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Current Status of Comprehensive Genomic Profiling（CGP） in Miyazaki Prefecture and Review of the Literature

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Background: Comprehensive Genomic Profiling（CGP）testing has been covered by insurance in Japan since 2019. Miyazaki Prefectural Hospital began CGP in January 2024 after designation as a Cancer Genome Collaboration Hospital in 2023. ***Methods:*** A retrospective study was conducted on 24 CGP cases from January to December 2024 to assess current status and future challenges. ***Results:*** Median patient age was 60 years（range: 39–82）, with female predominance（7 males, 17 females）. All tests used tissue samples and the FoundationOne® CDx platform. CGP was conducted at first-line in 12%（rare/unknown primary）, second-line in 46%, and third-line in 42%. Mean time from CGP submission to expert panel review was 32.1 days. Major tumor types were gastrointestinal（50%）and gynecologic（42%）cancers. DNA analysis was successful in all cases. The median number of actionable alterations was 5（IQR: 1–9; range: 1–15）. Common genomic alterations included *TP53* and *PIK3CA* mutations. In addition, high tumor mutational burden（*TMB high*）was frequently observed as a biomarker feature. All 24 cases harbored at least one actionable mutation. Drug-accessible alterations were found in 62%（15/24）, and 29%（7/24）received targeted treatments（treatment-matched rate）, including pembrolizumab and capivasertib. Implementation rates varied by tumor type: 60% in gallbladder, 14% in uterine, and 33% in intrahepatic cholangiocarcinoma. Targeted therapy showed a trend toward prolonged survival without statistical significance. One case required genetic counseling for *STK11* mutation. ***Conclusion:*** CGP has expanded opportunities to explore novel treatment strategies based on genomic alterations. It proved feasible and clinically valuable for identifying actionable mutations and guiding therapy. Future efforts should optimize timing, broaden access, and

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enhance data to advance precision oncology.

Keywords: Comprehensive Genomic Profiling (CGP), precision oncology, actionable genetic alterations, treatment-matched rate, overall survival.

INTRODUCTION

Precision medicine refers to medical care that is tailored to the individual characteristics of each patient, including their genetic profile. Comprehensive genomic profiling (CGP) is a key component of precision oncology, enabling the detection of clinically actionable genetic alterations in malignant tumors. Building on this basic foundation, the advent of precision oncology has transformed the paradigm of cancer treatment, aiming to tailor therapies based on the molecular characteristics of individual tumors rather than relying solely on histopathology or tumor location [1-4]. Advances in cancer genome analysis have enabled the identification of clinically relevant genomic alterations that can guide therapeutic decision-making and improve patient outcomes [2, 4].

Recent years have witnessed increasing efforts to integrate genomic profiling into routine oncology practice and clinical trials, particularly through the development of comprehensive cancer genome panels [1,3]. Large-scale real-world genomic datasets have further demonstrated the feasibility and clinical utility of this approach, providing evidence that supports genomics-informed treatment strategies across diverse cancer types [3, 5-8].

Nevertheless, significant challenges remain in the implementation of precision oncology, including disparities in access, timing of testing, and the translation of genomic data into actionable clinical decisions [2].

In Japan, CGP testing has been publicly reimbursed since 2019, and its adoption has been expanding through the national cancer genomic medicine framework. The clinical implementation of CGP tests has raised expectations for the realization of cancer genomic medicine; however, investigations into the regional circumstances and the clinical utility of CGP remain limited in Japan. The previous report by the Ministry of Health, Labour and Welfare (MHLW) has shown barriers to widespread CGP adoption in Japan, such as limited numbers of certified genetic counselors, uneven geographic distribution of testing facilities, and reimbursement restrictions [9]. However, most reports focus on national or large urban centers, and there is a lack of detailed data on CGP use and outcomes in regional areas.

In this study, we present a retrospective study of 24 CGP cases performed at Miyazaki Prefectural Miyazaki Hospital as a regional cancer genome collaboration hospital in Japan. By evaluating patient characteristics, mutation profiles, and clinical outcomes, we aim to assess the current status of CGP implementation and identify practical considerations for advancing precision oncology at the regional level in Japan.

PATIENTS AND METHODS

Establishment of Cancer Genome Medicine System

Our institution's cancer genome medicine system, comprising the Cancer Genome Clinic and the Genetic Counseling Division, was established as follows. Preparations for the program began in April 2022. By April 2023, our institution was officially recognized as a Cancer Genome Collaboration Hospital by the Ministry of Health, Labour and Welfare (MHLW), becoming the 249th facility to receive this designation. Subsequently, we established a collaborative partnership with Kyushu University, designated as a Core Center for Cancer Genomic Medicine by the Ministry. In January 2024, CGP testing was initiated at our institution.

Patient Information

We conducted a retrospective study of 24 patients who underwent CGP testing at Miyazaki Prefectural Hospital between January and December 2024.

