MedicalXpress

A new mathematical formula for cancer progression

November 9 2007

Tumor progression can now be mapped less to mathematical standards and more to individual patients according to a new study by researchers at Harvard and Johns Hopkins Universities. The study, publishing in *PLoS Computational Biology* on November 9, 2007, provides a new paradigm in calculating tumor development, showing that it appears to be driven by mutations in many genes.

Our understanding of the progression of cancer has long been based on streamlined models where cancer is driven by mutations in only a few genes. Niko Beerenwinkel et al. show how tumor progression can be driven by hundreds of genes. As many as 20 different mutated genes might be responsible for driving an individual tumor's development.

Beerenwinkel et al. used a case of colon cancer to derive their results. Cancer progression proceeds stochastically from a single genetically altered cell to billions of invasive cells through a series of clonal expansions. According to their model, cancer progression is driven by mutations in many genes, each of which confers only a small selective advantage. It was found that the time it takes for a benign tumor to transform into a malignant tumor is dominated by the selective advantage per mutation and by the number of cancer genes, whereas tumor size and mutation rate have smaller impacts.

This new model could help explain the large amount of variation between individual tumors that has long puzzled researchers and clinicians. The increasing amount of high-throughput molecular data that

is being generated has resulted in new challenges for understanding complex biosystems such as cancer. New mathematical models like this one can provide unique insights that simplify interpretation and at the same time answer important biomedical questions.

Source: Public Library of Science