INTRODUCTION AND OBJECTIVE: There are no series evaluating penile squamous cell carcinoma (pSCC) based on human papillomavirus (HPV)-status. Herein, we present national registry data on clinical and survival outcomes for pSCC based on HPV.

METHODS: We performed a retrospective review of 1,224 pSCC patients with known HPV-staining from the National Cancer Database. Patients with cM1 disease, did not receive treatment, and missing follow-up data were excluded. Logistic regression identified factors associated with locally aggressive disease. Univariable, multivariable and inverse probability of treatment weighting (IPTW)-Cox proportional hazards modeling were used to assess hazard ratios (HR) associated with overall survival (OS) with respect to HPV.

RESULTS: After exclusion criteria, we identified 825 cases of which 321 (38.9%) were HPV-positive. The HPV-positivity rate did not significantly change by year. HPV-positive patients were younger, had lower Charlson-Deyo performance score, and resided in areas with lower median household income and lower school education completion. HPV-positive tumors presented with lower American Joint Disease (cN) and presence of extranodal extension. Only tumor differentiation, LVI, and HPV status were independent predictors for locally aggressive disease. Etiologic classification based on HPV did not appear to impact survival.

CONCLUSIONS: In the largest series evaluating pSCC based on HPV status, HPV-positive tumors were associated with lower cT stages, less LVI, but more cN+ disease. Etiologic classification based on HPV did not appear to impact survival.

Table 4: Predictors for high-risk (cT3-cN+ disease) features (n=132)

|                | Univariable | Multivariable |
|----------------|-------------|---------------|
| **Variable**   | **OR (95%CI)** | **p** | **OR (95%CI)** | **p** |
| Age            | 1.00 (0.99-1.02) | 0.56 | 0.99 (0.98-1.01) | 0.34 |
| Tumor grade (Ref: Well differentiated) | Moderate | 4.46 (2.99-6.7) | <0.01 | 4.29 (1.58-11.56) | <0.01 |
|                | Poorly differentiated | 8.99 (4.28-18.15) | <0.01 | 8.58 (2.97-15.16) | <0.01 |
|                | Undifferentiated/Anaplastic | 0.64 (0.39-1.2) | 0.37 | 0.58 (0.25-1.35) | 0.065 |
| LVI (Ref: Not present) | Present | 6.54 (3.82-11.21) | <0.01 | 4.95 (2.34-7.33) | <0.01 |
|                | Unknown | 1.52 (0.94-2.45) | 0.09 | 2.71 (1.52-4.80) | <0.01 |
| Ethnicity (Ref: Non-Hispanic) | Hispanic | 1.06 (0.69-1.58) | 0.84 | 1.76 (0.91-3.38) | 0.09 |
|                | Unknown | 0.44 (0.11-1.6) | 0.33 | 0.83 (0.35-2.1) | 0.72 |
| Race (Ref: White) | Black | 1.53 (0.89-2.68) | 0.12 | 1.76 (0.91-3.38) | 0.09 |
|                | Other | 0.83 (0.33-2.04) | 0.68 | 0.83 (0.30-2.33) | 0.82 |
| Charlson-Deyo score (Ref: 0) | <1 | 1.31 (1.17-2.86) | <0.01 | 2.01 (1.19-3.39) | <0.01 |
|                | 1 | 0.78 (1.15-1.32) | 0.59 | 0.80 (0.23-1.39) | 0.30 |
|                | 3 | 1.48 (0.73-3.13) | 0.15 | 1.39 (0.43-4.49) | 0.59 |
|                | 3 | 1.14 (0.66-1.85) | 0.09 | 0.95 (0.59-1.53) | 0.85 |

Bold values indicate statistical significance.

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THE COMBINATION OF MICORRNA-371A-3P AND 375-5P CAN DISTINGUISH VIABLE GERM CELL TUMOR AND TERATOMA FROM NECROSIS IN POSTCHEMOTHERAPY RETROPERITONEAL LYMPH NODE DISSECTION SPECIMENS

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INTRODUCTION AND OBJECTIVE: To identify a combination of microRNAs (miRNA) to differentiate between viable tumor (V) or teratoma (T) and necrosis/fibrosis (N) in pcRPLND specimens of metastatic germ cell tumor (GCT) patients with residual masses ≥1cm after chemotherapy. Biomarker guided therapy could reduce overtreatment with pcRPLND in patients with only N.

METHODS: We selected 48 metastatic GCT patients who had undergone pcRPLND. V, pure T and N was shown in the resected tissue of 16 patients, respectively. Of these areas total RNA was isolated and miRNA expression was analyzed for miR-371a-3p, 375-3p, and 375-5p using qPCR. ROC analysis was performed for each miRNA and for all combinations in order to determine the discriminatory capacity of V and T vs. N.

RESULTS: On comparing V vs. N miR-371a-3p achieved the highest fold change (FC) of 31.1 (p=0.023) while for T vs. N miR-375-5p performed best (FC: 46.2; p<0.001). Likewise, the most accurate AUC for V was 0.75 using miR-371a-3p, for T 0.80 using miR-375-5p. Combining the best performing miRNAs for V and T resulted in an AUC of 0.94 with a sensitivity of 93.75, specificity of 93.75, PPV of 96.8 and NPV of 83.3.

CONCLUSIONS: By combining miR-371a-3p and miR-375-5p in pcRPLND tissue samples V and T could be distinguished from necrosis/fibrosis with great accuracy. This combination of miRNAs might serve as new biomarker in the future, in order to spare miRNA-negative patients from pcRPLND. However, further studies analyzing patient's serum are needed to confirm the clinical impact of these biomarkers.

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