

Dual-targeting strategy using trastuzumab and lapatinib in a patient with HER2 gene amplification in recurrent metachronous metastatic gallbladder carcinoma

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Abstract

Gallbladder carcinoma (GBC) is a rare and highly aggressive tumor. Early diagnosis is challenging, which results in a poor prognosis using systemic therapy. Recent studies have identified a subset of GBC patients with HER2 gene (ERBB2) amplification that could benefit from HER2-targeted therapy. Here, we report one patient with recurrent metachronous GBC with metastasis, who received the combination of trastuzumab and lapatinib. This approach achieved a partial response for both the brain and the lung metastases. This study demonstrated that HER2 inhibition is a promising therapeutic strategy for GBC with HER2 amplification and, combined with lapatinib, it can effectively target brain metastasis.

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Keywords

Gallbladder carcinoma, HER2 amplification, dual-targeted therapy, trastuzumab, lapatinib, tumor

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Introduction

Anti-HER2 molecular targeted agents are established for treating breast cancer, ¹⁻³ gastric cancer, ⁴ and metastatic colorectal cancer⁵ in patients with HER2 gene amplification (an increase in the copy number). A combination of two HER2-targeted therapies, such as trastuzumab and lapatinib, has also been demonstrated to have clinical efficacy in advanced HER2-positive metastatic breast cancers^{2,3} and colorectal cancers.⁵

Lapatinib (GW572016) is a selective inhibitor of epidermal growth factor receptor (EGFR) and HER-2 tyrosine kinase,⁶ and trastuzumab is a humanized monoclonal antibody that targets the HER-2 extracellular domain.⁷ The dual targeting of HER2-positive tumors using trastuzumab and lapatinib results from the primary and acquired resistance of these two drugs, their partly non-overlapping mechanisms of action, and the well characterized synergistic interaction between them in HER2 breast-cancer models. Clinically, trastuzuprimarily induces pro-apoptotic effects, while lapatinib inhibits proliferation.^{8,9} Clinical evidence shows indirect support for dual HER2 blockade. In patients with refractory breast cancer who are treated with trastuzumab, lapatinib plus trastuzumab prolonged the progression-free survival compared with lapatinib alone. Konecny et al. 10 analyzed the combination of trastuzumab plus lapatinib, and they observed synergistic drug interactions in four HER-2-overexpressing breast cancer cell lines. Additionally, similar results were obtained in the study reported by Baselga

et al., 11 which suggested complementary mechanisms of action and synergistic antitumor activity for the monoclonal antibody in a model of breast cancer that overexpressed HER2. Xu et al.3 conducted a systematic review and meta-analysis of randomized controlled trials (RCTs), and the results showed that lapatinib plus trastuzumab significantly prolonged the pathological complete response, overall survival, and event-free survival with tolerance in HER2-positive breast cancer patients. Moreover, the combination of trastuzumab and lapatinib was also effective and well tolerated in patients with HER2-positive metastatic colorectal cancer refractory disease.5

Gallbladder carcinoma (GBC) is a rare and highly aggressive tumor. Early diagnosis is challenging, which results in a poor prognosis in patients who receive systemic therapy. However, combination therapy with trastuzumab and lapatinib has not been reported in patients with GBC. Here, we present the case of a patient with dual-targeted HER2 therapy including lapatinib that was used to treat advanced GBC with brain metastases.

Case presentation

On 4 January 2016, a 48-year-old Chinese female patient was admitted to the Shaoxing People's Hospital because of nausea, vomiting, dizziness, headache, crooked mouth, and slurred speech. Magnetic resonance imaging (MRI) showed multi-site metastatic brain tumors (Figure 1a) and bilateral adrenal gland metastasis (data not shown).

