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WHOLE GENOME SEQUENCING OF RICE MUTANTS INDUCED BY GAMMA RAYS AND ION BEAMS

Gamma rays have been used for several decades in mutation breeding as a physical mutagen. Though gamma ray irradiation has been used to induce many mutants, detailed characteristics of mutated DNA sequence have not been clarified enough. A newly introduced physical mutagen, ion beams, has attracted breeders' attention. We present the results of analysis of DNA mutation of rice mutants induced by gamma rays and ion beams using whole genome sequencing.

Oryza sativa L. cv. Hitomebore was used for irradiation. Unhulled dry seeds were irradiated with 250Gy gamma rays, at dose rate 10Gy/h. Hulled dry seeds were irradiated with 220MeV carbon ions (LET 107KeV/ μ m), at dose rate 30Gy/h.

Seven and eight mutants induced by gamma rays and ion beams were selected, by morphological traits, respectively. All DNA in leaves of mutants in M4 or M6 generation were extracted and used for DNA library construction and whole-genome sequencing. Paired-end (2 \times 150 bp) sequencing was performed in Illumina X Ten to sequence the genome to about 30-fold depth for each sample.

Averagely, 81 single base substitution (SBS), 23 deletions and 11 insertions were detected in each rice mutant induced by gamma rays. In contrast, 65 single SBS, 17 deletions and 10 insertions were detected in each mutant induced by ion beams. A t-test showed that the numbers of SBS and deletions induced by gamma rays were significantly higher than those induced by ion beams. The structure variation (SV) analysis averagely detected one SV (large deletion, inversion or duplication) in each mutant induced by ion beams while none in that by gamma rays.

Gamma rays trend to induce more point mutations while ion beams induce more SVs, which might be due to notable difference in linear energy transfer (LET) value between these two types of radiations.

Country or International Organization

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