

Ubiquitylome study highlights ubiquitination of primary metabolism related proteins in fruit response to postharvest pathogen infection

Yulin Cheng, Xuehan Xia, Yunlong Lin, Haohao Cao, Juanni Yao and Zhengguo Li

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Abstract

As an important post-translational modification, protein ubiquitination is proven to be involved in plant resistance to pathogens. Postharvest diseases on fruit caused by fungal pathogens lead to huge economic losses worldwide, but fruit resistance remains relatively unexplored compared with well-studied leaf resistance and nothing is currently known about ubiquitination in fruit resistance. Here, we report ubiquitylome analysis of citrus fruit infected by *Penicillium digitatum* (*Pd*), a most harmful postharvest pathogenic fungus. *Pd* infection promoted ubiquitination of total proteins in citrus fruit. Based on proteome-wide enrichment of ubiquitination using the anti-K- ϵ -GG antibody, we identified 4168 Lys ubiquitination sites in 1726 citrus proteins, among which 3082 sites in 1377 proteins were quantified. A total of nine conserved motifs for 2581 unique sites were identified and there was a significant preference for aliphatic residues Ala and Glu at positions adjacent to ubiquitinated Lys residues. Compared with uninfected citrus fruit, 174 sites in 129 proteins and 102 sites in 91 proteins were up-regulated and down-regulated in infected citrus fruit, respectively. Further bioinformatic analysis indicated that ATPases, transporters or pyruvate kinases and dehydrogenases or thioredoxins were preferentially up-regulated and down-regulated, respectively. Noticeably, both up-regulated and down-regulated sites in citrus proteins were mainly enriched in primary metabolic pathways which were affected by *Pd* infection and are proven to involve in plant disease resistance by increasing evidences. Our results reveal the involvement of ubiquitination, especially ubiquitination of primary metabolism related proteins, in fruit response to postharvest pathogen infection.