OB-02

Classification of Wild Wheat (*Aegilops* L.) and Quantitative Trait Gene Mining

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[Introduction]
Rapid changes in the wheat planting environment caused by global warming pose challenges to food safety. Common wheat (*Triticum aestivum*) is a hexaploid plant (AABBDD) that shares a large number of quantitative traits and resistance genes in common with the B and D genomes of the genus *Aegilops* functioning in metabolism and biosynthetic processes and in particular plant adaptation to biotic and abiotic stresses. The abundance of the *Aegilops* gene pool is much higher compared with that of *Triticum*. Therefore, the purpose of this research is to sort out and classify *Aegilops*, record basic fertility data of *Aegilops*, and development *Aegilops* heading date genes in order to study the regulation mechanism of the growth cycle in *Aegilops*.

[Materials and Methods]
Therefore, we use 4 plant universal DNA barcodes (ITS2, matK, rbcL and psbA-trnH) and 6 chloroplast regions to construct a phylogenetic tree used for classify genus *Aegilops*. According to GBS data, 18 SNPs related to heading date were found using GWAS.

[Results and Discussion]
Total 14 species can be distinguished among 17 species, so we need other research to distinguish the other 3 species. We chose to use LM and SEM to observe the pollen morphology and surface. The observation results cannot distinguish these 3 species. Interestingly, pollen is classified into *Triticum*-type and *Avena*-type according to its surface ornamentation morphotypes. According to the distribution of 2 types of pollen in Section, it can be inferred: *Avena*-type stigmas are difficult to recognize and accept *Triticum*-type pollen, while *Triticum*-type stigmas are easier to accept *Avena*-type pollen. Based on this inference, the previous case study on the success rate of wild wheat-wheat hybridization can be explained. We also tried to use the SNPs selected in the GBS data for phylogenetic analysis. The resulting phylogenetic tree can only distinguish 7 species. Therefore, we have reached the conclusion that using the DNA barcode and pollen micro data used in this study, 14 of the 17 *Aegilops* can be distinguished. The other 3 species have gene introgressions from other species, but they can be classified using the morphological classification key. The GWAS results were identified by the function and expression level of SNP mapping genes, and two loci related to the heading date have been identified. The over-expressed DEAH-box helicase was found. DEAH-box helicase is a WW domain protein. A study showed that when such genes are mutated, plants show early flowering. The WW domain protein FCA is a regulator of flowering and controls the formation of the 3'end of certain transcripts. FCA needs to form a complex with FY to efficiently promote flowering, and the combination of ABA and FCA will inhibit the FCA-FY interaction. Therefore, we propose two hypotheses: 1. DEAH-box helicase replaces FCA, binds to FY-like proteins and participates in FLC down-regulation. 2. DEAH-box helicase replaces FCA and maintains the amount of FCA/FY by combining with ABA. A new FVE gene was also identified in this study. Povides a new direction and material for the regulation of wheat heading period.

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