NON-CODING RNA

The other face of PIWI


Credit: S. Bradbrook/Springer Nature Limited

Spermiogenesis involves gradual chromatin compaction and transcription shut-down. mRNAs that are transcribed in spermatocytes and early-round spermatids are stored as translationally inactive ribonucleoproteins until later during spermiogenesis, when their translation is activated, but how this activation occurs is largely unknown. PIWI proteins and PIWI-interacting RNAs (piRNAs) are essential for gametogenesis as they suppress the expression of transposons and mRNAs. Dai et al. now show that mouse PIWI (MIWI)–piRNAs are the core of a complex required for selective mRNA translation in spermatids.

MIWI–piRNAs target transcripts for silencing through base-pairing between the piRNA and the mRNA 3′ untranslated region (3′UTR). Working in cells derived from mouse spermatocytes, the authors were surprised to find five piRNAs that strongly upregulated reporters with 3′UTRs of the target mRNAs; reporter protein levels but not mRNA levels increased, implicating translation in reporter activation.

Activation of the target-mRNA reporters required piRNA–3′UTR base-pairing and 3′UTR binding by functional MIWI. Screening for MIWI-interacting proteins revealed that eukaryotic translation initiation factor 3f (eIF3f) directly interacted with MIWI and was also required for reporter activation. The activated 3′UTRs included AU-rich elements (AREs) that are bound by HuR, which is an RNA-binding protein known to interact with another translation factor, eIF4G3, for translation in spermatids. Together with the poly(A) binding protein PABPC1, they formed the MIWI–piRNA–eIF3f–HuR–eIF4G3–PABPC1 complex.

MIWI association with eIF3f–HuR was restricted to round spermatids, thus defining the stage of mRNA-specific translation activation. Translation of hundreds of mRNAs co-targeted by piRNA and HuR was dependent on MIWI, indicating that they are direct targets of this selective mechanism of translation activation.

> “MIWI–piRNAs… interact with eIF3f–HuR and other proteins to select a subset of ARE-containing mRNAs for translation activation”

The proteins encoded by two of the five original target mRNAs are essential for sperm acrosome formation. Indeed, severe acrosome defects were found in MIWI-depleted spermatids owing to considerable decrease in the levels of the two proteins.

Thus, although MIWI–piRNAs are mostly known for gene silencing, in round spermatids they interact with eIF3f–HuR and other proteins to select a subset of ARE-containing mRNAs for translation activation.

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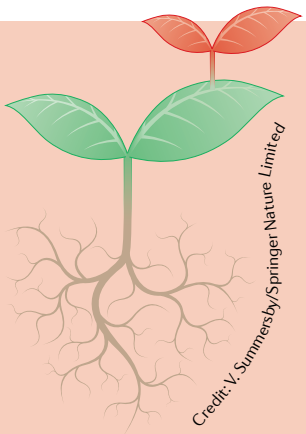
ORIGINAL ARTICLE Dai, P. et al. A translation-activating function of MIWI/piRNA during mouse spermiogenesis. *Cell* **179**, 1566–1581 (2019)

GENOME EDITING

Plant gene editing improved


Credit: V. Summersby/Springer Nature Limited

Gene editing in plants is usually achieved by modifying the genome of cultured cells and then regenerating whole plants by exposing the modified cultured cells to growth hormones. This method is inefficient, limited to a few species, and can also lead to undesired genome aberrations. Maher et al. now report that it is possible to overcome the tissue culture bottleneck by modifying somatic cells in whole plants and inducing the formation of shoot meristems — the plant stem cell niches that give rise to all the above-ground organs of the plant.

First, the authors developed a protocol (a high-throughput platform) to generate de novo meristems on the leaves of *Nicotiana benthamiana* in vitro-grown seedlings by expressing the developmental regulators *Wus2* and *STM* using *Agrobacterium*-mediated transient transformation. This transient expression led to the formation of callus-like growths. Even though many calli remained undifferentiated, some formed meristem-like structures that then differentiated into small shoots that could be transferred to a rooting medium, and then soil, to obtain full flowering plants (from which seeds could be harvested). Using a similar method on tomato seedlings, transient expression of *Wus2*, *ipt* and *STM* enabled the regeneration of whole tomato plants.

> “it is possible … to generate gene-edited shoots by transiently transforming stems of soil-grown plants”

This protocol was repeated using transgenic seedlings that constitutively expressed the nuclease Cas9. But in addition to developmental regulators, a single guide RNA (sgRNA, which targets the Cas9 nuclease to a specific sequence) was also expressed transiently to induce targeted mutations. This led to the generation of target gene-edited shoot meristems that developed into whole plants.

The authors could then show that it is possible to apply the same method to generate gene-edited shoots by transiently transforming stems of soil-grown plants. Moreover, they could modify agronomically important species such as potato and grape.

Thus, this study reports the successful generation of gene-edited plants without the need for time-consuming and inefficient sterile culture methods. Importantly, the developed high-throughput platform will enable the method to be tested on different plant species.

Kim Baumann

ORIGINAL ARTICLE Maher, M. F. et al. Plant gene editing through de novo induction of meritems. *Nat. Biotechnol.* https://doi.org/10.1038/s41587-019-0337-2 (2019)