

Transcriptome Analysis of Dry and Soaked Tomato (*Solanum lycopersicum*) Seeds in Response to Fast Neutron Irradiation

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Abstract : Fast neutron irradiation (FNI) can cause mutations on plant genome but, in the most of cases, these irradiated plants have not shown significant characteristics phenotypically. In this study, we utilized RNA-Seq to generate a high-resolution transcriptome map of the tomato (*Solanum lycopersicum*) genome effected by FNI. To quantify the different transcription levels in tomato irradiated by FNI, tomato seeds were irradiated by using MC-50 cyclotron (KIRAMS, Korea) for 0, 30 and 90 minutes, respectively. To investigate the effects on the pre-soaking condition, experimental groups were divided into dry and soaked seeds, which were soaked for 8 hours before irradiation. There was no noticeable difference in the percentage germination (PG) among dry seeds, while irradiated soaked seeds have about 10 % lower PG compared to the unirradiated control group. Using whole transcriptome sequencing by HiSeq 2000, we analyzed the differential gene expression in response to different time of FNI in dry and soaked seeds. More than 1.4 million base pair reads were mapped onto the tomato reference genome and the expression pattern differences between irradiated and unirradiated seeds were assessed. In 0, 30 and 90 minutes irradiation, 12,135, 28,495 and 28,675 transcripts were generated, respectively. Gene ontology analysis suggested the different enrichment of transcripts involved in response to different FNI. The present study showed that FNI effects on plant gene expression, which can become a new parameters for evaluating the responses against FNI on plants. In addition, the comparative analysis of differentially expressed genes in D and S seeds by FNI will also give us a chance to deep explore novel candidate genes for FNI, which could be a good model system to understand the mechanisms behind the adaption of plant to space biology research.

Keywords : tomato (*solanum lycopersicum*), fast neutron irradiation, RNA-sequence, transcriptome expression

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