Characterisation of breast tumors with a model-independent analysis of bolus-tracking MRI

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Introduction

Dynamic contrast enhanced MRI (DCE-MRI) using standard Gadolinium chelates reflects the properties of both intra- and extravascular compartments of tumor tissue [1,2]. Previously we demonstrated the feasibility of quantifying perfusion parameters in human breast tumors using a deconvolution analysis of DCE-MRI [2]. For this study we implemented and validated two methodological refinements (AIF filtering and R1 quantification), applied the final protocol to a larger cohort of patients and investigated the value of the measured parameters in terms of tumor characterization.

Materials and Methods

In vivo perfusion measurements were performed on 30 women with histologically proven breast tumors on a 1.5 T scanner (Philips Intera). The routine MR mammography protocol was applied first. It included T1-weighted DCE-MRI (30 ml of a 0.5 M Gd-DTPA solution) with high coverage and low temporal resolution, and high-resolution axial 3D T1 GE with fat suppression. The slice where the tumor enhanced maximally was identified on these data. At that slice position, the passage of a 20ml bolus of Gd-DTPA (2 ml/sec) was measured with an inversion-prepared FLASH sequence (TR 4.9 msec, TE 2.4 msec, flip angle 50°, TI 196 ms, 128x67 matrix reconstructed at 256x204, FOV 230x183 mm^2, slice thickness 6 mm, 600 images with a temporal resolution of 360 msec). For R1-quantification an additional measurement was performed immediately before second bolus injection with the same sequence, but with a flip angle of 5°.

Image post-processing was performed on a personal computer using software written in-house in IDL. The AIF was selected manually in the aorta and the flow-induced signal fluctuations were removed by filtering of the arterial signal-time courses [2]. The signals were converted to change in relaxation rate ($\Delta R1$) by a two-point method [3] and the $\Delta R1$ time courses were then deconvolved pixel-by-pixel, using standard-form Tikhonov regularization and an optimized minimization scheme for the L-curve criterion [4]. Finally, the parametric maps of tumor blood flow (TBF), tumor extracellular volume (TEV) and mean transit time (MTT) were generated from the Impulse Response Function [2]. Quantitative values for each patient were derived as an average over a ROI covering the whole lesion.

Results

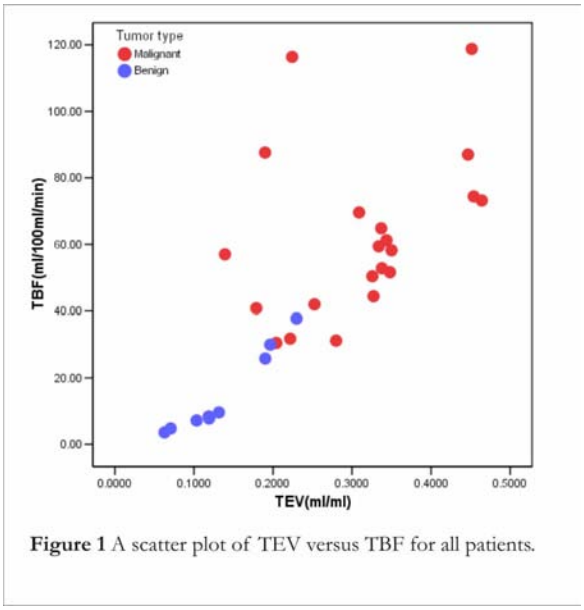

Figure 1 A scatter plot of TEV versus TBF for all patients.

Table 1	TBF (ml/100ml/min)	TEV (ml/ml)	MTT (sec)
Malignant	52	0.33	38
Benign	8	0.12	87

Histological analysis revealed 21 malignant and 9 benign tumors. In the malignant tumors, the parametric maps clearly delineated the tumor from the surrounding breast tissue. On the other hand, the benign tumor and some parts of breast parenchyma reveal identical perfusion status. Quantitative values for the perfusion parameters are given in table 1. The difference between both groups was significant ($p<0.05$) for all parameters, and the median TBF value in the malignant tumors lies within the literature range of 8-80 ml/100ml/min [5]. Figure 1 shows an overview of all patient data for TBF and TEV. Both parameters were positively correlated for each group ($p<0.05$), but the correlation was stronger for benign ($r^2= 0.95$) than for malignant tumors ($r^2=0.24$). Choosing cut-off values of 25 ml/100ml/min for TBF and 0.2 ml/ml for TEV, all except one benign lesion were separated from the malignant group. Histology revealed that this outlying benign lesion to be a proliferative sclerosing adenosis.

Conclusion

We conclude from these data that malignant and benign breast tumors may be characterized with the proposed measurement and post-processing protocol, in terms of their perfusion values. However, the number of patients is limited and the separation between the groups is not clear-cut. Hence additional parameters may be required to provide a clearer separation and improve the robustness of the procedure. Preliminary studies suggest that useful additional measures can be obtained by a modeling approach [1,6].

References

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