# ROLE OF MAGNETIC RESONANCE IMAGING IN PREDICTING ADVERSE PATHOLOGY POST-RADICAL PROSTATECTOMY

MP14-17

Alp Tuna Beksac, Ugo Falagario, Shivaram Cumarasamy, Akriti Gupta, Paige Xu, Sonya Prasad, Alberto Martini, Hari Thulasidass, Isuru Jayaratna, Ardeshir Rastinehad, Ash Tewari

*Department of Urology, Icahn School of Medicine at Mount Sinai*

## INTRODUCTION

- Multiparametric MRI can predict clinically significant prostate cancer, but its relationship with final pathology and genomic features is unclear
- Decipher genomic classifier (GC) is a validated gene signature of 22 genes, associated with postoperative outcome

## OBJECTIVES

- To evaluate the association of preoperative MRI features with final pathology and GC score in our radical prostatectomy cohort

## MATERIALS & METHODS

- We retrospectively analyzed the data of 206 patients who underwent RP between October 2013 and August 2017 with available preoperative MRI and postoperative GC score
- Primary analysis was the association between MRI and GC score
- Secondary analysis was the ability of MRI to predict adverse pathology. Adverse pathology was defined as Gleason Group >2, T3-4 disease or pN1 disease
- PI-RADS v2 was used in the analysis
- Categorical values were compared with chi-square and Fischer's exact tests. Mann-Whitney U, Kruskal-Wallis and ANOVA tests were used for analysis of independent variables associated with adverse pathology
- Multivariate analysis was done using linear regression and binomial logistic regression models

## RESULTS

**Table 1.** Baseline Characteristics and Their Association with GC Score

| Variable | Value/Frequency | Decipher Score | p Value |
|---|---|---|---|
| **Age** | 63±17.0 | | 0.757 |
| **Race** | | | 0.233 |
| **Caucasian** | 156 (83.9%) | 0.50±0.19 | |
| **Other** | 30 (16.1%) | 0.45±0.21 | |
| **BMI (km/m²)** | 27.3±4.0 | | 0.706 |
| **PSA (ng/mL)** | 8.6±5.3 | | 0.330 |
| **Max Core %** | 68.3±26.5 | | 0.080 |
| **Clinical Stage** | | | 0.011 |
| T1c | 106 (52.3%) | 0.46±0.18 | |
| T2a-T2b | 74 (37.2%) | 0.51±0.20 | |
| T2c-T3 | 19 (9.6%) | 0.61±0.24 | |
| **Gleason Group** | | | **<0.001** |
| 1 | 24 (11.7%) | 0.39±0.17 | |
| 2 | 72 (34.9%) | 0.45±0.16 | |
| 3 | 45 (21.8%) | 0.50±0.21 | |
| 4 | 39 (18.9%) | 0.55±0.20 | |
| 5 | 26 (12.6%) | 0.64±0.19 | |
| **PI-RADS** | | | **0.017** |
| 3 | 14 (6.9%) | 0.39±0.22 | |
| 4 | 95 (47.0%) | 0.47±0.17 | |
| 5 | 93 (46.0%) | 0.53±0.21 | |
| **T2** | | | 0.081 |
| 3 | 15 (9.0%) | 0.39±0.14 | |
| 4 | 76 (45.8%) | 0.48±0.18 | |
| 5 | 75 (49.5%) | 0.52±0.22 | |
| **DWI** | | | 0.076 |
| 3 | 18 (9.8%) | 0.42±0.20 | |
| 4 | 75 (40.8%) | 0.48±0.18 | |
| 5 | 91 (49.5%) | 0.53±0.21 | |
| **Lesion Size (mm)** | 15.8±7.8 | | **0.028** |
| **D'Amico Risk** | | | **0.001** |
| Low | 18 (9.0%) | 0.41±0.18 | |
| Average | 102 (50.7%) | 0.45±0.18 | |
| High | 81 (40.3%) | 0.21±0.16 | |
| **MRI EPE** | | | 0.10 |
| Absent | 159 (77.9%) | 0.47±0.19 | |
| Present | 45 (22.1%) | 0.57±0.22 | |

## RESULTS

- In final pathology, Gleason group (p<0.001), pT stage (p<0.001), pN stage (p<0.001), tumor percentage (p=0.007) and adverse pathology features (p<0.001) were associated with GC score
- In a multivariate model adjusting for age, race, PSA, cT stage and Gleason score, PI-RADS was not associated with GC score. Only Gleason group was associated with GC score (p<0.05)
- In a logistic regression model adjusting for age, race, PSA, cT stage and Gleason group (p<0.05), PI-RADS (p<0.05) was associated with adverse pathology

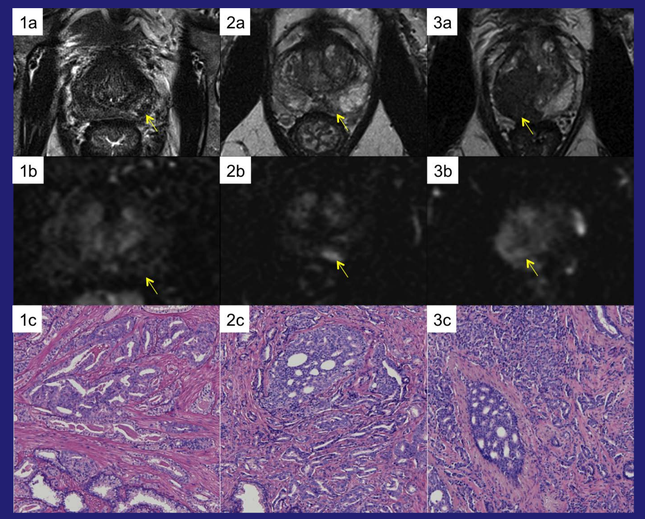


**Figure 1.** Sample Patients. Each column corresponds to a patient

## CONCLUSION

- Higher PI-RADS scores were associated with increased GC score on final pathology
- PI-RADS scores were associated with adverse pathologic features