In 2019, the Ministry of Health, Labour and Welfare (MHLW) in Japan approved insurance coverage for CGP testing in solid tumors under the condition that all standard treatment options had been exhausted. However, subsequent clinical guidance recommends that CGP testing may also be consid-

ered earlier in the disease course for patients with advanced malignancies lacking standard treatment options, provided that performance status (PS) and organ function are preserved [10, 11].

Based on these evolving recommendations, our institution has adopted a flexible approach to the timing of CGP testing. While adhering to national insurance regulations, we consider testing at an earlier stage, especially during second line or third line therapy, in cases where clinical appropriateness is determined based on the patient's general condition (including PS and organ reserve), the judgment of the attending physician, and the consensus of our institutional cancer genome board.

In practice, CGP testing during first-line therapy is limited to rare cancers without standard treatment. For gastrointestinal and gynecologic malignancies, which constitute the majority of our cases, we consider CGP testing during second-line therapy when standard options are nearing exhaustion, and routinely during third-line treatment and beyond. This institutional policy has been reviewed and approved by institutional cancer genome board.

Patient demographic data, including age and sex, as well as clinical information such as tumor type, were extracted from medical records.

Tumor Specimens and Next-Generation Sequencing

All CGP tests were performed using formalin-fixed paraffin-embedded (FFPE) tissue samples. Genomic analysis was conducted using the FoundationOne® CDx platform, an FDA-approved CGP assay that examines 324 cancer-related genes and key genomic signatures through next-generation sequencing. This assay is designed to identify actionable mutations to guide targeted therapy decisions in patients with solid tumors.

Data Collection

Clinical information collected from medical records included the timing of CGP testing, specimen source, tumor content rate as assessed by pathologists, identified genomic alterations, and subsequent therapeutic interventions. The timing of CGP was categorized into three groups: first-line (prior to initiation of systemic therapy), second-line (during ongoing standard therapy), and third-line (after completion of standard therapy). Expert panel (EP) meetings were held to evaluate the therapeutic relevance of CGP results. The interval between CGP sample submission and EP review was recorded.

Statistical Analysis

Survival outcomes were analyzed using Kaplan-Meier curves to compare patients who received recommended treatments based on CGP results with those who did not. The date of specimen submission was defined as the starting point, and the last follow-up date was used as the endpoint. Statistical significance was set at a p-value of less than 0.05.

Ethics Approval

This retrospective study was approved by the Institutional Review Board (IRB) under protocol number (24-20).

RESULTS

Patient Demographics and Specimen Characteristics

A total of 24 patients underwent CGP testing at our institution between January and December 2024 (Table 1). The median age was 60 years (range: 39–82), with a female predominance (7 males, 17 females). All CGP tests were performed using tissue samples analyzed via the FoundationOne® CDx platform (Table 2). Of the specimens, 20 (83%) were surgical and 4 (17%) were biopsy samples. Tumor content was ≥30% in 21 cases (88%), while 3 cases (12%) had tumor content ≤20%. In the latter group, tumor areas were marked by pathologists, and approximately 20 slides were submitted per case. DNA analysis was successfully completed in all cases.

Tumor Type Distribution

The most common tumor types were gastrointestinal and hepato-pancreato-biliary cancers (12 cases, 50%) and gynecologic tumors (10 cases, 42%) (Figure 1a). Among these, uterine and gallbladder cancers were the most frequent (Figure 1b). The remaining cases included intrahepatic cholangiocarcinoma, ovarian cancer, colorectal cancer, and others (Figure 1b).

