

Genetic variation of *TaMyb10* that affects both seed color and germination of wheat

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Abstract

Pre-harvest sprouting (PHS), the germination of grain before harvest, is a serious problem resulting in wheat yield and quality losses. We mapped the PHS resistance gene *PHS-3D* from synthetic hexaploid wheat to a 2.4 Mb presence-absence variation (PAV) region and found that its resistance effect was attributed to the pleiotropic *Myb10-D* by integrated omics and functional analyses. Three haplotypes were detected in this PAV region among 262 worldwide wheat lines and 16 *Aegilops tauschii*, and the germination percentages of wheat lines containing *Myb10-D* was approximately 40% lower than that of the other lines. Transcriptome and metabolome profiling indicated that *Myb10-D* affected the transcription of genes in both the flavonoid and ABA biosynthesis pathways, which resulted in increases in flavonoids and ABA in transgenic wheat lines. *Myb10-D* activates *NCED* by binding the secondary wall MYB-responsive element (SMRE) to promote ABA biosynthesis in early wheat seed development stages. We revealed that the newly discovered function of *Myb10-D* confers PHS resistance by enhancing ABA biosynthesis to delay germination in wheat. The homologous of *Myb10* from A, B, and D genomes have been characterized from 416 bread wheat and 302 *Ae. tauschii* accessions. Among them, 61.3% (255 out of 416) of *TaMyb10-A* sequences had a 214-305bp deletion in the signal and beginning of amino acid coding region; 79.3% (330 out of 416) of the *TaMyb10-B* sequences have 19bp deletion in the third exon region; 40.8% (293 out of 718) accessions don't have the 2.4Mb fragment (in/del mutations) on Chr3D that harbor *Myb10-D/PHS-3D*. For the 672 genes with full CDS, an SNP in *Myb10-A*, three SNPs in *Myb10-B*, and four SNPs in *Myb10-D* were identified. The divergence of *Myb10* showed little relationship with the geographical position. And the ability for different *Myb10* proteins binding the promoter of downstream flavonoid and ABA pathway genes *CHS*, *DFR*, and *NCED* was similar. We found that *Myb10-A*, *Myb10-B* and *Myb10-D* have redundant roles in the regulation of seed color and germination. Though, accessions carrying only *Myb10-D* can result in red seed color and lower germination percentages, which revealed that the function of *Myb10-D* has a stronger effect than *Myb10-A* and *Myb10-B*.