

New Insights into the Role of the NAC Family in Transcriptional Control of Seed Life

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Abstract

Seed life, including development, dormancy, and germination, is a complex process regulated by intricate networks of genetic and environmental factors. Among the numerous gene families involved in these processes, the NAC (NAM, ATAF, and CUC) transcription factor family stands out due to its critical role in regulating various aspects of plant development and stress responses. This mini review focuses on recent discoveries concerning the NAC family's function in seed life, highlighting their regulatory mechanisms and potential applications in agriculture.

Keywords: Transcription factor • Germination • Dormancy

Introduction

The NAC family is one of the largest families of plant-specific transcription factors, characterized by a highly conserved N-terminal DNA-binding domain (NAC domain) and a variable C-terminal transcriptional activation or repression region. Since the discovery of the first NAC genes, the family has expanded to include hundreds of members in various plant species, with *Arabidopsis thaliana* alone possessing over 100 NAC genes. These transcription factors are involved in diverse biological processes, including organ formation, secondary wall synthesis, and responses to biotic and abiotic stresses. During embryogenesis, NAC transcription factors play crucial roles in regulating the formation and differentiation of the embryo. The NAC genes SOMNUS (SOM), NAC1, and NAC2 in *Arabidopsis* have been shown to control cell division and differentiation, ensuring proper embryo development. For instance, SOM is involved in the repression of seed germination under unfavorable conditions, highlighting its role in seed dormancy.

Literature Review

The seed coat is essential for protecting the embryo and regulating seed dormancy and germination. NAC transcription factors like ANAC058 and ANAC092 are critical in the development of the seed coat. These transcription factors regulate the expression of genes involved in the synthesis and deposition of secondary cell walls in the seed coat, thus influencing seed hardness and permeability. Seed dormancy is a crucial adaptive trait that prevents germination under unfavorable conditions. Several NAC transcription factors have been implicated in the regulation of seed dormancy. For instance, the NAC gene ANAC060 in *Arabidopsis* regulates Abscisic acid (ABA) signaling, a key hormone in maintaining seed dormancy. ANAC060 modulates the expression of ABA-responsive genes, thereby enhancing seed dormancy under stress conditions [1].

Conversely, certain NAC transcription factors promote seed germination by antagonizing ABA signaling or enhancing Gibberellin (GA) signaling,

which promotes germination. ANAC089, for example, has been identified as a positive regulator of seed germination by promoting the degradation of ABA and enhancing GA biosynthesis. This balance between ABA and GA signaling orchestrated by NAC transcription factors is vital for the timely germination of seeds. Seed longevity, the ability of seeds to remain viable over extended periods, is influenced by both genetic factors and environmental conditions. NAC transcription factors contribute to seed longevity by regulating stress responses and protective mechanisms during seed maturation [2].

Seeds are often exposed to various stresses, including desiccation, oxidative stress, and pathogen attack. NAC transcription factors such as ANAC072 (RD26) enhance seed longevity by activating stress-responsive genes that confer protection against these stresses. ANAC072, for instance, regulates the expression of genes involved in antioxidant defense, thus mitigating oxidative damage during seed storage. NAC transcription factors also regulate the synthesis of protective compounds such as Late Embryogenesis Abundant (LEA) proteins and Heat Shock Proteins (HSPs), which stabilize cellular structures and protect against desiccation. ANAC019 and ANAC055 have been shown to activate the expression of LEA and HSP genes, thereby enhancing seed desiccation tolerance and longevity [3].

Discussion

NAC transcription factors function within complex transcriptional networks, interacting with other transcription factors and signaling molecules to fine-tune gene expression. For instance, ANAC092 (AtNAP) interacts with the transcription factor ABI3 to regulate seed dormancy and germination. These interactions highlight the integrative role of NACs in coordinating multiple signaling pathways. Post-Translational Modifications (PTMs) such as phosphorylation, ubiquitination, and sumoylation modulate the activity and stability of NAC transcription factors. For example, phosphorylation of ANAC019 by SnRK2 kinases enhances its stability and transcriptional activity under drought stress. These PTMs provide an additional layer of regulation, ensuring precise control of NAC functions in seed life [4].

Understanding the role of NAC transcription factors in seed life has significant implications for agriculture. By manipulating NAC genes, it is possible to improve seed traits such as dormancy, germination, and longevity, which are crucial for crop yield and quality. For crops where premature germination is problematic, such as during wet harvest conditions, enhancing seed dormancy through the overexpression of NAC genes like ANAC060 could be beneficial. This approach can prevent pre-harvest sprouting and ensure better seed quality. In contrast, for crops grown in challenging environments where rapid and uniform germination is desired, promoting seed germination by downregulating dormancy-inducing NAC genes or upregulating germination-promoting NAC genes like ANAC089 can be advantageous. This strategy can improve crop establishment and yield. Seed

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longevity is essential for seed storage and maintaining seed viability during transportation and storage. Overexpression of NAC genes involved in stress responses and protective mechanisms, such as ANAC072, can enhance seed longevity, ensuring better seed performance over time [5,6].

Conclusion

The NAC family of transcription factors plays a pivotal role in the transcriptional control of seed life, influencing seed development, dormancy, germination, and longevity. Recent insights into their regulatory mechanisms have uncovered their potential in improving seed traits through genetic manipulation. As research continues to unravel the complexities of NAC functions, these transcription factors hold promise for advancing agricultural practices and enhancing crop resilience to environmental stresses. By leveraging the knowledge of NAC transcription factors, breeders and biotechnologists can develop crop varieties with optimized seed traits, contributing to sustainable agriculture and food security. The integration of NAC-focused strategies with traditional breeding and modern biotechnological approaches will be key to unlocking the full potential of these versatile transcription factors in crop improvement.

Acknowledgement

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Conflict of Interest

None.

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