

D-D2-11**Allelic variation by domestication in wild and cultivated soybean using SSR markers****Tae-Hwan Jun¹, Kyujung Van¹, Moon Young Kim^{1,2}, Donghyun Kim¹, Suk-Ha Lee^{1,2,*}**¹Department of Plant Science, Seoul National University, Seoul, 151-921, Korea²Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

Soybean [*Glycine max* (L.) Merr.] is widely considered to have been domesticated from the wild soybean (*Glycine soja* Sieb. & Zucc.). However, many valuable genes of wild soybean for improvement have been eliminated by genetic bottlenecks during domestication. Distribution of alleles associated with seed protein content was characterized between 192 wild and 159 cultivated accessions. A total of eight simple sequence repeat (SSR) loci were tested including the three SSR loci showed significant allele variation between 48 "high protein (HP)" and 48 "lowprotein(LP)" accessions used for association analysis. In most of SSR loci, the number of alleles per locus and the level of genetic diversity in wild soybean were higher than those in cultivated soybean, representing the genetic bottlenecks occurred during domestication. A total of 122 of 125 alleles were present in wild soybean, but only 72 alleles were detected in cultivated soybean. The genetic diversity averaged 0.742 in wild soybean and 0.641 in cultivated soybean. Three SSR loci observed significant allele variation between HP and LP groups showed strong differentiation between wild and cultivated soybean with an average of 0.319 in F_{ST} value. Our results suggest that the predominant alleles at Satt384 (113 bp for wild soybean and 148 bp for cultivated soybean) clearly represented the result of domestication, and the predominant allele in HP group, 119 bp at Satt384, would be possible allele responsible for controlling soybean seed protein content.

*Corresponding author: Tel. 02-880-4545, e-mail: sukhalee@snu.ac.kr

D-D2-12**Genetic diversity of the *Waxy* gene in foxtail millet [*Setaria italica* (L.) P. Beauv.] accessions****Kyujung Van¹, Shiho Onoda¹, Moon Young Kim^{1,2}, Kyungdo Kim¹, Suk-Ha Lee^{1,2,*}**¹Department of Plant Science, Seoul National University, Seoul, 151-921, Korea²Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

The *Waxy* (*Wx*) gene product controls the formation of a straight chain polymer of amylose in the starch pathway. Dominance/recessiveness of the *Wx* allele is associated with amylose content, leading to non-waxy/waxy phenotypes. For a total of 113 foxtail millet accessions, agronomic traits and the molecular differences of the *Wx* gene among non-waxy, low amylose, and waxy phenotypes were surveyed. The expected size was produced by four specific primer sets in non-waxy (Type I) and the 440 bp insertion amplified by M5/R9 in low amylose (Type VI) and no detection of PCR amplicons with either ex1/ex2 or ex2int2/ex4r in waxy (Type IV or V) were observed. With directly sequenced PCR products, 17 single nucleotide polymorphisms (SNPs) were observed from non-coding regions, while 3 SNPs from coding regions were nonsynonymous. Interestingly, the phenotype of No. 88 was still non-waxy, although seven nucleotides (AATTGGT) insertion at 3,336 bp led to 78 amino acids shorter than other non-waxy accessions. The rapid decline of r^2 in the sequenced region with ex1 or ex2 suggested a low level of linkage disequilibrium and limited haplotype structure. K_s value between non-waxy and waxy phenotypes and estimation of evolutionary events indicate early divergence of *S. italica* in Panicoideae.

* Corresponding author: Tel. 02-880-4545, e-mail: sukhalee@snu.ac.kr