Data in Brief 31 (2020) 105712

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Dataset of voxelwise correlated signal values of ADC, rCBV and FAP-specific PET of 13 Glioblastoma patients

Manuel Röhrich[a,b,*], Lisa Loi[c], Ralf Floca[d,e], Uwe Haberkorn[a,b,f], Daniel Paech[c]

[a] Clinical Cooperation Unit Nuclear Medicine, German Cancer Research Center (DKFZ), Heidelberg, Germany
[b] Department of Nuclear Medicine, University Hospital Heidelberg, Germany
[c] Division of Radiology, German Cancer Research Center (DKFZ), Heidelberg, Germany
[d] Division of Medical Image Computing, German Cancer Research Center (DKFZ), Heidelberg, Germany
[e] Department of Radiation Oncology, University Hospital Heidelberg, Germany
[f] Translational Lung Research Center Heidelberg (TLRC), German Center for Lung Research (DZL), Heidelberg, Germany

ARTICLE INFO

Article history:
Received 20 April 2020
Revised 7 May 2020
Accepted 8 May 2020
Available online 15 May 2020

Keywords:
Glioblastoma
Fibroblast Activation Protein
FAP
PET
ADC
CBV

ABSTRACT

This dataset is based on multimodal MRI and FAP-specific PET/CT Imaging applied to 13 patients with histologically proven glioblastomas. Imaging Data was processed using Medical Imaging Interaction Toolkit (MITK) software. MRI images (contrast enhanced T1w, T2w/FLAIR, ADC, rCBV) were co-registrated with FAP-specific PET images. T2w/FLAIR hyperintensities and contrast enhancing lesions were segmented manually. Necrotic areas were segmented manually and subtracted from T2w/FLAIR hyperintensities and contrast enhancing lesions. Voxelwise ADC/rCBV and PET signal intensities in projection on T2w/FLAIR hyperintensities and contrast enhancing lesions were extracted using the pixel dumper function of the MITK software and stored as excel-files. The data presented in this article has been analysed and described in the article FAP-specific "PET signaling shows a

* Corresponding author.
E-mail address: Manuel.roehrich@med.uni-heidelberg.de (M. Röhrich).

https://doi.org/10.1016/j.dib.2020.105712

moderately positive correlation with relative CBV and no correlation with ADC in 13 IDH wildtype Glioblastomas" published in the European Journal of Radiology.

Specifications table

Subject	Radiology and Imaging
Specific subject area	We provide voxelwise signal intensities of FAP-specific PET-imaging and ADC/rCBV in projection on the T2w/FLAIR hyperintensities and contrast enhancing lesions of 13 glioblastomas.
Type of data	Table
How data were acquired	MRI and PET data were acquired during clinical routine. Data analysis was performed using Medical Imaging Interaction Toolkit (MITK) Workbench.
Data format	Raw
Parameters for data collection	Only imaging data of patients with histologically proven glioblastomas and sufficient MRI and PET data were included into the dataset.
Description of data collection	Imaging data was processed using Medical Imaging Interaction Toolkit (MITK) software. MRI image series (contrast enhanced T1w, T2w/FLAIR, ADC, rCBV) were co-registrated with FAP-specific PET images. T2w/FLAIR hyperintensities and contrast enhancing lesions were segmented manually. Necrotic areas were segmented manually and subtracted from T2w/FLAIR hyperintensities and contrast enhancing lesions. Voxelwise ADC/rCBV and PET signal intensities in projection on T2w/FLAIR hyperintensities and contrast enhancing lesions were extracted using the pixel dumper function of the MITK software.
Data source location	Institution: University Hospital Heidelberg City/Town/Region: Heidelberg Country: Germany
Data accessibility	With the article
Related research article	Manuel Röhrich et al.: FAP-specific PET signaling shows a moderately positive correlation with relative CBV and no correlation with ADC in 13 IDH wildtype Glioblastomas

Value of the data

- The data provided is useful for future correlation analyses of FAP-specific PET/CT imaging and MRI (ADC, rCBV) data.
- The data is of interest for research projects related to hybrid (MRI/PET) imaging that include publicly available data.
- The dataset could be included into similar hybrid imaging datasets with a higher number of individuals examined and used for correlation analyses of MRI parameters and FAP-specific PET signalling.

