

Champion racer's maneuver—m¹A mRNA modification accelerates transcription while restraining translation

Chenxi Guo¹, Shuangqing Jiang¹, Shikang Zhang¹ and Chengxiang Li^{1,2*} 

¹ Key Laboratory of Bio-Resource and Eco-Environment of Ministry of Education, Laboratory for Ex Situ Conservation and Resource Utilization of Mountain Plants, College of Life Sciences, Sichuan University, Chengdu, Sichuan 610065, China

² Chengdu Botanical Garden, Chengdu, Sichuan 610083, China

* Correspondence: chexiangli@scu.edu.cn (Li C)

Of the more than 100 chemical modifications catalogued on eukaryotic mRNA, only a handful are understood in functional detail. N⁶-methyladenosine (m⁶A) has anchored the plant epitranscriptomic field for over a decade: its writers, readers, and erasers have been characterized, and its roles in development and stress physiology are widely documented^[1–3]. Although N¹-methyladenosine (m¹A) has been detected in a few plant species, it has never been systematically characterized. A recent study by Ke et al. delivers the first single-nucleotide-resolution m¹A methylome across 10 Arabidopsis tissues, identifies the complete writer–reader–inhibitor toolkit, and demonstrates that m¹A regulates abscisic acid (ABA) signalling^[4]. It provides the most accurate m¹A map available for any plant species and establishes m¹A as only the second mRNA modification, after m⁶A, for which a full regulatory system with a defined physiological function has been described in plants.

A comprehensive, high-resolution m¹A atlas

The defining technical advance of this study is its detection strategy. Earlier plant m¹A studies in tomato and petunia relied on antibody-based enrichment alone, yielding broad, lower-resolution profiles^[5,6]. Zhou et al. coupled m¹A immunoprecipitation with the engineered RT1306 reverse transcriptase. This enzyme introduces a characteristic mutation signature at m¹A sites, enabling detection at single-nucleotide resolution when paired with AlkB demethylase treatment as a negative control^[7]. This approach yields a standard previously achieved only in mammalian systems.

The resulting atlas comprises 4,802 high-confidence m¹A sites across 2,947 genes, drawn from 10 tissues spanning the Arabidopsis lifecycle (Fig. 1a). The majority of methylated genes (83%) carry a single site, consistent with m¹A functioning as a position-specific mark, not a diffuse modification. In general, m¹A is ubiquitous in Arabidopsis, with m¹A/A ratios of 0.028%–0.043% detected from 25 different tissues. These values match those reported in mammals, yeast, and other eukaryotes. Such cross-kingdom conservation implies fundamental functional constraints on m¹A deposition, rather than species-specific idiosyncrasy. Notably, m¹A is preferentially enriched in 5'-UTRs, peaking roughly 100 nucleotides upstream of the start codon. This distribution mirrors the mammalian pattern and stands in marked contrast to the 3'-biased localization of m⁶A, pointing to a spatial division of regulatory labor between the two modifications. Ke et al. also identified a plant-specific feature: m¹A sites cluster closer to the start codon when they reside in the second exon rather than the first. This is the opposite of the trend in mammals^[8], and it suggests not only divergent

m¹A deposition mechanisms but also different regulatory mechanisms associating m¹A with transcription, splicing, or translation, at least between plants and animals.

A distinct regulatory logic: translational control via RNA structure

The spatial segregation of m¹A and m⁶A reflects fundamentally different regulatory strategies. Ke et al. demonstrated this functional distinction by integrating their methylome with publicly available proteomic data. m¹A-modified transcripts consistently exhibited higher mRNA and protein levels than those of unmodified transcripts. However, their protein-to-RNA ratio (PTR), a measure of translational efficiency, was significantly lower (Fig. 1b). Polysome profiling reinforced this picture: m¹A-marked mRNAs were enriched in ribosomal subunits and monosome fractions and were depleted from actively translating polysomes (Fig. 1c). The m¹A-modified 5' UTRs also exhibited higher minimum free energy than the unmodified ones. A positively charged N¹-methyl group that blocks base pairing is expected to stiffen the local RNA structure, making it harder for the 43S preinitiation complex to scan through^[4].

