Proteomics and Phosphoproteomicsof fruit ripening mechanisms in Tomato(*Solanum lycopersicum*)

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Abstract: Fruit ripening is a highly programmed regulation process, including a series of physiological and biochemical changes, such as color changes, the formation of aroma, flavor substances, nutrients and fruit softening. Tomato is a research model for fruit ripening. The MADS-box transcription factor RIN has been regarded as a key regulator responsible for the onset of ripening by acting upstream of both ethylene- and non-ethylenemediated controls. The rin (ripening-inhibitor) mutation that inhibits all measured ripening phenomena, including the respiratory climacteric and associated ethylene evolution, provitamin A carotenoid accumulation, softening, and production of flavor compounds. In this study, the proteomics and phosphoproteomics were used to detect the normal ripening fruits (AC) and rin mutant fruits of tomato, and the translation and posttranslational regulation mechanisms of tomato fruit ripening were investigated. A total of 6141 proteins and 4011 sites of 1996 proteins contain quantitative information, mainly in ethylene biosynthesis and signal transduction, photosynthesis regulation, carotenoid and flavonoid biosynthesis, chlorophyll degradation, and ribosomal subunit expression changes, MAPK pathway changes as well as more than 15 transcription factors. Although photosynthesis was inhibited, diverse primary and secondarymetabolic pathways were employed for fruit ripening, such as glycolysis, pentose phosphate pathway, amino acid metabolism, fatty acid metabolism, nucleotidemetabolism, vitamin metabolism, and isoprenoid biosynthesis. These data constitute the protein, protein phosphorylation and metabolic atlas in tomato fruit ripening regulation, which will springboard

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Abstract Citation: <u>Proteomics and Phosphoproteomics of fruit ripening mechanisms in Tomato(Solanum lycopersicum)</u>

Insights in Aquaculture and Biotechnology

Volume s1