Modeling therapy response and spatial tissue distribution of erlotinib in pancreatic cancer

Barbara M. Grüner,[1*] Isabel Winkelmann,[2] Annette Feuchtinger,[2] Na Sun,[2] Benjamin Balluff,[3] Nicole Teichmann,[1] Alexander Herner,[1] Evdokia Kalideris,[1] Katja Steiger,[4] Rickmer Braren,[5] Michaela Aichler,[2] Irene Esposito,[6] Roland M. Schmid,[1,7] Axel Walch,[2] Jens T. Siveke[1,7,8]

[1] 2. Medizinische Klinik, Technische Universität München, Munich, Germany

[2] Research Unit Analytical Pathology, Helmholtz Center Munich - German Research Center for Environmental Health, Neuherberg, Germany

[3] Center for Proteomics and Metabolomics, Leiden University Medical Center, Leiden, Netherlands

[4] Institute of Pathology, Technische Universität München, Munich, Germany

[5] Institute of Radiology, Technische Universität München, Munich, Germany

[6] Institute of Pathology, Heinrich-Heine-University, Düsseldorf, Germany

[7] German Cancer Consortium (DKTK) and German Cancer Research Center (DKFZ), Heidelberg, Germany

[8] Division of Solid Tumor Translational Oncology, German Cancer Consortium (DKTK) partner site Essen, West German Cancer Center, University Hospital Essen, Essen, Germany

[*] current address: Department of Genetics, Stanford University School Of Medicine, Stanford, USA

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*** Correspondence**:

Jens T. Siveke, MD, West German Cancer Center, University Hospital Essen, Hufelandstr. 55, 45147 Essen, Germany

email: j.siveke@dkfz.de, phone/fax: +49-201-723-4580/6725

Axel Walch, MD, Research Unit Analytical Pathology, Helmholtz Center Munich , German Research Center for Environmental Health, Ingolstädter Landstr. 1, 85764 Neuherberg, Germany

email: axel.walch@helmholtz-muenchen.de, phone/fax: +49-89-3187 2739 / 3360

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Abstract

Pancreatic ductal adenocarcinoma (PDAC) is likely the most aggressive and therapy-resistant of all cancers. The aim of this study was to investigate the emerging technology of matrix assisted laser desorption/ionization imaging mass spectrometry (MALDI IMS) as a powerful tool to study drug delivery and spatial tissue distribution in PDAC. We utilized an established genetically engineered mouse model of spontaneous PDAC to examine the distribution of the small molecule inhibitor erlotinib in healthy pancreas and PDAC. MALDI IMS was utilized on sections of single-dose or long-term-treated mice to measure drug tissue distribution. Histological and statistical analyses were performed to correlate morphology, drug distribution and survival. We found that erlotinib levels were significantly lower in PDAC compared to healthy tissue ($p = 0.0078$). Survival of long-term-treated mice did not correlate with overall levels of erlotinib or with overall histological tumor grade but did correlate both with the percentage of atypical glands in the cancer ($p = 0.021$, $r_s = 0.59$) and the level of erlotinib in those atypical glands ($p = 0.019$, $r_s = 0.60$). The results of this pilot study present MALDI IMS as a reliable technology to study drug delivery and spatial distribution of compounds in a preclinical setting and supports drug imaging-based translational approaches.

Introduction

Pancreatic ductal adenocarcinoma (PDAC) is likely the most aggressive and therapy-resistant of all cancers (1). PDAC is characterized by a large degree of inter- and intratumoral genetic heterogeneity and a strong desmoplastic reaction, factors that likely impede many therapeutic approaches. Modeling these hallmark characteristics of PDAC *in vivo* using xenograft models has been largely disappointing, while genetically engineered mouse models (GEMM) based on pancreas-specific activation of oncogenic mutant Kras faithfully recapitulate the morphological and molecular characteristics of human PDAC enabling sophisticated preclinical approaches (reviewed in (2)).

Recently, Olive and colleagues found transplanted xenografts to be highly responsive to gemcitabine treatment but not tumors in GEMM due to lower perfusion and high desmoplasia in the latter. These results support the view that GEMM recapitulate the clinically acknowledged stromal barrier potentially better than classical xenotransplant models (3).

Drug tissue distribution and metabolism are key factors for tumor responses to therapy. Despite their extensive use, autoradiography and tissue homogenate LC-MS analysis have limitations in providing a comprehensive assessment of tissue distributions. Matrix assisted laser desorption/ionization (MALDI) imaging mass spectrometry (IMS) allows the simultaneous label-free detection of multiple molecules while maintaining spatial distribution in tissues, thus allowing various translational approaches (overview in (4)). We thus aimed to establish a MALDI IMS based detection method for preclinical characterization of intratumoral drug delivery in PDAC.

