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ANALYSING THE SPECTRUM OF SPACEFLIGHT-INDUCED MUTAGENESIS VIA HIGH THROUGHPUT SEQUENCING

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Rice is an important staple food crop, and it is also the first crop that has been subjected to spaceflight-induced mutagenesis. In the present study, whole-genome sequencing of rice mutants selected following mutagenesis induced by space flight was conducted. The main results were as follows: (1). Three mutants named H153, H398 and H399 were selected following spaceflight-induced mutagenesis, the genome mutation number observed was more than 10000 via high throughput sequencing. Single nucleotide variation (SNV) and small insertion or deletion (Indel) shorter than 5 bp made up the most majority of all mutations. (2). Validation of mutations in the mutant H153, H398 and H399 were performed by using single molecule sequencing (SMRT). The validation revealed a very low false positive rate in the mutations detected, indicating that the mutation discovery by using illumina sequencing was highly accurate. Based on the discovered mutation data, the mutation rate in the H153, H398 and H399 was 7.1×10^{-4} , 6.8×10^{-5} and 6.6×10^{-5} , respectively. (3). Many structural variants (SVs) with size larger than 50 bp were detected in the three mutant H153, H398 and H399. Moreover, SNVs were densely distributed around the SVs and therefore formed many mutation clusters as revealed by visualized analysis. (4). Effects of all the mutations detected were analyzed and predicted, and the percentage of mutations that put highly impact on the gene was 1.98%. For these genes predicted to be highly impacted, nonsignificant GO term was found, indicating that the genomic mutations may put an unbiased impact on biological processes, cellular functions and pathways.

Country or International Organization

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