

Title Map position and functional allelic diversity of *Md-Exp7* , a new putative expansin gene associated with fruit softening in apple (*Malus × domestica* Borkh.) and pear (*Pyrus communis*)

Author F. Costa, W. E. Van de Weg, S. Stella, L. Dondini, D. Pratesi, S. Musacchi and S. Sansavini

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Abstract

Fruit ripening can be considered as a complex set of biochemical and physiological changes occurring at the end of the developmental stage. Ripe fruit texture notably affects overall quality and consumer appreciation. Excessive softening limits shelf-life and storability, thereby increasing disease susceptibility and economic loss. Fruit softening is a process due to the depolymerisation of different polysaccharide classes, an event controlled by a synergic and coordinated action of several enzymes among which expansins play a fundamental role. To date, six expansin genes are known to be expressed during apple fruit ontogeny, from full bloom up to fruit ripening. We identified a novel expansin apple homolog (*Md-Exp7*) sharing high sequence similarity with specific-ripening expansin genes of other crops. A functional marker (*Md-Exp7_{SSR}*) based on an SSR motif located within the untranslated region of the gene was developed and mapped on Linkage Group 1 of the apple and pear genomes in a region where one major apple QTL for fruit firmness had been previously identified. The allelic composition of 31 apple varieties for the SSR marker was associated with differences in fruit softening.

<http://www.springerlink.com/content/b0078455838885xp/fulltext.pdf>