

Elucidation of the biochemical pathways involved in two distinct cut-surface discolouration phenotypes of lettuce

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Abstract

To understand better the biochemistry and underlying genetic control of postharvest discolouration in lettuce, an F₇ recombinant inbred population (Saladin x Iceberg) was grown in field trials and phenotyped. We identified two distinct discolouration phenotypes, pinking and browning, which were negatively correlated at the phenotypic level and located six QTL associated with pinking and five QTL associated with browning plus two QTL associated with total discolouration which could not be attributed to either type, on an improved genetic map. Candidate genes underlying QTL were investigated. Plants showing extremes of discolouration were also grown under controlled environment conditions. Lines showing extreme phenotypes from both environments were used for transcriptome profiling and differentially expressed transcripts associated with pinking and browning were identified. Involvement of the phenylpropanoid, flavonoid and terpenoid biosynthesis pathways were indicated in the development of discolouration, with the point of divergence for development of the different discolouration phenotypes localised to the phenylpropanoid pathway. Other biochemistry including amino acid metabolism was also implicated with environmental factors including temperature, water availability and physical stress indicated as potential contributory factors. Differential transcriptional control may be involved in regulating discolouration, potentially through stereochemical selection.