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* Foundation items: National Key R&D Project of Chinese Ministry of Science and Technology (2018YFE0205100), Key Program of National Natural Science Foundation of China (11875299) and National Natural Science Foundation of China (11675234)

5 - 50 A Radiation Sensitivity Prediction Model

Jin Xiaodong

Clinical trials show that carbon ion radiotherapy has excellent antitumor effects. Moreover, it is suggested that carbon ion radiotherapy is an effective treatment for tumors that are resistant to conventional X-ray radiotherapy. However, the high cost of constructing the accelerator system limits its practical application. Carbon ion radiotherapy has the capacity to treat only 0.015% of the total patient population with a newly diagnosed cancer[1]. Therefore, selecting patients who can derive the greatest benefit from carbon ion radiotherapy is of great importance.

In previous study, we obtained a NSCLC cell line with raidoresistance through fractionated X-ray irradiation and its expression patterns of mRNAs were explored with high-throughput sequencing assays. We observed the expressions of circRNA ZNF208 and lincRNA H19 were significantly upregulated in the radioresistant NSCLC cells. Then, the biological characters of these noncoding RNAs in regulating radiosensitivity were evaluated. We found that circZNF208 could regulate NSCLC sensitivity to X-ray but had no effect on NSCLC cells exposed to carbon ions[2]. Meanwhile, the radiosensitivity of NSCLC cell line was substantially augmented upon exposure to low-LET X-ray and high-LET carbon ions when the expression of lncRNA H19 was decreased[3].

Based on the results mentioned above, we constructed a radiation sensitivity prediction model which facilitates appropriate selection of patients for carbon ion radiotherapy, as shown in Table 1.

Table 1 A radiation sensitivity prediction model.

	circZNF208	**lncRNA H19**	**Radiotherapy**
Type I	low	low	X-ray
Type II	high	low	Carbon ion
Type III	high	high	Carbon ion with other modalities such as chemotherapy

According the biological characteristics of circZNF208 and lncRNA H19 in tumor, the samples or patients with NSCLC could be divided into three types. Type I, which has low expressions of circZNF208 and lncRNA H19, was suitable for X-ray radiotherapy. And carbon ion radiotherapy will be the most beneficial for patients with high circZNF208 but low H19 expressions (Type II). Moreover, if both circZNF208 and H19 have the high expressions (Type III), patients with NSCLC should be treated with carbon ion radiotherapy combined with other modalities such as chemotherapy.

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5 - 51 The Function of RPS27a in Apoptosis of Non-small Cell Lung Carcinoma Cells Induced by Carbon Ion Radiation*

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Lung adenocarcinoma (LUAD) is the main histological subtype of lung cancer, and the 5-year overall survival rate of LUAD is less than 20%[1]. However, the mechanism of LUAD development is complex, and the effect of oncogenes on LUAD is still unknown. This study used the A549 cells of non-small cell lung carcinoma cells (NSCLC) as a model to address these questions. The present study revealed that ribosomal protein S27a (RPS27a) directly bound RPL11, and RPS27a knockdown enhanced the binding of RPL11 and MDM2, thereby inhibiting MDM2-mediated p53 ubiquitination and degradation in A549 cells.

The silver stained image of the binding proteins revealed a band at approximately 18 kDa (Fig. 1(a)). The band was further analyzed by MS, and a total of 133 proteins were identified in the IP protein sample. Among which 43 interactors were RPs (Fig. 1(b)). The combined degree of RPS27a was highest. 4 Gy carbon ion irradiation (CIR), a common experimental dose[2], was used to induce apoptosis of A549 cells. Then, the increased apoptosis of A549 induced by CIR was observed and the decreased expression of RPS27a were time dependent. The correlation analysis suggested that the RPS27a level was related to the late apoptotic ratio after CIR. Therefore, A549 cell apoptosis may be associated with decreased RPS27a expression, and we were able to induce apoptosis of A549 cells by decreasing RPS27a expression. The knockdown of RPS27a increased in MDM2 and p21 protein levels, G1-phase arrest and apoptosis of A549 cells. Therefore, RPS27a might be a potential target in the treatment of NSCLC.

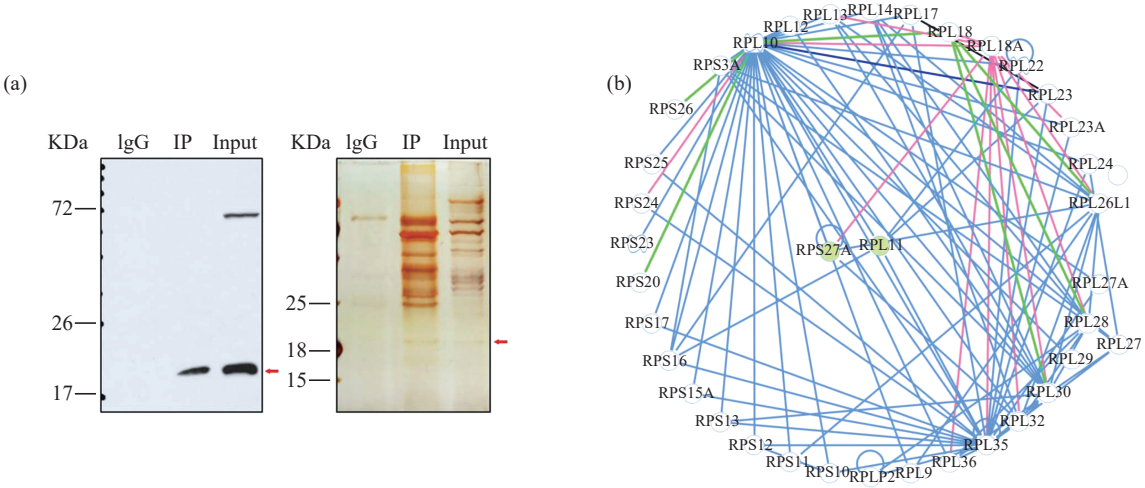

Fig. 1 (color online) Identification of RPs interacting with RPL11 in A549 cells. (a) The endogenous RPL11-interacting proteins were pulled down by anti-RPL11 antibody. The immunoprecipitates were separated by SDS-PAGE, then silver stained. The band (approximately 18 kDa) containing proteins strongly bound to RPL11 was digested with trypsin and analyzed with LC-MS/MS, (b) Interaction network of RPs with RPL11, on the basis of the STRING database.

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* Foondation item: National Key R&D Program of China (2018YFE0205100) and National Natural Science Foundation of China (11875061)