Table 1. Patient Characteristics, Genetic Alterations, and Treatment Outcomes

Case	Age	Gender	Diagnosis	Treatment Line	The treatment-matched genetic alterations	Matched Therapy	Matched Therapy Drug	Sample Date	EP Date	OS Date	OS Status
1	68	M	Rectal Cancer	3rd line	None	N	None	2024/1/4	2024/2/13	2024/12/11	Alive
2	52	F	Uterine Cancer	3rd line	None	N	None	2024/2/29	2024/4/8	2024/9/2	Dead
3	52	F	Cancer of Unknown Primary	1st line	TMB-high	Y	Pembrolizumab	2024/5/6	2024/6/17	2024/12/11	Alive
4	48	F	Uterine Cancer	2nd line	None	N	None	2024/5/22	2024/6/26	2024/12/11	Dead
5	69	F	Ovarian Cancer	2nd line	None	N	None	2024/6/5	2024/7/8	2024/10/2	Dead
6	52	F	Oral Cancer	1line	None	N	None	2024/6/19	2024/7/22	2024/12/11	Alive
7	52	F	Gallbladder Cancer	1st line	TMB-high/MSI-high	Y	Pembrolizumab	2024/7/4	2024/8/5	2024/12/11	Alive
8	79	F	Gallbladder Cancer	2nd line	None	N	None	2024/7/11	2024/8/5	2024/12/11	Dead
9	39	F	Uterine Cancer	3rd line	None	N	None	2024/8/8	2024/9/2	2024/12/11	Alive
10	82	M	Gallbladder Cancer	2nd line	KRAS G12D	N	Clinical Trial	2024/9/2	2024/9/30	2024/12/11	Alive
11	71	M	Gallbladder Cancer	2nd line	None	N	None	2024/9/5	2024/10/7	2024/12/11	Alive
12	52	F	Uterine Cancer	3rd line	None	N	None	2024/9/19	2024/10/15	2024/12/11	Alive
13	65	F	Gallbladder Cancer	2nd line	TMB-high	Y	Pembrolizumab	2024/9/26	2024/10/28	2024/12/11	Alive
14	58	F	Ovarian Cancer	3rd line	None	N	None	2024/10/3	2024/11/6	2024/12/11	Dead
15	73	M	Intrahepatic Cholangiocarcinoma	2nd line	None	N	None	2024/10/11	2024/11/18	2024/12/11	Alive
16	73	M	Intrahepatic Cholangiocarcinoma	2nd line	None	N	None	2024/10/11	2024/11/18	2024/12/11	Alive
17	48	F	Breast Cancer	3rd line	PIK3CA・TMB-high	Y	Capivasertib, Pembrolizumab	2024/10/31	2024/12/2	2024/12/11	Alive
18	48	F	Pancreatic Cancer	2nd line	None	N	None	2024/11/7	2024/12/9	2024/12/11	Alive
19	48	F	Intrahepatic Cholangiocarcinoma	2nd line	TMB-high	Y	Pembrolizumab	2024/11/21	2024/12/23	2024/12/11	Alive
20	57	M	Colon Cancer	2nd line	None	N	None	2024/11/21	2024/12/9	2024/12/11	Alive
21	63	F	Uterine Cancer	3rd line	TMB-high	Y	Pembrolizumab	2024/11/27	2024/12/9	2024/12/11	Alive
22	61	F	Uterine Cancer	3rd line	None	N	None	2024/11/27	2024/12/9	2024/12/11	Alive
23	48	F	Uterine Cancer	3rd line	None	N	None	2024/11/27	2024/12/9	2024/12/11	Alive
24	72	M	Colon Cancer	3rd line	None	N	None	2024/11/7	2024/12/9	2024/12/11	Alive

Abbreviations: EP Date = Date of Expert Panel; OS Date = Date of last follo-up day or death; OS Status = Overall Survival Status at OS Date.
Matched Therapy Column:
“Y” indicates the patient received a therapy matched to the genomic alteration identified by CGP.
“N” indicates no matched therapy was given.
Matched Therapy Drug: "Clinical Trial" indicates the patient was enrolled in a clinical trial based on CGP findings.

Table 2. Evaluation of Specimen Quality Submitted for Comprehensive Genomic Profiling（CGP）Testing（F1CDx）

	Surgical Specimens (20 cases)	Biopsy Specimens (4 cases)	Total (24 cases)
Successful Analysis	**20 cases (83.3%)**	**4 cases (16.7%)**	**24 cases (100%)**
Slightly Lower Quality			
・Qualified			
・TMB/MSI evaluation not possible	**0 cases (0%)**	**3 cases (12.5%)**	**3 cases (12.5%)**
・Tumor cell content（FM）<20%			
・Average sequencing depth <400			
Unsuccessful (Pre-sequencing)	**0 cases (0%)**	**0 cases (0%)**	**0 cases (0%)**

