Abstract

During long term storage of apple, physiological disorders may occur. One major group of internal disorders is characterized by flesh browning. The susceptibility to flesh browning is cultivar, batch and season dependent and is caused by a combination of pre and post harvest factors. This can result in considerable economic losses with incidence levels up to 40%. Braebum and Kanzi are commercial cultivars in Belgium that are prone to browning.

An important influencing factor is the controlled atmosphere (CA) storage of apple. The main objective of this experiment is to investigate how the proteome changes during storage. This will be related to the real browning incidence after prolonged storage, which was determined by picture analysis.

Apples (Malus x domestica Borlch., cv. Braeburn) were picked in the orchard of the Experimental Garden for Pome and Stone Fruits, pcfruit (Sint-Truiden, Belgium). Samples were taken immediately after harvest and after two weeks, two months and four months of storage under brown inducing conditions (2.5% O_2, 3.7% CO_2, 4°C). Proteins were extracted using a phenol extraction and quantified using a modified Bradford procedure. For each moment in storage the four least and four most brown apples were sampled and analysed after tryptic digestion using a nano-2D-UPLC-MS system. Data processing was performed with ProteinLynx and Progenesis software.

After optimization of the peptide extraction and gel-free two-dimensional separation, 24439 peptides could be detected and 145 different protein families could confidentially be identified via an optimized workflow. Further results will be presented focusing on the observed proteome differences as a function of brown incidence and storage time.