S2-1

Functional Genomics of Rice by T-DNA Tagging

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POSTECH

During the past four years we have produced over 100,000 transgenic rice lines that carry T-DNA insertion. T-DNA was inserted into rice chromosome at an average of 1.4 genetic loci per plant. It can be estimated that the probability of finding a T-DNA insertion within a given gene from our insertional lines is approximately 60%. The binary T-DNA vector used in the insertion contained the promoterless β-glucuronidase (gus) reporter gene. This gene trap vector is designed to detect a gene fusion between gus and the endogenous gene that is tagged by the T-DNA. It was shown that 2–5% transgenic plants were GUS positive in the tested organs. Analysis of the T-DNA flanking sequences resulted in identification of knockout genes, which are disrupted by T-DNA insertion. Some of these lines showed co-segregation of T-DNA and a mutant phenotype. For reverse genetics approach, DNA pools have been prepared from the T-DNA tagged lines. For more efficient use of the lines, we are systemically determining the border sequences of each T-DNA insertion. The data will be valuable in identifying insertional mutant lines and understanding functional roles of rice genes.

S2-2

Present and Future of Hot Pepper Genomics

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We have been conducting a genome research of hot pepper since 1996 as a comprehensive group effort. The objectives of our research is to construct a molecular linkage map based on RFLP, AFLP and SSR. Up to now, we have constructed an interspecific molecular linkage map of pepper using an F_2 population from a cross between Capsicum annuum cv.TF68 and C. chinense cv.Habanero. For physical analysis, we also constructed a 15$\times$ genome size BAC library from C. annuum cv.CM334, which is known for strong resistance against Phytophthora capsici. Based on this molecular linkage map, the mature fruit color determined by carotenoid pigments was investigated genetically and shown to be cosegregated with psy encoding phytoene synthase of carotenoid biosynthesis pathway. Understanding pungency at molecular level, placenta-specific cDNA clones were isolated from a highly pungent cultivar cv.Habanero using the suppression subtractive hybridization (SSH) method and are now being further investigated genetically and biochemically. To study quantitative resistance of Phytophthora and virus, we have analysed 100 F_2 plants as mapping population derived from a cross between cultivar CM334 and Chilsuncho.