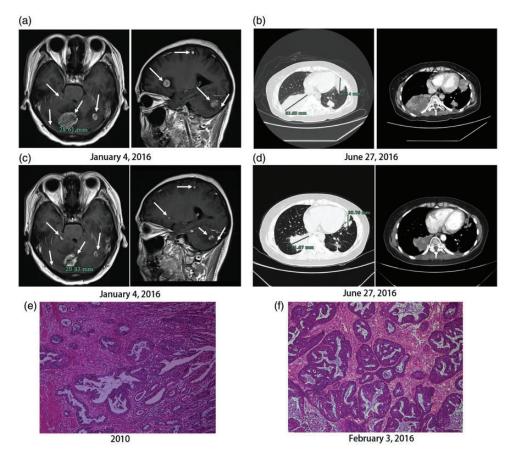


Figure 1. Dual-targeted therapy with trastuzumab and lapatinib were effective in advanced gallbladder carcinoma patients with multi-site brain and lung metastases.

Magnetic resonance imaging showed the status of brain metastases before (a) and after (c) three cycles of dual-HER2 targeted therapy with trastuzumab and lapatinib. Chest computed tomography scans showed the status of lung metastasis before (b) and after (d) three cycles of dual HER2-targeted therapy with trastuzumab and lapatinib. (e) A biopsy identified that the gallbladder tumor was moderate-differentiated adenocarcinoma (hematoxylin and eosin staining; original magnification \times 100). (f) A biopsy showed that the metastatic brain tumors were adenocarcinoma (hematoxylin and eosin staining; original magnification \times 100).

computed tomography (CT) scans revealed multi-site metastatic lung tumors (Figure 1b). This patient was diagnosed with GBC via cholecystectomy that was performed because of cholecystitis and gallstones in 2010 (pT3N0M0; TNM staging: IIB; Nevin staging: III) (Figure 1e). Lung metastasis was found in 2014, and brain metastasis was detected in 2015. The patient's medical history is shown in Figure 2.

One month after admission, the patient underwent surgery to remove one of the largest metastatic tumors (longest diameter in the transverse plane, 38.96 mm) in the left frontal lobe. The biopsy showed that the metastatic tumor was adenocarcinoma (Figure 1f). The patient was diagnosed with the GBC brain metastasis after a comprehensive review. Genetic profiling of 416 cancer-relevant genes was performed using

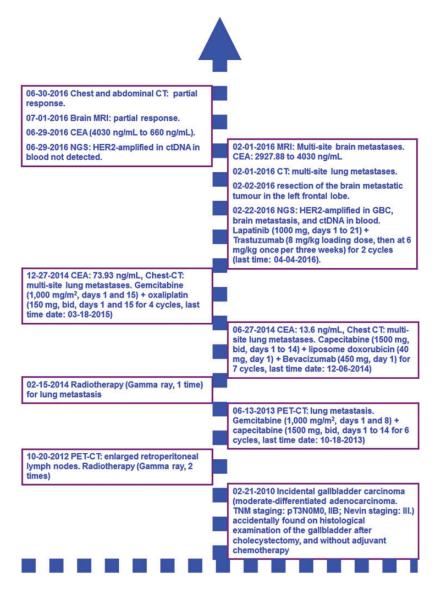


Figure 2. Medical history, clinical interventions, and metastasis development.

targeted next generation sequencing (NGS; see Materials and Methods) to develop potential molecular therapeutic approaches. GBC primary tumor and brain metastatic tissues, as well as the circulating tumor DNA (ctDNA) in the blood were collected from the patient for genetic profiling. The sequencing results showed

a significant increase in the HER2 copy number in the GBC primary tumor $(8.6\times)$, brain metastasis $(14.6\times)$, and ctDNA $(2.5\times)$ (Table 1). Thus, dualtargeted therapy was initiated on 6 March, 2016 using trastuzumab (administered intravenously at an initial dose of $8 \, \text{mg/kg}$, followed by subsequent doses of $6 \, \text{mg/kg}$

