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Proteomics Analysis of Strawberry Fruits Exposed to Essential Oils

Abstract

This study aims to identify the strawberry proteins that are responsive to surface treatments to delay or prevent fruit rot caused by the fungal infection. Four strawberry varieties including Albion, Allstar, Jewel, and Sweet Charlie, were planted in a high tunnel in September 2020. The fruits were harvested in spring 2021 and were packaged inside a tight-air container and exposed to 30 ul of vapor of five essential oils (thymol, cinnamon oil, eugenol, clove bud oil, and non-enal). Fungicide Switch (30 ul active ingredient) and no treatments were used as positive and negative controls respectively. After one week of storage at 4^0C, fruit tissues were taken out and homogenized in acetone containing 10% TCA (Trichloroacetic acid). Protein were precipitated after incubation at -20^0C overnight. The quality of proteins was examined by electrophoresis on 12.5% Tris-SDS-PAGE gels followed by Coomassie Blue Staining. Tryptic digested proteins were labeled using the 16Plex TMT kits. The proteomes were identified using real time search (RTS) selection and MS3 quantification. All MS and MS/MS raw spectra from each TMT experiment were processed and database searched using Sequest HT software within Proteome Discoverer 2.5 (PD 2.5, Thermo Scientific) against Strawberry database. Proteins showing significant differences in relative protein abundance between pairs of samples were taken as differentially expressed proteins (DEPs); these DEPs were used to identify the biological processes associated with fruit rot, and plant defense against fungal infection.