# SWATH-MS proteomics and postharvest analyses of mangosteen ripening revealed intricate regulation of carbohydrate metabolism and secondary metabolite biosynthesis

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Postharvest Biology and Technology, Volume 176, June 2021, 111493

## Abstract

Mangosteen (*Garcinia mangostana* L.) is a tropical fruit with numerous beneficial properties such as anti-cancer, anti-oxidant, and anti-microbial activity. This is due to the presence of potent secondary metabolites such as phenolics, and xanthones, which are differentially accumulated during ripening. However, the molecular regulation that governs mangosteen ripening and hence metabolic changes has not been fully elucidated, especially at the proteome level. This study details the first proteomic report on mangosteen ripening, particularly utilizing Sequential Windowed Acquisition of All Theoretical-Mass Spectra (SWATH-MS) analysis. Furthermore, postharvest analyses such as color changes, fruit firmness, anthocyanin content, total phenolic content, antioxidant activity, soluble solid content and titratable acidity were performed to further corroborate the proteome changes. Out of 3397 total identified proteins, 277 proteins were statistically measured as differentially expressed proteins (DEPs) and grouped into eight different expression clusters by *k*-means clustering analysis. Some of the key DEPs involved in ripening-related biological processes include 1-aminocyclopropane-1-carboxylate oxidase (ACO) (ethylene biosynthesis), pyruvate kinase (PK) (carbohydrate metabolism), polygalacturonase (PG) (cell wall modification) and phenylalanine ammonia-lyase (PAL) (secondary metabolite biosynthesis) which displayed increasing expression patterns during early (Stage 0 to Stage 2) and/or late (Stage 2 to Stage 6) ripening period. Coherently, the protein trends were also mostly consistent with the recorded postharvest characteristics, highlighting the underlying regulation contributing to the physiological changes of this unique fruit. Interestingly, all five benzophenone synthases (BPS) proteins involved in xanthone biosynthesis were not differentially expressed,

speculating that other enzymes within this pathway could be responsible for the compound regulation. Future work should identify and characterize poorly annotated proteins within this dataset to further enrich key metabolic pathways of this species such as the xanthone pathway. Nevertheless, the use of SWATH-MS for proteomics analysis on this non-model fruit has enabled us to comprehend the dynamicity and complexity of its ripening process. This report will certainly aid future molecular research in mangosteen and ultimately contribute to the advancement in postharvest ripening control and preservation of this fruit. The proteome data are available via ProteomeXchange with identifier PXD006295.