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MODIFICATION OF UNMETHYLATED CYTOSINE INTO THYMINE IN SD1 CAUSES SEMI DWARFING IN WHITE PONNI RICE MUTANT

Mutants of Improved white ponni rice (IWP) along with non-irradiated control lines were evaluated over 6 generations. Test lines and controls were genotyped using SNPs and a few haplotypes were identified. Bioinformatic analyses revealed the presence of multiple mutations in each locus and the presence of splice variants and multiple ORFs were analysed. DNA methylation at C5 of cytosine is a mechanism of gene expression regulation. This indicates the presence of chromatin modification and transcriptional gene silencing. From SNP data sets of the tested samples and control white ponni, the conversion of unmethylated Cytosine to Thymine were found in regions of SD1 gene located in chromosome 1. White ponni control sample was having two Cytosines (CC) which were completely converted into Thymines (TT) in Nipponbare. Whereas, in BRNS-WP-15-5 mutant conversion of C to A at second C is found. BRNS- WP-22-2 is exactly like white ponni control in three base positions vulnerable for mutations. The in-depth haplotype analyses of these SNPs revealed the presence of four different forms of SD1 with its three alternate forms viz. SD1 (protein kinase), SD1 isoform x2, SD1-8, SD1-8 isoform X1. With these four variants six more loci viz., Os01g0784700, ARK1, OsJ_19099, OsJ_11431, OsJ_03701, Os07g0550500 were found to exist in multiple ORFs. Conversion of unmethylated C into T changes the functional SD1 ORF into silenced locus. In chromosome 1 SD1 loci position 33252230 bases and 33253569 bases are vulnerable for CC to TC and TT mutation. This information could be very significant in terms of either generating desired phenotype by modifying the loci or by transfer by conventional breeding tools. The base change specific markers if developed could help in screening larger germplasm sources for identification of desirable genotype.

Country or International Organization

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