

Characterization of breast tumors with a model-dependent analysis of bolus-tracking MRI

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Introduction: Dynamic contrast enhanced MRI (DCE-MRI) of the breast using standard Gadolinium chelates has a high sensitivity for breast cancer detection, but varying specificity for tumor characterization [1]. Earlier we had shown that a pixel wise deconvolution analysis based on second bolus data leads to vascular parameters that could contribute to the effective characterization of suspicious breast lesions [2]. However, we observed no clear-cut separation between benign and malignant cases on the basis of these parameters alone. It was proposed that additional parameters may be required to provide a clearer separation and improve the robustness of the results [3].

It has been shown that a 2-compartment uptake model (2CUM) could efficiently fit tumor time courses covering a limited time window at high temporal resolution and thus could generate acceptable estimates of permeability [4]. The aim of this study was to investigate whether a 2CUM accurately describes high temporal resolution kinetics in breast pathology and also to evaluate the results of the measured parameters in terms of tumor characterization in a small cohort of patients.

Materials and Methods: In vivo perfusion measurements were performed in 22 women with histologically proven breast tumors (16 malignant and 6 benign) on a 1.5 T scanner (Philips Intera). The routine MR mammography protocol was applied first. The slice where the tumor enhanced maximally was identified on these data. At that slice position, 10 minutes later prebolus protocol was applied. 1ml of Gd-DTPA solution at 2ml/s was injected at the beginning of a dynamic axial single slice inversion-prepared (IR prepared) TFE acquisition. At the 400th dynamic, a high dose (10 / 20ml) of contrast agent is injected at 2ml/s and a further 400 dynamics were acquired with a temporal resolution 0.3s. Image post-processing was performed on a personal computer using software PMI 0.3 [5]. ROIs were placed manually in aorta and the region within the breast lesion with highest enhancement. The signals were converted to relative enhancement (RE) and analyzed using 2CUM to obtain estimates of plasma flow (PF), extraction flow (EF) and plasma volume (PV). Statistical comparison between malignant and benign groups for all three model parameters was performed using independent sample t-test.

Results: The 2CUM provides accurate fits to the data in malignant as well as benign tumors (Figure 1). The mean \pm std. dev of the parameters for both malignant and benign breast tumors are given in Table 1. Significant difference in mean values between groups is observed for PF and EF. Both parameters show a significant correlation for malignant tumors (Pearson $r = 0.713$; $p = 0.002$). However, we observe no sharp separation between benign and malignant cases on the basis of PF, PV and EF taken together on a 3D scatter plot (Figure 2).

Discussion & Conclusion: We conclude that inclusion of the permeability parameter does not improve the separation of malignant and benign breast tumors. In the malignant group, the overlap consisted of 2 in-situ carcinomas and 2 invasive lobular carcinomas (ILC). It has been proposed that angiogenesis plays a lesser role in the growth pattern of these cancers, which in turn can result in the observed contrast behavior [6]. MR spectroscopy detects the cellular markers of proliferation and could be a promising technique for aiding classification of breast lesions when DCE MRI results become equivocal [7]. Malignant tumors with identical histopathology can exhibit very different perfusion and permeability parameters, which points to the fact that DCE MRI can provide additional information that is not there in the histopathology.

References

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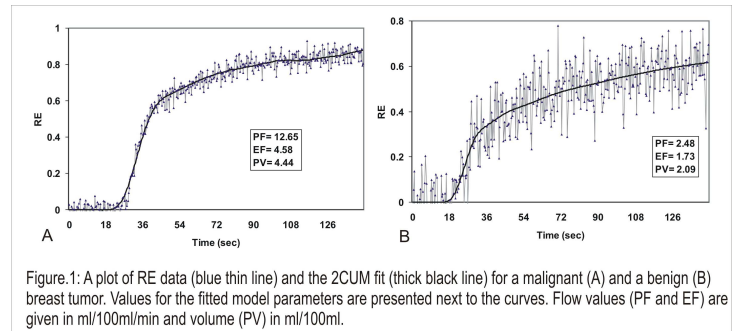


Table 1: Quantitative values of the three model parameters for both malignant and benign tumors			
	PF (ml/100ml/min)	EF (ml/100ml/min)	PV (ml/100ml)
Malignant	12.06 \pm 6.8	4.32 \pm 1.42	5.80 \pm 2.83
Benign	4.79 \pm 3.03	2.84 \pm 0.86	3.03 \pm 2.82
P value	0.003	0.01	0.07

