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Comparative analysis of cancer cell responses to targeted radionuclide therapy (TRT) and external beam radiotherapy (EBRT)

Michal Grzmil^{1*}, Paul Boersema², Ashish Sharma³, Alain Blanc¹, Stefan Imobersteg¹, Martin Pruschy³, Paola Picotti², Roger Schibli^{1,4} and Martin Behe¹

Abstract

The vast majority of our knowledge regarding cancer radiobiology and the activation of radioresistance mechanisms emerged from studies using external beam radiation therapy (EBRT). Yet, less is known about the cancer response to internal targeted radionuclide therapy (TRT). Our comparative phosphoproteomics analyzed cellular responses to TRT with lutetium-177-labeled minigastrin analogue [¹⁷⁷Lu]Lu-PP-F11N (β-emitter) and EBRT (γ-rays) in CCKBR-positive cancer cells. Activation of DNA damage response by p53 was induced by both types of radiotherapy, whereas TRT robustly increased activation of signaling pathways including epidermal growth factor receptor (EGFR), mitogen-activated protein kinases (MAPKs) or integrin receptor. Inhibition of EGFR or integrin signaling sensitized cancer cells to radiolabeled minigastrin. In vivo, EGFR inhibitor erlotinib increased therapeutic response to [¹⁷⁷Lu]Lu-PP-F11N and median survival of A431/CCKBR-tumor bearing nude mice. In summary, our study explores a complex scenario of cancer responses to different types of irradiation and pinpoints the radiosensitizing strategy, based on the targeting survival pathways, which are activated by TRT.

Keywords: CCKBR, Minigastrin, Phosphoproteomics, Radioresistance, Erlotinib

To the editor,

Systemic TRT employs radiopharmaceuticals that specifically target primary tumors and metastatic lesions [1]. Yet, the cancer radioresistance limits the efficacy in clinic. In 2018, FDA-approved lutathera for the first-in-class peptide receptor radionuclide therapy (PRRT) of somatostatin receptor-positive gastroenteropancreatic and neuroendocrine tumors and, recently, pluvicto has been approved for targeted radioligand therapy of PSMA-positive, metastatic castration-resistant prostate cancers [2, 3]. These advancements bring many opportunities and challenges. To explore TRT radiobiology

and identify radiosensitizing strategies, we analyzed cellular responses to radiolabeled minigastrin [¹⁷⁷Lu]Lu-PP-F11N that targets overexpressed cholecystokinin B receptor (CCKBR) in human cancers, including medullary thyroid carcinoma (MTC), gliomas, small cell lung and ovarian cancer [4], in comparison to EBRT (Fig. 1a). In both treatments, selected radiation doses had similar effect on cell proliferation (Additional file 1: Fig. S1). Phosphoproteomics quantified abundance of 6173 and 7293 phosphopeptides, whereas corresponding proteomics quantified 2567 and 2582 protein groups in response to TRT and EBRT, respectively (Fig. 1b). Abundance of 188 and 329 unique phosphopeptides (Fig. 1c, Additional file 2: Table S1–S4) and 25 and 15 proteins (Fig. 1c, Additional file 2: Tables S5 and S6) was significantly changed in response to TRT and EBRT, respectively (Fig. 1d). Of these, the phosphorylation of 34 proteins was common

*Correspondence: michal.grzmil@psi.ch

¹ Center for Radiopharmaceutical Sciences, Paul Scherrer Institute, Villigen, Switzerland