Epidermal growth factor receptor (EGFR) is a long-known target in many tumors including PDAC supported by a plethora of clinical and preclinical evidence (5). Erlotinib, a small molecule tyrosine kinase domain inhibitor directed against EGFR is to date the only approved targeted therapy for PDAC. However, its clinical benefit in combination with standard chemotherapy gemcitabine is very modest, arguing that additional factors co-determine therapy response. So far, no biomarker for a clinical response except a drug-induced skin rash has been identified. Besides multiple molecular resistance mechanisms (6, 7), inefficient drug delivery due to abundant desmoplasia and tumor-independent factors such as inter-individual variations in metabolism and modulation of immune responses may account for poor treatment response (8, 9). We thus aimed to utilize MALDI IMS to establish and characterize the delivery and distribution of erlotinib in healthy and tumorous pancreatic tissue using a GEMM-based approach.

Materials and Methods

Mouse strains

Kras$^{wt/LSL\text{-}G12D}$, *Ptf1a*$^{wt/Cre}$ and *Trp53*$^{fl/fl}$ strains have been described previously (10-12). Mice were interbred to obtain *Ptf1a*$^{wt/Cre}$;*Kras*$^{wt/G12D}$;*Trp53*$^{fl/fl}$ mice (named *Kras*^{G12D};*p53*^{KO}) and were backcrossed to C57BL/6J background for at least four generations. C57BL/6J mice served as wild-type controls. All animal experiments were in accordance with German Federal Animal Protection Laws and approved by the Institutional Animal Care and Use Committee at the Technical University of Munich.

Drug treatment of mice

Erlotinib (Roche) was dissolved in 0.5 % methylcellulose in water and was administered to mice by oral gavage in either a single dose for indicated time points or daily ± gemcitabine (Cellpharma) as indicated as soon as a tumor was detectable with MRI. For combination treatment, 4 doses of gemcitabine were administered i.p. each separated by three days in the concentration of 100 mg/kg.

MRI measurement of mice

To track tumor onset and end point volume, non-invasive MRI was performed with a clinical 1.5T MRT as previously described (5). MR imaging experiments were initiated at an age of 25-40 days and were performed weekly. Before imaging, mice were anesthetized by continuous gaseous infusion of 2% isoflurane (Abbott) for at least 10 minutes using a veterinary anesthesia System (Vetland Medical). During imaging, the dose was kept at 2% isoflurane, animal temperature was maintained and continuously monitored and eyes were protected with an eye ointment. Tumor growth kinetics changes were followed with T2 weighted imaging protocol using microscopy surface coil inside a Philips 1.5T or 3.0T clinical scanner. An axial multi-slice T2-weighted (T2w) TSE sequence (resolution 0.3x0.3x0.7 mm3, minimum 30 slices, TE=90 ms, TR>3 s) was applied for tumor detection. Solid tumor volumes were calculated using in house optimized ImageJ based software that differentiates between solid and cystic parts of the tumor.

MALDI-TOF IMS measurement of erlotinib on pancreatic sections

Pancreata were resected and snap frozen in liquid nitrogen without fixation. 10 µm cryosections were cut and transferred to Indium-Tin-Oxide (ITO) coated glass slides pretreated with poly-lysine (0.1 %) 1:1 in water with 0.1% NP-40. Sections were dried for 30 min at RT and α-cyano-4-hydroxycinnamic acid (CHCA) matrix (7 g/l CHCA in 70% methanol) was applied to the glass slide with the ImagePrep™ station (Bruker Daltonics). Mass spectra were measured using the MALDI TOF/TOF Analyzer Ultraflex III (Bruker Daltonics) with a spatial resolution of 70 µm in reflector mode. Ions were detected in a mass range of m/z 200 to 500 with a sampling rate of 0.1

GS/s. Calibration for each measurement was performed using the first isotope of the matrix dimer (CHCA: $2MH^{+}+1 = 380.09$) as calibration point. MALDI-TOF IMS data were obtained and analyzed using the FlexControl 3.0 and FlexImaging 3.0 software (Bruker Daltonics).

Co-registration of morphology and spectra for MALDI measured sections

After MALDI measurements, slides were washed in 70% ethanol to remove the matrix and counterstained with hematoxylin/eosin (H&E). High-resolution images of stained sections were taken using the Mirax Scan system (Carl Zeiss) and co-registered with the MALDI IMS data to correlate mass spectra with the histological features of the same section.

Statistical analysis of MALDI IMS data

With the FlexImaging software regions of interest (ROI) were defined and 80 to 500 randomly chosen single spectra (depending on sample number and ROI size) per mouse per ROI-group were exported to ClinProTools 2.2 software for further analysis. Extracted mass spectra were recalibrated on common “background” peaks (spectral alignment), normalized to their total ion count and the relative signal intensities for selected ions per ROI were calculated.

Average peak intensities for erlotinib were exported from ClinProTools and compared using the Wilcoxon-test for non-normally distributed paired data using the GraphPad Prism5 statistical software. For correlation analyses Spearman correlation coefficients for non-parametric data and corresponding p values for linear regression were calculated. P values ≤ 0.05 were considered significant.