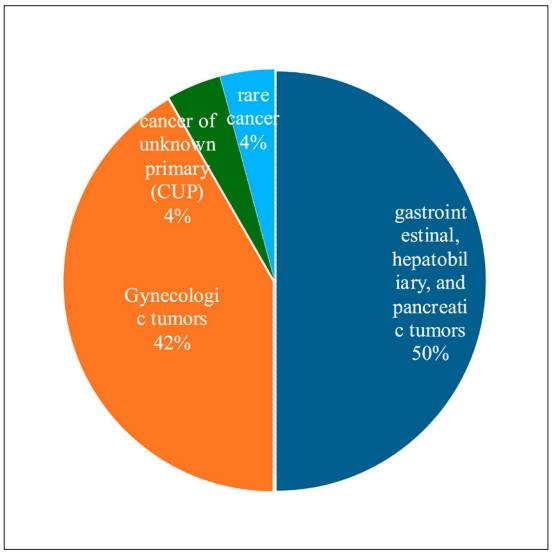


Figure 1a. Distribution of CGP Testing by Cancer Type at Our Institution

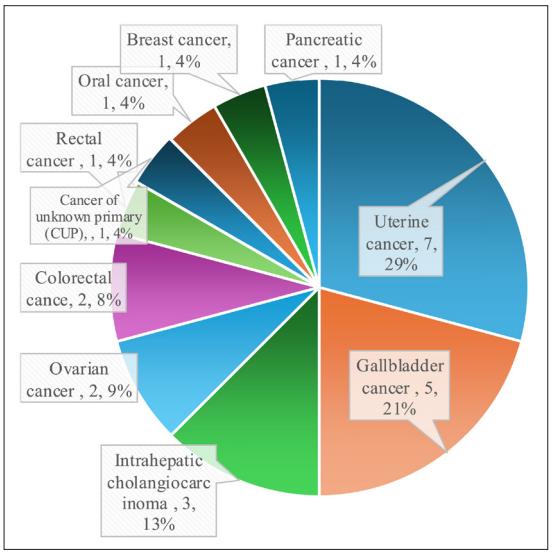


Figure 1b. Detailed Breakdown of CGP Testing by Cancer Type

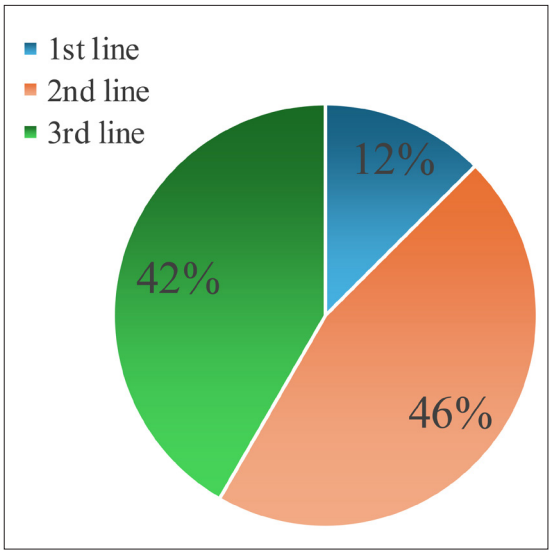


Figure 1c. Analysis of the Timing of CGP Testing

Figure 1. Analysis of Cancer Type and the Timing in Comprehensive Genomic Profiling（CGP）Testing

Timing and Turnaround of CGP Testing

CGP testing was conducted at the first-line setting in 3 cases (12%), primarily involving rare cancers or cancers of unknown primary origin where no standard therapies were available (Figure 1c). Second-line testing was performed in 11 cases (46%), and third-line in 10 cases (42%), mainly for gastrointestinal and gynecologic malignancies (Figure 1c). The average duration from CGP sample submission to expert panel (EP) discussion was 32.1 days (range: 25–42 days).

Actionable Genomic Alterations and Their Associations

The median number of actionable genomic alterations per case was 5 (IQR: 1–9; range: 1–15), with some cases exhibiting up to 15 alterations (Figure 2). The most frequently observed gene alterations included *TP53* (15 cases), *PIK3CA* (7 cases), *ARID1A* (6 cases), *CDKN2A* (6 cases), and *KRAS* (6 cases) (Figure 3). *TP53* mutations were most common in gallbladder cancer (5 of 15 cases), whereas *PIK3CA* mutations were predominantly seen in uterine cancer (4 cases) and breast cancer (1 case) (Figure 4). In addition, high tumor mutational burden (*TMB high*) status, which is a genomic biomarker, was detected in 6 cases across multiple tumor types, suggesting its tumor agnostic relevance (Figure 4).

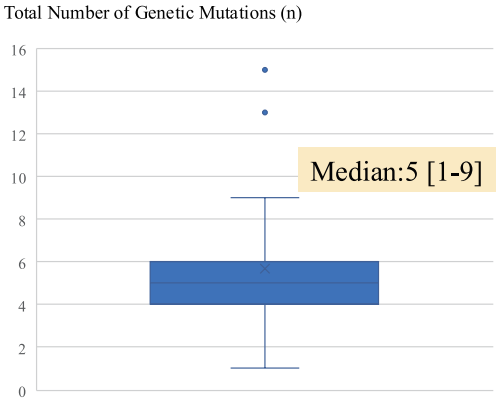


Figure 2A. Analysis of the Distribution of Total Number of Genetic Mutations per Case

