

Plant Mitochondrial Genome Map (PMGmap): A Software Tool for Comprehensive Visualization of Coding, Non-coding and Genome Features of Plant Mitochondrial Genomes

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Abstract

Genome visualization tools are important for exploring genomic features and their interactions. Currently, visualization of the plant mitochondrial genomes (mitogenome) depends on those tools designed originally for animal mitogenomes and plant plastomes. These tools cannot faithfully present features unique to the plant mitogenomes, such as non-linear exon arrangement for genes, prevalence of functional non-coding features, and complex chromosomal architectures. To address these challenges, a software package plant mitochondrial genome map (PMGmap), was developed using Python programming language. PMGmap can draw genes at exon levels, draw cis- and trans-splicing gene maps, draw non-coding features, draw repetitive sequences, scale the genic regions using a scaling the genic regions on the genome (SGM) algorithm, and draw multiple chromosomes simultaneously. We compared PMGmap with other leading tools on 405 plant mitogenomes and found that PMGmap allowed the visualization of the above-mentioned features better than those tools. We believe PMGmap will become an invaluable tool for plant mitogenome research. The web and container versions and the source code of PMGmap can be accessed at <http://www.lkmpg.cn/pmgmap>.

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02.PMGmap-maintext.docx available at <https://authorea.com/users/675182/articles/673251-plant-mitochondrial-genome-map-pmgmap-a-software-tool-for-comprehensive-visualization-of-coding-non-coding-and-genome-features-of-plant-mitochondrial-genomes>