To correlate erlotinib distribution and morphology, Definiens Developer XD2 (Definiens AG, Munich) was used. A rule set was developed in order to detect and quantify semantic classes. In a first step the algorithm segments pictures iteratively, recognizing groups of pixels as objects. The objects are classified further based on staining intensity, morphology, neighborhood and special color features to distinguish the morphological classes “glandular” and “desmoplastic” and their percentage of total area was calculated. With the same software, the presence of erlotinib on mass-visualization pictures, provided by the Bruker FlexImaging Software, was classified and overlay with the above-defined morphological classes was calculated.

MALDI-FT-ICR IMS measurement of erlotinib and related metabolites on pancreatic sections

FT-ICR measurements were performed using the Solarix 7T (Bruker Daltonics). Mass spectra were acquired in positive mode using 300 laser shots at a frequency of 1 kHz. MSI data were recorded with a 50 µm spatial resolution. The digital resolution of the MALDI FT-ICR was 150,000 at *m/z* 400. Consequently, MALDI-FT-ICR enables simultaneous imaging of the low abundant metabolites of erlotinib, including M13, M14, M16 and M6 (13).

Results

Determination of time point for highest drug concentration

To analyze the distribution and pharmacokinetics of *in vivo* administered erlotinib in the pancreas, 25 mg/kg erlotinib diluted in methylcellulose were administered orally to WT mice (n = 3 mice for each time point plus one vehicle only treated control for each time point to determine baseline levels). The average peak intensity for erlotinib ([M+H+] = 394.18 Da) could be detected in pancreata of mice treated with the drug 0.5h, 1h, 4h, 12h after drug administration. No peak corresponding to the mass of erlotinib could be detected in pancreata of control (vehicle-treated) mice, ensuring specific drug detection. 24h after drug administration the relative levels of erlotinib returned to untreated control levels, showing full metabolic elimination of the drug.

One hour after drug application, average peak intensities were highest (Figure 1A) and this time point was chosen for further analysis in PDAC bearing mice.

Erlotinib levels are higher in healthy pancreas than in PDAC

To determine the distribution and relative peak intensities of erlotinib in normal, preneoplastic and tumor tissue, 8 *Ptf1a*$^{wt/Cre}$;*Kras*$^{wt/LSL\text{-}G12D}$;*p53*$^{fl/fl}$ (named *Kras*^{G12D};*p53*^{KO} hereafter) mice at approximately 6 weeks of age were treated with a single dose of erlotinib. At this age mice display well-differentiated PDAC with abundant stroma (14, 15) next to still healthy acinar tissue. The 2-dimensional tissue distribution image of relative erlotinib peak intensities for each of the analyzed tumor sections depicted differences in drug distribution between healthy pancreatic tissue and PDAC with increased amounts of erlotinib in healthy acinar tissue but only low average peak intensities in tumor areas (example in Figure 1B). Statistical analysis revealed significantly less average erlotinib peak intensities ($p = 0.0078$) in tumorigenic tissue than in acinar tissue within each mouse (Figure 1C), supporting impaired delivery of erlotinib into the tumor tissue. High levels of drug peak intensities at the outer borders of the lymph nodes and nearly no signal in the middle of the nodes indicate that the drug uptake follows the lymph flow in the lymph nodes from subcapsular sinus to medulla (Figure 1B). “On tissue” spotting of erlotinib confirmed the differences in peak intensities were not due to ion suppression (Supplementary Figure S1A and Supplementary Materials and Methods). “On tissue” MS/MS spectrum of erlotinib (*m/z* 394) comparison to reference erlotinib confirmed the specific identification of erlotinib (Supplementary Figure S1B and Supplementary Materials and Methods). Additionally, we performed high mass resolution MALDI FT-ICR analysis on selected sections to visualize the differences in intensities of the parent drug erlotinib and its main metabolite M13/14 between tumor and acinar areas (*m/z* 380.1065, Figure 2A) as well as additional metabolites M16 and M6 (Figure 2B).

Relative erlotinib levels in tumors do not correlate with overall survival or differentiation status

Next, we investigated whether survival or tumor differentiation correlate with erlotinib peak intensities and distribution in PDAC. Therefore, we subjected 12 $Kras^{G12D};p53^{KO}$ mice to weekly MRI exams starting at week 5 of age to determine tumor onset. Upon a defined tumor burden (200-400 mm^3), mice were treated with either only 100 mg/kg erlotinib daily (n = 5 mice) or with 50 mg/kg erlotinib daily plus four single doses of gemcitabine separated each by three days (n = 7). Mice were treated daily and received one additional single dose of erlotinib upon reaching no-go criteria one hour before sacrifice (schematic treatment overview Figure 3A). Parameters obtained included survival time, overall erlotinib peak intensities in two independent randomly chosen pancreatic tumor sections that were at least 5mm apart and tumor grade as determined by a pancreatic pathologist (Table 1). Survival and histological analysis of the tumor sections did not show significant differences between mono- or combination treated tumor-bearing animals as previously reported (5) (Supplementary Figure S2A).

Overall, average erlotinib peak intensities between two sections from different regions of individual mice showed high correlation, indicating representative drug distribution in single sections (Supplementary Figure S2B). However, overall intratumoral erlotinib peak intensities did not correlate with either overall survival or tumor grade (Figure 3C and Supplementary Figure S2C).