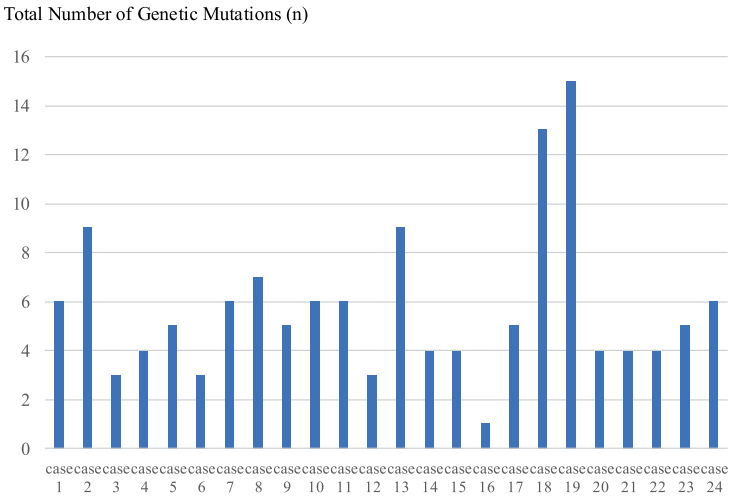


Figure 2B. Analysis of the Total Number of Genetic Mutations per Case

Figure 2. Analysis of Actionable Genetic Mutations in CGP Testing

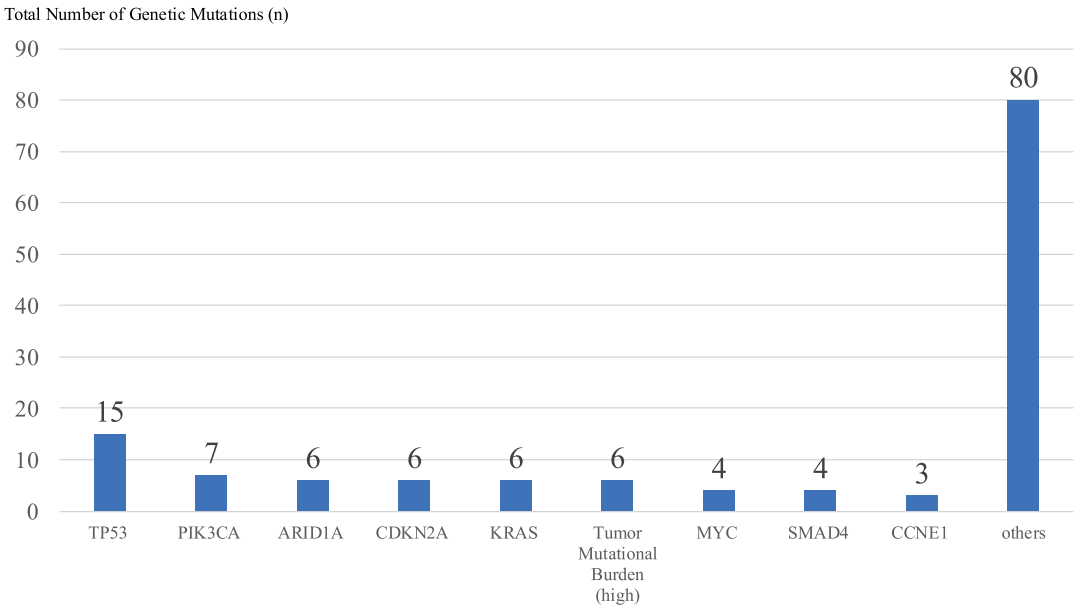


Figure 3. Analysis of Actionable Genetic Mutation Types in CGP Testing

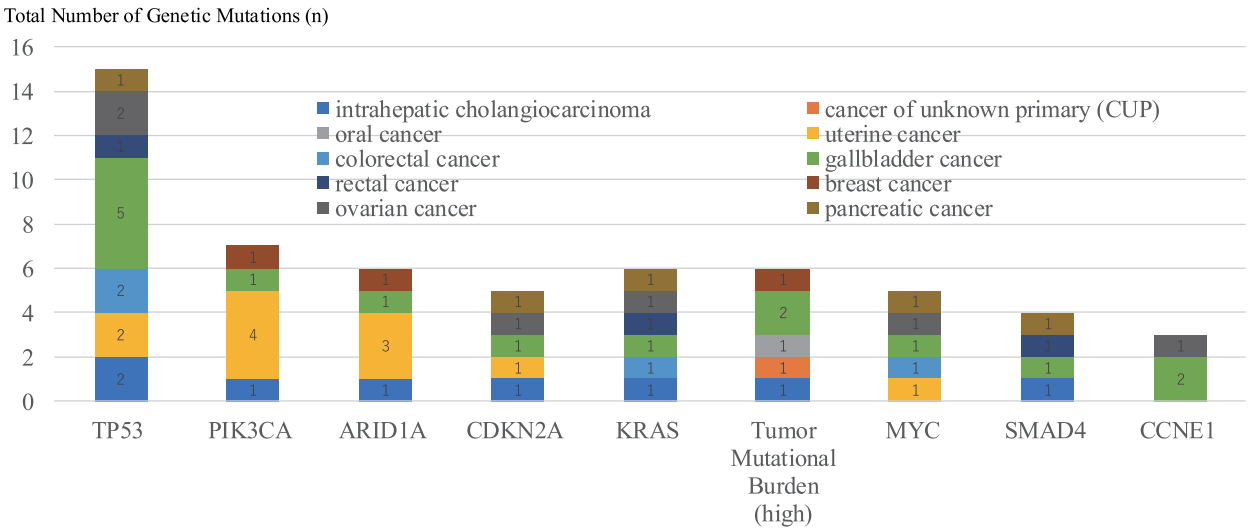


Figure 4. Analysis of the Relationship Between Actionable Genetic Abnormalities Detected in CGP Testing and Diseases

