20(S)-PPD induces vasorelaxation via an endothelium-independent pathway. The inhibition of voltage-dependent Ca^{2+} channels and receptor-operated Ca^{2+} channels and the activation of Ca^{2+}-activated K^{+} channels are probably involved in the relaxation.

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4 - 60 Study on Protein Marker of Hepatotoxicity Induced by Iron Ion Radiation in Mice

Li Hongyan and Zhang Hong

It is important to determine whether exposure to cosmic radiation induces disease or toxicity in astronauts and space travellers[1]. In this investigation, we used a comparative proteomics approach based on a 2-DE reference map to detect alterations in protein expression in the serum of Swiss–Webster mice following exposure to iron ion radiation (IIR), and to identify biomarkers of liver toxicity. The results reveal the underlying molecular mechanisms of liver disease or toxicity following exposure to IIR.

Compared with the control (Fig. 1), the irradiated mice showed inflammatory cell in filtration, blood vessel congestion and dilatation, hepatic necrosis in the liver lob-ules, and the hepatic portal vein had obvious pathological changes. The pathological evidence demonstrated that IIR resulted in long-term liver injury in mice. Differential serum protein spots between irradiated mice and controls were screened using 2-DE and the differentially expressed protein spots detected by PDQuest 8.0 software based on the ± over 1.5-fold difference in the protein quantities (normalized spot volume) was used as the standard to determine differential spots. A total of 11 differentially expressed spots were enlarged to show in Fig. 2. We profiled serum proteome alterations in mice after IIR exposure using 2-DE, and identified potential biomarkers of toxicity in liver tissues. To the best of our knowledge, this is the first study to demonstrate the serum proteomic profiles underlying liver toxicity in mice after IIR.

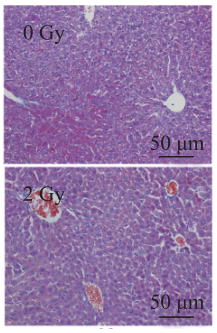

Fig. 1 (color online) Hepatic histological examination in male mice at 3 months after IIR. Photomicrographs of sections stained with H&E (magnification 200 ×), bar= 50 μm.

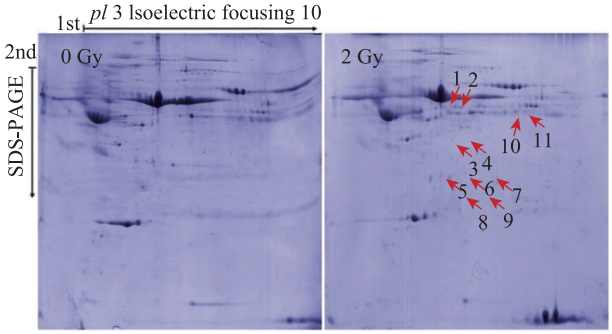

Fig. 2 (color online) The protein profiles and differentially expressed spots of mice serum at 3 months after IIR. 10 μL serum were separated using IEF of pH 3∼10, followed by 12% SDS-PAGE and visualized by CBB-R 250 staining. Red arrows represent increased expression.

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