

Genomic clusters of transcription factor binding sites in plants

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Crop breeding has entered a new era using high-throughput technologies, such as transcriptomics, genomics, and metabolomics. Integration of omics data provides a comprehensive understanding of the biological processes underlying plant traits and their interactions. We have studied regulatory transcription networks in model plants. The distribution of the number of links in the network of protein-protein interactions follows certain statistical patterns. The distribution of the number of hub genes in such a network for transcription factors also has an exponentially decreasing character. We discuss the hypothesis about the general nature of the distribution of clusters of binding sites in the genome according to the number of different transcription factors, which is determined by the structure of the regulatory gene network. A method and computer tool for searching for regulatory regions based on the statistics of the distribution of binding sites in plant genomes were presented (Dergilev et al., 2021). The existence of nonrandom clusters of binding sites in all studied plant genomes has been shown.

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The main publications of authors on the subject of the abstract:

Dergilev A.I., Orlova N.G., Dobrovolskay O.B., Orlov Y.L. *Statistical estimates of transcription factor binding site clusters in plant genomes based on genome-wide data. Journal of Integrative Bioinformatics. 2022; 18, 20200036 doi: 10.1515/jib-2020-0036*