10

KNOCKDOWN OF TRANSFORMING GROWTH FACTOR BETA REGULATOR 4 (TBRG4) PROMOTES APOPTOSIS IN HUMAN LUNG CANCER CELL LINE H1299 VIA REGULATING DDIT3, CAV1 AND RRM2

¹Ansheng Wang, ²Xuegang Liu, ³Wen Su, ⁴Guixin Duan, ⁵Zongyu Xie, ⁶Shanshan Chu. ¹Department of Thoracic Surgery, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ²Department of Cardiac Surgery, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ³Medical Oncology, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ⁴Department of Thoracic Surgery, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ⁵Department of Radiology, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ⁶Department of Thoracic Surgery, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China; ⁶Department of Thoracic Surgery, The first affiliated hospital of Bengbu Medical College, Bengbu, Anhui, China

10.1136/jim-2017-MEBabstracts.10

Abstract Transforming growth factor beta regulator 4 (TBRG4) gene is located on 7 p14-p13, a region correlated with many cancer types, such as hematologic malignancies, head and neck squamous cell carcinoma, and multiple myeloma. However, the role of TBRG4 in human lung cancer is largely unknown. Thus, in the present study, the TBRG4 mRNA level was evaluated in the lung cancer cell line H1299 by quantitative PCR (qPCR) after knocking down TBRG4 using lentivirus-mediated small interfering RNA (siRNA). The result showed that TBRG4 was significantly inhibited in H1299 by RNAi. Microarray analysis revealed 586 differentially-expressed genes after TBRG4 silencing. Analysis of the dataset with differentiallyexpressed genes using Ingenuity Pathway Analysis (IPA) software showed that infectious diseases, cancer, organismal injury and abnormalities were functions associated with the highest rated network. Further analysis of this network by IPA revealed that TBRG4 knockdown in H1299 cells changed the levels of downstream genes, including the upregulation of DDIT3 and downregulation of CAV1 and RRM2. These results have been validated by qPCR and Western blotting. Moreover, TBRG4 was shown to be highly expressed in carcinoma by immunohistochemstry compared with adjacent carcinomatous normal tissue. However, there were no associations between TBRG4 expression and clinicopathological characteristic, including sex, age, distant metastasis, TNM stage, and tumour grade. Taken together, TBRG4 plays an anti-apoptotic role in tumorigenesis of lung cancer via regulating DDIT3, CAV1 and RRM2 expression. The present findings are potentially significant to advance the understanding of TBRG4 as a candidate for the treatment of lung cancer.

11

META-ANALYSIS OF PROGNOSTIC VALUE OF TRANSFORMING GROWTH FACTOR-BETA (TGF- β) IN PATIENTS

F Wang. Zhoukou Normal University, Henan, China

10.1136/jim-2017-MEBabstracts.11

Objectives Transforming growth factor-beta (TGF- β) is associated with a higher incidence of distant metastasis and decreased survival. Whether TGF- β can be used as a prognostic indicator of colorectal cancer (CRC) remains controversial. Methods The Medline, EMBASE and Cochrane databases were searched from their inception to March 2016. The studies

that focused on TGF-β as a prognostic factor in patients with CRC were included in this analysis. Overall survival (OS) and disease-free survival (DFS) were analysed separately. A meta-analysis was performed, and hazard ratios (HR) with 95% confidence intervals (CI) were calculated.

Results Twelve studies were included in the analysis, of which 8 were used for OS and 7 for DFS. In all, 1622 patients with CRC undergoing surgery were included. Combined HRs suggested that high expression of TGF-β had a favourable impact on OS (HR=1.68, 95% CI 1.10 to 2.59) and DFS (HR=1.11, 95% CI 1.03 to 1.19) in CRC patients. For OS, the combined HRs of Asian studies and Western studies were 1.50 (95% CI 0.61 to 3.68) and 1.80 (95% CI 1.33 to 2.45), respectively. For DFS, the combined HRs of Asian studies and Western studies were 1.42 (95% CI 0.61 to 3.31) and 1.11 (95% CI 1.03 to 1.20), respectively.

Conclusions This meta-analysis demonstrates that TGF- β can be used as a prognostic biomarker for CRC patients undergoing surgery, especially for CRC patients from Western countries.

12

THE IGCA STAGING SYSTEM COMPARED WITH AJCC7 SYSTEM IN STRATIFYING SURVIVAL OF PATIENTS WITH CANCER

F Wang. Zhoukou Normal University, Henan, China

10.1136/jim-2017-MEBabstracts.12

Objectives A new staging system recently proposed by the IGCA has demonstrated a better capacity for stratifying different prognoses for gastric cancer than the 7th edition AJCC staging system (AJCC7). The aim of this study was to evaluate the efficacy of the IGCA system in Chinese patients.

Methods Medical records of patients with gastric cancer who received curative surgery in our centre from January 2003 to December 2011 were reviewed retrospectively. All the lesions were staged according to both AJCC7 and IGCA staging systems. Overall survival (OS) of the patients was used as the observation endpoint.

Results One thousand five hundred and twenty-six cases were included in this study. By comparing the AJCC7 system with the IGCA system, 395 cases were stratified into different stages, most of which were in stage III. The IGCA system could better stratify stage IIIB and IIIC patients (5-year OS, 38.1% vs. 29.0%; p=0.005) than the AJCC7 system (5-year OS, 38.2% vs. 35.9%; p=0.148). T3N3bM0, T4aN2M0 and T4aN3bM0 made up 97.5% (385/395) of the stage shift. T3N3bM0, which was stratified to stage IIIB in the AJCC7 system, showed a significantly poorer prognosis than T4aN2M0 and T4aN3aM0, which were staged to IIIB and IIIC in the same system. The improper staging was revised in the IGCA staging system.

Conclusions The IGCA staging system can stratify stage III gastric cancer patients more correctly than the AJCC7 system. Acknowledgement Supported by the National Natural Science Foundation of China (Grant No. 14B520013) and the Scientific Research Project from the open fund of Henan Key laboratory (Grant No. 172400410344).