

Global Consortium Completes Tumor Analyses Project

Japanese participation to lead to clinical development

6 February 2020 National Cancer Center Japan

- Over 1300 researchers from 37 countries explored the entire cancer genome of 2658 human tumors, across 38 types of cancer
- Driver mutations and specific fingerprint of damages in Non-coding DNA elucidated a comprehensive picture of the human cancer genome
- Driver mutations were not found for rare cancers, comprising 5% of the tumors, leaving room for further explorations
- Research data is made available to the public, and to cancer researchers globally
- With further research with Japanese samples, clinical development leading to treatment of cancers specific to the Japanese population is anticipated

The National Cancer Center Japan took part in the Pan-Cancer Analysis of Whole Genomes (PCAWG) Consortium Project, initiated by the International Cancer Genome Consortium (ICGC). The project explored the entire cancer genome of 2658 human tumors across 38 types of cancer. Results were published on *Nature*, 5 February 2010 edition, in which contributions from the NCC Japan team made way into six of the papers.

The project accomplished the sequencing and analyses at an unprecedented scale, looking into noncoding DNA, the previous unexplored 'dark matter' comprising 99% of the genome. The new findings from mutations, chromosomal variants, elucidated the nature of how human tumors form, and are anticipated to lead to new diagnostics such as cancer gene panel tests and treatments.

In this project, Japanese samples only amounted to 286, although driver mutations are known to have respective links to ethnicity. Samples of cancer types prevalent in Asia and Japan, such as those of the stomach, esophageal squamous cell carcinoma, and biliary tract were also insufficient to lead to conclusions. To realize cancer genomic medicine tailored to Japanese ethnicity, large scale whole genome sequencing of Japanese samples are called for. Combined with accurate clinical information, whole genome big data will drive clinical development.

For 5% of the tumors, driver mutations could not be identified. Possibly this was because rare cancer sample numbers were also insufficient, calling for more research into a wider variety of individual types of cancer.

This project is also significant in that new analytic methods were developed and standardized, establishing a research framework for the next generation, with raw genome sequencing data stored on

the cloud portal, allowing integrated analyses with expressions and epigenomic data.

The International Cancer Genome Consortium (ICGC) has initiated the Accelerating Research in Genomic Oncology (ICGC-ARGO), a more ambitious larger scale project with whole genome sequencing and analyses of 200,000 tumors with clinical data. The National Cancer Center will participate in this succeeding project, advancing cancer research.

[Publications]

22 scientific papers were published from this research on *Nature*. Of the following, 1-3 exhibits the largest contribution from researchers at National Cancer Center Japan.

- 1. <u>Pan-cancer analysis of whole genomes</u>
- 2. The Repertoire of Mutational Signatures in Human Cancer
- 3. Genomic basis of RNA alterations in cancer
- 4. Patterns of somatic structural variation in human cancer genomes
- 5. <u>Analyses of non-coding somatic drivers in 2,693 cancer whole genomes</u>
- 6. The evolutionary history of 2,658 cancers

Author : The ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium

[Support]

Practical Research for Innovative Cancer Control - Japan Agency for Medical Research and Development (AMED) National Cancer Center Japan

[International Cancer Genome Consortium (ICGC)]

https://icgc.org

Established in 2008, the ICGC launches and coordinates large numbers of comprehensive and detailed analysis of cancer research projects, towards the common goal of unraveling the genomic changes present in many forms of cancer. 17 countries take part looking into 90 types of cancer. National Cancer Center Japan sequences and analyses liver, biliary tract, and gastric cancers.

[International Cancer Genome Consortium- Accelerating Research in Genomic Oncology (ICGC-ARGO)] https://www.icgc-argo.org

The second initiative launched by the ICGC, to address challenges of central importance to improving outcomes for people affected by cancer. Other than Japan, USA, Canada, UK, Germany, France Italy, Switzerland, Korea, China, Hong Kong, Saudi Arabia have also formalized their participation.

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