Full list of author information is available at the end of the article



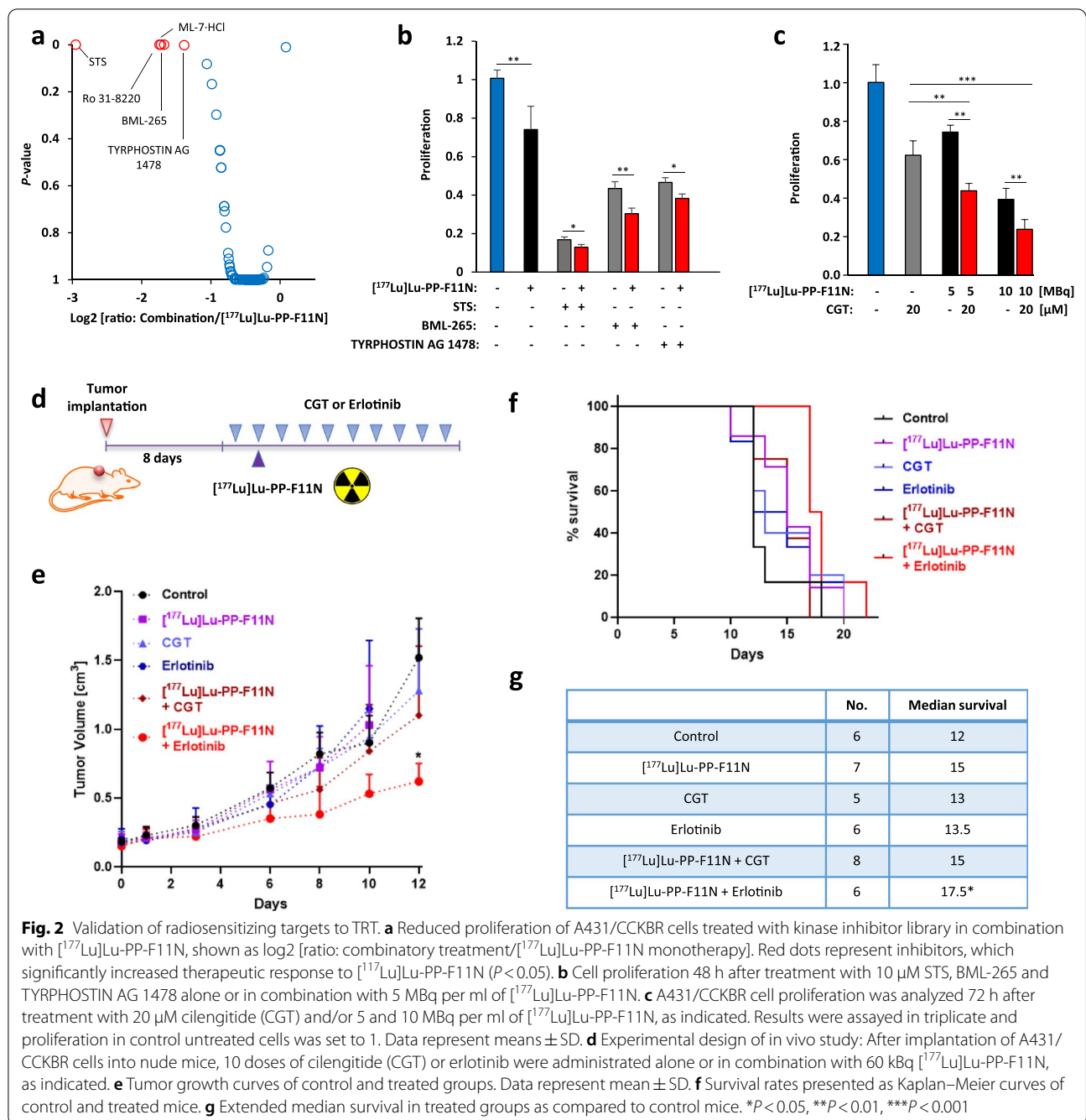
(See figure on next page.)