Druggable and Treatable Alterations Identified by CGP: Therapeutic Implications and Real-World Treatment Outcomes

Drug-accessible genomic alterations were identified in 15 patients (62%), of whom 6 were eligible for insurance-covered targeted therapies and 9 were considered for clinical trial enrollment (Table 3). The identified gene alterations included *PIK3CA*/PTEN pathway alterations (11 cases), *BRAF* (1 case), *ERBB2* (2 cases), *IDH* (1 case), *FGFR* (2 cases), *KIT* (1 case), *CDK4* (1 case), and *KRAS G12D* (2 cases). In addition, two genomic biomarkers were detected, namely *TMB high* in 5 cases and microsatellite instability-high (MSI high) in 1 case.

Targeted therapies based on treatable alterations were successfully administered in 7 patients (29%) (Table 4). Five received pembrolizumab for *TMB-high* status, one received capivasertib for a *PIK-3CA* mutation, and one was considered for a *KRAS G12D*-specific inhibitor. Among those not receiving targeted therapy, most continued subsequent chemotherapy, while some transitioned to best supportive care (BSC). In contrast, the treatment-matched rates by tumor type were as follows: 60% for gallbladder cancer (3 of 5), 33% for intrahepatic cholangiocarcinoma (1 of 3), and 14% for uterine cancer (1 of 7) (Table 5). Furthermore, patients with cancer of unknown primary and breast cancer achieved a 100% treatment rate (1 case each). Notably, patients receiving targeted therapy showed a trend toward improved overall survival, although the difference was not statistically significant, likely due to the small sample size (24 cases) (Figure 5).

Secondary findings

Among the 24 cases analyzed, 2 cases (8%) were suspected of having hereditary tumors based on family history. One involved mucocutaneous pigmentation in both the patient and her father, suggesting Peutz-Jeghers syndrome. The other involved pancreatic tumors in both the patient's mother and daughter. Both patients received genetic counseling before CGP. CGP revealed an *STK11* mutation in the case suspected of Peutz-Jeghers syndrome, while no pathogenic variants, including BRCA, were found in the other. Confirmatory germline testing was performed only in the *STK11* case and confirmed a mutation. This patient had uterine cancer.

DISCUSSION

In this study, we analyzed 24 cases of CGP at our institution and found promising results that align with or exceed those reported in previous studies (Table 6) [6-9]. The detection rates of actionable genetic alterations (100%), druggable alterations (62%), and the treatment achievement rates (29%) are comparable to or better than those of other institutions, supporting the clinical utility of CGP in routine oncology practice. Notably, this may be the

Table 3. Drug-Accessible Genetic Alterations in Our Institution

Genetic Alteration Type	Genetic Alteration / Biomarker	Drug	Insurance-Covered Drugs（the number）	Clinical Trials（the number）
Genomic Biomarker	**TMB high**	**PD-1 Inhibitor**	**5**	0
	MSI high	**PD-1 Inhibitor**	**1**	0
Gene Alteration	BRCA1/2 Mutation	PARP Inhibitor	0	0
	HRD-Related（RAD54L, RAD51C, ATM, CDK12）	PARP Inhibitor	0	0
	AKT/PIK3CA/PTEN Mutation	**AKT Inhibitor / mTOR Inhibitor**	**1**	**10**
	BRAF Mutation	**BRAF Inhibitor + MEK Inhibitor**	0	**1**
	ERBB2 Amplification	**Anti-HER2 Antibody**	0	**2**
	NTRK Fusion Gene	TRK Inhibitor	0	0
	EGFR Mutation	EGFR Inhibitor	0	0
	TSC2 Mutation	mTOR Inhibitor	0	0
	MET Mutation	MET Inhibitor	0	0
	IDH1/2 Mutation	**IDH1 Inhibitor / IDH2 Inhibitor**	0	**1**
	FGFR Fusion Gene / Mutation	**FGFR Inhibitor**	0	**2**
	ALK Mutation	ALK Inhibitor	0	0
	KIT Mutation	**KIT Inhibitor**	0	**1**
	SMARCB1 Mutation	EZH2 Inhibitor	0	0
	CDK4 Mutation	**CDK4/6 Inhibitor**	0	**1**
	NF1 Mutation	MEK Inhibitor	0	0
	KRAS G12D Mutation	**KRAS G12D Inhibitor**	0	**2**

Footnote:
The number in the Insurance-covered drugs column indicates the number of cancer types in which the listed drug is covered by the Japanese national insurance.
The number in the Clinical Trials column indicates the number of clinical trials available at our institution targeting the respective genetic alteration.

