

DEVELOPMENTAL REGULATION OF THE GA BIOSYNTHESIS GENES, *GA20ox*, *GA3ox*, and *GA20ox* DURING GERMINATION AND YOUNG SEEDLING GROWTH OF PEA (*Pisum sativum* L.)

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ABSTRACT

To understand the role of gibberellins (GAs) during germination and early post-germinative stages of large-seeded dicotyledonous plants, we profiled the expression pattern of genes encoding three regulatory GA biosynthesis enzymes (*PsGA20ox1*, *PsGA3ox1* and *PsGA2ox1*) in pea (*Pisum sativum* L.) using real-time RT-PCR. To broaden our inferences on the role of GAs in these processes, we compared the GA biosynthesis gene expression patterns in two distinctly different genotypes of pea ('Alaska' a model cultivar for vining pea containing the wild-type internode length gene *LE* and 'Carneval' a model cultivar for semi-leafless field pea containing the *le* mutation producing shorter internodes), both of which germinate readily on imbibition under normal environmental conditions. Residual amounts of *PsGA20ox1*, *PsGA3ox1*, and *PsGA2ox1* transcripts were detected in the mature embryos (0 days after imbibition; DAI) of both genotypes. Transcription of *PsGA20ox1*, *PsGA3ox1*, and *PsGA2ox1* mRNAs occurred in all tissues examined (cotyledons, embryo axis, shoots and roots from 0.5 to 6 DAI) and was developmentally regulated within each tissue. Cotyledonary GA biosynthesis gene transcript patterns suggest that a signal from the axis triggers GA biosynthesis in the cotyledon. The high levels of *PsGA20ox1* and *PsGA3ox1* mRNA in the embryonic axis at 1 DAI suggests that the embryo axis is a major site for GA biosynthesis for stimulation of axis expansion. GA biosynthesis gene expression in 2 to 6 DAI shoots and roots (when their growth in fresh weight and length increased linearly) indicates a key role for *de novo* GA biosynthesis in early growth of seedlings. Supported in part by NSERC grant #138166.

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