

Genetic diversity of the Waxy gene in foxtail millet (*Setaria italica* (L.) P. Beauv.)

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With a total of 113 foxtail millet accessions, agronomic traits were surveyed and the molecular differences among non-waxy, low amylose, and waxy phenotypes were clarified with genomic DNA of *Waxy* (*Wx*) gene. After approximately 4kb portion of the *Wx* gene was amplified using four specific primer sets, PCR types were determined with the patterns of PCR amplification depending on phenotypes. The expected size produced by four specific primer sets in non-waxy landraces (Type I), the 440 bp insertion amplified by M5/R9 in low amylose phenotype (Type VI) and no detection of PCR amplicons with either ex1/ex2 or ex2int2/ex4r in waxy accessions (Type IV or V) were observed. With directly sequenced PCR products, single nucleotide polymorphisms, mostly located at 5' UTR and intron were observed. Three polymorphisms in coding regions were nonsynonymous. Interestingly, the phenotype of No. 88 was still non-waxy, although seven nucleotides long (AATTGGT) of insertion at 3,336 bp in No. 88, leading to 78 amino acids shorter than other accessions. The rapid decline of r^2 in the sequenced region with ex1 or ex2 suggested this study used a low level of linkage disequilibrium and limited haplotype structure. K_s value between non-waxy and waxy phenotypes was 0.77 and waxy phenotypes were diverged from non-waxy phenotype at 27.6 MYA.

Construction of introgression lines carrying wild rice (*Oryza rufipogon* Griff.) segments in cultivated rice (*Oryza sativa* L.) background and QTL dissection of agronomic and domesticated traits

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A set of 126 introgression lines (ILs) carrying variant introgressed segments from a presumed wild progenitor, *O. rufipogon* Griff. Acc. W1944, collected from China, in the background of an elite Korean japonica cultivar (*O. sativa* L.), Hwayeongbyeon, was constructed using marker assisted selection technique. The 126 ILs have different W1944 segments on each chromosome, 100% of chromosome 1 carried with *O. rufipogon* introgressed segments, while for chromosome 10, the coverage was only 33.3%. The mean number of homozygous and heterozygous donor segments were 3 (ranging 0-7) and 4.7 (ranging 1-14.5), respectively, and 31.6% of introgressed segments had sizes less than 10.5 cM. A total of 54 quantitative trait locus (QTLs) and three loci associated with qualitative variation for pericarp coloration were identified and confirmed using single point analysis. The number of QTLs per trait ranged from 2 to 7. Phenotypic variation associated with each QTL varied from 8.6% to 52.2%, with an average of 17.13%. For 14 (25.9%) of the QTLs detected in this study, the *O. rufipogon*-derived allele contributed a desired agronomic effect despite the overall inferior characteristics of the wild phenotype. Favorable alleles from *O. rufipogon* were identified for panicle number, panicle length, days to heading, secondary branches, spikelet per panicle, 1000 grain weight, and yield per plant.