Fig. 1 Cellular responses to TRT and EBRT. **a** A431/CCKBR cells were treated with [¹⁷⁷Lu]Lu-PP-F11N or exposed to EBRT and the generated tryptic peptides and phosphopeptide enriched samples were subjected to mass spectrometry analysis. **b** Charts display phosphopeptide (upper panels) and protein (lower panels) abundance changes shown as log₂ transformed fold change (FC). Red dots represent phosphopeptides or proteins with significantly altered abundance. *FDR* < 0.05. **c** Hierarchical clustering of identified changes in phosphopeptide and protein abundance. **d** Number of phosphopeptides and protein abundance changes. Arrows indicate up-regulated (purple) or down-regulated (blue) phosphorylation or protein levels. **e** MS2-based quantification of abundance changes was shown as Log₂ transformed radiation/control ratios for CYR61, GAPDH, ERK2 and P53 protein levels and phosphorylation of ERK, P53 and JUN after exposure to [¹⁷⁷Lu]Lu-PP-F11N and EBRT in A431/CCKBR cells. **f, g** Expression and phosphorylation levels of the same proteins were validated by quantitative WB analysis on total protein lysates isolated from untreated (control) and [¹⁷⁷Lu]Lu-PP-F11N- or EBRT-treated cells. Each treatment was performed in triplicate (Exp 1–3). Quantification of signal intensities (in **f**) is shown as Log₂ transformed radiation/control ratios as described above. **P* < 0.05, ***P* < 0.01, ****P* < 0.001. **h** WB analysis for CYR61 and P53 phosphorylation in total protein lysates isolated from A431/CCKBR cells untreated (control) and treated with 1, 2, 4, 6 and 8 Gy at indicated time points. Blot was re-probed with antibody against GAPDH and total P53

to both types of radiation. Bioinformatics analysis identified interaction networks (Additional file 1: Fig. S2) and over-represented terms for gene ontology and signaling pathways among proteins with altered level or phosphorylation in response to TRT and EBRT. Both radiotherapies influenced responses to DNA damage, signal transduction by p53, cell cycle regulation, RNA processing and metabolism as well as cellular transport, morphology and adhesion (Additional file 2: Table S7). TRT influenced DNA repair via translesion synthesis (TLS), whereas EBRT induced both double-strand break repair via non-homologous end joining (NHEJ) and homologous recombination (HR) as well as base-excision repair (BER) and interstrand cross-link repair (ICLR). Signaling of TGFβR, EGFR, HGFR, mTOR, MAPK, RAS homologous (Rho), integrin and estrogen receptors was influenced by TRT, whereas EBRT induced RAS signaling as well as ATM, PYK and MAP kinases. Consistently with (phospho)proteomics data (Fig. 1e) WB analysis (Fig. 1f, g) confirmed elevated level of integrin receptor ligand, cysteine-rich angiogenic inducer 61 (CYR61), phosphorylation of EGFR and ERK1/2 and transcription factor c-JUN in response to TRT, whereas EBRT did not increase CYR61 protein level, ERK1/2 phosphorylation and decreased c-JUN phosphorylation. Next, to investigate whether the differences between TRT and EBRT result from different energy dose or time after irradiation, CYR61 expression was analyzed in the cells treated with 1–8 Gy and at different time points (Fig. 1h).

As expected, P53 phosphorylation was increased, whereas CYR61 protein level was marginally affected by EBRT indicating that elevated CYR61 level is TRT-specific and that cancer responses differ among various types of radiations. These differences could be explained by the different ratios of various DNA strand breaks or/and types of DNA lesions or by diverse activation of DNA damage-unrelated signaling pathways. Previously, x-ray spectroscopy determined structures of DNA lesions caused by UVA light or protons and

