

BitBiome to analyse gut bacteria related to cancer

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Announces collaborative research agreement with National Cancer Center



bitBiome, Inc., a start-up company from Waseda University in Japan, and National Cancer Center of Japan have signed a collaborative research agreement on the analysis of gut bacteria related to cancer on November 22nd.

This collaborative research is an incidental study in the third phase of SCRUM-Japan, MONSTAR-SCREEN, by conducting shotgun metagenome analysis and single cell genome analysis of gut microbiome using a part of the sample of patients who participated in the project. It adds further value to the research.

In particular, single cell genome analysis of the gut microbiome is by the world's first technical platform (bit-MAPTM) from bitBiome. By using bit-MAPTM, in relationship between cancers and gut microbiome, it is possible to make a new attempt in the world to identify new types of bacteria that could not be achieved before, and to evaluate clinical outcomes from differences in strain-level bacterial genome sequences and functions.

In addition to oncogene analysis using blood (liquid biopsy) and gut microbiome analysis (16S rRNA metagenome), gut microbiome analysis using bit-MAP makes it possible to further understand the relationship between cancers caused by various somatic gene mutations and gut microbiome at a single cell level.

Furthermore, by investigating clinical information such as treatment progress of patients obtained through research, we aim to elucidate biomarkers related to the effects and side effects of immunotherapy and other drug treatments, and to further accelerate the development of new treatments.

NCC began research in Phase 3 of Japan's first Industry-academia collaboration cancer genome screening project, SCRUM-Japan (Project representative: Director of NCC East Hospital Atsushi Ohtsu) targeting a wide range of solid cancers.

In the research project MONSTAR-SCREEN (Max Onco-Network with STARS-SCREEN), for patients with a wide range of solid cancers except lung cancer, the effects and side effects of various drug treatments are analyzed through oncogene analysis using blood (liquid biopsy) and gut microbiome analysis (16S rRNA metagenome). The project aims to elucidate related biomarkers and develop new therapies.