Genome Biology

INVITED SPEAKER PRESENTATION Open Access

Next-generation cancer genomics

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The combined discovery power of next-generation sequencing instruments and the associated somatic variation discovery of bioinformatics, applied to clinically characterized cancer samples, is changing our understanding of this disease. Since the 1930s, scientists have considered cancer a disease of the genome after observing novel chromosomal structures upon cytogenetic examination of tumor nuclei. As the resolution and sensitivity of methods for genomic examination have now permitted a nucleotide-level view of cancer genomes, we have the capability to understand somatic variation at unprecedented detail. Central to this capability is the human reference genome sequence and its annotation, which are ever improving. During the past year, our laboratory has undertaken a Cancer Genome Initiative that has produced data and analysis of 150 cancer cases (300 matched tumor and normal genomes), focusing primarily on acute myeloid leukemia, breast and lung cancers. My presentation will describe our results to-date and some technical advances developed during this project.

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