Nuclear dynamics

https://doi.org/10.1038/s41477-023-01458-1

Dynamic nucleoskeleton in stress

Yiling Fang & Yangnan Gu

The nucleoskeleton maintains nuclear integrity and chromatin organization at the inner nuclear surface. Here, Wang et al. revealed a disassociation of nuclear skeleton proteins from the nuclear periphery upon heat stress, which affects genome architecture and alters gene expression.

The nucleoskeleton provides mechanical stability to the plant cell nucleus by forming a mesh-like network beneath the inner nuclear membrane and helps to organize and position chromosomes within the nucleus, which facilitates proper gene expression and genome integrity[1]. Specifically, the *Arabidopsis* nucleoskeleton protein CROWDED NUCLEI 1 (CRWN1) defines plant nuclear-lamina-associated domains (PLADs), which are regions of chromatin bound to CRWN1 with limited accessibility and repressed transcription activities[2]. Disruption of CRWN1 and its homologues, as well as their association with other nuclear membrane structures such as the nuclear pore complex, leads to increased expression of stress-related genes[3–5]. Additionally, mutations in a potential plant chromatin tethering factor PLANT NUCLEAR ENVELOPE TRANSMEMBRANE 2 (PNET2), which coordinates perinuclear chromatin organization, display a similar stress-responsive gene-expression pattern[6]. These findings underscore the importance of maintaining proper chromatin localization and architecture at the nuclear surface. However, the contribution of chromatin reorganization to stress-related gene activation and the precise role of nucleoskeleton proteins in this process remain largely unknown. In this issue of *Nature Plants*, Wang et al. discovered an unforeseen migration of CRWN1 and its homologue CRWN4 from the nuclear periphery to the nuclear interior during heat stress. This phenomenon coincides with the redistribution of PLADs and changes in the expression of genes associated with heat stress[7] (Fig. 1).

To investigate the underlying mechanism that drives stress-induced chromatin dynamics, Wang et al. focused their study on heat stress — a condition that is known to induce substantial reorganization of chromatin in plant cells[8]. Using fluorescence in situ hybridization, they demonstrated the relocation of multiple PLADs from the nuclear periphery to the nuclear interior, accompanied by considerable chromatin decondensation. Chromatin immunoprecipitation (ChIP) experiments conducted with CRWN1 targeting the selected PLAD loci revealed that the interactions between CRWN1 and these loci remained unchanged. This finding indicates that the repositioning of genomic loci is not caused by dissociation from CRWN1.

To examine potential alterations in the localization of CRWN1 during heat stress, the researchers monitored the dynamics of nucleoskeleton proteins. Their observations revealed that not only CRWN1 but also its homologue CRWN4 and the nucleoskeleton-associated protein KAKU4 underwent relocation from the nuclear surface to the nuclear interior in response to heat stress. Notably, this phenomenon was also observed under salt and osmotic stress, which indicates that nucleoskeleton dynamics occur in response to diverse abiotic stress

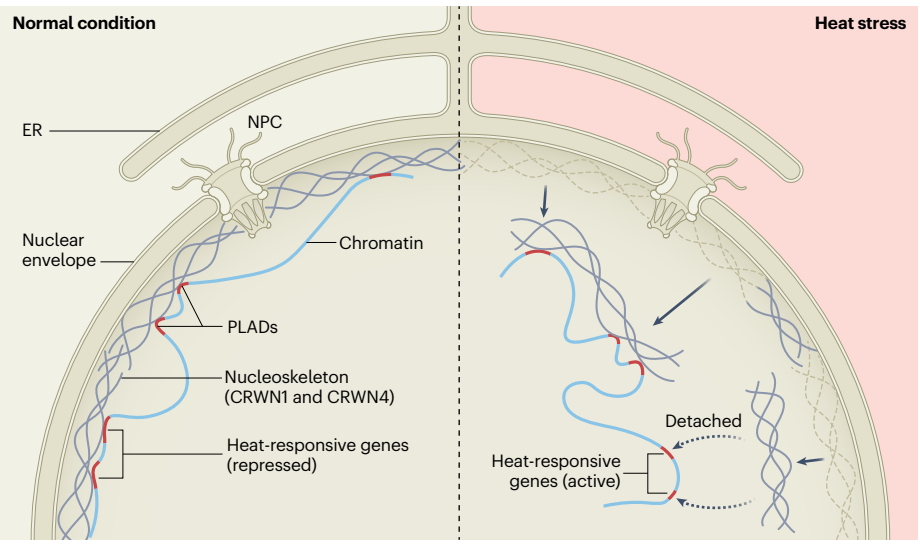

Fig. 1 | Nucleoskeleton-chromatin reorganization induced by heat stress. Under normal conditions, the nucleoskeleton proteins CRWN1 and CRWN4 are found at the nuclear periphery, where they contribute to the formation of PLADs and transcription repression of stress-induced genes. In heat-stressed plants, CRWN1 dissociates from the nuclear periphery, which potentially drives considerable nuclear reorganization of chromatin associated with it. Furthermore, partial detachment of PLADs in chromosome arm regions from CRWN1 occurs, resulting in the activation of heat-responsive genes. NPC, nuclear pore complex; ER, endoplasmic reticulum.