Localization of erlotinib treated mice correlates with overall survival

We next examined drug distribution in PDAC of the 12 long-term treated mice in more detail. Tumor areas with more atypical glands showed higher average peak intensities of erlotinib than areas with a higher stroma content. To test this hypothesis we developed a tissue image analysis algorithm that classified morphological features as “glandular”, i.e. having a more differentiated epithelial morphology, or as “desmoplastic”, i.e. with no obvious epithelial proportions and high stroma content, based on the density and relative distance of cell nuclei to each other (Figure 3B). A second algorithm was implemented to quantify the percentage of tissue that showed the presence of the relative erlotinib peak intensity in the 2-dimensional tissue distribution overlay image as exemplified in Figure 3B middle (overlay of histology and average peak intensity) and quantified as a binary function of being present in that morphological area or not (Figure 3B right side). We next determined the percentage of erlotinib-presence in glandular or desmoplastic areas of the tumors and correlated these with the duration of study treatment. Both, the overall percentage of glandular areas in the tumors and the percentage of drug found in these areas significantly correlated with the survival of the treated mice (n = 12, Figure 3C), although the amount of glandular complexes in the tissue and the percentage of them containing drug did not correlate (Supplementary Figure S2D). This indicates that the higher the percentage of atypical glands in PDAC tissue, the higher the amount of intratumoral drug and also the higher the survival in respective individual mice.

Discussion

In this study we evaluated MALDI-based drug imaging for morphological analysis of drug tissue distribution on a cellular level in a complex tumor using a well-established GEMM of aggressive PDAC with high desmoplasia. Underlying evidence for this approach stems from increasing evidence for the tumor microenvironment as a major factor in drug delivery determining outcome as previously described in PDAC with its abundant desmoplasia (3, 8, 9). However, other variables affecting drug metabolism and stabilization of the respective drug have been described (16) and thus, the clinical translation remains challenging.

Because of its practical simplicity and ability to gain reliable information, even from the smallest tissue amounts, which may also originate from endoscopic biopsies from patients for MALDI drug imaging, the application of MALDI IMS to determine the tissue distribution of drugs could have a dramatic impact on both drug discovery and development and, as shown by our study, for therapy response prediction.

In this study we focused on imaging of erlotinib, which is approved for targeted therapy in PDAC albeit with only moderate effectiveness (17). Small molecule inhibitors have been analyzed using this method including lapatinib and nevirapine in a mimetic tissue model with parallel dosed tissue sections to quantify drug amounts and to determine a tissue's effects on analyte extraction and ion suppression (18). Erlotinib has previously been studied using MALDI IMS,(19), albeit not in a long-term treated complex disease model. Its distribution in healthy rat liver, spleen and muscle resembled autoradiographic results. In 2011, differences in distribution of erlotinib in three different lung cancer tumor phenotypes were reported (20) and in 2013 drug distribution of erlotinib and other molecules in the microenvironmental tissue compartments of lung cancer that were either submerged or spotted with the compounds was investigated (21).

In our study, erlotinib was administered orally as used in clinical administration. This way, tissue delivery and distribution of erlotinib are dependent on the metabolism of the drug *in vivo*, therefore allowing us to draw biologically meaningful conclusions about erlotinib distribution. We observed rapid tissue elimination of the parent drug already after one hour in wild type mice. To correlate intratumoral erlotinib tissue distribution patterns with effectiveness of the drug in a preclinical trial setting – which has to our knowledge not been reported before -, we thus decided to administer one more single dose of erlotinib to mice before sacrifice, assuming –although not proven -that distribution of this last erlotinib dose would more reliably reflect drug distribution in the tumors. Even though we cannot follow tissue distribution over time, which would be potentially possible by procuring biopsies over the treatment course, our study describes reliable spatial distribution of erlotinib in a clinically relevant setting.

The method described here enables multimodal analysis of intratumoral drug levels including high spatial resolution and drug metabolism (22, 23). Application of MALDI IMS for imaging of pharmaceutical unlabeled compounds has been of great interest since introduction of the technology (24, 25). The emerging technique of MALDI imaging mass spectrometry has the capability to distinguish between parent drug and metabolites while maintaining spatial distribution in tissues. MALDI Drug imaging is often considered as a targeted approach in MSI, because the method is designed to detect specific drugs of interest within a sample. Autoradiography is also used to examine *in situ* distribution either in whole animals (whole-body autoradiography) or on the cellular level (microautoradiography). As these methods need labeling of the drug in contrast to MALDI IMS, they are not very suitable for long-term treatment studies. Homogenization- and separation-based LC-MS of tissue samples effectively and accurately allow for the identification and quantification of drugs and their metabolites, but result in the loss of spatial information. Absolute quantification is highly desired for pharmacological studies. However, quantification using MSI is still a challenging research area due to the limitations of MSI technology, such as substance-specific extraction and ionization, tissue-specific ion suppression and matrix-specific deposition and properties. We have instead used relative quantification, which sufficiently revealed the potential impact of erlotinib levels in glandular structures on the survival of mice.