Sample type	Sample ID	Genetic alterations identified	MAF (%)/ Fold change (\times)
Before HER2-targeted the	rapy		
ctDNA	P16020611144	TP53: p.K291X (c.A871T)	4%
		CDK12: amplification	2.87×
		ERBB2: amplification	2.48×
FFPE sample of	F16020611145	TP53: p.K291X (c.A871T)	31%
gallbladder tumor		CDK12: amplification	9.03×
		ERBB2: amplification	8.40×
FFPE sample of	F16020611146	TP53: p.K291X (c.A871T)	72%
brain tumor		CDK12: amplification	11.28×
		ERBB2: amplification	14.60×
		RBI: Single-copy loss	0.53×
After three cycles of anti-	HER2 targeted therapy	· · ·	
ctDNA	P16051918361	TP53: p.K291X (c.A871T)	0.5%
		CDK12: amplification	Not detected
		ERBB2: amplification	Not detected
		RB1: Single-copy loss	Not detected

Table 1. Genetic alterations identified in samples before/after HER2-targeted therapy.

MAF, mutant allele frequency; ctDNA, circulating tumor DNA; FFPE, formalin-fixed paraffin-embedded.

once per week for 3 weeks) and lapatinib (administered orally each day at a dose of 1000 mg per day in 21-day treatment cycles), based on previously published work in breast cancer^{2,3} (i.e., one dose of trastuzumab each week and one dose of oral lapatinib each day). No concurrent chemotherapy was administrated.

Three weeks after dual HER2 targeted therapy with trastuzumab and lapatinib, the follow-up chest and brain MRI revealed that the patient achieved a partial response in brain metastatic tumors (Figure 1c) and lung metastatic tumors (Figure 1d), after three cycles of treatment based on the Response Criteria Evaluation in Solid Tumors (RECIST) version 1.1. The MRI results showed that the metastatic tumors had shrunk. A concurrent blood sample was collected for genetic testing of ctDNA using targeted NGS. The HER2 copy numbers did not increase at this time (Table 1), suggesting that the tumors were cleared after trastuzumab and lapatinib dual therapy. It was also accompanied by a carcinoembryonic antigen (CEA) response (CEA levels decreased from 4030 ng/mL to 660 ng/mL). The patient developed grade 3 adverse reactions including fatigue, skin rash, and increased bilirubin concentration, but no grade 4 or 5 adverse reactions were observed. In summary, dualtargeted therapy with trastuzumab and lapatinib offered a chemotherapy-free option and achieved tumor suppression with an acceptable safety profile for this patient with HER2 amplification in GBC.

Materials and methods

Patient information

The patient provided written informed consent. The study was approved by the ethics committee at the institute and was performed in strict accordance with the principles of the Declaration of Helsinki and the International Conference on Harmonization and Good Clinical Practice guidelines.

Tumor assessment

Tumor measurements were performed by a radiologist (ZXL) before treatment and were assessed every 2 months in accordance with RECIST (version 1.1). The patient was examined using a CT of the chest, abdomen, or pelvis, and MRI brain scans when clinically indicated in accordance with the protocol. All tumor measurements were reviewed by a radiologist (ZXL) who read the MRI or CT scans, and collected, stored, and interpreted the imaging results.

Adverse reaction assessment

The patient's health was continuously monitored and graded in accordance with the Common Terminology Criteria for Adverse Events (CTCAE) version 4.0. Laboratory test assessments (hematology, serum chemistry, urine analysis, and tumor markers) were performed at baseline (day 1 of every cycle), and at the end of treatment. The left ventricular ejection fraction was examined at baseline (day 1 of every cycle) and at the end of treatment.

