malignant tumor of the urinary system. Early detection is the effective way to improve the prognosis of patients with renal cell carcinoma. In the development and progression of cancer accompanied by metabolic changes, so metabolomics has special advantages in diagnosis of RCC. The aim of this study is to find discriminating metabolites from RCC through a non-target metabolomics method.

Methods: We extracted the serum samples of RCC patients and controls for HPLC-MS detection, and used quantitative analysis of multivariate statistical methods were employed to analyze the data.

Results: In this study, we found that the metabolite in RCC significantly different from the controls, metabolic pathways including arachidonic acid and sphingolipid metabolism were found to be disturbed in RCC patients compared with controls.

Conclusions: Metabolite concentration in cells of the system change is most likely to switch to immune response and energy balance. This study indicates that metabolomics may be a valuable tool for the discovery of novel cancer biomarkers in the future.

Keywords: Renal cell carcinoma (RCC); metabolomics; metabolite

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AB205. Deep sequencing reveals intensive interindividual and intraindividual heterogeneity in TCR-beta repertoire across multiple renal cell carcinoma subtypes

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Objective: Tumor immunogenicity has been proved to have an essential role in tumor development and metastasis. Cancer cell recognition of T cells can be potentially utilized in tumor prognosis and immunotherapy. However, the understanding of immune responses and T cell receptor (TCR) repertoires in many types of tumor is yet to be complete. Our aim was to explore the TCR beta-chain (TCRb) heterogeneity across renal cell carcinoma (RCC) patients, as well as the TCRb heterogeneity between tumor-infiltrating lymphocytes (TILs) and peripheral blood mononuclear cells (PBMCs).

Methods: Tumor and blood samples of thirty-nine treatment-naïve RCC patients, and blood samples of two renal neoplasm patients and ten healthy volunteers were obtained. Genomic DNA was extracted from the frozen tumor tissues and the isolated PBMCs. To prepare the TCRb library, primers were designed to amplify the CDR3 region of the *TCRb* gene for the followed high-throughput sequencing. The sequencing data was analyzed by an in-house immune repertoire analyzing pipeline, including Shannon diversity, clonotype abundance, pair-wise overlap and distance, and other analyses.

Results: TCRb repertoires in the RCC tumor tissues have lower diversity compared to the RCC PBMC samples while the TCRb repertoires in the non-carcinoma PBMC samples possess the highest diversity among them. The abundance of highly expressed clonotypes (HECs) in the RCC tumor samples is higher than the HECs in the RCC PBMC samples, whereas the abundance of HECs in the non-carcinoma PBMC samples was the lowest. The pair-wise distance data generated by comparing the overlap of any two included samples suggest that TCRb repertoires in RCC do not produce distinguishable pattern across pathologically classified subtypes. The comparison of two cladograms generated from the pair-wise distances with or without the HECs suggests that HEC was a major contributor to the intraindividual difference in TCRb repertoires between TILs and PBMCs.

Conclusions: Intensive interindividual and intraindividual heterogeneity in TCRb repertoire across multiple RCC subtypes can be observed in the aspect of diversity, abundance of HECs, and pair-wise distance; the intraindividual heterogeneity in RCC is mainly contributed by HECs.

Keywords: Renal cell carcinoma (RCC); immune repertoire; T cell receptor (TCR)

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AB206. Expression and clinical significance of CCAT2 in renal cell carcinoma and bladder cancer

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Objective: To research the expression of CCAT2 in renal cell carcinoma (RCC), bladder cancer and paired normal tumor-adjacent tissues and investigate the correlations between expression of CCAT2 and clinicopathologic characteristics for further study of the role of CCAT2 in RCC and bladder cancer.

Methods: Total RNA isolated from 40 RCC and 37 bladder cancer tissues and paired normal tumor-adjacent normal tissues which random selected from specimen bank was used for obtaining cDNA by performing reverse transcription. Using real-time PCR (RT-PCR) to detect the expression of CCAT2 in specimen, then use statistical method to analysis the relationships between the expression of CCAT2 and clinicopathologic characteristic.

Results: The expression of CCAT2 in RCC tissues was significantly lower than in paired normal tumor-adjacent tissues (P<0.01), with 33 cases (82.5%) showing down-regulation of CCAT2. While the expression of CCAT2 in bladder cancer tissues was significantly higher than in paired normal tumor-adjacent tissues (P<0.01), with 31 cases (83.8%) showing up-regulation of CCAT2. No relationships were found between the expression of CCAT2 and patients' age, gender, histology, TNM stage or AJCC stage.

Conclusions: CCAT2 is up-regulated in bladder cancer and down-regulated in RCC, indicating it may participate in the tumorigenesis and development of RCC and bladder cancer and be used as a tumor marker.

Keywords: CCAT2; expression; bladder cancer; renal cell cancer (RCC)

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AB207. RNA expression analysis of different sample storage time profiled by RNA sequencing in human bladder cancer

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Objective: Gene expression analysis is widely used in most of studies of transcriptomic. Whether the cryopreserved samples' storage time may influence the expression levels of genes is unknown. We aim to test the status of gene expression of different sample storage time during the cryopreserved processing by RNA sequencing.

Methods: We selected one tissue sample of bladder cancer to be cryopreserved. Firstly the sample was prepared to cell suspension divided into five centrifuge tube. One of five was undergone RNA sequencing processing immediately. The rest of them were storage in –80 ℃ by temperature gradient cooling method, and performed RNA sequencing after 18 h, 66 h, 10 d, 30 d of storage. Then, we calculated the RPKM and FPKM of all mapped genes and those of 12 housekeeping genes.

Results: Less than 30 d tissue storage had little effect on the total gene expression but induced changes in the transcript levels of stress-responsive genes as COX family after 18 h. Among the house keeping genes tested, the chosen 12 genes is stable.

Conclusions: This study shows that the bladder cancer sample storage in –80 ℃ can be used in related research refer to RNA sequencing. The most genes expressions are stable except several stress-responsive genes.