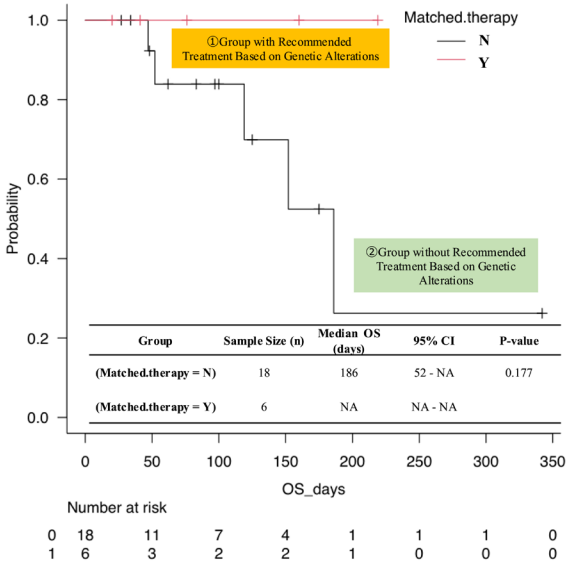
Table 4. The Treatment-Accessible Genetic Alterations in Our Institution

Genetic Alteration Type	Genetic Alteration / Biomarker	Drug	Insurance-Covered Drugs（the number）	Clinical Trials（the number）
Genomic Biomarker	**TMB high**	**PD-1 Inhibitor**	**5**	0
	MSI high	**PD-1 Inhibitor**	**1**	0
Gene Alteration	BRCA1/2 Mutation	PARP Inhibitor	0	0
	HRD-Related（RAD54L, RAD51C, ATM, CDK12）	PARP Inhibitor	0	0
	AKT/PIK3CA/PTEN Mutation	**AKT Inhibitor / mTOR Inhibitor**	**1**	0
	BRAF Mutation	BRAF Inhibitor + MEK Inhibitor	0	0
	ERBB2 Amplification	Anti-HER2 Antibody	0	0
	NTRK Fusion Gene	TRK Inhibitor	0	0
	EGFR Mutation	EGFR Inhibitor	0	0
	TSC2 Mutation	mTOR Inhibitor	0	0
	MET Mutation	MET Inhibitor	0	0
	IDH1/2 Mutation	IDH1 Inhibitor / IDH2 Inhibitor	0	0
	FGFR Fusion Gene / Mutation	FGFR Inhibitor	0	0
	ALK Mutation	ALK Inhibitor	0	0
	KIT Mutation	KIT Inhibitor	0	0
	SMARCB1 Mutation	EZH2 Inhibitor	0	0
	CDK4 Mutation	CDK4/6 Inhibitor	0	0
	NF1 Mutation	MEK Inhibitor	0	0
	KRAS G12D Mutation	**KRAS G12D Inhibitor**	0	**1**

Footnote:
The number in the Insurance-covered drugs column indicates the number of cancer types in which the listed drug is covered by the Japanese national insurance.
The number in the Clinical Trials column indicates the number of clinical trials available at our institution targeting the respective genetic alteration.

Table 5. Analysis of Treatment Accessibility by Tumor Type

Tumor Type	Number of Cases	Treatment Accessibility	Treatment Accessibility Rate (%)
Uterine Cancer	7	1	14.30%
Gallbladder Cancer	5	3	60.00%
Intrahepatic Cholangiocarcinoma	3	1	33.30%
Ovarian Cancer	2	0	0.00%
Colorectal Cancer	2	0	0.00%
Rectal Cancer	1	0	0.00%
Cancer of Unknown Primary	1	1	100.00%
Oral Cancer	1	0	0.00%
Breast Cancer	1	1	100.00%
Pancreatic Cancer	1	0	0.00%



Factor	Group	Matched.therapy N	Matched.therapy Y	p.value
n		18	6	
Diagnosis (%)	Oral cancer	1 (5.6)	0 (0.0)	0.573
	Breast cancer	0 (0.0)	1 (16.7)	
	Gallbladder cancer	3 (16.7)	2 (33.3)	
	Intrahepatic cholangiocarcinoma	2 (11.1)	1 (16.7)	
	Pancreatic cancer	1 (5.6)	0 (0.0)	
	Ovarian cancer	2 (11.1)	0 (0.0)	
	Uterine cancer	6 (33.3)	1 (16.7)	
	Colorectal cancer	2 (11.1)	0 (0.0)	
	Rectal cancer	1 (5.6)	0 (0.0)	
	Cancer of unknown primary (CUP)	0 (0.0)	1 (16.7)	
Gender (%)	Female	11 (61.1)	6 (100.0)	0.13
	Male	7 (38.9)	0 (0.0)	
OS (%)	Alive	13 (72.2)	6 (100.0)	0.28
	Dead	5 (27.8)	0 (0.0)	
Age		60.67 (12.14)	61.17 (9.75)	0.928
OS (days)		97.28 (79.50)	92.83 (79.23)	0.907

Abbreviations: OS Date = Date of last follo-up day or death;
Matched Therapy Column:
"Y" indicates the patient received a therapy matched to the genomic alteration identified by CGP.
"N" indicates no matched therapy was given.
Matched Therapy Drug:"Clinical Trial" indicates the patient was enrolled in a clinical trial based on CGP findings.

