

MP 08-13: Metabolomic characterization of renal cell carcinoma using high resolution magic angle spinning magnetic resonance spectroscopy

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Objective

- *To investigate the metabolomic profile of renal cell carcinoma and compare it to that of adjacent benign renal parenchyma using high resolution magic angle spinning (HRMAS) magnetic resonance spectroscopy (MRS).*

Methods

- **Samples:** 38 RCC samples from partial or radical nephrectomy were stored in frozen tissue bank
 - 16 clear cell, 11 papillary, 11 chromophobe and 13 adjacent normal tissue specimens = 13 matched pairs
- **Outcome:** Metabolites indicative of renal cell carcinoma
- **Statistics:** False discovery rates (FDR) were used from the response screening to account for multiple testing. Regions of interest (ROI) with FDR <0.05 were selected as potential predictors of malignancy

Table 1. Baseline characteristics and metabolomic predictors of malignancy

	RCC (N=38)	Adjacent benign parenchyma (N=13)	P-value			
Age (years)	55.3 ± 11.4	50.8 ± 7.3	0.1818			
Males (n, %)	27 (71.1)	8 (61.5)	0.7302			
Race (n, %)	37 (97.4)	13 (100)	1.00			
Median MRS relative intensities (IQR)				FDR P-value	Odds ratios (OR, 95% CI)	P-value for OR
4.07-4.05 (Myo-Inositol)	0.80 (0.48, 1.32)	1.84 (1.27, 2.24)	0.0026	0.027	0.38 (0.18, 0.82)	0.013
4.02-4.00 (TBD)	1.21 (0.68, 2.07)	0.50 (0.06, 0.88)	0.0073	0.034	3.12 (1.10, 8.84)	0.032
3.99-3.96 (Histidine, Phenylalanine, Phosphocholine, Serine)	1.26 (0.84, 1.93)	2.56 (1.19, 3.50)	0.0092	0.013	0.34 (0.16, 0.71)	0.004
3.95-3.94 (Serine, Phosphocreatine)	0.77 (0.33, 1.24)	0.30 (0, 0.53)	0.0006	0.003	29.2 (2.47, 345.24)	0.007
3.93-3.91 (Creatine, Glycerophosphocholine)	1.28 (0.90, 1.61)	0.69 (0.24, 1.34)	0.0071	0.012	8.17 (1.77, 37.78)	0.007
3.61-3.59 (Myo-Inositol, Glycerophosphocholine, Phosphocholine, Valine)	0.96 (0.63, 1.24)	1.68 (1.39, 1.96)	0.0006	0.005	0.13 (0.03, 0.49)	0.003
3.55-3.52 (Glycine)	1.92 (0.77, 3.17)	4.02 (2.87, 4.42)	0.0019	0.024	0.59 (0.39, 0.90)	0.014
3.36-3.34 (Scylla-Inositol)	0.55 (0.35, 0.78)	1.34 (0.75, 1.54)	0.0019	0.005	0.08 (0.02, 0.42)	0.003
3.24-3.23 (Myo-Inositol, Taurine)	5.86 (3.95, 9.46)	4.32 (2.43, 5.40)	0.0267	0.030	1.35 (1.04, 1.76)	0.027
3.22-3.21 (Phosphocholine, Glycerophosphocholine, Histidine)	0.69 (0.22, 2.16)	4.23 (3.05, 5.53)	<0.001	<0.001	0.41 (0.35, 0.67)	<0.001
3.15-3.13 (Spermine, Histidine, Phenylalanine)	0.21 (0.11, 0.35)	0.83 (0.49, 1.02)	<0.001	<0.001	4 x10 ⁻⁵ (7.42x10 ⁻⁸ , 0.02)	0.001
2.84-2.82 (TBD)	0.28 (0.18, 0.45)	0.18 (0.10, 0.23)	0.0021	0.009	7158.67 (6.3, 8.3x10 ⁶)	0.013
2.45-2.42 (Glutamine)	0.51 (0.30, 0.74)	0.32 (0.21, 0.38)	0.0098	0.017	121.5 (2.16, 6820)	0.02
2.15-2.11 (TBD)	1.45 (1.15, 1.97)	1.95 (1.46, 2.50)	0.0370	0.035	3.96 (1.18, 13.28)	0.026
1.93-1.92 (Acetoacetate)	0.31 (0.18, 0.67)	0.77 (0.54, 2.83)	0.0008	0.012	0.38 (0.13, 1.09)	0.072
1.35-1.33 (Lactate)	8.74 (5.26, 13.23)	5.2 (3.06, 8.30)	0.0150	0.033	1.22 (1.03, 1.45)	0.023

*TBD denotes that the specific metabolites characterizing this region remain to be identified