Tumor functional mapping using synchrotron radiation computed tomography

Balvay D.[1], Troprès I.[2], Billet R.[3], Joubert A.[3], Péoc'h M.[3], Cuenod C.A.[1], Le Duc G.[3]

[1] *LRI, PARCC, Inserm 970 – Service Radiologie HEGP, Paris, France*
[2] *IFR1, Université Joseph Fourier – Unité IRM 3T, CHU Grenoble, France*
[3] *Biomedical Beamline & Facilities, ESRF, Grenoble, France*

Dynamic contrast enhanced medical imaging (DCE-MI) is a promising technique for the detection, the characterization and the follow up of many lesions such as solid tumors. Its use has recently increased in order to allow the in vivo assessment of the microcirculatory function of the tissues. The intravenous bolus of contrast agent (CA) is followed as a function of time in tissues through local variations of gray levels in pixels or in regions of pixels. The evolution of the CA concentration depends on microcirculatory characteristics which are assessed by using pharmacokinetic modeling. However, in practice, the variability in data acquisition techniques and data analysis is so important that results cannot be easily compared.

To test the potential of DCE-MI in terms of microcirculatory parameters quantification, we acquired and analyzed images issued from a well controlled DCE-MI protocol. We tested if it was possible to characterize different structure elements of C6 rat brain tumors by their different microcirculatory behaviors. The acquisition was provided in stereotaxic conditions with the monochromatic Synchrotron Radiation CT (SRCT) technique available at the Biomedical Beamline (ID17). Hence, it was possible to avoid several biases associated with other techniques: low signal to noise ratio, beam hardening, no direct relation between image intensities and CA concentrations. The analysis was provided by selecting the more relevant pharmacokinetic model among several compartmental models, for the set of selected anatomic region. The model selection was guided by using quality criteria which tested the consistence between original data and modeling information provided by each pharmacokinetic model. This analysis avoids any potential misinterpretations of results and helps in evaluating the consistence of the final parametric results.

DCE-SRCT sequences were analyzed by using home-made software. The software provided parametric maps of tumors and surrounding brains, each map corresponding to different microcirulatory parameters: blood flow, blood volume, mean transit time, capillary permeability index and artery to tissue delay. It provided also quality maps for the quality control. Moreover structure region were selected in the original sequences and microcirculatory parameters in the defined regions were compared.

Remarkably, the regional organization of the tumor zones, visible on the hematoxylin-eosin-stained slices, was reproduced on parametric map for which high quality criteria were found. Quantitative results in the selected regions indicated that each type of tumor tissue is characterized by (1) an abnormal capillary permeability and intravascular transit time. Quantitative results indicated also that the structures of the tumor could be characterized by their specific blood flow and blood volume values, increasing in this order: center, intermediate, periphery and hot spots.

The consistence between DCE-SRCT and histological maps such as the ability of DCE-SRCT to significantly differentiate microcirculatory behaviors between tumor elements could position this technique as a reference. Especially, the assessment of absolute concentrations allows comparison between centers and estimation of calibration factors.