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International Journal of Plant Biology & Research

Mini Review

High Throughput Next Generation Sequencing to Study Epigenetics of Plant Stem Cells

Rwik Sen*

Active Motif, USA

***Corresponding author**
Active Motif, Inc., 1914 Palomar Oaks Way, Suite 150, Carlsbad, CA 92008, USA, Email: rsen@activemotif.com

Submitted: 15 December 2020

Accepted: 24 December 2020

Published: 26 December 2020

ISSN: 2333-6668

Plant stem cells are innately undifferentiated reservoir of cells found in plant meristems which renew themselves and continuously supply precursor cells that differentiate to plant tissues and organs [1,2]. Research has focused on several aspects of plant stem cells but a lot of information about their epigenetic regulations are unknown. Hence, this mini-review of current literature presents elegant next generation sequencing (NGS) technology like ChIP-sequencing, ATAC-sequencing, and RNA-sequencing to understand the epigenetic regulations and mechanisms in plant stem cells (Figure 1).

Transcriptional profile analysis of plant stem cells shed new insights into gene regulation

Orchestration of gene expression programs among various plant stem cells lead to well-coordinated cellular communication and gene regulatory network for development. In this direction, RNA sequencing is used as a powerful tool to study the expression patterns of genes in plant stem cells. Clark et al. dissected genes that are specifically expressed in individual stem cell types versus all stem cells that regulate maintenance and division of stem cells in the root of *Arabidopsis thaliana* [3].

The study reports RNA sequencing (seq) of root-tip stem cells, differential gene expression analysis by PoissonSeq, followed by Gene Regulatory Network (GRN) analysis using Regression Tree Pipeline to predict probable networks. Ordinary Differential Equation (ODE) modeling was used to study gene expression changes in predicted networks. Overall, the study reports 9266 stem cell-enriched genes, transcriptomic profiles and timing of various stem cell populations leading to division and maintenance.

Epigenomic profiling reveals dynamic patterns of histone modification

Since epigenetic regulations regulate transcription, epigenetic processes like histone modifications need to be properly understood in order to study plant stem cells and development. Histone modifications across various stages of development of *Arabidopsis* have been reported by Engelhorn et al. [4]. In this study, modifications like H3K4me3 and H3K27me3 are studied by ChIP sequencing which show that these chromatin signatures are extremely dynamic during early development of plants, and hence crucial for stem cells. The ChIP seq reads were mapped to Columbia reference genome, and SICER V1.1 clustering approach was used to assess ChIP enriched regions and differentially enriched regions. Approximately 8000 and 5000 genes were identified with H3K4me3 and H3K27me3, respectively. The study combines ChIP seq with RNA seq, to report the prevalence of H3K4me3 changes in early flower development, H3K27me3 changes in later stages, and temporal tissue-specific epigenetic regulations.

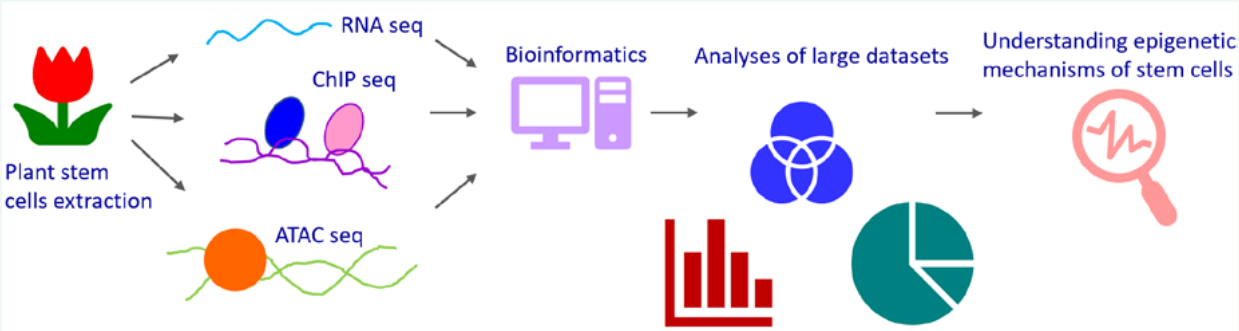

Figure 1 Plant stem cells are extracted and subjected to NGS technology like RNA seq, ChIP seq, and ATAC seq, and bioinformatics analysis of large datasets to understand novel epigenetic regulations.

Assay for open chromatin identify new cell-type specification and regulatory elements

Apart from histone modifications, epigenomics are regulated by various other factors that open and close chromatin. ATAC seq is an assay to analyze regions of open versus close chromatin to correlate with transcriptionally accessible/active versus inaccessible regions. Using ATAC seq, Frerichs et al. analyzed lateral organ founder cells (LOFCs) of *Arabidopsis* inflorescence meristem to find remarkable correlations between transposase hypersensitive sites (THSs) and DNase I hypersensitive sites (DHSs) [5]. They found 26 538 THS and 25 565 DHS frequency, with an overlap between 19 111 DHSs and 19 896 THSs, spanning 12.09 Mbps of open chromatin. The study provides important insights into chromatin dynamics during cell-type specification and identifies regulatory elements in plant genomes.

CONCLUSION

Hence, the future of plant research can be improved by future applications and modifications of the elegant NGS techniques discussed above that produce large datasets. Overall, the studies show that plant stem cell research can significantly benefit from high-throughput next generation sequencing technology to understand epigenetic regulations and mechanisms.

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Cite this article

Sen R (2020) High Throughput Next Generation Sequencing to Study Epigenetics of Plant Stem Cells. Int J Plant Biol Res 8(2): 1124.