

A View to a Kill: Markers for Developmentally Regulated Cell Death in Plants

Although paradoxical, the selective killing of cells by programmed cell death (PCD) is an integral part of life (Ameisen, 2002). In this issue of *Plant Physiology*, Olvera-Carrillo et al. (2015) identify a conserved gene signature of PCD in plants.

PCD is the process by which the execution of a genetically encoded, actively controlled sequence of steps leads to the suicide of a cell. PCD differs from necrosis, which is generally described as an uncontrolled, chaotic mode of death (van Doorn, 2011). PCD serves diverse functions during development, cell differentiation, cell number homeostasis, and immune response (van Doorn, 2011; Van Hautegeem et al., 2015).

PCD is an integral element of the plant lifecycle. Development-related programmed cell death (dPCD) encompasses the selective elimination of cells as part of the differentiation process, the most prominent examples being the differentiation of the xylem and the rapid turnover of the root cap (Bollhöner et al., 2012; Kumpf and Nowack, 2015). dPCD is also associated with the senescence of whole organs (Thomas, 2013). Environment-related programmed cell death (ePCD) includes the hypersensitive response where the rapid death of cells in the local region surrounding an infection prevents the spreading of pathogens (Coll et al., 2011), but it can also be triggered in response to abiotic stresses, such as UV and salt (Nawkar et al., 2013; Petrov et al., 2015).

Our understanding of PCD has been shaped by research on animal PCD, particularly apoptosis. Although plant and animal PCDs share numerous characteristics (for instance, nuclear DNA degradation), several differences exist. The presence of a cell wall and the absence of phagocytosis imply that corpse clearance is a cell-autonomous process in plants. The dying cell synthesizes substances to break itself down and places them in the vacuole that ruptures as the cell dies (van Doorn, 2011). At the molecular level, apoptosis initiation and execution in animals relies on the antagonistic action of pro- and antiapoptotic members of the B-cell lymphoma2 family and the cascade activation of Caspases proteases (Fuchs and Steller, 2011). None of these components exist in plants, pointing to the existence of specific mechanisms. Plant PCD has been so far mostly investigated using morphological and biochemical characteristics (Reape et al., 2008), with a notable lack of molecular information.

Olvera-Carrillo et al. (2015) report on the *in silico* meta-analysis of transcriptomic data sets associated with

diverse instances of dPCD and ePCD in *Arabidopsis* (*Arabidopsis thaliana*). Their main finding is that, although ePCD and dPCD harbor distinct transcriptional signatures, a conserved core of PCD-associated genes is commonly regulated in diverse dPCD contexts. In planta validation using transcriptional reporters of the expression profile of some of these core dPCD genes confirmed their finding. Interestingly, most of these core dPCD genes are conserved in green plants, hinting at the existence of a conserved machinery of dPCD.

These reporters represent powerful tools for the future investigation of PCD in plants. They will allow for visualizing PCD at the tissue level. They will also allow obtaining PCD-specific transcriptomes and combined with genetic screens, dissection of the genes networks coordinating, preparing, and executing plant PCD.

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