Materials and methods: We retrospectively analyzed the records of 103 patients with suspicion of prostate cancer (PCa) who underwent a mpMRI showing at least one PIRADS 3 lesion, who were referred to our Institution for a prostate biopsy between October 2017 and April 2019. Before biopsy, all patients underwent also a mUS examination. The PRI-MUS protocol was used identify targets within the prostate. Subsequently, patients were subjected both to MRI/US fusion biopsy and to mUS-targeted biopsies. Additionally, systematic randomized biopsies were also performed. The presence of overall PCa and of clinically significant PCa (csPCa) defined as Gleason score ≥7 was determined. Finally, multivariable logistic regression models were fitted to test the predictors of PCa.
Results: Median age was 63.0 years, median total PSA was 6.0 ng/mL and median prostate volume was 50.5 mL. Of the 103 patients, 23 (22.3%) did not show any lesion at mUS (PRIMUS 1–2) while in the remaining 80 (77.7%) patients at least one target was identified (PRI-MUS ≥3). Among patients without lesions at mUS, 18 (78.3%) of did not harbor PCa, while, 5 (21.7%) harbored a PCa, but none of these was defined as csPCa. Among patients with at least one PRI-MUS ≥3 lesion, 43 (53.7%) had a negative biopsy while 37 (46.3%) had harbored PCa and 21 (26.2%) harbored csPCa. MicroUS showed an extremely high sensitivity and negative predictive value (100%), while its specificity and positive predictive value were 28.1% and 26.2%, resepctively. In multivariable logistic regression models, the PRI-MUS score emerged as the only independent predictor of PCa, with patients with at least one PRI-MUS ≥3 showing a 3.8-fold higher risk of harboring PCa as compared to their counteparts without any lesion at mUS (p = 0.021).
Conclusions: According to our results, mUS is capable of stratifying the presence of PCa in patients with an equivocal mpMRI. Further prospective studies are urgently needed to determine whether mUS could be adopted as a supplementary diagnostic tool in patients with at least one PIRADS 3 lesion.

SC34 Using a machine learning algorithm to predict prostate cancer grade

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Introduction: Several nomograms have been developed to predict prostate cancer however, very little machine learning (ML) tools are available for this purpose. Our study aimed to develop a ML based methodology to predict prostate cancer in patients undergoing prostate biopsies.
Materials and methods: From 2012 onwards, we consecutively enrolled, in 12 centers in Italy, men undergoing prostate needle biopsy (SB) plus target biopsy in patients with a positive MRI. Demographic, clinical, and histopathological data were collected. Two different tree-based ML techniques (XGBoost and Random Forest) were trained to predict PCa risk. The models output 1 value in order to predict the PCa risk as a categorical value among no-cancer, low-grade cancer, and high-grade cancer. High-grade cancer was defined as Grade ≥3. The ML models were trained using the following variables: age, DRE, prostate volume, 5ARI treatment, previous prostate surgery, previous biopsies, PIRADS score. The area under the curve (AUC) for the multiclass problem were finally assessed for both models.
Results: Overall 1022 patients were enrolled. The median age was 66 (61/70) years, median prostate volume was 49 (39/66) ml, and median PSA was 7.4 (5.5/11) ng/ml. For both models we evaluated the micro-average and the macro-average ROC curves in addition to the ROC curve for each of the target class. XGBoost presented a micro-average and a macro-average AUC of 0.81 and 0.80 respectively. Moreover, the AUC for class 0 (no-cancer), class 1 (low-grade-cancer) and class 2 (high-grade-cancer) were 0.82, 0.68, 0.89 respectively. Random Forest presented slightly lower performances. The micro-average and the macro-average AUC were both equal 0.79. The AUC for class 0 was 0.82, for class 1 was 0.68 while for class 2 the AUC was equal to 0.85.
Conclusions: Our experience confirmed that ML technology can be applied to prostate diagnosis and it can be used to counsel patients about the risk of caring high grade prostate cancer. ML has also the possibility to continously improve accuracy of the model by including new data and new patients over time. Implementation/validation of our ML model and relative App could confirm our results and establish its role in clinical practive.

SC35 TMPRSS2: ERG expression in prostate cancer: Imaging and clinico-pathological correlations

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Introduction: The TMPRSS2:ERG gene fusion (T:E) is found in up to 50% of prostate cancers (PCa) and results in androgen dependent over-expression of ERG, which has been demonstrated to promote tumor growth. Early identification of this fusion may be helpful for an optimal management of patients, even in low-risk PCa. Although T:E can be non-invasively detected in urine, its correlation with new imaging tools (MRI and high-frequency ultrasound) and clinical outcome remains vague. This study aims at investigating T:E expression in patients scheduled for random/software-assisted MRI or micro-ultrasound (MICRO-US), 29Mhz (ExactVu™) fusion biopsy (bx).
Materials and methods: This is a prospective cohort study of men with suspected PCa enrolled between 2016 and 2019 at our institution. The study was approved by authorities (Prot. N. 336/19, 14/5/19). All patients signed written informed consent. Patients underwent systematic US-guided bx, plus targeted bx if they presenting with ≥1 suspicious lesion (PIRADS V.2 >2) at mpMRI or Prostate Risk Identification Using Micro-Ultrasound (PRIM-US) >2 at MICRO-US assessment. For each patient, one prostatic core from the highest PIRADS or PRIMUS lesion was collected for T:E analysis. If imaging findings were negative a core from the right lobe was collected. All histological analyses were performed by experienced genitourinary pathologists. RNA was extracted from a dedicated fresh biopsy and RT-PCR was performed with different primer couples to detect the most frequent T:E fusions. All amplified products were checked by sequencing.
Results: The cohort consists of 157 patients (median PSA 7.83 ng/ml, IQR 5.34–14.3) with an average age of 66 years, 131 (83.4%) of which had a diagnosis of PCa after biopsy. mpMRI was performed on 104 (66.2%) patients and positive in 98 (94.2%) men who underwent fusion biopsy. MICRO-US was performed on 67 (42.6%) men and positive in 89% of men. T:E fusion transcripts were detected in 23.0% of individuals with a diagnosis of PCa. Among 43 patients who underwent prostatectomy, all those with positive T: E had a grade ≥2 group. Among patients positive for T:E, mpMRI was positive in all man (72% PIRADS ≥4) while MICRO-US was positive in 91%. Sensitivity of the T:E assay for any PCa was 22%, specificity 100%, positive predicting value 100% and negative predicting value 21%; while sensitivity for clinically significant PCa was 24%, specificity 100%, negative predicting value was 38% and positive predicting value was 100%. Interestingly there was no statistical correlation between T:E and family history, PSA, PIRADS, PRI- MUS and Gleason score results.
Conclusions: Our finding showed a 100% of specificity making T:E an attractive tool for early cancer detection in a selected population. In the future, the identification of T:E in the seminal fluid could represent a screening test for clinical stratification of patients with suspected PCa.