

Spatial mapping revealed the spatiotemporal expression of genes during wheat grain development and expression variation in response to heat stress

Yuxin FU¹, Mengping CHENG¹, Jirui WANG¹

¹State Key Laboratory of Crop Gene Exploration and Utilisation in Southwest China, Sichuan Agricultural University, Chengdu, China.

Program theme: Genetics and Epigenetics.

Oral

Abstract

The grain-filling stage was identified as the most vulnerable to the detrimental effects of rising temperatures, resulting in reduced wheat yield. In this study, we employed spatial transcriptomics and bulk RNA sequencing (RNA-seq) techniques to analyze the transcriptomic landscape of wheat grain throughout its developmental stages, explicitly focusing on the grain-filling stage under heat-stress conditions. We identified 11 distinct clusters by profiling 21618 spots from wheat grain, including various tissue components such as the nucellus projecter (NP), exocarp (EXC), mesocarp (MEC), endocarp (ENC), aleurone layer (AL), endosperm (EN), endosperm transfer cell (ETC), endosperm cavity (EC), embryo (EM), embryo adjacent to scutellum (EAS), and germ. The analysis revealed a clear separation of cell clusters originating from the endosperm compared to those derived from the pericarp and embryo. Genes specifically expressed in the aleurone layer (AL) were found to be primarily associated with lipid transport functions. The endocarp (ENC) cells were responsible for photosynthesis, converting light energy into chemical energy. In contrast, cells derived from the exocarp (EXC) were found to contribute to multicellular organism development processes. Interestingly, unexpected divergence in gene expression within the same tissue was also observed. This indicated a dynamic shift in gene localization among different cells. Among them, half of the genes encode histone protein whose expression was elevated exclusively in the embryo, demonstrating that histone modifications might regulate gene expression by their dynamic variation in response to HS, which enables wheat to respond more effectively and efficiently to recurring stress and prepare offspring for potential future stresses. Moreover, we noted a significant upregulation of heat shock proteins in the endosperm transfer cells (ETC) and embryos under heat stress conditions, suggesting a transcriptional regulatory response in these specific tissues. Our results provide a strategy for studying gene regulation networks at the cellular level of seed grain development, incredibly high heat stress during the grain-filling stage, characterize the cellular composition, and elucidate the potential origin and regulation in pericarp cell development.