AgroSpectrum ASIA
Envisaging Future | Updating Present

Scientists in ChinaÂ discover Transcriptional Regulatory Network of Wheat Endosperm development to enhance breeding

05 July 2024 | News

Regulating endosperm development is an important strategy for increasing crop yield and quality, as well as addressing the trade-off between these two factors

Regulating endosperm development is an important strategy for increasing crop yield and quality, as well as addressing the trade-off between these two factors

Improving yield and quality are central goals of wheat breeding. The endosperm is the main nutrient storage organ of wheat grain and the primary source of flour. Seed storage proteins (SSP) and starch are the main components of the endosperm, and the balance between them directly affects wheat grain yield and its end-use quality. Regulating endosperm development is an important strategy for increasing crop yield and quality, as well as addressing the trade-off between these two factors.

In a recent study led by Prof. XIAO Jun from the Institute of Genetics and Developmental Biology (IGDB) of the Chinese Academy of Sciences, a new discovery was made in elucidating the transcriptional regulatory network during wheat endosperm development and identifying key regulatory factors impacting this process.

By integrating transcriptome data, chromatin accessibility, and various histone modification sequencing at eight key developmental stages, researchers mapped the dynamic transcriptional and epigenetic modification landscape of wheat endosperm development. The epigenetic regulatory regions were found to be significant for driving the expression regulation of SSP and starch genes and for shaping the diversity of grain weight and quality phenotypes within wheat populations.

In this work, the researchers constructed a hierarchical transcriptional regulatory network, identifying 436 core regulatory factors, including a set of transcription factors that synergistically or antagonistically regulate the expression of SSP and

starch synthesis genes. Additionally, they also conducted a comprehensive evaluation of novel genes, screening 42 reliable candidate genes for regulating storage protein and starch synthesis, with support from GWAS signal, expression-phenotype correlations, and morphological defects of TILLING mutants.

Among these candidate genes, *TaABI3-A1* negatively regulated starch biosynthesis while activating storage protein accumulation, and it has been selected during the wheat breeding process in China as a key factor potentially balancing wheat yield and quality.

This study elucidates the epigenetic and molecular regulatory mechanisms of the coordinating SSP and starch synthesis in wheat grains, providing essential gene resources and selection targets for breeding wheat varieties with high yield and good end-use quality.