

Scientists Reveal Role of RNA Helicase in Zygote Activation and Stem Cell Homeostasis in Plants

After double fertilization, zygotic activation occurs that initiates a new life cycle, followed by cell divisions, cell differentiation and organogenesis. During post-embryonic development, stem cells located in shoot apical meristem (SAM) and root apical meristem (RAM) allow plants to continuously generate new tissues and organs. Therefore, understanding the role of zygote activation and stem cell homeostasis is a long-standing interest to scientists.

Recently, researchers led by Prof. LIU Chunming from the Institute of Botany of the Chinese Academy of Sciences (IBCAS) found that DEAD-box RNA helicase

27 (RH27) plays critical roles in miRNA biogenesis, zygote activation, and stem cell homeostasis.

The Arabidopsis genome has 58 genes encoding DEAD-box RNA helicases, some of which are implicated in RNA-related events including mRNA export, mRNA splicing and rRNA processing. However, the role of DEAD-box RNA helicases in miRNA biogenesis has not been reported in plants.

In this study, a zygote-lethal mutant *zyg4-1* was identified, and map-based cloning showed that the mutation was caused by a point mutation in the *RH27* gene.

Interestingly, a weak allele of *rh27-2* exhibited

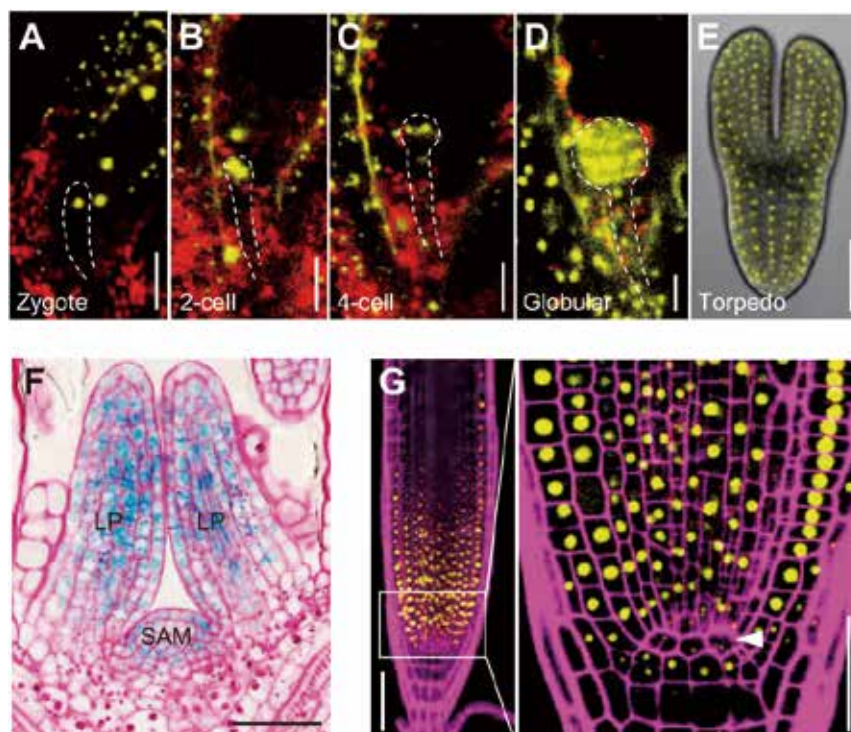


Figure 1. RH27 is expressed in embryos of Arabidopsis, a small flowering mustard, from the zygote stage onwards, and in the shoot apical meristem (SAM) and root apical meristem (RAM). (Image by IBCAS)

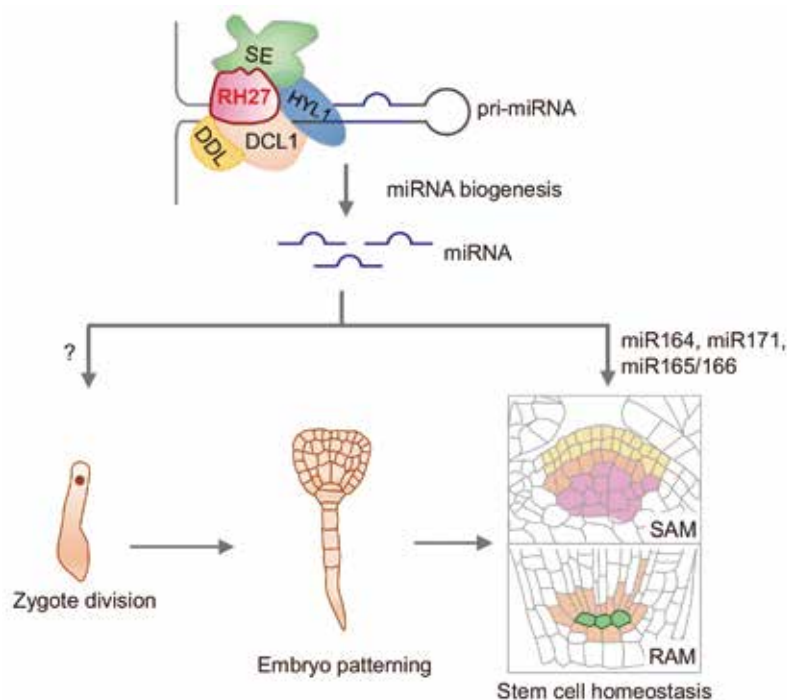


Figure 2. RH27 regulates zygote division and stem cell homeostasis through miRNA biogenesis. (Image by IBCAS)

compromised stem cell homeostasis, in both the SAM and RAM. In *rh27-2* plants, the expression of stem cell homeostasis-related genes was up-regulated, alongside with reduced levels of their regulatory miRNAs. Small RNA sequencing and RT-qPCR analyses showed reduced accumulations of a large subset of miRNAs and their pri-miRNAs in *rh27-2*.

RH27 was found to be expressed in embryos from the zygote stage onwards, and in the SAM and RAM (see figure 1). Confocal examination of roots showed that RH27 was localized primarily in the nucleolus, indicating the site it can exert influence.

Further biochemical studies revealed that RH27 is associated with pri-miRNAs *in vivo* and directly interacts with miRNA biogenesis components, DCL1, DDL, HYL1 and SE.

Based on the data, they proposed a model for the role of RH27 in zygote division and stem cell homeostasis, as illustrated in figure 2. It should be noted that direct evidence for the involvement of miRNAs in zygote division is still lacking; therefore, a question mark is used.

These data together demonstrate that RH27 is a new component of the microprocessor complex, and is required for zygote division and stem cell homeostasis. This work indicates a potential role of miRNA in zygote activation and stem cell homeostasis.

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(IBCAS)

Reference

Xiu-Li Hou, Wen-Qiang Chen, Yifeng Hou, Hua-Qin Gong, Jing Sun, Zhen Wang, . . . Chun-Ming Liu, (2020) DEAD-BOX RNA HELICASE 27 regulates microRNA biogenesis, zygote division, and stem cell homeostasis. *The Plant Cell* 33, 66. doi: 10.1093/plcell/koaa001.