conditions. The authors demonstrated that this movement was specific to the nucleoskeleton proteins and did not involve other nuclear lamina-associated components such as the nuclear pore complex, nor did it result from general disorganization of the nuclear membrane. Further analysis using ChIP-seq with *CRWN1*-transgenic plants indicated that, despite the chromatin rearrangement triggered by heat stress, the overall interaction between CRWN1 and PLADs remained largely intact. This finding implies that the stress-induced dynamics of nucleoskeleton proteins may be responsible for driving the nuclear rearrangement of chromatin.

Despite the preservation of the general CRWN1–PLAD interaction, the effect of heat stress manifests locally. Wang et al. made a notable discovery that heat stress enhances the interactions between CRWN1 and pericentromeric regions, while reducing interactions with chromosome arms. They provided compelling evidence that genes showing compromised interaction with CRWN1 tend to exhibit higher expression levels, and several of these genes are functionally associated with heat responses. These data establish a connection between the release of CRWN1 and the upregulation of gene activity during heat stress, which sheds light on the regulatory role of CRWN1 in heat-responsive gene expression. Last but not least, the researchers used high-throughput chromosome conformation capture analysis to show that the absence of CRWN1 and CRWN4 considerably affected chromatin compartmentalization during heat stress, which further supports the involvement of CRWN1 and CRWN4 in the regulation of genome organization during heat stress.

Our comprehension of the plant nucleoskeleton and nuclear lamina has been expanding substantially, particularly in terms of their intricate involvement in regulating chromatin organization and gene expression during stress conditions. This growing knowledge highlights the complex functions of CRWN proteins in these vital processes. Previous studies have demonstrated that CRWN1 predominantly binds to transcriptionally inactive chromatin regions[2], and it physically associates with the POLYCOMB REPRESSIVE COMPLEX 2 (PRC2) to facilitate the repressive H3K27me3 modification[9]. However, there are also reports that indicate that CRWN1 binds to copper-associated genes, promoting their localization to the nuclear periphery for activation[10]. This seemingly contradictory effect of CRWN1 in regulating gene expression might arise from its distinct local environment at the nuclear periphery, where both transcriptionally active regions (such as the basket region of the nuclear pore complex) and inactive regions (such as PLADs) coexist. The findings presented by Wang et al. provide insights into a mechanism of CRWN1-mediated chromatin rearrangement that is dependent on stress-induced nucleoskeleton relocation. It would be fascinating to investigate whether the CRWN1-dependent chromatin-reorganization pattern differs under diverse environmental stimuli, including both abiotic and biotic stresses. Understanding how these dynamics may contribute to stress resistance and exploring the conservation of this regulatory mechanism across eukaryotic species would be of great interest as well. Nevertheless, it is important to note that the relocation of CRWN1 and CRWN4 does not necessarily imply complete disruption of the nuclear surface-localized nucleoskeleton, as compensatory mechanisms that involve other nucleoskeleton proteins (for example, CRWN2 and CRWN3) may come into play. Future experiments will be essential to unravel the intricate interplay and distinct functions of CRWN1 and CRWN4 versus CRWN2 and CRWN3 during stress-mediated chromatin reorganization.

Yiling Fang & Yangnan Gu ✉
Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA.
✉e-mail: guyangnan@berkeley.edu

Published online: 3 July 2023

References

1. Graumann, K. *J. Exp. Bot.* **72**, 6077–6080 (2021).
2. Hu, B. et al. *Genome Biol.* **20**, 87 (2019).
3. Choi, J., Strickler, S. R. & Richards, E. J. *Plant Physiol.* **179**, 1315–1329 (2019).
4. Guo, T. et al. *Mol. Plant* **10**, 1334–1348 (2017).
5. Tang, Y., Ho, M. I., Kang, B. H. & Gu, Y. *PLoS Biol.* **20**, e3001831 (2022).
6. Tang, Y., Dong, Q., Wang, T., Gong, L. & Gu, Y. *Dev. Cell* **57**, 19–31.e6 (2022).
7. Wang, N. et al. *Nat. Plants* https://doi.org/10.1038/s41477-023-01457-2 (2023).
8. Sun, L. et al. *Nat. Commun.* **11**, 1886 (2020).
9. Mikulski, P. et al. *Plant Cell* **31**, 1141–1154 (2019).
10. Sakamoto, Y. et al. *Nat. Commun.* **11**, 5914 (2020).

Competing interests

The authors declare no competing interests.