These data identify m¹A as a translational brake at highly active transcripts; it permits transcript production while limiting protein output. When the restraint is lifted, protein products can be synthesized without waiting for new rounds of transcription. Much like an accomplished race car driver who skillfully balances the throttle and the brake to navigate a complex racetrack, m¹A appears to fine-tune gene expression by simultaneously preserving responsiveness and preventing excessive output. In plants, constantly changing environmental conditions and the accompanying reconfiguration of phytohormone signaling pathways represent precisely such a 'complex racetrack'. Adaptive responses must be deployed rapidly, yet remain sufficiently restrained, reversible, and flexible to accommodate subsequent environmental fluctuations. The regulatory mode uncovered for m¹A is remarkably well suited to these biological demands, providing an elegant mechanism for balancing rapid response with controlled gene expression.

An ancient enzyme repurposed: from tRNA to mRNA modification

TRM6 and TRM61 are known to form the tRNA m¹A methyltransferase complex in Arabidopsis. Loss of this essential activity results in embryo lethality^[9,10]. Ke et al.^[4] now show that the same complex also methylates mRNA, but only under stringent structural

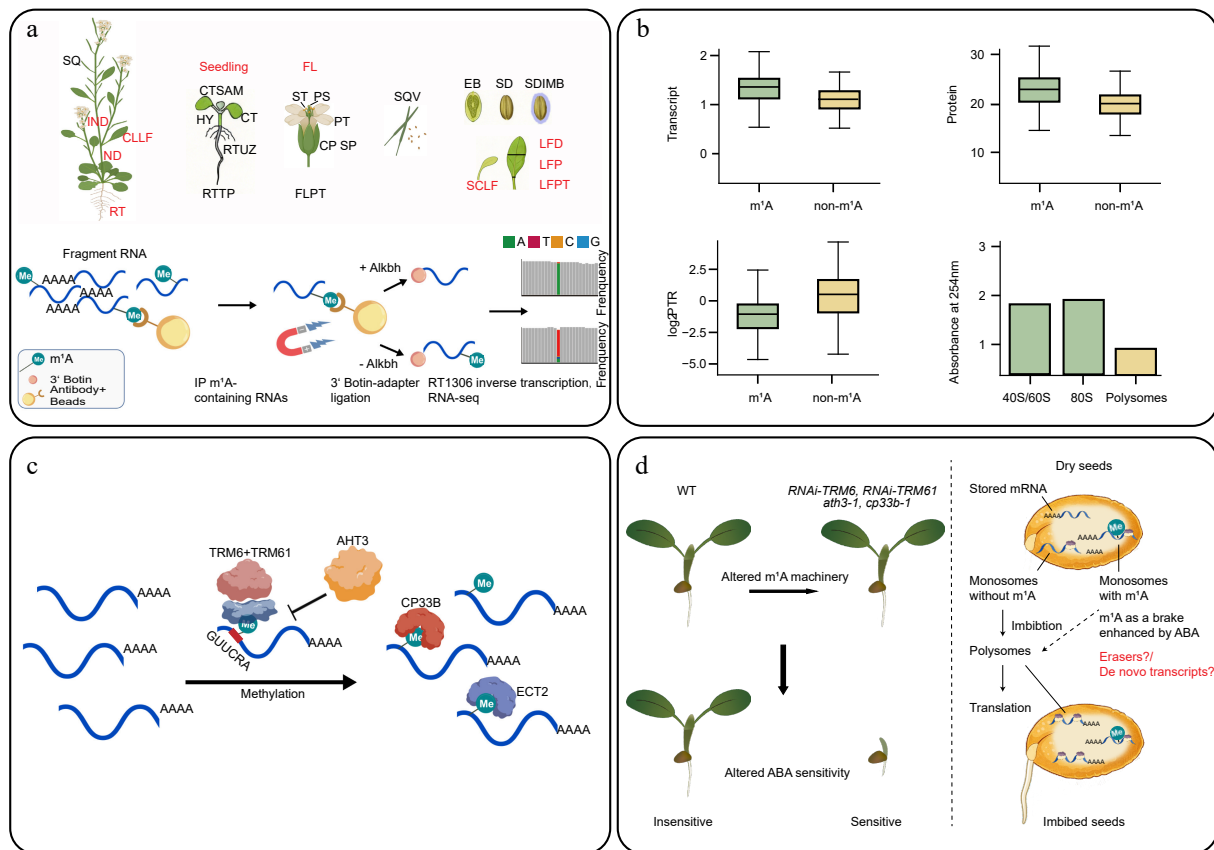


Fig. 1 Foundational m¹A epitranscriptomic atlas and regulatory system in Arabidopsis. (a) Schematic of 25 Arabidopsis tissues collected in the m¹A atlas and m¹A-IP-seq workflow. Tissues abbreviations: EB, embryo; CP, carpel; CT, cotyledons; CTSAM, shoot tip; FL, flower; FLPT, flower petiole; HY, hypocotyl; IND, internode; LFD, leaf distal; LFP, leaf proximal; LFPT, leaf petiole; ND, node; PS, pistil; PT, petal; RT, root; RTTP, root tip; RTUZ, root upper zone; SCLF, senescent leaf; SD, seed; SDIMB, seed imbibed; SP, sepal; SQ, silique; SQV, silique valves; ST, stamen. All these 25 tissues were used in the m¹A level detection, while the 10 tissues used in m¹A-IP-seq were labelled in red abbreviations. For m¹A detection at single-nucleotide resolution, m¹A-modified mRNA fragments are immunoprecipitated, and one aliquot is treated with AlkB to remove m¹A. Both aliquots were reverse-transcribed using RT1306. The enzyme's elevated mismatch rate at m¹A sites in the untreated sample, relative to the AlkB-treated control, enables single-nucleotide detection of m¹A. (b) m¹A regulates events from transcription to translation. m¹A-modified transcripts show higher mRNA and protein abundance but lower protein-to-RNA ratios (PTR). m¹A is enriched in monosome fractions and depleted from polysomes. (c) m¹A writer–reader network. TRM6–TRM61 catalyses m¹A deposition on substrates bearing a tRNA-like stem-loop with the GUUCRA motif. ATH3 inhibits this complex by impairing the RNA-binding of the TRM6–TRM61 complex. CP33B and ECT2 read m¹A; ECT2 additionally binds m⁶A. (d) Genetic disruption of any m¹A pathway component results in ABA hypersensitivity (left panel) and m¹A as a translational brake on stored mRNAs at germination (right panel). The figure was created in BioRender. Guochenxi, G. (2026), <https://BioRender.com/d9bmi84>, and with BioGDP (biogdp.com).