MALDI-TOF (Ultraflex) has limited mass resolution and accuracy and only the parent drug can be detected using the Ultraflex. However, information regarding related metabolites are also highly informative and an increasingly recognized influencing factor. To ensure specificity, we performed additional high mass resolution MALDI FT-ICR analysis. Additionally, a previous study by Huber et al (26) has proven the high sensitivity and specificity of the applied method to detect erlotinib in tissue.

In our study we find considerably less erlotinib in PDAC compared to healthy pancreatic tissue. Relative erlotinib peak intensities within the tumors vary highly, suggesting additional factors that influence drug distribution and intensity. Although overall tumor grading did not differ between the mice, we found that mice harboring PDAC with increased numbers of atypical glands and higher intra-glandular erlotinib peak intensities showed an increased survival. Whether this is due to less aggressive tumors, tumors with less stroma and potentially lower interstitial pressure, differences in drug response or indeed the measured increased drug presence remains to be determined.

There are further limitations to be considered. Survival in this aggressive GEMM is short and effects on survival are difficult to address. Second, we did not acquire suitable biopsy tissue early after therapy start, as one would envision in a clinical trial and needed for evaluation of intratumoral erlotinib as a predictive biomarker. This study shows that drug distribution as well as metabolism in tumors is highly complex and needs to be investigated in great detail on a cellular level, for which we find

MALDI IMS a highly suitable method. Investigating the influence of the desmoplastic reaction in low versus high desmoplastic tumors or the effect of stroma-modulating drugs on drug distribution and therapy-response are clinically highly anticipated study aims that could potentially be approached using this method.

In conclusion, MALDI drug imaging provides an excellent approach to study drug delivery, spatial distribution and drug metabolism in great detail in complex preclinical models and foreseeable in clinical trials.

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Table 1: Overview of mice in the preclinical therapy trial.

mouse number	group	Responder according MRI	age in days	relative intensity erlotinib region1	relative intensity erlotinib region2	tumor stage	anaplastic or sarcomatoid	ADM	Necrosis
60884	M		49	2.167	1.8032	G2			
60894	M	x	65	3.7494	3.2366	G2	s	x	
60895	M		58	5.8275	5.4462	G2			x
60908	M		63	6.613	12.5681	G2	a	x	
60904	M		72	4.7134	3.9381	G2	a + s	x	
60911	C		72	10.3315	4.2725	G2 + G3			
60950	C		64	4.3307	5.1656	G1 + G2 + G3			x
60965	C		71	3.3149	5.2965	G2		x	x
61018	C	x	74	2.3313	3.0282	G2			
61029	C	x	62	2.9096	3.1248	G2		x	
61025	C		40	3.7528	2.5548	G2 + G3		x	
61021	C	x	68	6.2353	4.2742	G2			

M monotherapy erlotinib only, C combination therapy erlotinib and gemcitabine, x happened event, G1 G2 G3 tumor staging according to pathologist, ADM acino-ductal metaplasia, a anaplastic, s sarcomatoid

Table 1. Overview of mice in the preclinical therapy trial.

Depicted are assigned mouse number, treatment group, MRI response, age in days, relative overall erlotinib levels in two independent regions and tumor grading according to expert pancreatic pathologists (I.E., K.S.). $Kras^{G12D};p53^{KO}$ mice were treated as indicated in Figure 3A.

Figure legends

Figure 1

(A) Time course of relative levels of erlotinib (*m/z* 394, green line) in murine WT pancreata at indicated time points after oral application. Untreated mice served as baseline, while mice treated with the vehicle methylcellulose only were measured at each time point to ensure specificity of the measured peaks. 600 spectra per mouse were extracted and imported into ClinProTools to determine relative mass intensities for erlotinib; n = 3 mice per time point. (B) Representative average mass spectrum, histology and corresponding re-visualizations of erlotinib (*m/z* 394) in a pancreatic section of a 6 week old $Kras^{G12D};p53^{KO}$ mouse containing an area with invasive PDAC, normal acinar tissue and a lymph node. Scale bar represents 2mm. (C) Erlotinib (*m/z* 394) showed significantly (p = 0.0078) higher intensities in normal appearing acinar areas than in tumor tissue. Regions of interest (ROIs) were defined for healthy acinar tissue and PDAC and 500 randomly chosen spectra per region extracted and processed with ClinProTools to obtain visual and statistical data about distribution of erlotinib.

