PROTEOMICS AND FUNCTIONAL GENOMICS APPROACHES TO EXPLORE CHLOROPLAST-CHROMOPLAST TRANSITION IN TOMATO FRUIT


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Chloroplast to chromoplast transition has been investigated in tomato (Solanum lycopersicum) fruit. Our results reveal that only “green” fruit have photosynthetically active tissues releasing O2, while low PSII activity was measured also in “orange” fruit, but not in “red” fruit. In order to explore changes at protein level during chloroplast-chromoplast transition, we applied a detailed proteomic analysis on plastids purified from tomato berries at four different developmental stages. Using a MudPIT (Multidimensional Protein Identification Technology) LC/MS proteomic technique we identified more than 400 different polypeptides present in the four ripening stages. Our results show a strong decrease of photosynthetic proteins during fruit maturation, while heat shock proteins, chaperonins and plastid lipid associated proteins (PAP) increase. Together with an accumulation of stress related proteins we also detected an increase of Reactive Oxidative Species in plastids during chloroplast-chromoplast transition. Interestingly, the early steps of photosynthetic machinery reduction during fruit maturation affect the same photosynthetic proteins (LHCII, CP24, PSI-LHCI) decreased in leaves during acclimation to high light conditions. These results suggest a common mechanisms of photosynthetic proteins turnover modulation during chloroplast-chromoplast transition and high light acclimation. In order to better understand the role of the differentially expressed proteins during fruit ripening, we started a functional study by RNA interference (RNAi). For this purpose we are using hairpin RNAi (hpRNAi) vectors based on the Gateway™ recombinational cloning which facilitates high-throughput applications. In particular, hpRNAi constructs under the control of the constitutive 35S promoter were generated to induce gene silencing of HSP, PAP and protease differentially expressed proteins.