Investigation of Prostate Cancer Metabolomics with Prostate Biopsy Cores

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Background: Our prior studies of intact prostate tissue samples from PCa patients suggest the existence of metabolic or metabolomic fields within and surrounding PCa lesions. These field effects likely create PCa "metabolomic lesions" that are larger than the histologic lesions and are detectable by *ex vivo* MR spectroscopy. In the present study, we evaluate these 'field effects' using prostate biopsy samples from patients suspected of harboring PCa.

Methods: One prostate biopsy core from each of 138 patients undergoing standard trans-rectal ultrasound (TRUS) guided biopsy for suspicion of PCa or for active surveillance was used for the study. High-resolution magic angle spinning MR spectroscopy was carried out on a Bruker AVANCE spectrometer operating at 600 MHz (14.1T). Spectra were recorded at 4ºC with the spectrometer frequency set on the water resonance and analyzed using an in-house developed MatLab based program. 75 spectral regions were identified and used in principal component analysis (PCA) and canonical analysis (CanCor). After spectroscopy, biopsy cores were analyzed with traditional histopathology. The volume percentages of histological features were quantified by a pathologist. Based on the complete pathology report for each patient, and the subsequent clinical follow-up, we categorized patients into the groups in Table 1.

Results: Metabolic and metabolomic results indicate the ability of differentiating the E5 (with >5-year follow-up after MRS analysis of biopsy core) patient group from other groups. In addition to a number of individual metabolic peaks, such as creatine (3.026ppm), PCA results (Figure 1A) clearly distinguish E5 group as demonstrated by PC2. Furthermore, CanCor results (Figure 1B) obtained by using groups B and D as the training cohort, and groups A and C as the testing cohort, clearly present the diffusiveness of PCa metabolomic field from PCa foci to their surrounding histologically benign structures.

Conclusions: Our data further demonstrate metabolomic profiles within and surrounding prostate cancer lesions and suggest that patient PCa characteristics can be obtained from surrounding histologically benign tissue through the presence of PCa metabolomic fields. We are currently investigating these metabolomic signatures in our patients undergoing MR-ultrasound fusion biopsy and anticipate that these signatures may be translatable to *in vivo* MR spectroscopy allowing for improved non-invasive detection.

Conflict of Interest: None

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Table 1 – Analysis Groups

Group	Diagnosis	Case #
A	Cancer in the analyzed core	*15*
B	Cancer in same quadrant as the analyzed core	*18*
C	Cancer in adjacent quadrant from the analyzed core	*32*
D	Cancer in far quadrant the analyzed core	*21*
E	No PCa detected Histologically Benign (<5-year)	*33*
E5	Histologically Benign, no PCa after >5-year	*9*
U	PCa Diagnosis but location unknown	*10*
	Total	**138**

Figure 1: