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Difference of proteomics vernalization-induced in bolting and flowering transitions of *Beta vulgaris*

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ABSTRACT. Sugar beet (*Beta vulgaris*) is a biennial crop that accounts for 30% sugar production of the world. Vernalization is an essential factor for sugar beet reproductive growth under long days. Although genes association with bolting and flowering were well explored, the difference of proteomics in the two growth stages were still poorly understood. To address the molecular mechanism at the level of proteins, an isobaric tags for relative and absolute quantification (iTRAQ)-based quantitative proteomics approach was employed to the three different growth stages (germination, bolting, flowering) of vernalized samples and the corresponding stage germination (17W weeks), 19W and 20W of nonvernalized samples. A total of 1110 peptides, 842 unique peptides and 570 proteins were identified. Most of them were assigned to phenylpropanoid biosynthesis, hormone metabolism and protein processing pathway. IAA and Gibberellins (GA3) promoted growth and development in a threshold manner at growth stage germination after vernalization. A novel discovery was that IAA biosynthetic pathway of sugar beet was the Trp-dependent. In addition, two predominant pathways of protein processing association with vernalization were also identified in sugar beet at growth stage flowering. This study provided an in-depth understanding of the molecular mechanism of vernalization at the level of proteomics.

Keywords: vernalization, nonvernalization, proteomics, iTRAQ, sugar beet

1. Introduction

Developmental transition from vegetative to reproductive growth of plant species were induced by environmental signals such as vernalization and photoperiods. Flowering plant *Arabidopsis thaliana* perceived vernalization stimuli to initiate flowering transition, which process had been extensively