疾患プロテオゲノム研究センター
テクニカルセミナー
Institute for Genome Research, The University of Tokushima

BGI における次世代シーケンスを用いた疾患研究紹介

BGI: 世界的なゲノム解析センター。Top Journal に多数のゲノム解析論文を掲載。最近では慶應冨田教授の日本人初個人ゲノムの解析に関与。

日時　平成 24 年９月 19 日（水）16：00～17：30
場所　疾患ゲノム研究センター1F　交流室
講師　Mr. Guangliang YIN[1] and Mr. Shida ZHU[2] (BGI)

1.Epigenomics and Transcriptomics Studies in Cancer Researches

Next generation sequencing (NGS) provides promising means to study human personal genomes and human diseases, like cancers. Although cancers are widely recognized to be an accumulative process with somatic mutations, the epigenetics alterations in last decades are becoming clear that has an important role involved in various stages of cancer development. In addition, dysregulations of gene expression as well as structural variations in cancer cells were identified to be as biomarkers for diagnosing and classification of subtypes of cancers. Many experimental approaches and analytical tools were developed for epigenetics studies and transcriptome studies. BGI, as a leading genomics institute in multidisciplines research in world, is also focusing on these fields in cancer studies. We believed that epigenomics and transcriptomics analyses in cancer studies are indispensable for not only tumorigenesis studies, but personalized treatments for cancer patients by using NGS as well.

2.Acquisition of anti-estrogen resistance in breast cancer cells is associated with specific genomic alterations

Endocrine therapy has proven effective in estrogen receptor positive (ER+) breast cancer, however, drug resistance both in the adjuvant and advanced setting remain a major clinical problem leading to disease progression and death. The acquisition of resistance still remains poorly understood. With the advent of Next Generation Sequencing (NGS) technologies, newer large-scale and more data-driven types of research are now making it possible to explore disease mechanisms through many “omic” levels using sophisticated data integration methods. With the aim of obtaining further insight into the molecular mechanisms of endocrine resistance we applied exome sequencing and global gene expression analysis to study the acquisition of somatic mutations in an isogenic MCF-7 derived breast cancer cell model for acquired tamoxifen and fulvestrant resistance.

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