

Division-4-06

Genetic Insights into Domestication Loci Associated with Awn Development in Rice

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[Abstract]

Rice (*Oryza sativa* L.) is a widely studied domesticated model plant. Seed awning is an unfavorable trait during rice harvesting and processing. Hence, awn was one of the target characters selected during domestication. However, the genetic mechanisms underlying awn development in rice are not well understood. In this study, we analyzed the genes for awn development using a mapping population derived from a cross between the Korean *indica* cultivar ‘Milyang23’ and NIL4/9 (derived from a cross between ‘Hwaseong’ and *O. minuta*). Two quantitative trait loci (QTLs), *qAwn4* and *qAwn9* were mapped on chromosome 4 and 9, respectively, increased awn length in an additive manner. Through comparative sequencing analyses parental lines, *LABA1* was determined as the causal gene underlying *qAwn4*. *qAwn9* was mapped to a 199-kb physical region between markers RM24663 and RM24679. Within this interval, 27 annotated genes were identified, and five genes, including a basic leucine zipper transcription factor 76 (*OsZIP76*), were considered candidate genes for *qAwn9* based on their functional annotations and sequence variations. Haplotype analysis using the candidate genes revealed tropical *japonica* specific sequence variants in the *qAwn9* region, which partly explains the non-detection of *qAwn9* in previous studies that used progenies from interspecific crosses. This provides further evidence that *OsZIP76* is possibly a causal gene for *qAwn9*. The *O. minuta qAwn9* allele was identified as a major QTL associated with awn development in rice, providing an important molecular target for basic genetic research and domestication studies. Our results lay the foundation for further cloning of the awn gene underlying *qAwn9*.

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