

Redox proteomic analysis reveals the involvement of oxidative post-translational modification in tomato fruit ripening

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Abstract

Fruit ripening is a complicated biological process, in which the levels of reactive oxygen species (ROS) fluctuate. However, the molecular mechanisms of ROS in the regulation of fruit ripening are still unclear. Here we utilized an iodoacetyl tandem mass tag (iodoTMT)-based redox proteomic approach to detect the redox dynamics of proteins during tomato fruit ripening. A total of 70 cysteine (Cys)-containing peptides from 51 proteins were identified in fruit at different ripening stages. Determination of oxidation levels indicated that Cys-containing peptides at the later stage of fruit ripening were generally more oxidized than those at the early stage. Of these proteins, 13 were identified as redox-sensitive proteins, whose oxidation levels changed significantly during fruit ripening, including polygalacturonase 2A (PG2A) involved in cell wall degradation and 1-aminocyclopropane-1-carboxylate oxidase-like protein (E8) involved in ethylene biosynthesis. Immunodetection of oxidized Cys residues demonstrated that Cys-307 in E8 was a redox-sensitive site, whose oxidation is likely to affect the function of E8. These data suggest that ROS may regulate fruit ripening by targeting critical enzymes via oxidative post-translational modifications. Our findings uncover the mechanisms of ROS in the regulation of fruit ripening and contribute to the regulatory networks controlling ripening.