

## GENES CONTROLLING FRUIT DEVELOPMENT IN *ARABIDOPSIS*

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### ABSTRACT

The *Arabidopsis* fruit is typical of several thousand members of the *Brassicaceae* family and consists of two valves that are separated by a thin structure called the replum. A narrow stripe of valve margin cells differentiates at the valve/replum boundary and is necessary for fruit opening at maturity. We have used molecular and genetic approaches to identify the genes that control valve margin specification to understand how the valve margin cells are precisely positioned at the valve/replum boundary during fruit development. The *SHATTERPROOF* (*SHP*), *INDEHISCENT* (*IND*) and *ALCATRAZ* (*ALC*) genes encoded transcription factors that are expressed in the valve margin where they act to promote valve margin differentiation, and mutants lacking the activities of these gene fail to disperse their seeds at maturity. The *FRUITFULL* (*FUL*) gene encodes a transcription factor that is expressed in valve cells and functions to negatively regulate expression of the valve margin identity genes in the valves. The *REPLUMLESS* (*RPL*) gene encodes a transcription factor that is expressed in the replum where it functions to negatively regulate valve margin identity gene expression. Together, negative regulation by *FUL* and *RPL* leads to a narrow stripe of expression of *SHP*, *IND* and *ALC*, thus positioning valve margin formation precisely at the valve/replum border. Two additional genes, *FILAMENTOUS FLOWER* (*FIL*) and *YABBY3* (*YAB3*), previously shown to encode transcription factors that pattern lateral organs, function to positively regulate expression of the *FUL* and *SHP* genes. Together, these studies have led to a model for the regulatory interactions among genes that pattern the *Arabidopsis* fruit.

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