Figure 2

(A) Relative quantification of erlotinib and the demethylative metabolites M13/M14. MALDI FT-ICR MSI detects erlotinib and related metabolites M13/M14 in acinar tissue and tumor in a 6 week old $Kras^{G12D};p53^{KO}$ mouse. With relative quantification, both erlotinib and the metabolites M13/M14 show higher intensity in acinar regions. Moreover, M13/M14 represent lower abundancy compared with the parent drug erlotinib. M14 is the pharmacologically active metabolite of erlotinib. Scale bar represents 500 µM. (B) MALDI FT-ICR imaging data and representative average MS spectrum of erlotinib and related metabolites, M13, M14, M16 and M6. H&E staining of a pancreatic section of a 6 week old *Kras*^{G12D};*p53*^{KO} mouse shows invasive PDAC, normal acinar tissue and a lymph node. Erlotinib is present at moderate levels in the tumor area, while we found higher levels of erlotinib in acinar region and the subcapsular sinus of lymph node. MALDI FT-ICR MSI enables simultaneous detection of low abundant metabolites peaks, M13, M14, M16 and M6, which represent similar distributions as the parent drug. Please note that M13 and M14 are isomers with identical molecular mass, which cannot be distinguished by current MALDI MS imaging analysis. Scale bar represents 500 µM.

Figure 3

(A) Schematic of treatment and measurements in long-term treated *Kras*^{G12D};*p53*^{KO} mice. Below the representative MRI scan shows the pancreas at start of the measurement and during progression at indicated time points. White dotted line indicates pancreas/tumor area. (B) Representative image of pancreatic histology (left), erlotinib re-visualization measured with MALDI-Imaging (green, middle picture) and tissue analysis cluster algorithm (right picture, light green indicating areas with detectable erlotinib mass, dark red indicating areas classified as “glandular” and dark green indicating areas with an overlap between those). Scale bars represent 200 µM. (C) Correlation analysis of survival with overall drug levels in tissue (left, p = ns, r_s = 0.08 with percentage of atypical glands in tumor areas (middle, p = 0.021, r_s = 0.59) and percentage of drug (right, p = 0.019, r_s = 0.60). Each data point represents one analyzed section per mouse (n = 12 mice total).

