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ANALYSIS OF MULTIPLE DIFFERENCES ASSOCIATED WITH CHLOROPLAST IN THE SPACEFLIGHT-INDUCED WHEAT LEAF COLOUR MUTANTS

Chloroplast development is an integral part of plant survival and growth, and occurs in parallel with chlorophyll biosynthesis. We have obtained three novel wheat leaf colour mutants mtg, mts, and mta from spaceflightinduction. To explore the genetic variations under space environment and uncover the mechanisms, which cause the leaf colour mutations, we performed chloroplast ultra-structural observation, photosynthetic pigments assays, leaf transcriptome sequencing, chloroplast proteomic analyses and chloroplast genome sequencing. Compared to wild type, chloroplast of mts and mta exhibit abnormal morphology and distribution. The photosynthetic pigments content was also significantly decreased. From transcriptome and chloroplast proteome profiling, a total of 4,588 differentially expressed genes (DEGs) and 48 differentially chloroplast expressed proteins (DEPs) were identified between mta and wild type, most of which were involved in chloroplast development, chlorophyll biosynthesis, or photosynthesis. The correlation analysis between DEGs and DEPs revealed that the transcript-to-protein abundance was functioned into photosynthesis and chloroplast relevant groups. Chloroplast genome sequencing revealed the impact of spaceflight environmental forces on the variations in the whole plastome sequences. The complete plastomes of three leaf colour mutants mtg, mts, mta and WT were obtained, and the cp genomes were highly conserved in organization. However, the totally length and boundaries of cp genome were slightly distinct. Besides, many variations and gene mutation were found and might affect the leaf colour traits. Integrated omics analyses revealed the main molecular mechanisms regulating leaf colour formation, involving chloroplast development, chlorophyll biosynthesis, and photosynthesis. In addition, plastome variations were identified in the leaf colour mutants. The alterations were induced by space environment, which would be fully utilized of mutagenesis in crop breeding.

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