explored. Small-interfering RNA (siRNA) was used to suppress CENPH expression in RCC cell lines. *In vitro* assays were performed to further explore its role in tumor progression.

Results: The expression level of CENPH was higher in ccRCC tissues and cell lines than in corresponding adjacent normal tissues and normal human proximal tubule epithelial cell line HK-2. IHC analysis revealed high expression levels of CENPH in ccRCC specimens. The ccRCC patients with higher CENPH expression had an advanced clinical stage and poorer prognosis than those with lower CENPH expression. CENPH expression was an independent prognostic marker of overall RCC patient survival in a multivariate analysis. *In vitro* assays indicated that knockdown of CENPH reduced cell proliferation, apoptosis, and cell cycle arrest at G0/G1.

Conclusions: High expression of CENPH in ccRCC indicates poor prognosis. CENPH is a novel molecule involved in ccRCC progression, which provide a potential prognostic biomarker and therapeutic target.

Keywords: Clear cell renal cell carcinoma (ccRCC); centromere protein H (CENPH); proliferation; apoptosis

doi: 10.3978/j.issn.2223-4683.2015.s202

Cite this abstract as: Wu S, Wu X. Overexpression of centromere protein H is associated with tumor progression and prognosis of clear cell renal cell carcinoma. Transl Androl Urol 2015;4(S1):AB202. doi: 10.3978/j.issn.2223-4683.2015.s202

AB203. The mutational landscapes of adrenal cortex aldosterone-producing adenoma (APA) diversified between different populations

Song Wu[1,2], Peide Huang[1,2], Meng Zhang[1,2]

[1]Shenzhen Luohu People's Hospital, Shenzhen 518001, China; [2]Shenzhen Huada Gene Research Institute, Shenzhen 518083, China

Objective: The genetic determinants of aldosterone-producing adrenal adenoma (APA), one of the most common causes of secondary hypertension, had been studied intensively in European patients but its mutational landscapes in Asian populations remained unclear. We aim to further understand the genetic determinants of APA in East Asian patients.

Methods: We perform Whole-exome sequencing and comprehensive data analyses in tumors and matched normal tissues from 22 Chinese APA patients.

Results: Notably, we identified KCNJ5 as an ultra-high frequency mutation gene (72.7%) in our cohort compared with previous studies, which highlights the importance of KCNJ5 mutations in the diagnosis and targeted therapy for East Asian APA patients. We also identified somatic mutations in another potassium channel gene and other four cancer relative genes in our APA cohort.

Conclusions: These findings extend our knowledge about the genetic mechanism of APA development and would contribute to the diagnosis and targeted therapy for East Asian APA patients.

Keywords: Adrenal adenoma; whole-exome sequencing; genetic; East Asian

doi: 10.3978/j.issn.2223-4683.2015.s203

Cite this abstract as: Wu S, Huang P, Zhang M. The mutational landscapes of adrenal cortex aldosterone-producing adenoma (APA) diversified between different populations. Transl Androl Urol 2015;4(S1):AB203. doi: 10.3978/j.issn.2223-4683.2015.s203

AB204. Application of HPLC-MS metabolomics to the characterization and possible detection of renal cell carcinoma

Song Wu[1,2], Shupeng Wang[1,2], Junyan Zhong[1,2], Meng Zhang[1,2]

[1]Shenzhen Luohu People's Hospital, Shenzhen 518001, China; [2]Shenzhen Huada Gene Research Institute, Shenzhen 518083, China

Objective: Renal cell carcinoma (RCC) is a common

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

doi: 10.3978/j.issn.2223-4683.2015.s204

Cite this abstract as: Wu S, Wang S, Zhong J, Zhang M. Application of HPLC-MS metabolomics to the characterization and possible detection of renal cell carcinoma. Transl Androl Urol 2015;4(S1):AB204. doi: 10.3978/j.issn.2223-4683.2015.s204

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

Song Wu[1,2], Yongqiang Wang[1,2], Fusheng He[1,2], Meng Zhang[1,2]

[1]Shenzhen Luohu People's Hospital, Shenzhen 518001, China; [2]Shenzhen Huada Gene Research Institute, Shenzhen 518083, China

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)

doi: 10.3978/j.issn.2223-4683.2015.s205