demonstrated that the cyclobutane pyrimidine dimers were almost exclusively detected in UVA-exposed samples [5]. Consequently, different types of DNA lesions can lead to the activation of different DNA repair and survival mechanisms [6] and thus, may require design of radiation-specific radiosensitizing strategies. To investigate the influence of signaling pathway activation on the survival of [¹⁷⁷Lu]Lu-PP-F11N-treated cells, we employed small-molecule kinase inhibitor library. The screen identified Staurosporin (STS) as well as two EGFR inhibitors BML-265 and Tyrphostin AG 1478, which significantly enhanced therapeutic response to TRT as compared to the monotherapy and reached 12 (*P* = 0.027), 30 (*P* = 0.005) and 38% (*P* = 0.012) proliferation of control, respectively (Fig. 2a, b). STS is highly cytotoxic, whereas the combinations of [¹⁷⁷Lu]Lu-PP-F11N with two other identified inhibitors Ro 31-8220 or ML-7-HCL were not superior to the monotherapy (Additional file 1: Fig. S3), and thus, their further development was not considered. Next, we analyzed the potential of cilengitide (CGT), a cyclized Arg-Gly-Glu (RGD)-containing pentapeptide, which selectively blocks activation of the αvβ3 and αvβ5 integrin receptors [7]. Combination of 5 or 10 MBq of [¹⁷⁷Lu]Lu-PP-F11N with CGT significantly increased therapeutic response as compared to the monotherapy and reduced cell proliferation to 43 (*P* < 0.001) or 23% (*P* = 0.006) of control, respectively (Fig. 2c, Additional file 1: Fig. S4). In vivo, the average tumor volume, on the last day when all mice were alive, reached 1.52 cm³ in the control, whereas in mice treated with [¹⁷⁷Lu]Lu-PP-F11N, CGT and EGFR inhibitor erlotinib alone was 1.03, 1.28 and 1.15 cm³, respectively (Fig. 2d, e). The tumor volume in [¹⁷⁷Lu]Lu-PP-F11N-treated mice in combination with CGT was 1.15 cm³, whereas combination with erlotinib led to reduced tumor volume (*P* ≤ 0.002) to 0.65 cm³ as compared to the control. The increased survival was significant (*P* ≤ 0.026) in erlotinib and [¹⁷⁷Lu]Lu-PP-F11N-treated mice (Fig. 2f, g). During therapy, there was no significant decrease in body weight (Additional



mutations of EGFR drive carcinogenesis, and its hyper-activation has been associated with poor prognosis and outcomes [10]. Erlotinib is approved for non-small-cell lung carcinoma (NSCLC) treatment [11] suggesting that its combination with TRT with radiolabeled minigastatin is clinically feasible. Nevertheless, radiosensitizing potential of erlotinib for other radioligands requires further investigation. In conclusion, our signaling network analysis reveals TRT-activated cellular responses, in

comparison to EBRT, and identifies molecular targets for cancer radiosensitization (Additional file 3).

Abbreviations

ATM: Ataxia–telangiectasia mutated; CGT: Cilengitide; CYR61: Cysteine-rich angiogenic inducer 61; EBRT: External beam radiation therapy; EGFR: Epidermal growth factor receptor; ERK: Extracellular signal-regulated kinase; GAPDH: Glyceraldehyde 3-phosphate dehydrogenase; HGFR: Hepatocyte growth factor receptor; LET: Linear energy transfer; MAPK: Mitogen-activated protein kinase; mTOR: Mammalian target of rapamycin; PRRT: Peptide receptor

radionuclide therapy; PSMA: Prostate-specific membrane antigen; PYK: Pyruvate kinase; TGF β R: Transforming growth factor beta receptor; TRT: Targeted radionuclide therapy.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13045-022-01343-y>.

Additional file 1. Supplementary Figure S1–S5.

Additional file 2. Supplementary Table S1–S7.

Additional file 3. Supplementary Methods.

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Authors' contributions

MG, PB, PP, MP, MB and RS design the research methods and provided the academic environment of the research work. MG, PB, AS, AB and SI conducted the experiments and acquired and analyzed the data. MG prepared the manuscript. MG, MB, RS, PP and MP reviewed the manuscript. MG, MB and RS conceived and funded the study. All authors read and approved the final manuscript.

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Availability of data and materials

Generated phosphoproteomics and proteomics peptide and protein data analyzed during this study are included in this published article and its supplementary information files (Additional file 2: Tables S1–S7). All other data used during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate

All animal experiments were performed in accordance with Swiss Animal Protection Laws.

Consent for publication

Not applicable.

Competing interests

MB and RS are inventors of the patent WO2015/067473: Minigastrin analogue, in particular for use in CCK2 receptor positive tumor, diagnosis and/or treatment. No other potential conflict of interest relevant to this article was reported.

Author details

¹Center for Radiopharmaceutical Sciences, Paul Scherrer Institute, Villigen, Switzerland. ²Institute of Molecular Systems Biology, Department of Biology, ETH Zurich, Zurich, Switzerland. ³Department of Radiation Oncology, University Hospital Zurich, Zurich, Switzerland. ⁴Department of Chemistry and Applied Biosciences, ETH Zurich, Zurich, Switzerland.

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