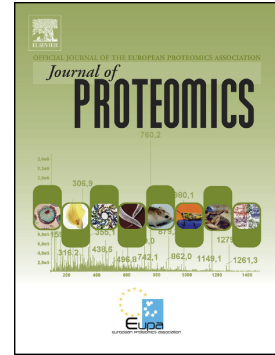


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TMT-based quantitative proteomics analysis reveals the response of *Camellia sinensis* to fluoride

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ABSTRACT

The tea plant is a fluoride hyperaccumulator, and fluoride accumulation in its leaves is closely related to human health. To dissect molecular mechanisms underlying fluoride accumulation/detoxification, the leaves of tea seedlings exposed to different fluoride treatments for 30 days were sampled for physiological and proteomics analyses. The results showed that fluoride had no adverse effects on the growth of tea seedlings in spite of high content fluoride accumulation in their leaves. Through TMT coupled with UPLC MS/MS, 189 differentially accumulated proteins were quantified, of which 41 and 148 were localized in the cell wall and cellular compartments respectively. 41 cell wall proteins were mainly conducive to cell wall structure rearrangement, signaling modulation and the protection the cells from damages; 148 cellular compartments proteins mainly contributed to diverse metabolisms reprogramming, energy reallocation and plant defense. Notably, upregulation of several proteins including smHSPs, DRT100, YLS2-like, primary amine oxidase, GDSL esterase/lipases and citrate synthase probably enhanced the defense of tea seedlings against fluoride. Collectively, our results presented a comprehensive proteomics analysis on the leaves of tea seedlings in response to fluoride, which would contribute to further deciphering of molecular mechanisms underlying fluoride accumulation/detoxification in tea plant.

Keywords:

Tea plant; Fluoride; Cell wall proteins; cellular compartments proteins; Quantitative proteomics

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