Mass genome sequencing likely best shot for cancer ‘magic bullet’

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As breast cancer specialist George Sledge, M.D., said in his presentation at the Personalized Medicine World Conference in 2015, “It turns out that we don’t need a magic bullet to cure cancer. We need a magic shotgun.”

Dr. Sledge, professor and chief of medical oncology at Stanford University Medical Center, was referring to the avalanche of genomic studies that have begun to reveal multiple potential drug targets in individual tumors.

In their 2013 Cancer Discovery review, Matthew J. Ellis, M.D., of the Washington University School of Medicine, and Charles M. Perou, Ph.D., at Charles University of North Carolina’s Lineberger Comprehensive Cancer Center, observed that “Deep genomic analysis will drive treatment decisions based on … cell type and pathway-matched therapies.”

The etiological events that drive breast cancer, they said, “Are finally coming into focus and should be used to set priorities for clinical trials.”

The authors noted that during a six-month span in 2012, four papers published in Nature described the application of massively parallel sequencing techniques to hundreds of breast cancer samples providing a comprehensive catalog of somatic mutations that cause this disease.

Next-generation sequencing (NGS) mutational profiling methods have revealed that treatment-naïve triple-negative breast cancers (TNBCs) display a complete spectrum of mutational and clonal evolution, with some patients’ tumors showing only a few somatic coding sequence point mutations involving a limited number of molecular pathways. Other patients’ tumors however exhibit considerable additional mutational involvement.

Read full, original post: Finer Cancer Screens Catch More Cancer Clues