Figure 5. Analysis of Overall Survival（OS）in All 24 Cases

Table 6. The Summary of Domestic and International CGP Studies

	Total Cases	Actionable (%)	Druggable (%)	Insurance-Covered Treatment (%)	Clinical Trial Enrollment (%)	Treatment Attainment (%)
MSK-IMPACT（International）	10,336	37%	36%	9%	27%	10.50%
NCC Oncopanel（TOP-GEAR, Japan）	187	59%	13%	3%	10%	13%
Project HOPE（Japan, JCGA 2014–2016）	5,143	72%	58%	11.30%	18.70%	-
C-CAT（Japan, 2019–2022）	30,822	-	44.50%	-	-	9.40%
Present Study (2024)	**24**	**100%**	**62%**	**25%**	**37.50%**	**29%**

first validated report from Japan to highlight the clinical utility of CGP in relation to regional factors, with no prior studies identified in major English-language databases searched via PubMed, Cochrane Library, and Scopus of April 19, 2025.

First, in comparison with domestic studies such as the TOP-GEAR trial (2019), Project HOPE (2019), and the C-CAT database (2024), as well as international data from MSK-IMPACT (2019) [6-9], our findings demonstrate comparable or favorable outcomes. The detection rate of actionable mutations at our institution was 100%, exceeding the reported range of 37%–97% [6-9]. The detection rate of druggable mutations was 62%, which is within the previously reported range of 13%–69% [6-9]. Notably, the treatment achievement rates at our institution was 29%, which is markedly higher than the reported range of 9%–15% [6-9], suggesting favorable clinical translation.

Several factors may contribute to this favorable outcome. First, a substantial number of patients with druggable mutations were able to access clinical trials conducted at Kyushu University, owing to its geographic and institutional accessibility. Second, a relatively high proportion of patients exhibited *TMB-high* across multiple tumor types, frequently resulting in the administration of pembrolizumab.

Second, it is noteworthy that actionable mutations were identified in all 24 cases. A detailed analysis revealed that the number of genetic alterations per case had a median of 5 (IQR: 3–7; range: 1–15), with some cases exhibiting up to 15 mutations. Frequently altered genes included *TP53* (15 cases), *PIK3CA* (7 cases), *ARID1A*, *CDKN2A*, *KRAS* (6 each), *MYC* and *SMAD4* (4 each), and *CCNE1* (3 cases). In addition, *TMB high* was observed in 6 cases as a genomic biomarker, independent of specific gene mutations. These findings are consistent with Singh *et al.* (2023) [5], which associated mutations in *TP53*, *KRAS*, *CDKN2A*, and *SMAD4* with clinical significance in pancreatic cancer. In particular, the high prevalence of *TP53* mutations in our cohort supports its potential role in tumor progression and poor prognosis. Furthermore, mutations in genes such as *PIK3CA*, *ARID1A*, and *KRAS*, along with the presence of *TMB high*, were observed at notable frequencies, suggesting opportunities for targeted therapies tailored to individual genomic profiles. The observed alterations and biomarkers may serve as a basis for personalized treatment strategies.

Finally, in this study, approximately 8% of cases were suspected to have hereditary tumors based on CGP results. Genetic counseling was provided to both patients, and confirmatory testing identified a germline mutation in the *STK11* gene in one case (4%), associated with Peutz-Jeghers syndrome. This highlights the value of CGP in detecting hereditary mutations, which can inform treatment decisions and guide family counseling. The detection of a germline mutation in uterine cancer underscores the importance of personalized care and monitoring for other hereditary cancer manifestations.

In the future, it is crucial to optimize the timing of CGP implementation based on updated guidelines, as well as to expand its applications to include hematologic malignancies, a point not covered in this study.

Despite these strengths, our study has limitations, including a relatively small sample size and the single-institutional nature of the cohort. Nevertheless, our findings demonstrate the feasibility and clinical utility of CGP, and highlight the importance of systemic infrastructure—including access to molecular tumor boards and clinical trials—in translating genomic findings into patient care.

CONCLUSION

This retrospective study of 24 CGP cases demonstrated the feasibility of cancer genome profiling in routine oncology practice. High detection rates of actionable (100%) and druggable (62%) alterations were observed, with a 29% treatment achievement rate. These outcomes were supported by access to clinical trials and a high proportion of *TMB-high* cases, enabling pembrolizumab treatment. CGP has expanded personalized treatment options, and further optimization of its timing and inclusion of hematologic malignancies in testing is essential for advancing precision oncology.

Author's contribution

N.K. and I.K. designed the study and wrote the

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Conflict of interest disclosure

All authors declare no conflicts of interest.

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