Figure 1

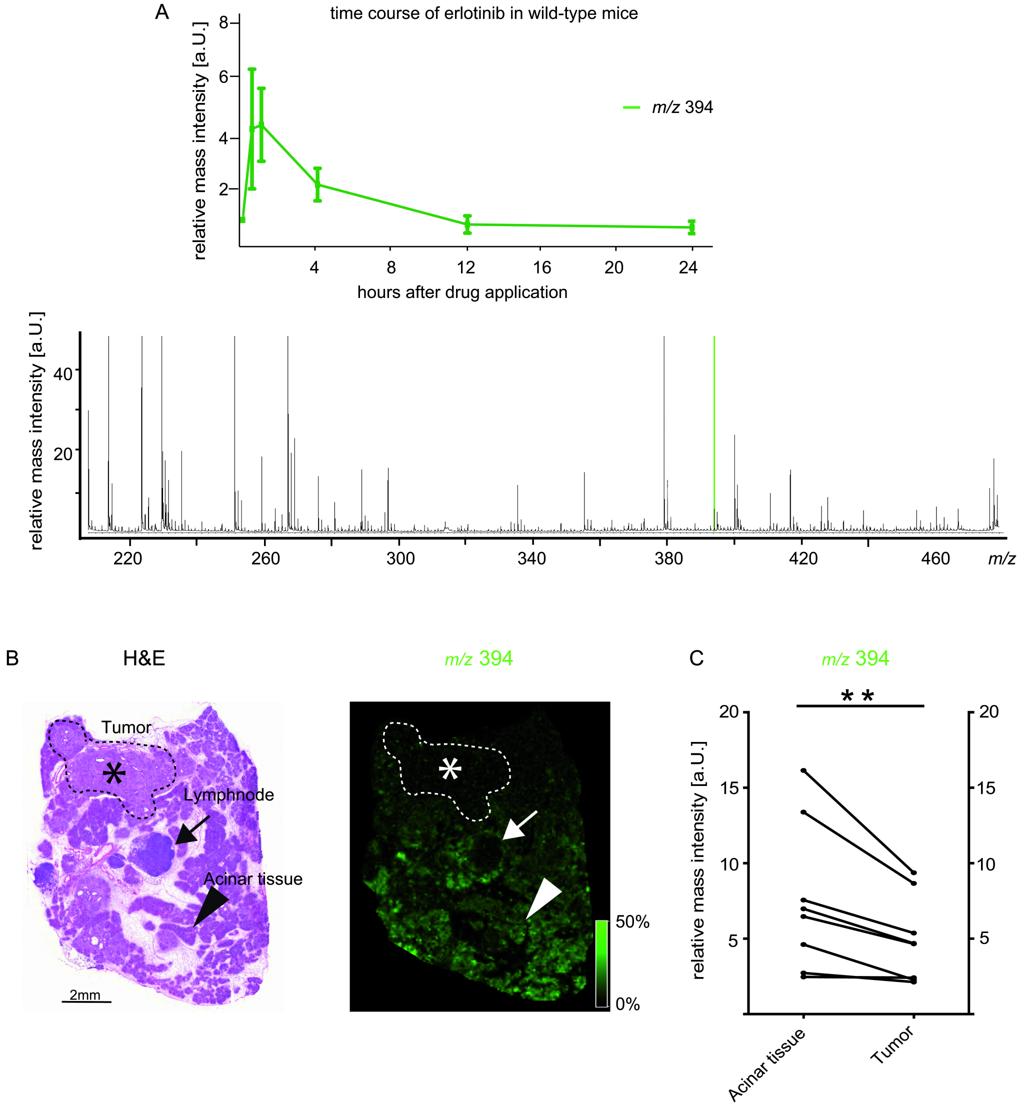

A
time course of erlotinib in wild-type mice
relative mass intensity [a.U.]
8
6
4
2
m/z 394
4
8
12
16
20
24
hours after drug application
relative mass intensity [a.U.]
40
20
220
260
300
340
380
420
460
m/z
B
H&E
Tumor
Lymphnode
Acinar tissue
2mm
m/z 394
50%
0%
C
m/z 394
**
relative mass intensity [a.U.]
20
15
10
5
Acinar tissue
Tumor

Figure 2

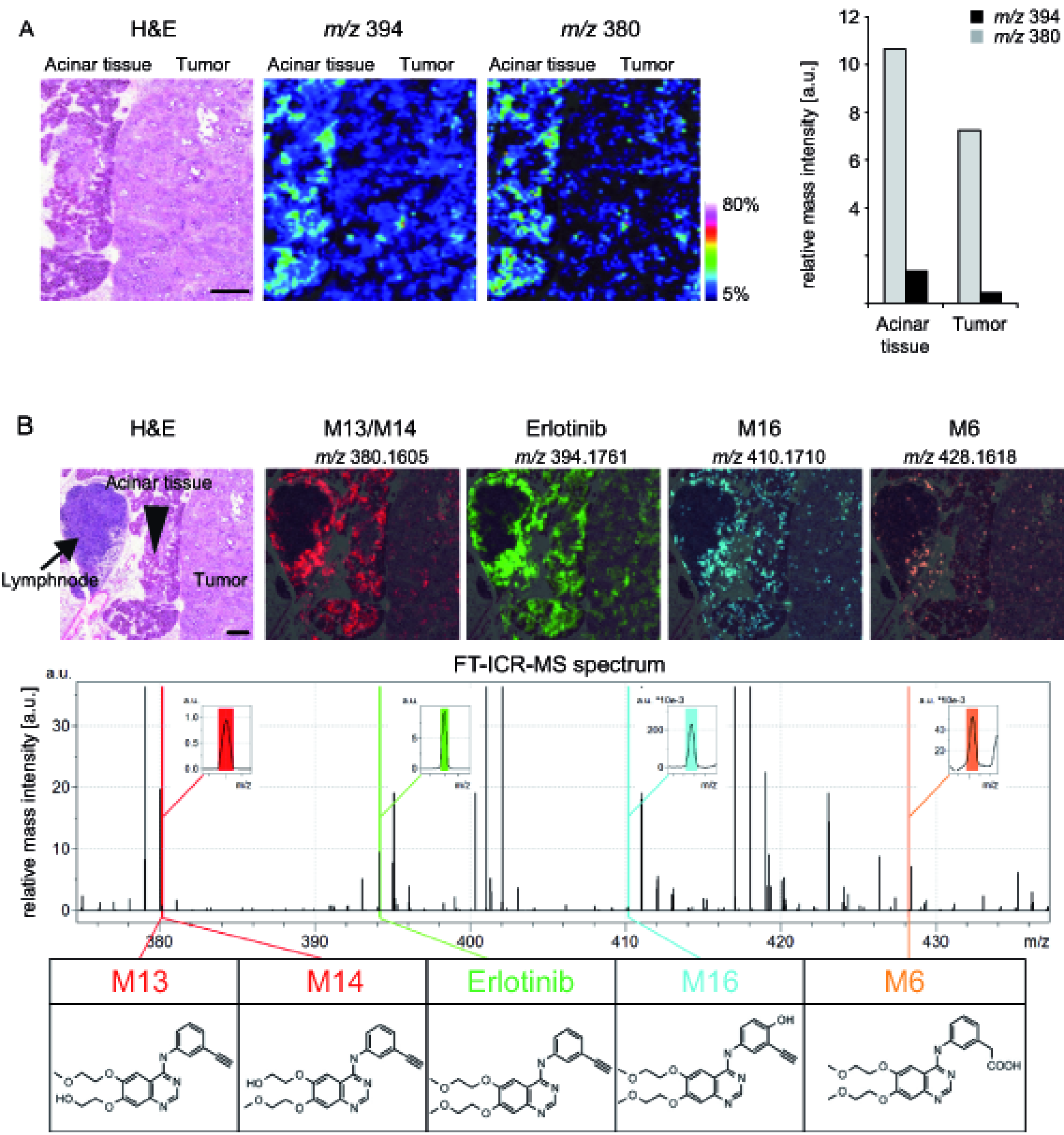
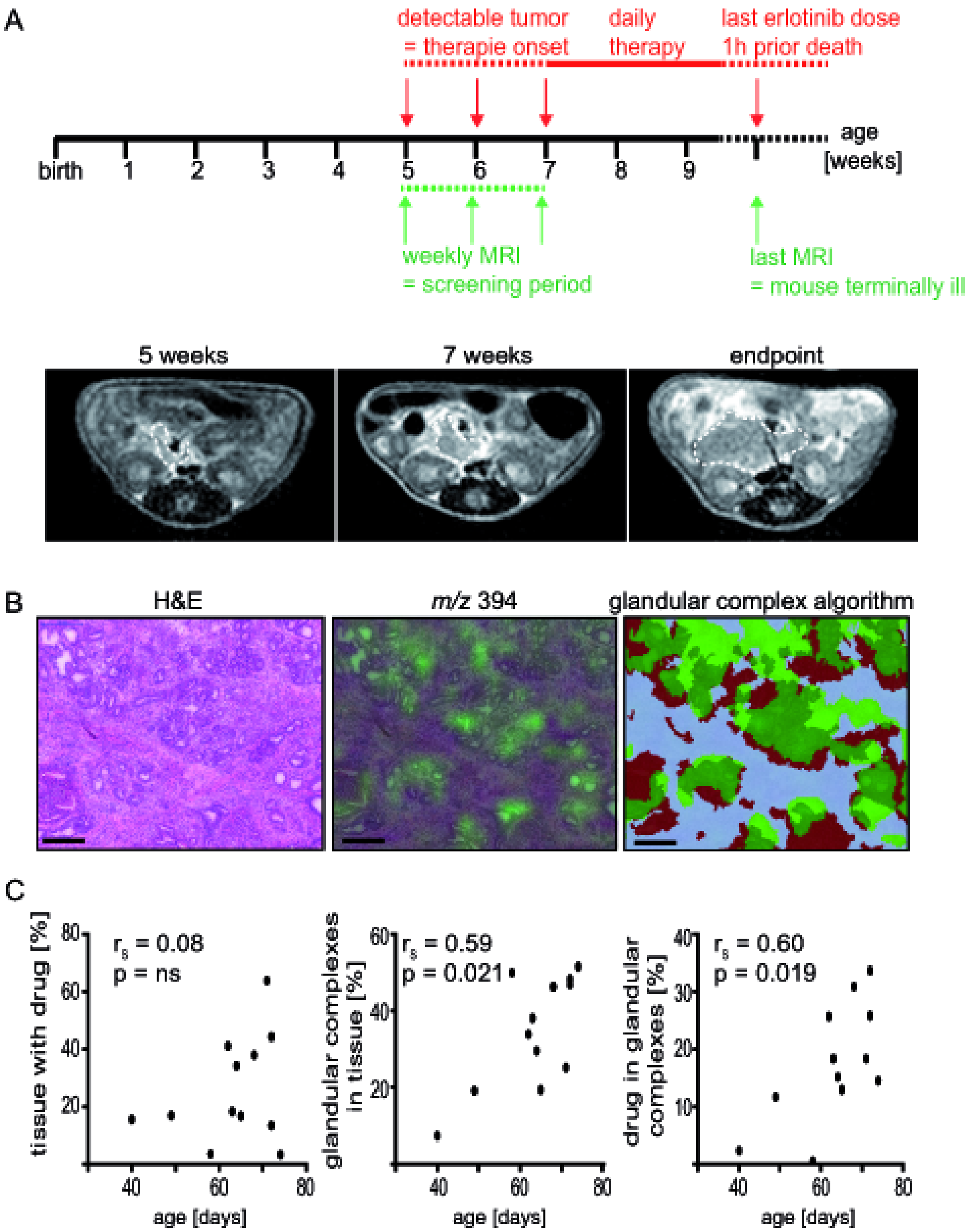