DNA extraction

Formalin-fixed paraffin-embedded (FFPE) tissues were sectioned, and hematoxylin and eosin (H&E)-stained slides reviewed by surgical pathologists (FL and AJS). Tumor tissue areas were dissected from ten serial sections (4 µm) guided by H&E slides as templates. The FFPE tissues were deparaffinized with xylene and genomic DNA was extracted using a QIAamp DNA FFPE tissue kit (Qiagen, Valencia, CA, USA). The concentration of DNA was determined using a Qubit dsDNA HS assay the Qubit 3.0 (Life kit on Technologies, Carlsbad, CA, USA), in strict accordance with the manufacturer's protocol. DNA (A260/280 and A260/230) was measured using the Nanodrop-2000 (Thermo Fisher Scientific, Waltham, MA, USA).

Whole blood (8 mL) was collected using **EDTA** blood collection tubes Biosciences, San Jose, CA, USA) that were centrifuged within 2 hours at $1800 \times g$ for 10 minutes at $\geq 4^{\circ}$ C to collect the plasma. ctDNA was extracted from plasma using a QIAamp circulating nucleic acid (Qiagen). The purified ctDNA was quantified using a Qubit dsDNA HS assay kit on the Qubit 3.0 Fluorometer (Life Technologies).

Library construction

The sequencing library was prepared using **KAPA** Hyper Prep Kit (Kapa Biosystems, Boston, MA, USA), in accordance with the manufacturing protocol. Briefly, 1 µg genomic DNA sample was fragmented into 350 bp in an Adaptive Focused Acoustics (AFA) fiber snap-cap microTUBE using Covaris M220 (Covaris, Woburn, MA, USA) or 10-50 ng ctDNA underwent end repairing, A-tailing, adapter ligation, size selection, and finally PCR amplification. Library concentration was determined using a Qubit dsDNA HS assay kit on the Qubit 3.0 Fluorometer (Life Technologies).

Hybrid capture and ultra-deep next generation sequencing

The 5'-biotinylated probe solution was used as capture probes, which targeted 416 cancer-related genes (Table 2). The capture reaction was performed using NimbleGen SeqCap EZ hybridization and Wash Kit (Roche) with 1 µg of pooled libraries, 5 µg of human Cot-1 DNA, 1 unit of adapter-specific blocker DNA, and the capture probes. The solution hybridization was performed for 16–18 hours at 65°C. The captured targets were selected by pulling down the biotinyprobe/target lated hybrids using

Table 2. Gene targeted in hybridization capture.

