# 🧐 National Cancer Center Japan

# To the press

# SCRUM-Japan GI-SCREEN Aims for Realizing of Cancer Precision Medicine Utilizing Liquid Biopsy by Analyzing Comprehensive Cancer

Genome Alterations in Blood

March 13, 2018 National Cancer Center, Japan

In February 2018, National Cancer Center (President, Dr. Hitoshi Nakagama, Tokyo, Japan) and National Cancer Center Hospital East(Director, Dr. Atsushi Ohtsu, Kashiwa, Japan) launched a new project "Research on Liquid Biopsy in Patients with Advanced Gastrointestinal Cancers". This study is conducted using a highly sensitive genetic analysis technology "Guardant360<sup>®</sup> assay" as part of a Nationwide cancer genome screening project for various gastrointestinal cancer, "SCRUM–Japan GI–SCREEN". The Guardant360<sup>®</sup> assay, developed by Guardant Health in the U.S. is a new diagnostic technique capable of analyzing fragments of tumor DNA circulating in the blood by next–generation sequencer technology, and providing cancer genetic information accurately and quickly. As conventional tumor tissue biopsies are highly invasive, biopsies of multiple regions and repeated biopsies can cause significant risk to the patients and delays in reaching a treatment decision. However, liquid biopsy is minimally invasive and enables the analysis of fragments of tumor DNA circulating in the blood. For these reasons, it can overcome the problems faced by tumor tissue biopsy.

## Background/social significance

Various genetic alterations have been being discovered in gastrointestinal cancers with the progress of genetic analysis; findings are applicable to clinical treatments. For instance, anti-epidermal growth factor receptor (anit-EGFR) antibodies such as cetuximab and panitumumab are used for treating colorectal cancers, but they are ineffective if the *RAS* gene has a mutation. Thus, the *RAS* gene test is now carried out before starting the anti-EGFR antibody therapy. However, alterations of various genes other than *RAS* have been reported to be related with resistance to anti-EGFR antibodies, such as *BRAF*, *PIK3CA*, *HER2*, and *MET* genes. At the moment, it is not clear whether anti-EGFR antibody preparations are completely ineffective in clinical treatment if these genetic alterations are found. Thus, the testing of these genes is presently not covered by National Health Insurance. For other gastrointestinal cancers, such as gastric, esophageal, liver, biliary tract, pancreatic, small intestine, appendicitis, anal canal cancers, gastrointestinal neuroendocrine tumor/cancer, and gastrointestinal stromal tumor (GIST), the only treatment option based on genetic alterations available in the clinical scene is *HER2* gene amplification for gastric cancer. Presently, new drugs for digestive system cancers with these genetic alterations are being developed, thus the importance of the analysis of these genetic alterations is gradually being recognized.

These genetic alterations have been gradually known to change according to the tumor region and treatment effects. Conventional tumor tissue biopsies are highly invasive and impose considerable stress on patients,

making it difficult to analyze genes by the biopsies of multiple regions and repeated biopsies. On the other hand, fragments of tumor DNA are known to circulate in the blood, allowing analysis by liquid biopsy using sampled blood. It can overcome the problems faced by tumor tissue biopsy. If the usefulness of genetic analysis using minimally invasive liquid biopsy for gastrointestinal cancers can be confirmed, even more precise personalized medicine based on genetic analysis using liquid biopsy will be established soon.

#### Outline of study

The joint industry-academia Nationwide cancer genome screening project "SCRUM-Japan GI-SCREEN" is a genetic alteration screening project for patients with gastrointestinal cancers, undertaken by the National Cancer Center Hospital East in collaboration with medical facilities all over the country and pharmaceutical companies, in the aim to provide the best medical care to each and every patient. If specific genetic alterations are found in patients in this study, they may participate in clinical studies of corresponding treatment drugs, which gives opportunities for new treatments. As of December 2017, more than 5,000 patients with gastrointestinal cancers have been registered since 2014.

