## **Discovery of Key Genes Regulating Wheat Leaf**

## **Stomatal Traits and Their Superior Sites**

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**Abstract: [Background]** Wheat is one of the three major food crops in the world. The stable and high yield of wheat is of great significance to ensure food security in China. Stoma is widely distributed on the surface of leaves, which is an important channel for gas and water exchange between plants and the external environment, and directly affects the photosynthesis and transpiration of plants.

**(Method)** Four wheat stomatal traits were measured under two wheat seasons and two environments using 189 wheat populations as natural populations. Genomewide association analysis of stomatal traits was performed using wheat 660 K SNP chip combined with Blink, CMLM, MLMM and MLM models.

**【 Result 】** 445 genetic loci significantly associated with wheat stomatal traits were found. Finally, seven candidate genes directly or indirectly regulating stomatal traits were obtained by annotation. They encode signal recognition particle 54 kDa protein, protein IQ-DOMAIN 1, SOUL heme-binding family protein, 26S protease regulatory subunit, G-box binding factor, Aldose 1-epimerase-like and malate dehydrogenase. These candidate genes may regulate wheat stomatal traits by regulating the development of stomatal structure and the metabolism of guard cells. At the same time, five candidate genes regulating stomatal index and one homologous gene related to stomatal density were found. These genes encode O-methyltransferase, chalcone synthase, protein kinase, WD40 repeat-like protein, Mitochondrial import inner membrane translocase subunit TIM9 and 60S ribosomal protein L28. Through genome-wide association analysis, seven candidate genes previously discovered were also found. **【Conclusion】** These results will help to strengthen the in-depth understanding of wheat stomatal traits and provide reference for the screening and innovation of wheat stomatal traits.