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Unraveling the 3D Genome Architecture in Plants: Present and Future

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摘要	<p>The eukaryotic genome has a hierarchical three-dimensional organization with functional implications in DNA replication, DNA repair, and transcriptional regulation. Over the past decade, scientists have endeavored to elucidate the spatial characteristics and functions of plant genome architecture using high-throughput chromatin conformation capturing technologies such as Hi-C, Chromatin Interaction Analysis by Paired-End Tag sequencing (ChIA-PET), and HiChIP. Here, we systematically review current discoveries in chromatin organization in plants at multiple scales. We also discuss the emerging opinions and concepts in 3D genome research, focusing on state-of-the-art 3D genome techniques, RNA-chromatin interactions, liquid-liquid phase separation (LLPS), and dynamic chromatin alterations. We propose the application of single-cell/single-molecule multi-omics, multiway (DNA-DNA, DNA-RNA, and RNA-RNA interactions) chromatin conformation capturing methods, and proximity ligation-independent 3D genome-mapping technologies to explore chromatin organization structure and function in plants. Such methods could disclose the spatial interactions between the trait-related SNPs and their target genes at various spatiotemporal resolutions, and elucidate the molecular mechanisms of the interactions among DNA elements, RNA molecules and protein factors during key trait formation in plants.</p>
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