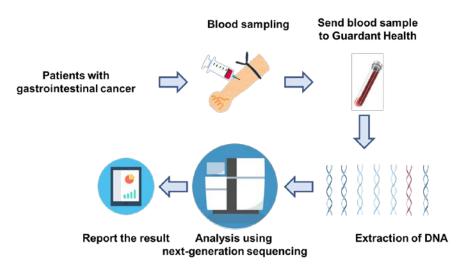
As part of SCRUM-Japan GI-SCREEN, a new Project "Research on Liquid Biopsy in Patients with Advanced Gastrointestinal Cancers" will start. The project will adopt Guardant360® assay, a new genetic analysis technology capable of measuring alterations in 73 genes all at once from blood. To date, cancer tissue specimens has been used for genetic analysis, but this study will attempt at genetic analysis using the blood (20 mL) of patients with gastrointestinal cancers. Specimens will be sent to Guardant Health who will conduct the genetic analysis to determine if the 73 cancer-related genes such as *RAS*, *BRAF*, *PIK3CA*, *HER2*, and *MET* are abnormal. The results of the genetic analysis will take about two weeks. The study will first be conducted on about 200 patients with advanced colorectal cancer who underwent treatment with anti-EGFR antibody. In upcoming year, the study will be expanded to appropriately 2,000 patients with all advanced gastrointestinal cancers to verify the clinical utility of genetic analysis using liquid biopsies. If specific genetic alterations are found in patients in this study, they may participate in clinical studies of corresponding treatment drugs.

AKT1         ALK         APC         AR         ARAF         ARID1A         ATM         BRAF         BRCA1         BRCA2           CCND1         CCND2         CCNE1         CDH1         CDK4         CDK6         CDK02A         CTNNB1         DDR2         EGFR           ERBB2         ESR1         EZH2         FBXW7         FGFR1         FGFR2         FGFR3         GATA3         GNA11         GNAQ           GNAS         HNF1A         HRAS         IDH1         IDH2         JAK2         JAK3         KIT         KRAS         MAP2K1           MAP2K2         MAPK1         MAPK3         MET         MLH1         MPL         MTOR         MYC         NF1         NFE2L2           NOTCH1         NPM1         NRAS         NTRK1         NTRK3         PDGFRA         PIK3CA         PTEN         PTN11         RAF1           RB1         RET         RHEB         RH0A         RIT1         ROS1         SMAD4         SMO         STK11         TERT**           TP53         TSC1         VHL	Point Mutations and Splice Site-Disrupting Alterations - 73 Genes										
ERBB2         ESRI         EZH2         FBXW7         FGFR1         FGFR2         FGFR3         GATA3         GNA11         GNAQ           GNAS         HINF1A         HRAS         IDH1         IDH2         JAK2         JAK3         KIT         KRAS         MAP2K1           MAP2K2         MAPK1         MAPK3         MET         MLH1         MPL         MTOR         MYC         NF1         NFE2L2           NOTCH1         NPM1         NRAS         NTRK1         NTRK3         PDGFRA         PIK3CA         PTEN         PTN11         RAF1           RB1         RET         RHEB         RHOA         RIT1         ROS1         SMAD4         SMO         STK11         TERT**           TP53         TSC1         VHL <td>AKT1</td> <td>ALK</td> <td>APC</td> <td>AR</td> <td>ARAF</td> <td>ARID1A</td> <td>ATM</td> <td>BRAF</td> <td>BRCA1</td> <td>BRCA2</td>	AKT1	ALK	APC	AR	ARAF	ARID1A	ATM	BRAF	BRCA1	BRCA2	
GNAS     HNF1A     HRAS     IDH1     IDH2     JAK2     JAK3     KIT     KRAS     MAP2K1       MAP2K2     MAPK1     MAPK3     MET     MLH1     MPL     MTOR     MYC     NF1     NF2L2       NOTCH1     NPM1     NRAS     NTRK1     NTRK3     PDGFRA     PIK3CA     PTEN     PTN11     RAF1       RB1     RET     RHEB     RHOA     RIT1     ROS1     SMAD4     SMO     STK11     TERT**       TP53     TSC1     VHL              Indels - 23     Genes                KIT     MET     MLH1     MTOR     NF1     PDGFRA     PTEN     RB1     SMAD4     STK11     TERT**       Indels - 23     Genes                  IATM     APC     ARIDIA     BRCA1     BRCA2     CDH1     CDKN2A     EGFR     ERB2     GATA3       KIT     MET     MLH1     MTOR     NF1     PDGFRA     PTEN     RB1     SMAD4     STK11       TP53     TSC1     VHL	CCND1	CCND2	CCNE1	CDH1	CDK4	CDK6	CDKN2A	CTNNB1	DDR2	EGFR	
MAP2K2     MAPK1     MAPK3     MET     MLH1     MPL     MTOR     MYC     NF1     NF2L2       NOTCH1     NPM1     NRAS     NTRK1     NTRK3     PDGFRA     PIK3CA     PTEN     PTN11     RAF1       RB1     RET     RHEB     RHOA     RIT1     ROS1     SMAD4     SMO     STK11     TERT**       TP53     TSC1     VHL              Indels - 23     Genes     Genes     ATM     APC     ARIDIA     BRCA1     BRCA2     CDH1     CDKN2A     EGFR     ERB82     GATA3       KIT     MET     MLH1     MTOR     NF1     PDGFRA     PTEN     RB1     SMAD4     STK11       TP53     TSC1     VHL             ATM     APC     ARID1A     BRCA1     BRCA2     CDH1     CDKN2A     EGFR     ERB82     GATA3       KIT     MET     MLH1     MTOR     NF1     PDGFRA     PTEN     RB1     SMAD4     STK11       TP53     TSC1     VHL              Amplifications - 18 Genes        MYC	ERBB2	ESR1	EZH2	FBXW7	FGFR1	FGFR2	FGFR3	GATA3	GNA11	GNAQ	
NOTCH1     NPM1     NRAS     NTRK1     NTRK3     PDGFRA     PIK3CA     PTEN     PTN11     RAF1       RB1     RET     RHEB     RHOA     RIT1     ROS1     SMAD4     SMO     STK11     TERT**       TP53     TSC1     VHL               Indels - 23     Genes                   Indels - 23     Genes </td <td>GNAS</td> <td>HNF1A</td> <td>HRAS</td> <td>IDH1</td> <td>IDH2</td> <td>JAK2</td> <td>JAK3</td> <td>KIT</td> <td>KRAS</td> <td>MAP2K1</td>	GNAS	HNF1A	HRAS	IDH1	IDH2	JAK2	JAK3	KIT	KRAS	MAP2K1	
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FGFR2     KIT     KRAS     MET     MYC     PDGFRA     PIK3CA     RAF1       Fusions - 6     Genes	Amplifications - 18 Genes										
Fusions - 6 Genes	AR	BRAF	CCND1	CCND2	CCNE1	CDK4	CDK6	EGFR	ERBB2	FGFR1	
	FGFR2	KIT	KRAS	MET	MYC	PDGFRA	PIK3CA	RAF1			
ALK FGFR2 FGFR3 RET ROS1 NTRK1	Fusions - 6 Genes										
	ALK	FGFR2	FGFR3	RET	ROS1	NTRK1					