ABCBI	CDK4	ERBB4	HGF	MSH2	PTEN	STKII
(MDRI) ABCC2	CDK6	ERCCI	HNFIA	MSH3	PTPNII	STMNI
(MRP2)	CDIA	ED C C 2	LINIELD	MOLIC	DTD\ IO	CTX
ACTB	CDK8	ERCC2	HNFIB	MSH6	PTPN2	STXII
ADHIB	CDKNIB	ERCC3	HRAS	MTHFR	PTPN6	STXBP2
AIP	CDKNIC	ERCC4	ID3	MTOR	PTPRO	SUFU
AKTI	CDKN2A	ERCC5	IDHI	MUTYH	QKI	SUZ12
AKT2	CDKN2B	ESRI	IDH2	MYC	RACI	SYN3
AKT3	CDKN2C	ETVI	IGFIR	MYCLI	RAD21	TCN2
ALDH2	CEBPA	ETV4	IGF2	MYCN	RAD50	TEK
ALK	CEP57	EWSRI	IKBKE	MYD88	RAD51	TEKT4
AMER I	CHD4	EXTI	IKZFI	MYNN	RAD51C	TERC
AP3B1	CHEKI	EXT2	IKZF2	NBN	RAD51D	TERT
APC	CHEK2	EZH2	IKZF3	NCSTN	RAFI	TET2
AR	CKSIB	FANCA	IL13	NFI	RARA	TGFBR2
ARAF	CREBBP	FANCB	IL7R	NF2	RASGEFIA	TLEI
ARIDIA	CRKL	FANCC	INPP4B	NFKBIA	RBI	TLE4
ARID2	CROT	FANCD2	INPP5D	NKX2-I	RECQL4	TMEM127
ARID5B	CSFIR	FANCE	IRFI	NOTCHI	RELN	TMPRSS2
ASXLI	CSF3R	FANCF	IRF2	NOTCH2	RET	TNFAIP3
ATM	CTCF	FANCG	IRF4	NPMI	RHBDF2	TNFRSF14
ATR	CTLA4	FANCI	IRF8	NQOI	RHOA	TNFRSF17
ATRX	CTNNBI	FANCL	JAKI	NRAS	RICTOR	TNFRSF19
AURKA	CUXI	FANCM	JAK2	NRGI	RNF146	TOPI
AURKB	CXCR4	FATI	JAK3	NSDI	RNF43	TOP2A
AXINI	CYLD	FBXOII	JARID2	NT5C2	ROSI	TP53
AXL	CYPI9AI	FCGR2B	JUN	NTRKI	RPTOR	TP63
B2M	CYP2B6*6	FGF19	KDM2B	PAGI	RRMI	TPMT
BAPI	CYP2C19*2	FGFRI	KDM5A	PAK3	RTELI	TRAF2
BARDI	CYP2C9*3	FGFR2	KDR	PALB2	RUNXI	TRAF3
D/ (ND)	C11 2C7 3	TOTAL	(VEGFR2)	17 LDZ	NOT VI	110 (13
BCL2	CYP2D6*3	FGFR3	KIFIB	PARK2	SBDS	TRAF5
BCL2L1	CYP2D6*4	FGFR4	KIT	PAX5	SDHA	TSCI
BCL2L2	CYP2D6*5	FH	KMT2B	PBRMI	SDHAF2	TSC2
BCORLI	CYP2D6*6	FIPILI	KMT2C	PC	SDHB	TSHR
BCL2L11 (BIM)	CYP3A4*4	FLCN	KRAS	PDCDI	SDHC	TTFI
BLM	CYP3A5*I	FLT I (VEGFR I)	LEFI	PDCD1LG2 (PD-L2)	SDHD	TUBB3
BMPRIA	CYP3A5*3	FLT3	LMOI	PDGFRA	SERP2	TYMS
BRAF	DAB2	FLT4	LSPI	PDGFRB	SETBPI	TYR
DIVAL		(VEGFR4)	L31 1	100110	JE I DI I	1110
BRCAI	DAXX	GADD45B	LYN	PDKI	SETD2	U2AFI
BRCA2	DDR2	GATAI	LYST	PHF6	SF3B1	UGTIAI
BRD4	DDXI	GATA2	LZTRI	PHOX2B	SGKI	UNC13D
BRIPI	DHFR	GATA3	MAP2K I (MEK I)	PICK3R1	SH2D1A	VEGFA

(continued)

Table 2. Continued.

BTG2	DICERI	GATA4	MAP2K2 (MEK2)	PIK3C3	SLX4	VHL
BTK	DIS3L2	GATA6	MAP2K4	PIK3CA	SMAD2	WISP3
BTLA	DLG2	GNATI	MAP3K1	PIK3CD	SMAD3	WRN
BUBIB	DMNT3A	GNA13	MCLI	PIK3R1	SMAD4	WTI
cllorf30	DNM2	GNAO	MDM2	PIK3R2	SMAD7	XIAP
CALR	DOCKI	GNAS	MDM4	PLCEI	SMARCA4	XPA
CBL	DOTIL	GPC3	MECOM	PLKI	SMARCBI	XPC
CCNDI	DPYD	GRIN2A	MED12	PMSI	SMCIA	XPOI
CCNEI	DUSP2	GRM3	MEF2B	PMS2	SMC3	XRCCI
CCT6B	EBFI	GSTMI	MENI	POLDI	SMO	YAPI
CD22	ECT2L	GSTPI	MET	POLD3	SOX2	ZAP70
CD274	EED	GSTTI	MGMT	POLE	SPOP	ZBTB20
(PD-LI)		33111		. 011	5. 5.	25.520
CD58	EGFR	HBAI	MITF	POTI	SRC	ZNF217
CD70	EGRI	HBA2	MLHI	PPP2RIA	SRSF2	ZNF703
CDA	EP300	HBB	MLL	PRDMI	STAG2	ZRSR2
CDC73	EPCAM	HDACI	MLLT10	PRFI	STAT3	
CDHI	EPHA3	HDAC2	MLPH	PRKARIA	STAT5A	
CDK10	ERBB2	HDAC4	MPL	PRKCI	STAT5B	
	(HER2)		·			
CDK12	ERBB3	HDAC7	MREIIA	PTCHI	STIL	

