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Space environment induced mutations prefer to occur at polymorphic sites of rice genomes»

Y. Li^a, M. Liu^b, Z. Cheng^{a, b} and Y. Sun^{a, b}, 🛃 🖂

^aDepartment of Life Science and Engineering, Harbin Institute of Technology, Harbin, PR China ^bInstitute of Environmental Systems Biology, Dalian Maritime University, Dalian, PR China Received 11 September 2006; revised 12 March 2007; accepted 16 April 2007. Available online 16 May 2007.

Abstract

To explore the genomic characteristics of **frice** mutants induced by space environment, space-induced mutants 971-5, 972-4, and R955, which acquired new traits after space flight such as increased yield, reduced resistance to **frice** blast, and semi-dwarfism compared with their on-ground controls, 971ck, 972ck, and Bing95-503, respectively, together with other 8 japonica and 3 indica **frice** varieties, 17 in total, were analyzed by amplified fragment length polymorphism (AFLP) method. We chose 16 AFLP primer-pairs which generated a total of 1251 sites, of which 745 (59.6%) were polymorphic over all the genotypes. With the 16 pairs of primer combinations, 54 space-induced mutation sites were observed in 971-5, 86 in 972-4, and 5 in R955 compared to their controls, and the mutation rates were 4.3%, 6.9% and 0.4%, respectively. Interestingly, 75.9%, 84.9% and 100% of the mutation sites identified in 971-5, 972-4, and R955 occurred in polymorphic sites in **frice genomes** and might share a common **fmechanism** with other types of mutagens. It also implies that polymorphic sites in **formers** are potential "hotspots" for mutations induced by the space environment.

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Abstract

To explore the genomic characteristics of rice mutants induced by space environment, space-induced mutants 971-5, 972-4, and R955, which acquired new traits after space flight such as increased yield, reduced resistance to rice blast, and semi-dwarfism compared with their on-ground controls, 971ck, 972ck, and Bing95-503, respectively, together with other 8 japonica and 3 indica rice varieties, 17 in total, were analyzed by amplified fragment length polymorphism (AFLP) method. We chose 16 AFLP primer-pairs which generated a total of 1251 sites, of which 745 (59.6%) were polymorphic over all the genotypes. With the 16 pairs of primer combinations, 54



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