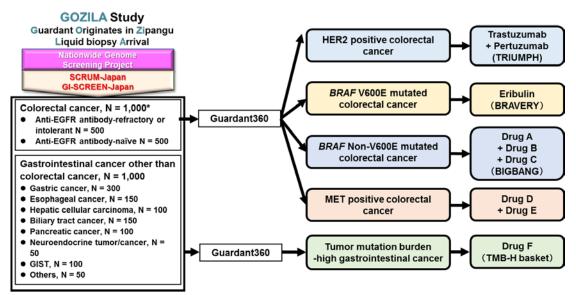
Figure 1. List of genetic alterations that can be analyzed by Guardant360® assay

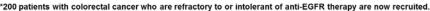
Point Mutations and Splice Site-Disrupting Alterations - 73 Genes

Figure 2. Outline of study



#### Figure 3. Future plan





#### Prospects

If the study results can identify different genetic alterations linked to cancer treatment in the blood and the differences from genetic alterations in the tumor tissue, it will help understand the changes in genetic alterations linked to cancer, as well as enable reviews for realizing of cancer precision medicine using liquid biopsies.

## SCRUM-Japan GI-SCREEN

SCRUM-Japan GI-SCREEN (Principal investigator, Dr. Takayuki Yoshino, Director of the Department of Gastroenterology and Gastrointestinal Oncology in National Cancer Center Hospital East) is the Nationwide cancer genome screening project for patients with advanced gastrointestinal cancers, undertaken by the National Cancer Center Hospital East in collaboration with medical facilities all over the country and pharmaceutical companies. It was established to identify cancer patients with orphan-fractionated cancer genome alteration who likely to have promising therapeutic drugs and to prepare easy-to-access platform where the patients can receive new treatment, in collaboration with major cancer hospitals and universities in Japan since February 2014. At the time of the start, it

aimed to find orphan-fractionated advanced colorectal cancer, but since February 2015, it became a member of the joint industry-academia nationwide cancer genome screening project "SCRUM-Japan", which expanded to not only colorectal cancer but also the whole gastrointestinal cancer, such as gastric and esophageal cancer.

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