1. Data Description

The dataset consists of 13 folders each containing 2 excel-files. One excel file consists of voxelwise correlated signal values of ADC, rCBV and FAP-specific PET-signal in projection on the T2w/FLAIR hyperintensities (after subtraction of necrotic voxels). The other excel file consists of voxelwise correlated signal values of ADC, rCBV and FAP-specific PET-signal in projection on the contrast enhancing lesion (after subtraction of necrotic voxels).

2. Experimental Design, Materials, and Methods

2.1. Clinical PET/CT Imaging

Diagnostic imaging was performed under the conditions of the updated declaration of Helsinki, § 37 (unproven interventions in clinical practice) and in accordance to the German Pharmaceuticals Law §13 (2b) for medical reasons using 68Ga-FAPI-02 (2 Patients) and -04 (11 Patients), which was applied intravenously (200+/-50 MBq), 10 min, 1 and 3 hours post tracer administration in 2 patients examined with FAPI-2 and 30 minutes after tracer administration in the other 11 patients examined with FAPI-4. For the two patients that have undergone PET imaging at three different time points, images after 1 hour were chosen for further analysis. The PET/CT scans were performed with a Biograph mCT Flow^{TM} PET/CT-Scanner (Siemens Medical Solutions, Berlin and Munich, Germany) using the following parameters: slice thickness of 5 mm, collimation of 5 mm, increment of 3-4 mm, soft-tissue reconstruction kernel, care dose. Immediately after CT scanning, a whole-body PET was acquired in 3D (matrix 200x200) in FlowMotion^{TM} with 0.7 cm/min. The emission data were corrected for random, scatter and decay. Reconstruction was conducted with an OSEM algorithm with 2 iterations/21 subsets and Gauss-filtered to a transaxial resolution of 5 mm at full-width half-maximum. Attenuation correction was performed using the low-dose non-enhanced CT data. The quantitative assessment of standardized uptake values (SUV) was done using a ROI technique. SUV values were corrected for healthy appearing contralateral brain parenchyma as background (SUV/BG). The imaging protocol was approved by the Institutional Review Board (Study number S-016/2018) and conducted according to the guidelines of the Institutional Review Board and to good clinical practice.

2.2. MRI Acquisition

The acquisition of MRI exams was performed at 3T, employing the following protocol parameters: T1-weighted GdCE MRI (GdCE-T1) (echo time[TE] = 4.04 ms; repetition time [TR] = 1710 ms; field of view [FoV] in mm2: 256×256; matrix: 512×512; slice thickness: 1 mm), T2 fluid attenuated inversion recovery (TE = 135 ms; TR = 8500 ms; FoV: 230×172 mm2; matrix: 256×192; slice thickness: 5 mm), and T2-weighted MRI turbo spin echo (TSE) (TE = 86 ms; TR = 5550 ms; FoV: 229×172 mm2; matrix: 384×230; slice thickness: 5 mm). Apparent diffusion coefficient (ADC) maps were generated from diffusion-weighted imaging (DWI). DWI was performed using a single-shot spin-echo (SE) echo-planar (EPI) sequence with the following parameters: echo time (TE) = 86–109 ms, repetition time (TR) = 4700–5300 ms, flip angle (FA) = 90°, slice thickness (ST) = 5 mm, field of view (FOV) = 229×229 mm, echo train length (ETL) = 1, number of slices (NS) = 25–26, spacing between slices (SS) = 5-6 mm, acquisition matrix (matrix) = 130/0/0/130 mm, number of averages (NA) = 3–4, parallel-acquisition-technique factor (PAT) = 2. Diffusion sensitizing gradients were applied sequentially in the x, y, and z directions with b values of 0 and 1200 s/mm2. Relative cerebral blood volume (rCBV) maps were generated from dynamic susceptibility contrast-enhanced perfusion weighted Imaging (DSC-PWI).Prior to acquisition of the DSC-PWI sequence either dynamic-contrast-enhanced MRI (DCE-MRI) or acquisition of a T2-w sequence was performed. In both cases a 0.1 mmol/kg prebolus dose of intravenous gadoterate meglumine (Gd-DOTA, DOTAREM, Guerbet, France) was administered 4 min prior to acquisition of the DSC-PWI sequence (injection was performed after a 20-s delay from the start of the DSC-MRI or prior to acquisition of the T2-w sequence) to diminish T1 effects that might result from agent extravasation. Timing of the prebolus with regard to the start of DSC-PWI was comparable in both cases, and allowed for contrast agent saturation within the extravascular space. DSC-PWI was obtained with a T2*-weighted gradient-echo EPI sequence and was started simultaneously with bolus injection of a standard dose (0.1 mmol/kg) of intravenous gadoterate meglumine. Bolus and prebolus injection was performed through a pneumatically driven injection pump at an injection rate of 5 ml/s. Twenty-six to 28

