Transcriptomic changes during carbon ion radiotherapy of prostate cancer patients detected by RNA-seq

Jin Meng [1] Ping Li[1] Shen Fu [1,2#]

1 Radiation Oncology Dept, Shanghai Proton and Heavy Ion Center (SPHIC), 4365 Kang Xin Rd, Pudong New District,Shanghai 201321, China
2 Radiation Oncology Center, Fudan University Shanghai Cancer Center (FUSCC)
399 LingLing Rd, Xu Hui District, Shanghai 200032, China
correspondence authors: Shen Fu E-mail: shen_fu@hotmail.com

Clinics:GU
Biology:Biomarkers
Words: 296

Purpose: Identifying novel molecular markers for assessing dynamic changes during carbon ion radiotherapy is necessary for understanding the mechanism of carbon ion and may help in improving the clinical outcome of treatment. We aimed to detect the global gene expression profile of carbon ion therapy in prostate cancer patients by RNA-seq.
Materials and methods: Sixteen patients with pathologically confirmed prostate cancer were treated with carbon ion therapy from June to Sep 2014 at Shanghai Proton and Heavy Ion Center (SPHIC). The patients with intermediate or high risk disease received neo-adjuvant hormone therapy for 2~3 months, followed by concurrent hormone and carbon ion irradiation. (63-66GyE/23-24Fx with one fraction per day and five days per week). The carbon ion related transcriptomes were determined by RNA-Seq, and differentially expressed genes (DEGs) were compared before and after the treatment. In view of further validation of our results, we investigated the effects of irradiation with 2GyE carbon beams on gene expression changes in the DU145 human prostate cancer cell line, and the expression of selected DEGs was validated by quantitative RT-PCR.

Results: A total of 474 DEGs were identified using peripheral blood mononuclear cell(PBMC) of prostate cancer patients by RNA-Seq, while 1854 DEGs were identified in the DU145 human prostate cancer cell line. Of these genes, 48 were common DEGs. DEGs were retrieved for Gene Ontology(GO) and pathway analysis. We first demonstrated that immune response and microtubule formation related genes showed significant expression changes during carbon ion treatment. Gene co-expression network analysis identified 6 core regulatory factors (IL7R, TNF, TUBA1B, UBC, TUBB4B and LMNA) that are involved in carbon ion radiotherapy.

Conclusion: This study provides the first RNA-Seq-based transcriptome study of dynamic changes in carbon ion radiotherapy. Many novel candidate genes may have functional significance during treatment of prostate cancer patients.