OPEN ACCESS Freely available online

ISSN: 2329-6682
Gene Technology

Perspective

Accessible Chromatin Regions and Sorghum Genome with Epigenetic Alterations

Arthur Kurt*

Department of Biotechnology, University of Houston, Texas, United States

DESCRIPTION

The study of heritable phenotype changes that do not involve changes in the DNA sequence is known as epigenetics. Epigenetics most commonly refers to changes in gene activity and expression, but the term can also refer to any heritable phenotypic change. Such effects on cellular and physiological phenotypic traits could be the result of external or environmental factors, or they could be a normal part of development. The term also refers to changes to the genome that are functionally relevant but do not involve a change in the nucleotide sequence. Examples of such mechanisms include DNA methylation and histone modification, both of which alter gene expression without changing the underlying DNA sequence. Gene expression can be regulated by repressor proteins that bind to silencer regions of the DNA. These epigenetic changes may continue though the cell divisions and for multiple generations, despite the fact that they do not involve changes in the organism's underlying DNA sequence; rather, non-genetic factors that cause the organism's genes [1].

In multiple plant species, Accessible Chromatin Regions (ACRs) act as physiological implants to recruit transcriptional co-regulators and displace their nearby nucleosomes. Characterization of ACRs and study of their biological effects in *Sorghum bicolor* has been slow. The transcriptional co-regulators that are recruited to ACRs to affect epigenome modifications of surrounding nucleosomes are responsible for gene expression regulation. Humans used transposable chromatin sequencing to identify ACRs and determine how their presence affects gene expression and epigenetic signatures in the Sorghum genome. ACR profiling on gene organized sector a narrow and sharp peak around the gene promoter, with relatively weak and broad signals covering the entire gene body, and an explicit but broad peak from the transcription termination site to its down-stream regions. The presence of genic ACRs boosts the transcriptional activity of intergenic ACR-associated genes. Furthermore, integrating multiple-omics analyses of whole-genome bisulphite sequencing, 6mA immune precipitation followed by sequencing, RNA sequencing, chromatin immune precipitation sequencing, and DNase I hypersensitive sites sequencing datasets revealed a ACRs, gene expression, and epigenetic marks all interact in a complex way [2].

The degree to which nuclear macromolecules physically contact chromatinized DNA and are topologically organized by nucleosomes and other chromatin-binding factors is referred to as chromatin accessibility. The topological organization of nucleosomes across the genome is not uniform histones are depleted at regulatory loci, including intergenic regions and transcribed gene bodies, despite densely wrapping within facultative and constitutive heterochromatin. Transposase-accessible chromatin sequencing has recently been developed as a reliable tool for profiling Accessible Chromatin Regions (ACR) across multiple plant species and cell types, requiring less labor and fewer starting nuclei than DNase 1 treatment of nuclei combined with high-throughput sequencing. ATAC-seq used isolated nuclei to cleave accessible DNA and insert adapters for high-throughput sequencing with an engineered Tn5 transposase [3].

S. bicolor L. is the fifth-largest cereal crop on the planet. It offers a genetic model for C4 grasses with the benefits of a small genome, diploid genetic factors, diverse genetic variability, and co-linearity with other C4 grass genomes. The forecast nucleosome residence probabilities in sorghum are comparable to those in maize, suggesting that the distributions in both genomes may vary across each chromosome. Interestingly, nucleosomes immediately downstream of the TSS are present in varying densities across chromosomes. The advancement of plant epigenetics has recently probed genome-wide characterization of chromatin accessibility and chromatin modifications in sorghum, revealing involved in the regulation functions of ACRs and some chromatin marks in plants. Specific chromatin regulatory patterns and mechanisms in the sorghum genome, on the other hand, must be discussed. Furthermore, it is unclear whether and to what extent dynamic interactions of ACRs and epigenetic modifications play a role in

Correspondence to: Arthur Kurt, Department of Biotechnology, University of Houston, Texas, United States, E-mail: arthurkurt@gmail.com

Received: 06-Jun-2022, Manuscript No. RDT-22-17296; **Editor assigned:** 09-Jun-2022, PreQC No. RDT-22-17296 (PQ); **Reviewed:** 24-Jun-2022, QC No. RDT-22-17296; **Revised:** 01-Jul-2022, Manuscript No. RDT-22-17296 (R); **Published:** 08-Jul-2022, DOI: 10.35248/2329-6682.22.11.193

Citation: Kurt A (2022) Accessible Chromatin Regions and Sorghum Genome with Epigenetic Alterations. Gene Technol. 11:193.

chromatin accessibility in sorghum. We used ATAC-seq-coupled strategies to identify ACRs from sorghum seedling aboveground tissues and characterize their genomic distributions and organizations. We investigated the relationships between various types of ACRs and gene expression activity [4].

In this study, we used ATAC-seq to characterize ACR distribution patterns in the sorghum genome, and then we dissected ACR chromatin roles using genome-wide transcriptional profiling and characterization of multiple epigenetic modifications. Our findings showed that ACRs were widely distributed across all chromosomes and were relatively enriched in the sorghum genome's euchromatin. The findings suggest that nucleosome positions are not the only determinants of ACRs that are influenced by epigenome marks. ACR density was significantly higher at TSSs, which nucleosomes frequently occupy, but only slightly higher at TTSs. This pattern is consistent with the previous research by Lu and colleagues. Furthermore, we discovered that ACRs prefer to be found upstream of TSSs in some reported plant species, such as *A. thaliana*, *Asparagus officinalis*, and *Eutrema salsugineum* [5].

REFERENCES

1. Bolger AM, Lohse M, Trimmomatic BU. Trimmomatic: A flexible trimmer for Illumina sequence data. Bioinformatics. 2014:30(15); 2114-2120.
2. Buenrostro JD, Giresi PG, Zaba LC, Chang HY, Greenleaf WJ. Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. Nat. Methods. 2013:10(12);1213-1218.
3. Corces MR, Trevino AE, Hamilton EG, Greenside PG, Sinnott-Armstrong NA, Vesuna S, et al. An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nat. Methods. 2017:14(10);959-962.
4. Frerichs A, Engelhorn J, Altmüller J, Gutierrez-Marcos J, Werr W. Specific chromatin changes mark lateral organ founder cells in the Arabidopsis inflorescence meristem. J. Exp. Bot. 2019:70(15); 3867-3879.
5. Kim D, Pertea G, Trapnell C, Pimentel H, R. Kelley, Salzberg SL: Accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. Genome Biol. 2013:14(4);36.