**ABSTRACT SUBMISSION FORM**

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<tr>
<th>Name (First, last)</th>
<th>Felix Raschke</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mailing address (including province/state, country, postal/zip code)</td>
<td>Fetscherstr. 74, PF 41, 01307 Dresden, Germany</td>
</tr>
<tr>
<td>Institution/organization</td>
<td>National Center for Tumor Diseases (NCT), Partner Site Dresden, Germany:</td>
</tr>
<tr>
<td>Position</td>
<td>PostDoc</td>
</tr>
<tr>
<td>Telephone (including country prefix)</td>
<td>+493514586538</td>
</tr>
<tr>
<td>Email</td>
<td><a href="mailto:felix.raschke@oncoray.de">felix.raschke@oncoray.de</a></td>
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**PRESENTATION TITLE**

Comparison of metabolic abnormality extension from MR spectroscopy with clinical target volume in glioma patients.

**AUTHOR(S)**

F. Raschke3,2,6; A. Werner4; H. Wahl4; T. Wesemann4; S. Appold6; M. Krause1,2,3,5,6; J. Linn4; E.G.C. Troost1,2,3,5,6

1 Institute of Radiooncology - OncoRay, Helmholtz-Zentrum Dresden-Rossendorf, Rossendorf, Germany;
2 OncoRay - National Center for Radiation Research in Oncology, Faculty of Medicine and University Hospital Carl Gustav Carus, Technische Universität Dresden, Helmholtz-Zentrum Dresden-Rossendorf;
3 National Center for Tumor Diseases (NCT), Partner Site Dresden, Germany; German Cancer Research Center (DKFZ), Heidelberg, Germany; Faculty of Medicine and University Hospital Carl Gustav Carus, Technische Universität Dresden, Dresden, Germany, and; Helmholtz Association / Helmholtz-Zentrum Dresden - Rossendorf (HZDR), Dresden, Germany;
4 Institute of Neuroradiology, University Hospital Carl Gustav Carus and Medical Faculty of Technische Universität, Dresden, Germany;
5 Department of Radiotherapy and Radiooncology, University Hospital Carl Gustav Carus and Medical Faculty of Technische Universität, Dresden, Germany;
6 German Cancer Consortium (DKTK), Partner Site Dresden, and German Cancer Research Center (DKFZ), Heidelberg, Germany;

**ABSTRACT**

**Purpose**: Gliomas are often characterised by heterogeneous and infiltrative growth, and anatomical MRI cannot visualise the actual tumour extent. In radiation treatment planning, this uncertainty leads to a significant extension of the gross tumour volume (GTV)/tumour bed volume (TBV) to the clinical target volume (CTV), particularly in high-grade gliomas. MR spectroscopy is able to identify infiltrative tumour growth, albeit at limited spatial coverage and resolution [1]. The aim of this study was to compare the abnormality extension defined by MR spectroscopic imaging (MRSI) with the actual CTV defined according to conventional MRI in glioma patients.

**Materials & Methods**: MRSI datasets (2D PRESS TR/TE=1300/97ms, single slice 15mm, voxel size 10x10mm) from 31 glioma patients post-resection but pre-radiotherapy from an ongoing longitudinal MR study were available. However, only in 17 patients (2 grade II, 9 grade III, 6 grade IV) the MRSI location and quality was deemed good enough for further spatial analysis. Each MRSI dataset was analyzed with LCModel and subsequently “radial-Choline-to-NAA indexing” (rCNI) was performed using a z-score threshold of two [2]. Resulting rCNI maps were interpolated inplane by a factor of 5 and clinical CTV masks were resampled to match the rCNI resolution and slice thickness. Tissue was defined abnormal for rCNI≥2 and used to create binary abnormality masks. In three cases, areas of...
clear misclassification in gray matter and the cerebellum were manually removed. CSF was manually masked out from both the CTV and rCNI masks. The CTV was trimmed to match the size of the usable MRSI coverage.

**Results:** Seven out of 17 patients showed an extension of the rCNI margins outside the CTV. Most of these extensions appeared to follow white matter tracts reaching towards or across the genu/splenium towards the contralateral hemisphere (Figure 1). In the remaining cases, the CTV was significantly larger than the rCNI abnormality (Figure 2). 50% ± 21% (mean ± std) of the masked CTV included areas with apparent normal rCNI values, albeit only a small proportion of the actual CTV, also limited to a 15mm slice, was investigated in this study.

A limitation of this study is the use of a single 2D MRSI slice to calculate the rCNI maps. This may lead to a low number of normal appearing MRSI voxels, which are needed to determine a reliable Choline-to-NAA-ratio threshold to identify tumour infiltration. However, this would only potentially bias our analysis towards a lower sensitivity but stable specificity. Consequently, the observed rCNI extension beyond the CTV is plausible or even an underestimation of the metabolically abnormal volume. Further work is thus required to validate our results with patterns of tumour progression and recurrence.

**Conclusions:** We identified extension of metabolically abnormal tissue beyond the CTV in seven out of 17 glioma patients. Longitudinal follow-up is now needed to correlate areas of recurrence to these areas and the actually received radiation dose.

**References:**

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**Figure 1:** Example of abnormal rCNI extension along the genu outside the CTV. Individual MRSI voxels are magnified and rCNI extension (red) is shown relative to FLAIR imaging. CTV – green; abnormal rCNI – red; available MRSI – yellow.

**Figure 2:** Example with rCNI abnormality extension closely matching the FLAIR hyperintensity and visibly larger CTV.

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