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Multi-omics analysis of abscisic acid roles in the control of *Arabidopsis* seed dormancy

Annie Marion-Poll

Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, 78026 Versailles Cedex, France
Annie.marion-poll@inra.fr

Frédéric Chauffour¹, Marlène Bailly¹, François Perreau¹, Boris Collet¹, Anne Frey¹, Gwendal Cueff¹, Gilles Clément¹, Ludivine Taconnat², Loïc Rajjou¹

¹ Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, 78026 Versailles Cedex, France;

² Institute of Plant Sciences - Paris-Saclay, 91192 Gif-sur-Yvette Cedex, France

Abstract

Abscisic acid (ABA) is a key hormone 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.

ABA is derived from cleavage of carotenoid precursors, which is a key regulatory step of the biosynthesis pathway. In *Arabidopsis*, the 9-*cis* epoxycarotenoid dioxygenase (NCED) that cleaves the *cis*-isomers of violaxanthin and neoxanthin is encoded by a multigene family. ABA inactivation occurs either by oxidation or conjugation and the major route is 8' hydroxylation by the CYP707A subfamily of P450 monooxygenases. A multi-omics analysis was performed on seeds of *nced* and *cyp707a* multiple mutants, which respectively exhibit reduced or increased seed dormancy, compared to wild type, in good correlation with their seed ABA contents. Hormone profiles in developing seeds revealed specific contributions of the different seed compartments to ABA production. Combined transcriptomic, proteomic and metabolomic data in wild type and mutant seeds highlighted important biological pathways that were differentially regulated by ABA levels, giving insights into a potential link with dormancy induction.

Key words: abscisic acid, *Arabidopsis thaliana*, dormancy, seed, omics