genesis and progression of solid tumors. Genome-wide detection and characterization of these structural mutations will aid in the discovery of genes critical to cancer progression and can also be used to guide therapy choices in a clinical setting. Using the optical mapping system, we have characterized the fine-scale genomic structure of the model breast cancer cell line MCF-7. Over 1,115,000 restriction maps have been generated, each from a single molecule of MCF-7 DNA. Analysis of these restriction maps has yielded 1,800 discrete mutations, including SNPs as well as small (few kb) and large (hundreds of kb) genomic insertions and deletions. Complex translocations have also been identified, and since the resolution of optical mapping is subgenic (5 kb), we can identify the genes at these breakpoint boundaries without additional analysis or experimentation. In parallel, Hidden Markov Model analysis is used to identify intervals that show aberrant optical map coverage across the entire genome—these results are being compared to copy number assessment via Affymetrix and maskless-array chips (Prof. Paul Lizardi, Yale), which when coupled with detailed structural analysis will identify potential tumor suppressors, oncogenes, and clinically relevant targets.
