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Cancer gene somatic mutation detection-A tool for personalized cancer therapy

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Substantial advances have been made in understanding critical molecular mechanisms driving tumor initiation, maintenance, and progression in many types of cancer. Specifically, allelic variations in cancer-related genes result in the expression of proteins that can affect the sensitivity of tumors to targeted therapeutics. For example, non-small cell lung cancer (NSCLC) tumors that express activating alleles of the Epidermal Growth Factor Receptor (EGFR) are more sensitive to EGFR kinase inhibitors such as Tarceva. Conversely, in metastatic colorectal cancer, activating alleles of the KRAS gene render tumors resistant to EGFR inhibitors. Furthermore, drugs that target specific allelic variants of cancer related targets have recently become available such as Vemurafenib that inhibits activated B-Raf in melanoma and potentially other forms of cancer. The challenge is that theseallelic variants often exist in a small minority (<1%) of tumor cells making direct sequencing of tumor DNA impractical. There is a need for simple and robust methodologies to quickly identify important mutations in cancer related genes.

In this presentation I will review the available technologies for cancer gene mutation detection and describe a new technology that can rapidly and accurately identify allelic variants in as little as 0.1% of tumor cells. The technology will allow the rapid screening of a patients tumor to provide the oncologist with information to use in the selection of appropriate therapy and treatment regimen on a patient specific basis.

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