

Abstract

Spatial distribution of proteins and metabolites in developing wheat grain and their differential regulatory response during the grain filling process

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Grain filling and grain development are essential biological processes in the plant's life cycle, eventually contributing to the final seed yield and quality in all cereal crops. Studies of how the different wheat (*Triticum aestivum* L.) grain components contribute to the overall development of the seed are very scarce. We performed a proteomics and metabolomics analysis in four different developing components of the wheat grain (seed coat, embryo, endosperm, and cavity fluid) to characterize molecular processes during early and late grain development. In-gel shotgun proteomics analysis after anthesis (DAA) revealed identified and quantified proteins, out of which 410 differentially expressed proteins were identified in the seed coat, 815 in the embryo, 372 in the endosperm, and 492 in the cavity fluid. The abundance of selected protein candidates revealed spatially and temporally resolved protein functions associated with development and grain filling. Multiple wheat protein isoforms involved in starch synthesis such as sucrose synthases, starch phosphorylase, granule-bound and soluble starch synthase, pyruvate phosphate dikinase, 14-3-3 proteins as well as sugar precursors undergo a major tissue-dependent change in abundance during wheat grain development suggesting an intimate interplay of starch biosynthesis control.

Biography

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