GENOMICS OF HETEROGENEITY IN LOCALISED NON-SMALL CELL LUNG CANCER

ABSTRACT:

Cancers are composed of populations of cells with distinct molecular and phenotypic features, a phenomenon termed intratumor heterogeneity (ITH). ITH in lung cancers has not been well studied. We applied multiregion whole-exome sequencing (WES) on 11 localized lung adenocarcinomas. All tumors showed clear evidence of ITH.

On average, 76% of all mutations and 20 out of 21 known cancer gene mutations were identified in all regions of individual tumors, which suggested that single-region sequencing may be adequate to identify the majority of known cancer gene mutations in localized lung adenocarcinomas.

With a median follow-up of 21 months after surgery, three patients have relapsed, and all three patients had significantly larger fractions of subclonal mutations in their primary tumors than patients without relapse. These data indicate that a larger subclonal mutation fraction may be associated with increased likelihood of postsurgical relapse in patients with localized lung adenocarcinomas.

ABOUT THE SPEAKER:

Andrew Futreal is currently Professor of Genomic Medicine at University of Texas MD Anderson Cancer Center, and co-leader of MD Anderson's Moon Shots Program, an innovative effort launched in 2012 to significantly reduce cancer deaths and transform care. Before accepting this position, from 2002 to 2012, Dr Futreal was joint head of the Cancer Genome Project with Professor Mike Stratton, and became head of Cancer Genetics and Genomics at the Sanger Institute in 2011.

Dr Futreal is collaborating with the Institute to investigate the molecular genetics of cancer and identify of cancer-causing genes. Before joining the Sanger Institute in 2002, Professor Futreal's work was most heavily focused on identification of susceptibility genes for breast and ovarian cancers and on characterising somatic genetic alterations in breast cancer and gynaecologic malignancies.

After his arrival, Dr Futreal worked closely with Mike Stratton within Cancer Genome Project, and he was instrumental in identifying somatic mutations in human cancer via large-scale genomic approaches, which led to the identification of the BRCA1 and BRCA2 breast/ovarian cancer susceptibility genes, BRAF mutations in melanoma, ERBB2 mutations in non-small cell lung cancer and multiple new cancer genes in renal cell carcinoma.

His Institute-based research also encompassed the application of molecular genetics to potential elucidation of therapeutic targets in cancer, the potential role of somatic genetics in patient stratification to conventional cancer therapies and the functional investigation of mutations identified in the Cancer Genome Project.

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DUKE NUS GRADUATE MEDICAL SCHOOL SINGAPORE

VENUE: Duke- NUS Room 7C, Level 7
DATE: 19 March 2015 (Thursday)
TIME: 1000 - 1130

All are welcome. No registration is required.