Title Effects of postharvest storage and dormancy status on ABA content, metabolism, and expression of genes involved in ABA biosynthesis and metabolism in potato tuber tissues

Author Luis Destefano-Beltrán, Donna Knauber, Linda Huckle and Jeffrey C. Suttle

Citation Plant Molecular Biology 61 (4-5): 687-697. 2006.

Keywords ABA; Dormancy; Gene expression; Potato; *Solanum tuberosum* L.; Tuber; qRT-PCR

Abstract

At harvest, and for an indeterminate period thereafter, potato tubers will not sprout and are physiologically dormant. Abscisic acid (ABA) has been shown to play a critical role in tuber dormancy control but the mechanisms controlling ABA content during dormancy as well as the sites of ABA synthesis and catabolism are unknown. As a first step in defining the sites of synthesis and cognate processes regulating ABA turnover during storage and dormancy progression, gene sequences encoding the ABA biosynthetic enzymes zeaxanthin epoxidase (ZEP) and 9-*cis*-epoxycarotenoid dioxygenase (NCED) and three catabolism-related genes were used to quantify changes in their relative mRNA abundances in three specific tuber tissues (meristems, their surrounding periderm and underlying cortex) by qRT-PCR. During storage, *StZEP* expression was relatively constant in meristems, exhibited a biphasic pattern in periderm with transient increases during early and mid-to-late-storage, and peaked during mid-storage in cortex. Expression of two members of the potato NCED gene family was found to correlate with changes in ABA content in meristems (*StNCED2*) and cortex (*StNCED1*). Conversely, expression patterns of three putative ABA-8′-hydroxylase (*CYP707A*) genes during storage varied in a tissue-specific manner with expression of two of these genes rising in meristems and periderm and declining in cortex during storage. These results suggest that ABA synthesis and metabolism occur in all tuber tissues examined and that tuber ABA content during dormancy is the result of a balance of synthesis and metabolism that increasingly favors catabolism as dormancy ends and may be controlled at the level of *StNCED* and *StCYP707A* gene activities