

P021

The peduncle-specific expression during floral transition by high-throughput transcriptome analysis in wheat

Cheol Won Lee, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea university, Anam-ro 145, Seong-Buk, Seoul, Korea.

Abstract

Flowering time of either early or late is one of the crucial parameters that determine the crop productivity. Therefore, elucidation of regulatory mechanisms of flowering time should contribute to breeding for yield enhancement. However, comprehensive explanation on molecular mechanism of flowering has not yet been reported in hexaploidy common wheat (*Triticum aestivum* L.). The mechanism of flowering in wheat has been studied mostly using flag leaf or floral meristem. The exposed peduncle, which is a shoot part between bottom of the spike and flag leaf, could be an important tissue that is responsible for flowering through various molecules expressing. To clarify for transcriptomic dynamics in the wheat peduncle that was uncovered by leaf sheath of flag leaf, RNA sequencing and transcriptomic analysis were conducted. With this, we also analyzed other transcriptomic results deposited in the public DB to identify genes specially expressed in peduncle tissue at transition from vegetative to reproductive phase. The obtained results will provide valuable information to understand the role of peduncle for flowering regulation in wheat aiming for elucidation of the regulatory mechanism of wheat flowering.

Acknowledgement: This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)” Rural Development Administration. Republic of Korea.

Keywords : Wheat, peduncle, flowering, RNA sequencing

Corresponding author*

Yong Weon Seo

Address : Department of Biosystems and Biotechnology, Korea university

Tel : +82 2 3290 3005

E-mail : seoag@korea.ac.kr