The identification of specific cDNA clones from tall and dwarf rice plants

The use of dwarfing genes in rice breeding has proceeded for several years without a clear understanding of the genetic, hormonal and physiological mechanisms involved. This issue was addressed by focussing on the isolation of specific clones from tall- and dwarf-derived cDNA libraries. The materials used include near-isogenic lines of the tall rice cultivar "Shiokari", differing at the DGWG or "Tanginbozu" dwarfing gene loci. Also used were tall and dwarf "Ginbozu" rice, the latter having been induced by treatment with 5-azacytidine, a potent demethylating agent. Subtractive and differential hybridisation have, to date, identified several candidate tall- and dwarf-specific clones. Their further characterisation is currently underway.

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Linkage analysis for the gametic lethal gene of a rice variety "Koshihikari" and the semi-dwarfing gene induced in "Koshihikari"

"Koshihikari", a Japanese tall variety, is now most widely cultivated in Japan because of its good quality and taste, but is extremely poor in lodging resistance. In order to create a semi-dwarf "Koshihikari", large scale mutation breeding was carried out at Hokuriku Agricultural Experiment Station, resulting in the production of an excellent semi-dwarf mutant strain "Hokuriku 100." It has extensively been used as cross parent. Genetic analyses revealed that the semi-dwarfness of "Hokuriku 100" is controlled by two mutant genes, a recessive semi-dwarfness gene sd(t) and a non-gametic lethal gene lt^m mutated from the genetic lethal gene of "Koshihikari" lt, which would cause abortion of both male and female gametes when it occurs together with sd(t). Further analyses led to conclude that lt is located on chromosome 9, sd(t) on chromosome 10.

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Identification of four loci for genetic male sterility in rice

The five spontaneously mutated sterile lines, Line 5495ms, Line 5683ms Milyang 55ms, Milyang 67ms and Milyang 77ms, and the male sterile line Milyang 54ms, bred by transferring the artifically induced genetic male sterility of IR 36ms, were tested for inheritance and allelism relations. The F_1 from crossing the male sterile and the original line exhibited normal seed fertility. The segregation ratio in F_2 showed that the male sterile mutants were controlled each by a single recessive gene. Allelism test with those six recessive male sterility genes revealed that Line 5495ms, Line 5683ms and Milyang 54ms are controlled by the common gene, and Milyang 55ms, Milyang 67ms and Milyang 77ms each by a different gene. Thus, four different loci for male sterility in rice were found from the six male sterile lines tested. Many male sterile rices reported in literature were mutants induced by EI, x-rays or γ-rays. Most remained unidentified in their allelic relationship. There is a need for international co-operation to genetically identify reported male sterilities.

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