

FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



Contribution ID: 48

Type: Poster

GENOMIC VARIATION CHARACTERISTICS OF GAMMA RADIATION-INDUCED MUTATIONS IN M1 POPULATION OF THE RICE JAPONICA VARIETY GAOGENGUO

Radiation-induced mutation can generate useful genetic variation in crops and has been widely used for rice germplasm innovation. To determine the pattern of DNA polymorphism in radiation-induced mutations in M1 population, we performed whole genome sequencing of rice cultivar Gaogengnuo lines treated with 300 Gy and 400 Gy ⁶⁰Co-gamma radiations. The Gaogengnuo resequencing data of 4×fold coverage was 96.24% compared with the *Oryza sativa* L. Japonica Nipponbare reference genome, in Gaogengnuo genome, a total of 1,002,114 polymorphic sites were detected, including 878,381 single nucleotide polymorphisms (SNPs), 123,733 insertion/deletion polymorphisms (InDels), and 12,805 structural variations. Compared with Nipponbare, the two M1 populations that received the different doses of gamma radiation, 300 Gy and 400 Gy, contained 429,809 and 684,221 polymorphic sites, and 9,075 and 8,852 structural variations, respectively. Through integrative analysis of resequencing data, we identified polymorphisms between Gaogengnuo and 300 Gy and Gaogengnuo and 400 Gy. We identified 67,885 and 69,899 InDels and 609,209 and 632,745 SNPs between 300 Gy and Gaogengnuo and between 400 Gy and Gaogengnuo, respectively. We identified 2,682 homozygous SNPs and 2,988 homozygous InDels present in Gaogengnuo, 300Gy and 400Gy. These genetically stable variants will be useful for rice breeding and functional research. Gene ontology analysis revealed that genes associated with metabolic process, binding function, and membrane may be susceptible to gamma radiation.

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Track Classification: New challenges and technologies in plant genomics and breeding