Title Role of members of the tomato ethylene receptor family in determining the timing of ripening

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Abstract

Tomatoes are an economically important crop and a significant dietary source of important phytochemicals, such as carotenoids and flavonoids. While it has been known for many years that the plant hormone ethylene is essential for ripening of climacteric fruits, its role in fruit growth and maturation is much less understood. In an attempt to better understand tomato fruit ripening we utilized both biotechnology and traditional breeding strategies. The multigene ethylene receptor family has been shown to negatively regulate ethylene signal transduction and suppress ethylene responses. Here, we demonstrate that a reduction in the levels of either of two family members, *LeETR4* or *LeETR6* , causes an early ripening phenotype. We provide evidence that the receptors are rapidly degraded in the presence of ethylene and that degradation likely occurs through the 26S proteasome-dependent pathway. Ethylene exposure of immature fruits causes a reduction in the amount of receptor protein and earlier ripening. Fruit-specific suppression of the ethylene receptor *LeETR4* causes early ripening while fruit size, yield and flavor-related chemical composition are largely unchanged. These results demonstrate that ethylene receptors likely act as biological clocks regulating the onset of tomato fruit ripening.

In order to better understand the mechanism controlling the timing of ripening we screened a *Lycopersicon hirsutum* introgression population for QTLs responsible for reduced time from 11 anthesis to breaker and/or increased ripening-associated ethylene biosynthesis. The *L. hirsutum* population was chosen because of unusual ripening characteristics and significantly higher levels of ethylene biosynthesis at maturity of *L. hirsutum.* A number of lines were identified that showed statistically significant differences from the control for both phenotypes. These lines are currently being refined for possible map-based cloning of loci controlling these phenotypes. These results demonstrate the power of using both molecular biology and traditional breeding for gene isolation/characterization and crop improvement.