

## CULTIVAR-SPECIFIC CHANGES OF APPLE METABOLITE PROFILE DURING COLD STORAGE DETERMINED BY GCxGC-QMS

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The apple (*Malus domestica* Borkh.) belongs to the most popular and most consumed types of fruit. Many cultivars show excellent storability, even under normal atmosphere. Although the typical changes of major quality parameters during storage are well known, a comprehensive investigation of changes in the metabolite profile during storage is still missing. Here we present the results of a GCxGC-MS metabolome analysis of eight cultivars before and after cold storage. Seven newly bred cultivars and the reference cultivar Elstar were grown in a pesticide-reduced cultivation system. Before and after a cold storage period of 27-29 weeks (ca. 6.5 months) under normal atmosphere at 1 °C, eight samples pooled from 5 fruits each were taken per cultivar, with peel and flesh being sampled separately. After lyophilization and grinding in a ball mill, samples were extracted with methanol, evaporated to dryness and finally derivatized (methoximation and trimethylsilylation). Untargeted metabolome analysis was performed with a GCxGC-qMS instrument. A wide range of compounds like amino, organic and phenolic acids, sugars, polyols, alkanes, fatty alcohols, fatty acids and wax esters, phytosterols and triterpenes was separated using a common apolarxmedium-polar column set. Storage-dependent changes were observed in both tissues but changes in the peel were generally more pronounced. The expected typical changes (increase in sugars, decrease in acids) could only partly be confirmed: the members of these compound classes didn't behave uniformly. Furthermore, in case of metabolites like ethanolamine, succinate, citrate, phosphate, ribose, sucrose, several amino acids and many unknowns, changes during storage were highly cultivar-specific. In summary, the results of this study may enable a deeper insight into the biochemical processes during apple storage.