conditions. Consistent with observations in humans, both a tRNA-like stem-loop and the GUUCRA consensus motif are required for substrate recognition (Fig. 1c). This structural mimicry of the tRNA T-loop represents an elegant example of evolutionary exaptation: the co-option of an ancient tRNA modification enzyme for a new regulatory function on mRNA. This stringent structural requirement also helps explain why m¹A has remained difficult to characterize systematically in plants, where it is also far less abundant than m⁶A. Unlike m⁶A, whose RRACH consensus motif enables straightforward sequence-based prediction, m¹A deposition depends on the three-dimensional RNA structure that cannot be inferred from the primary sequence alone.

Shared toolkit, different tunes: regulatory specificity of m¹A and m⁶A

The regulatory mechanism diverges further from the m⁶A paradigm with the discovery of ATH3 (AtTrxh3; Arabidopsis

thioredoxin H-type protein)^[4]. It physically associates with the TRM6–TRM61 complex and inhibits its RNA-binding activity. m¹A levels are elevated when ATH3 is deleted *in vivo*. An inhibitor protein of an mRNA methyltransferase has not been described for any other mRNA modification writer complex. Its existence implies that m¹A deposition is subject to active, tunable negative regulation.

On the reader side, CP33B and ECT2 were identified as m¹A readers. ECT2 is a YTH-domain protein that was previously characterized as an m⁶A reader^[11]. Given the distinct distributions of m⁶A and m¹A along mRNAs, ECT2 may exert context-dependent regulatory effects depending on the modification it engages. Whether these two marks compete for ECT2 occupancy, or cooperate to produce integrated regulatory outputs, is a central open question that the tools provided by Ke et al. now make experimentally tractable. These findings further raise the possibility that additional m⁶A readers also recognize m¹A.

However, global m⁶A levels did not change in m¹A pathway mutants upon ABA treatment, indicating that the two modifications operate independently at the deposition level. Previous studies

have shown that ECT2/3/4 function redundantly to negatively regulate ABA signaling through recognition of m⁶A-modified transcripts^[12]. In addition, the stress-inducible reader ECT8 promotes the degradation of m⁶A-modified transcripts encoding negative regulators, thereby acting as a molecular sensor of stress^[13]. Together, these findings suggest that functional crosstalk between m¹A and m⁶A is more likely to occur at the level of reader-mediated decoding and downstream target regulation than through coordinated methylation deposition.