A
H&E
m/z 394
m/z 380
Acinar tissue
Tumor
Acinar tissue
Tumor
Acinar tissue
Tumor
80%
5%
relative mass intensity [a.u.]
12
10
8
6
4
m/z 394
m/z 380
Acinar tissue
Tumor
B
H&E
Acinar tissue
Lymphnode
Tumor
M13/M14
m/z 380.1605
Erlotinib
m/z 394.1761
M16
m/z 410.1710
M6
m/z 428.1618
FT-ICR-MS spectrum
a.u.
relative mass intensity [a.u.]
30
20
10
0
380
390
400
410
420
430
m/z
M13
M14
Erlotinib
M16
M6
OH
COOH
HO
N

Figure 3


A
detectable tumor
= therapie onset
daily
therapy
last erlotinib dose
1h prior death
age
[weeks]
birth
1
2
3
4
5
6
7
8
9
weekly MRI
= screening period
last MRI
= mouse terminally ill
5 weeks
7 weeks
endpoint
B
H&E
m/z 394
glandular complex algorithm
C
tissue with drug [%]
r_s = 0.08
p = ns
age [days]
glandular complexes in tissue [%]
r_s = 0.59
p = 0.021
age [days]
drug in glandular complexes [%]
r_s = 0.60
p = 0.019
age [days]
80
60
40
20
40
60
80
40
30
20
10

Molecular Cancer Therapeutics

Modeling therapy response and spatial tissue distribution of erlotinib in pancreatic cancer

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