streptavidin-coated magnetic beads, and the off-target library was removed by washing with wash buffer, followed by PCR amplification of the target-enriched libraries. Sequencing libraries were quantified by using the KAPA Library Quantification kit (KAPA Biosystems, Boston, MA, USA), sized on a Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA, USA), and then deep-sequenced on an Illumina HiSeq 4000 using the PE150 kit (Illumina Inc., San Diego, CA, USA).

Sequence alignment and data processing

Quality control was applied using Trimmomatic. High quality reads were mapped to the human genome (hg19, GRCh37 Genome Reference Consortium Human Reference 37) using a modified Burrows-Wheeler Aligner (BWA) version 0.7.12¹³ with BWA-MEM algorithm and default parameters. The Genome Analysis

Toolkit¹⁴ (GATK, version 3.4-0) was modified and used to locally realign the BAM files at intervals with insertion/deletion (indel) mismatches and to recalibrate the BAM file read base quality scores. Single nucleotide variants (SNVs) and short indels were identified using VarScan2 2.3.9¹⁵ with a minimum variant allele frequency threshold set at 0.01 and a p-value threshold for calling variants set at 0.05 to generate variant call format (VCF) files. All SNVs/indels were annotated using ANNOVAR, and each SNV/indel was manually checked using the integrative genomics viewer (IGV). 16 Copy number variations (CNVs) were identified using ADTEx 1.0.4.17 The analysis and data are presented as copy number changes in all Tables.

Discussion

Recent studies have identified a subset of patients who are undergoing treatment for advanced GBC with HER2 overexpression or amplification that could potentially benefit from HER2-targeted therapy.^{6,7} Some studies previously reported the use of HER2-targeted treatment to treat HER2positive gallbladder cancers. One case included a significant reduction in lung metastasis in patients with amplified metastatic cholangiocarcinoma that was treated with trastuzumab and paclitaxel.8 Another study retrospectively reviewed GBC patients who received HER2-directed therapy with trastuzumab, lapatinib, or pertuzumab, and showed that HER2 blockage was a promising treatment strategy in HER2-positive GBC patients.⁷ Most of those patients received a single HER2-targeted reagent combined with chemotherapy.

Clinical trials have demonstrated that lapatinib can be used as a therapeutic option for advanced HER2 alterations in metastasis.9 cancers with brain Considering the multi-site brain and lung metastases of the GBC patients, we administrated dual-targeted HER2 therapy with trastuzumab and lapatinib and achieved PR after 4 months of treatment without concurrent chemotherapy. In summary, this is the first study to administer dualtargeted HER2 therapy including lapatinib to treat patients with advanced GBC with brain metastases. Patient follow-up and further multi-center clinical trials are necessary to investigate the long-term efficacy.

Conclusion

HER2 inhibition is a promising therapeutic strategy for GBC with HER2 amplification and used in combination with lapatinib, it can effectively target brain metastasis.

Declaration of conflicting interest

The authors declare that there is no conflict of interest.

Disclosure

Xue Wu, Yichuan Liu, and Yang W. Shao are the shareholders or employees of Geneseeq Technology Inc.

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