Squamous-cell carcinoma variant histology (SCC-VH) in muscle-invasive bladder cancer (MIBC): a comprehensive clinical, genomic and therapeutic assessment from multiple datasets

CONQUER CANCER® MERIT AWARD RECIPIENT

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Within patients with SCC, 4 pT0 (33.3%) and 10 pT≤1 (83.3%) were obtained, and no SCC pts died after a median follow-up of 10.4

months, TURB samples from all patients

nts which underwent IHC demonstrated PC

"The most significant differences in the frequency of gene alterations between SCC and UC groups involved CDKN2A, PI3KCA, and NFEZL2, all of

which were more frequently altered i SCC" Pathologic response

Achieved pT0

BACKGROUND

Pure or predominant SCC-VH is observed in MIBC. Nevertheless, limited data is available about the efficacy of neoadjuvant chemotherapy (NAC) or novel agents for this entity. We undertook this study which combined multiple clinical and genomic datasets to assess the genomic landscape of SCC, and to examine the efficacy of NAC in this disease, and present results for SCC-VH cases from PURE-01, a trial of pembrolizumab in the negadiuvant setting.

PATIENTS AND METHODS

The combined databases of the Urological Research Institute (URI, n=2,209) of San Raffaele Hospital and the Retrospective International Study of Invasive/Advanced Cancer of the Urothellum (RISC, n=2598) were queried for patients with non-metastatic MIBE treated with RC between January 1990 and September 2017 (Figure 1). The criteria for initial patient selection included: any histology, clinical Tu_nN_mMo Stage, and radical cystectomy performance with or without perioperative chemotherapy¹.

An external cohor was also analysed including 1,894 by 1 with UC 97 patients with SCC who

had their tumor assessed with an hybrid capture-based comprehensive genomic profiling (CGP) as routine finicinal partices. CGP was performed in a Clinical laboratory improvement Amendments (CLIA)-entified, College of American Pathologists (CAP)-accredited laboratory (Coundation Medicine, Inc., Cambridge, MA). The samples were assayed by CGP using adaptor-ligation and hybrid capture performed for all coding exons of from 287 (version 1) as 15 (version 2) cancer related general puls select introns from 19 (version 1) 22 (version 2) genes frequently rearranged in cancer. Sequencing of captured libraries was performed creations of the control of a control of the control of the

Finally, the Interim results of the PURE-0.1 study⁴ (NCT02736266) were recently published, experience application of 24% among the first 50 patients that of 24% among the first 50 patients that 50 patients with the same state. All of the control of 14% among the first 50 patients with the same state. All of the inclusion of non-ordan state of 14% and allow the inclusion of non-ordan state of 14% and allow the inclusion of non-ordan state of 14% and allow the inclusion of non-ordan state of 14% and 14% are the state of 14% and 14% and 14% are the first of 14% and 14% and 14% are the first of 14% are t

STATISTICAL ANALYSIS

Analyses on the URI/IRISC database were performed by grouping variant histologies into 6 categories, where pure and mised cases of each histological variant were respectively combined. Furthermore, we analysed data by separating pure from mixed cases of each variant histology. Here, 11 histological subgroups were tested as independent predictors. For example, SCC was analysed combining pure and mixed cases, and also as pure SCC and UC with SCC component, separately. The primary study endpoint was the cancer-specific survival (CSS), which was analysed across all different histological variants and according to treatment delivered. Here, UC was used as reference category while all others histological variants were compared with (Figure 2).

The secondary endpoint was the clinical-to-pathological downstaging, which was defined as a pathologic not obtained that was at least on the stage lows that have not related to a pathologic not obtained to the stage lows that the pre-NAC clinical N stage. When no variation of the N stage occurred, we used the above-mentioned criteria using the tumous stage (pre-NAC c 1 and p.T). Kaplan-Meier method was used for estimation of CSS, both defined as the period of survival from RC. Logistir regression and Cox regression of CSS, both defined as the period of survival from RC. Logistir regression and cox regression of CSS and p.T. Kaplan supportive subrevous nailves were run.

Within the FMI data, hybrid-capture based CGP of 97 patients with squamous-cell carcinoma patients were examined (Figure 9.). Tile plot was generated for SCC patients (Figure 9.). Finally, clinical-relevant gene frequency were reported according to UC and SCC histologies with associated p values (Figure 9.). All statistical tests were two-sided with a level of significance set at p-0.05. Analyses were performed using the R software environment for

CONCLUSIONS

- · SCC was the variant histology exhibited the lowest effect of neoadjuvant chemotherapy in terms of activity and CSS.
- · Genomic profiling revealed opportunities for targeted immunotherapy.
- Genomic correlates of SCC chemotherapy resistance warrant further investigation
- Finally, data coming from the PURE-01 study show un unprecedented benefit of neoadjuvant immunotherapy on SCC.

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