

【Grant-in-Aid for Scientific Research(S)】

Integrated Science and Innovative Science (New multidisciplinary fields)



Title of Project : An integrated genomic analysis on evolution of cancer cell population

Hiroyuki Aburatani

(The University of Tokyo, Research Center for Advanced Science and Technology, Professor)

Research Area : Genome science, Medical science

Keyword : Genome, epigenome, cancer, evolution, transcriptional regulation

【Purpose and Background of the Research】

Recent advances in genomic technology have enabled us to reveal driver somatic mutations in cancer genome during cancer initiation and progression. Various mutations have been identified in chromatin remodeling and epigenetic regulation genes, implicating that dysregulation of chromatin dynamics in somatic cells will lead to cancer. Sequential analysis of somatic events in cancer cell population will identify genomic and epigenomic alterations involved in clonal evolution of cancer. Elucidation of genetic and epigenetic heterogeneity in cancer cell population will be essential in understanding cancer evolution and its resistance mechanisms against anti-cancer drugs.

【Research Methods】

We will study genomic alterations and epigenomic profiles in cancer and xenograft cells, and elucidate genetic heterogeneity of cancer cell population and characteristic epigenetic features in drug resistant clones and cancer initiating cells.

1. genetic heterogeneity in cancer cell population
2. dysregulation of chromatin dynamics in cancer
3. evolution of cancer cell population

【Expected Research Achievements and Scientific Significance】

This study will identify the pathways involved in cancer progression and maintenance of cancer stem cells, by revealing genetic/epigenetic heterogeneity in cancer cell population. Such discovery will help develop drugs that inhibit cancer metastasis and conquer drug resistance.

【Publications Relevant to the Project】

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Genome Research 22(2):208-19. 2012

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【Term of Project】 FY2012-2016

【Budget Allocation】 167,500 Thousand Yen

【Homepage Address and Other Contact Information】

<http://www.genome.rcast.u-tokyo.ac.jp>
haburata-tky@umin.ac.jp