Abstract:

We have isolated two peach (Prunus persica) genes, Pp-ETR1 and Pp-ERS1, homolog to the Arabidopsis ethylene receptor ETR1 and ERS1. Pp-ETR1 is identical, in terms of exons number and introns position, to At-ETR1 although the first and fifth intron are 5 and 20 times longer, respectively. In addition two putative polyadenilation sites, that may cause an incomplete splicing at the 3' terminus, are present into the fifth intron. Translation of such a truncated transcript would lead to a product missing a large portion of the receiver domain. The coding region of Pp-ERS1 is organized in five exons interrupted by four introns, but unlike Pp-ETR1 no marked differences in terms of intron length between At-ERS1 and Pp-ERS1 have been detected. Into the promoter region of Pp-ERS1 a motif of 28 nt, which shows high homology with binding ethylene-factors detected in genes up-regulated by ethylene, is present. The deduced protein of both genes contain a sensor domain and the Histidine kinase domain, in which residues, thought to be important for the normal function of ETR1 and ERS-type proteins as ethylene receptors are conserved. These results indicate that Pp-ETR1 and Pp-ERS1 could be functional ethylene receptors with the ability to bind ethylene. Expression analysis, carried out by quantitative RT-PCR, was performed during fruit ripening (cv Maria Marta). The level of Pp-ETR1 transcripts remained unchanged throughout ripening, whereas Pp-ERS1 mRNA increased in parallel with the ethylene climacteric.