

Title Mining the apple genome reveals a family of nine ethylene receptor genes
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Abstract

Ripening in apple is mediated through the hormone ethylene in a dose-dependent manner. From work in model plants, it is known that the ethylene receptors are negative modulators of the ethylene signal, and therefore likely to play an important part in apple fruit ripening. Our mining of the recently completed whole apple genome identified a total of nine receptor genes, including three new sequences. Phylogenetic comparisons with other fruit species identified each of the homeologous pairs. Using *ACC OXIDASE 1*-suppressed apple fruit induced with ethylene, eight genes were expressed in fruit, while the ninth gene remains a predicted gene model with no current supporting evidence for expression. Five genes were upregulated by ethylene within 12 h of treatment. This study demonstrates the potential for the whole genome sequence to be used as a resource for determining large multi-gene families important for postharvest responses in apple.