From catalogue to function: m¹A responds to phytohormone and gate ABA signalling

Ultimately, the importance of any RNA modification is determined by its physiological function. Major phytohormones, including abscisic acid (ABA), auxin, gibberellin, cytokinin, and ethylene, significantly increased the relative m¹A level. A range of abiotic stresses was further examined, while only nitrogen deficiency, high pH, and light altered the relative m¹A level under the experimental conditions.

ATH3 was previously reported as an ABA-binding protein^[4], and m¹A levels responded most strongly to ABA. Echoing these clues, knocking down the writers (*RNAi-TRM6/61*), deleting the inhibitor (*ath3-1*), or the reader (*cp33b-1*) all altered ABA sensitivity (Fig. 1d). The transcript of *SnRK2.2*, a key positive regulator of ABA signalling, contains an m¹A site. Collectively, these observations suggest that m¹A dynamics are physiologically important for ABA signalling, although the precise mechanism remains to be fully resolved. Since m¹A may permit transcript accumulation while restraining translation, the dual role of the m¹A mark may maintain ABA signaling within an optimal dynamic range, balancing responsiveness with reversibility under fluctuating environmental conditions.

m¹A as a translational brake on stored mRNAs during germination

These ABA phenotypes were evaluated in germination assays (Fig. 1d), and germination may be one of the contexts in which m¹A's translational brake matters. Mature dry seeds accumulate many long-lived stored mRNAs, most of them kept as translationally silent monosomes, while the steady-state mRNA pool may not reflect the protein output^[14]. On imbibition, a subset of these stored mRNAs is loaded onto polysomes and translated before the requirement of transcription^[15]. *De novo* transcription resumes later, chiefly to sustain post-germinative growth. Newly produced transcripts face a further gate before translation: SAM8 condensation under low water potential can hold them in the nucleus^[16]. Transcript accumulation and translation thus run on different schedules during germination, and it is in this window that Ke and Balarynová et al. observed altered ABA sensitivity in m¹A pathway mutants. If m¹A decorates stored mRNAs too, the mark could keep germination-related transcripts in reserve until water releases them, setting both how quickly and how reversibly a seed commits to germinating. Recent data point in the same direction: m¹A is the most abundant RNA modification in *Arabidopsis* seeds, more so in a non-dormant accession than in a deeply dormant one, and its levels rise during after-ripening^[17]. Whether m¹A truly controls the translation of stored mRNAs, and how this intersects with ABA signalling, remains

to be seen. The answer bears directly on dormancy and on uniform germination in crops.

Conclusions

Ke et al. provide the plant research community with high-quality m¹A resources that it did not have before. The immediate priorities are structural and comparative studies. A cryo-EM structure of the TRM6–TRM61 holoenzyme would clarify how the GUUCRA motif and tRNA-like fold are recognized and whether tRNA and mRNA methylation activities can be experimentally uncoupled. Defining the dynamic interactome of the TRM6–TRM61 holoenzyme may help explain the differential m¹A deposition in various developmental or environmental contexts. Beyond the model plant *Arabidopsis thaliana*, extending high-resolution m¹A profiling to crop species will reveal whether translational control via m¹A is a conserved strategy for tuning hormone responses under field-relevant conditions.

Another intriguing observation is that m¹A and m⁶A may partially share the eraser and/or reader system. Identification of an m¹A eraser in *Arabidopsis*, as they do in mammals^[4], would complete the writer–reader–eraser framework. The dual-affinity reader ECT2 opens the door to a broader question that extends beyond m¹A and m⁶A. A broader challenge now lies in defining the regulatory logic that emerges when multiple RNA modifications converge on shared effector proteins.

Author contributions

The authors confirm their contributions to the paper as follows: conceptualized the manuscript: Guo C, Li C; draft manuscript preparation: Guo C, Jiang S, Zhang S, Li C. All authors reviewed the results and approved the final version of the manuscript.

Data availability

Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Acknowledgments

This work was funded by the Fundamental Research Funds for the Central Universities and the National Natural Science Foundation of China (Excellent Young Scientists Fund, Overseas) to Li C.

