**Analysis of 3D Chromatin Architecture Dynamics in Rice Under Drought Conditions**

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**Background**

The spatial organization of chromatin within the nucleus plays a crucial role in gene regulation and stress responses in eukaryotes. However, in plants, our understanding of how 3D chromatin architecture is remodeled upon exposure to environmental stress remains limited. In this study, we aim to investigate the structural dynamics of chromatin in rice (Oryza sativa) under drought conditions.

**Methods**

High-resolution three-dimensional (3D) chromatin contact maps of Oryza sativa under standard growth conditions have been previously generated using advanced chromatin conformation capture techniques, including Pore-C, Hi-C, and Micro-C. These intrachromosomal contacts have been shown to facilitate the identification of potential regulatory interactions between cis-regulatory elements and their target genes. To detect the dynamics in architecture between standard and drought conditions, we aim to first complement our current dataset by constructing a 3D chromatin interaction map of rice under drought conditions. We will compare the chromatin organization of drought-stressed and control growth conditions. Primary, we will focus on the structural dynamics of topologically associated domains (TADs), which are genomic regions characterized by high intra-domain interactions and play a crucial role in gene regulation. We will determine whether drought stress induces significant remodeling of chromatin architecture.

**Conclusion**

This study will enhance our understanding of how 3D chromatin architecture is remodeled in response to drought stress and its impact on gene regulation in rice. By identifying structural alterations in topologically associated domains and chromatin interactions under drought conditions, we aim to uncover regulatory mechanisms that facilitate stress-responsive gene expression.