ELUCIDATING THE REGULATORY ROLE OF *Arabidopsis thaliana* ARID-HMG PROTEIN ATHMGB15 IN POLLEN DEVELOPMENT

The development of male gametophytes in angiosperms is a highly intricate and synchronized process, governed by a sophisticated interplay between various hormonal signaling pathways that ensure the successful progression of fertilization. This process encompasses multiple critical events, including pollen maturation, anther dehiscence, pollen release, and the germination of pollen tubes. Central to these regulatory mechanisms are phytohormones, which act as master integrators of both internal developmental signals and external environmental cues, thereby orchestrating the fine-tuning of plant growth, reproduction, and adaptive responses. Jasmonic acid (JA) and its derivatives are critical, modulating processes like pathogen resistance, root growth, and senescence, while playing a vital role in male reproductive development, including stamen differentiation, pollen viability, and essential transcriptional networks for pollen maturation.

The *Arabidopsis thaliana* genome features a family of High Mobility Group (HMG) chromatin remodelers known to act as transcriptional activators, pivotal for the regulation of numerous genes. AtHMGB15 stands out as an ARID-HMG protein characterized by an AT-rich interaction domain alongside the canonical HMG-Box DNA-binding domain, with its expression predominantly elevated in flowers and pollen grains. This research delves into the molecular and biological mechanisms by which AtHMGB15 regulates pollen development, focusing on its integration with the JA hormone pathway. Detailed phenotypic analysis of the *athmgb15-4* mutant uncovered notable reproductive defects, including delayed flowering, shorter siliques, reduced seed set, and compromised pollen viability. Mutant pollen grains exhibited abnormal morphology, delayed germination, and impaired tube growth. Molecular profiling and *in silico* analysis revealed a significant down-regulation of genes involved in JA biosynthesis and signaling in *athmgb15-4* plants, accompanied by a roughly tenfold reduction in jasmonic acid and its derivatives in floral tissues. Remarkably, exogenous application of methyl jasmonate rescued pollen morphology and germination, reinstating the expression of JA signaling genes, which underscores the essential role of AtHMGB15 in JA-mediated developmental processes. Furthermore, biochemical assays suggest a direct physical interaction between AtHMGB15 and the MYC2 protein (a MYC2 transcription factor crucial in the JA pathway), forming a transcriptional activation complex that upregulates critical JA-responsive genes, including *MYB21* and *MYB24*, integral to stamen and pollen development.

These findings highlight AtHMGB15 as a crucial positive regulator of JA signaling, orchestrating the precise spatial and temporal expression of developmental regulators. Our work provides compelling insights into the interplay between chromatin architecture and hormone signaling in plant reproductive biology, positioning AtHMGB15 as a key player in ensuring successful male gametophyte development. By shedding light on how JA coordinates developmental and environmental signals, this study not only advances our understanding of plant reproductive biology but also presents promising implications for improving crop fertility and resilience in changing environmental conditions.

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