Conflict of interest

The authors declare that they have no conflict of interest.

Dates

Received 7 August 2026; Revised 11 September 2026; Accepted 16 September 2026; Published online 19 October 2026

References

- [1] Liang Z, Riaz A, Chachar S, Ding Y, Du H, et al. 2020. Epigenetic modifications of mRNA and DNA in plants. *Molecular Plant* 13:14–30
- [2] Shen L, Liang Z, Wong CE, Yu H. 2019. Messenger RNA modifications in plants. *Trends in Plant Science* 24:328–341
- [3] Cai J, Shen L, Kang H, Xu T. 2025. RNA modifications in plant adaptation to abiotic stresses. *Plant Communications* 6:101229
- [4] Ke Y, Huang H, Hou Z-Y, Zhang M, Zhang X, et al. 2026. N¹-methyladenosine mRNA methylation in *Arabidopsis*. *Nature Plants* 12(7):1403–1416

- [5] Ma L, Zuo J, Bai C, Fu A, Wang Q, et al. 2024. The dynamic N¹-methyladenosine RNA methylation provides insights into the tomato fruit ripening. *The Plant Journal* 120:2014–2030
- [6] Yang W, Meng J, Liu J, Ding B, Tan T, et al. 2020. The N¹-methyladenosine methylome of *Petunia* mRNA. *Plant Physiology* 183:1710–1724
- [7] Zhou H, Rauch S, Dai Q, Cui X, Zhang Z, et al. 2019. Evolution of a reverse transcriptase to map N¹-methyladenosine in human messenger RNA. *Nature Methods* 16:1281–1288
- [8] Dominissini D, Nachtergaele S, Moshitch-Moshkovitz S, Peer E, Kol N, et al. 2016. The dynamic N¹-methyladenosine methylome in eukaryotic messenger RNA. *Nature* 530:441–446
- [9] Aslam M, Huang X, Yan M, She Z, Lu X, et al. 2022. TRM61 is essential for *Arabidopsis* embryo and endosperm development. *Plant Reproduction* 35:31–46
- [10] Tang J, Jia P, Xin P, Chu J, Shi DQ, et al. 2020. The Arabidopsis TRM61/TRM6 complex is a *bona fide* tRNA N¹-methyladenosine methyltransferase. *Journal of Experimental Botany* 71:3024–3036
- [11] Wei LH, Song P, Wang Y, Lu Z, Tang Q, et al. 2018. The m⁶A reader ECT2 controls trichome morphology by affecting mRNA stability in *Arabidopsis*. *The Plant Cell* 30:968–985
- [12] Song P, Wei L, Chen Z, Cai Z, Lu Q, et al. 2023. m⁶A readers ECT2/ECT3/ECT4 enhance mRNA stability through direct recruitment of the poly(A) binding proteins in *Arabidopsis*. *Genome Biology* 24:103
- [13] Cai Z, Tang Q, Song P, Tian E, Yang J, et al. 2024. The m⁶A reader ECT8 is an abiotic stress sensor that accelerates mRNA decay in *Arabidopsis*. *The Plant Cell* 36:2908–2926
- [14] Bai B, van der Horst N, Cordewener JH, America AHP, Nijveen H, et al. 2021. Delayed protein changes during seed germination. *Frontiers in Plant Science* 12:735719
- [15] Bai B, van der Horst S, Cordewener JHG, America TAHP, Hanson J, et al. 2020. Seed-stored mRNAs that are specifically associated to monosomes are translationally regulated during germination. *Plant Physiology* 182:378–392
- [16] Wang Y, Zhu L, Yang Y, Li X, Zhang X, et al. 2026. Cellular water-potential sensing through biomolecular condensation. *Nature* 655:1320–1329
- [17] Balarynová J, Klčová B, Čegan R, Raabe K, Krejčí P, et al. 2025. Translational and epitranscriptomic regulation of seed germination in *Arabidopsis thaliana* genotypes with contrasting dormancy phenotypes. *Plant Molecular Biology* 115:135



Copyright: © 2026 by the author(s). Published by Maximum Academic Press on behalf of Hainan Yazhou Bay Seed Laboratory. This article is an open access article distributed under Creative Commons Attribution License (CC BY 4.0), visit <https://creativecommons.org/licenses/by/4.0/>.