

## TISSUE-SPECIFICITY OF ABA BIOSYNTHESIS IN RELATION TO ITS ROLES DURING ARABIDOPSIS SEED DEVELOPMENT AND GERMINATION

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Abscisic acid (ABA) is a key element in seed development and germination as well as adaptive responses to environmental stresses. The tissue-specific modulation of its endogenous levels by fine-tuning of synthesis and catabolism determines its physiological action. In seeds, ABA is synthesized in genetically distinct tissues, the testa is constituted of maternal tissues derived from ovule integuments, whereas the triploid endosperm and the diploid embryo result from two separate nuclear fusions, called double fertilization.

ABA is derived from carotenoid precursors. To date, genes encoding enzymes responsible for most steps of the ABA biosynthesis pathway have been identified in Arabidopsis. Our group has studied the regulation of genes involved in the conversion and cleavage of carotenoids, specifically zeaxanthin epoxidase, neoxanthin synthase and 9-*cis* epoxy-carotenoid dioxygenase (*NCED2*, *3*, *5*, *6* and *9*). *NCED* enzymes cleave the *cis*-isomers of violaxanthin and neoxanthin to a C15 product, xanthoxin, which is then converted into ABA by two successive enzyme reactions. In contrast to other enzymes of the ABA pathway, the cleavage enzyme is encoded by a multigene family, which potentially allows the precise regulation of xanthoxin production. We have characterized multiple *nced* mutants whose ABA deficiency is restricted to seeds and gained new insights into ABA origin. Analysis of hormone levels showed that *NCED6* specific expression in the endosperm is the major source of ABA during seed development, in contrast to the minor amount produced by other *NCEDs* expressed in the embryo or mother plant. "Omics" approaches were performed on developing seeds of *nced2 nced5 nced6 nced9* (*qnced*), severely ABA deficient in all seed tissues, and *nced2 nced5 nced9* in which ABA is still produced in the endosperm. Reduced ABA levels were correlated with differences in the accumulation of transcripts associated with signaling networks, in addition to genes involved in seed maturation and desiccation tolerance. Furthermore decreased or increased ABA levels in biosynthesis (*qnced*) or catabolism (*cyp707a1 a2*) mutants modulated the oxidized proteome in dry seeds suggesting a link between the regulation of oxidative processes and dormancy depth by ABA.