slices with a thickness of 5 mm were acquired with fat suppression (TE = 36 ms, TR = 2220 ms, FA = 90°, FOV = 240*240 mm, matrix = 128/0/0/128 mm). In total, 50–75 dynamic measurements were performed (including at least 8–10 prebolus measurements prior to bolus arrival). Subsequently, post-contrast MPRAGE data was acquired with inversion time (TI) = 1100 ms, TE = 4 ms, TR = 1710 ms, FA = 15°, ST = 1 mm, FOV = 250 × 250 mm and matrix = 256/0/0/256 mm. Both DWI and DSC-PWI have previously been described in detail [1,2]

2.3. Co-Registration of FAP-specific PET Scans and MRI Scans

For all patients, a corresponding MRI scan for the FAP-specific PET/CT scan (up to 4 weeks before PET/CT, no change of treatment between the examinations) was available. T2w/FLAIR sequences were available for all 13 patients, contrast enhanced T1 sequences were available for 12 patients.

ADC maps were available for all 13 patients and rCBV maps were available for 11 patients. A post-process co-registration using a multi modal rigid registration algorithm was done [3]. Thereby, contrast enhanced T1 weighted, T2w/FLAIR, ADC and rCBV images were co-registered on the corresponding FAP-specific PET images using the software Medical Imaging Interaction Toolkit (MITK) Workbench [4].

2.4. Image Analysis

T2w/FLAIR hyperintensities and contrast enhancing lesions and necrotic areas were delineated manually within co-registrated MRI slides on T1-w contrast enhanced images and T2-Flair images. Segmentations have been performed in consensus by D.P. and M.R. with eight years and five years of experience in brain tumor imaging. To generate volumes of interest (VOIs) necrotic areas were subtracted from T2w/FLAIR and contrast enhancing areas. Pixelwise signal intensity values of FAP-specific PET signaling, ADC and rCBV within T2w/FLAIR based and contrast enhancement based VOIs were extracted using the software Medical Imaging Interaction Toolkit (MITK) Workbench.

Acknowledgments

None.

Conflict of Interest

This work was funded by the Federal Ministry of Education and Research, grant number 13N 13341. The scientific guarantators of this study are Manuel Röhrich and Daniel Paech. We mention that Uwe Haberkorn declares the following conflict of interest: Patent application for quinoline based FAP-targeting agents for imaging and therapy in nuclear medicine. All other authors disclose any financial or other conflict of interest.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2020.105712.

References

[1] D Paech, J Windschuh, J Oberhollenzer, et al., Assessing the predictability of IDH mutation and MGMT methylation status in glioma patients using relaxation-compensated multipool CEST MRI at 7.0 T, Neuro Oncol 20 (2018) 1661–1671.
[2] K Deike, B Wiestler, M Graf, et al., Prognostic value of combined visualization of MR diffusion and perfusion maps in glioblastoma, J Neurooncol 126 (2016) 463–472.
[3] R. F., MatchPoint: on bridging the innovation gap between algorithmic research and clinical use in image registration, in: World Congress on Medical Physics and Biomedical Engineering, September 7-12, 2009 Munich, Germany, 2009, pp. 1105–1108.
[4] M Nolden, S Zelzer, A Seitel, et al., The Medical Imaging Interaction Toolkit: challenges and advances : 10 years of open-source development, Int J Comput Assist Radiol Surg 8 (2013) 607–620.