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Bioinformatics and Expression Study of CHI Genes in Sweet Potato

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Introduction

Sweet potato is an important staple crop with high nutritional value and multiple health benefits. The Chalcone Isomerase (CHI) gene family plays a crucial role in the flavonoid biosynthesis pathway, contributing to plant growth, stress response, and secondary metabolite production. Bioinformatics and expression analysis of the CHI gene family in sweet potato can provide valuable insights into their function and regulation, supporting genetic improvement efforts for enhanced yield, stress tolerance, and nutritional quality. A comprehensive bioinformatics analysis was performed to identify and characterize CHI genes in the sweet potato genome. Genome-wide identification was conducted using sequence homology searches against known CHI genes from model plants. Phylogenetic analysis classified the identified CHI genes into distinct subfamilies, revealing evolutionary relationships and functional diversification. Conserved domain analysis confirmed the presence of the CHI catalytic domain, ensuring the reliability of gene annotations. Structural analysis, including exon-intron organization and motif prediction, provided insights into the genetic architecture of CHI genes in sweet potato.

Description

Expression profiling of CHI genes was conducted using transcriptomic data from various sweet potato tissues, including leaves, stems, roots, and storage tubers. Differential expression analysis revealed tissue-specific expression patterns, suggesting specialized roles of CHI genes in different physiological processes. Notably, some CHI genes exhibited higher expression in tubers, indicating their potential involvement in flavonoid accumulation and storage organ development. The response of CHI genes to biotic and abiotic stresses was also investigated using publicly available RNA-seq datasets and Quantitative Real-Time PCR (qRT-PCR) validation. Several CHI genes were upregulated under drought, salinity, and pathogen attack, highlighting their importance in stress adaptation and defense mechanisms. To further explore the regulatory mechanisms governing CHI gene expression, promoter analysis was performed to identify cis-regulatory elements associated with stress responsiveness and hormone signaling. Binding motifs for transcription factors such as MYB, WRKY, and bZIP were detected, suggesting complex regulatory networks controlling CHI gene activity. Co-expression network analysis revealed interactions between CHI genes and other key enzymes in the flavonoid biosynthesis pathway, emphasizing their coordinated role in metabolic flux regulation [1].

Functional annotation of CHI genes was supported by Gene Ontology (GO) enrichment analysis, which confirmed their involvement in flavonoid metabolism, response to oxidative stress, and cellular signaling pathways. Comparative genomics analysis with other plant species provided additional insights into the conservation and divergence of CHI gene functions across different lineages. Structural modelling of CHI proteins was conducted to predict their three-dimensional conformations and substrate-binding affinities, offering valuable information for potential biotechnological applications. The findings from this study contribute to a deeper understanding of the CHI gene family in sweet potato and their potential role in improving crop traits through genetic engineering or breeding strategies. Future research should focus on functional validation of candidate CHI genes using gene editing approaches such as CRISPR-Cas9 and metabolic engineering to enhance flavonoid content for improved nutritional and medicinal properties. Integrating multi-omics approaches, including metabolomics and proteomics, will further elucidate the functional significance of CHI genes and their impact on sweet potato physiology and agricultural performance. The knowledge gained from this study lays the foundation for harnessing CHI genes in sweet potato improvement programs, benefiting both food security and human health [2,3].

Expression analysis of CHI genes in sweet potato involves the use of RNA sequencing (RNA-seq) data and quantitative PCR experiments to determine when and where these genes are active. Expression profiles across different tissues, such as leaves, stems, roots, and storage tubers, provide insights into the functional roles of individual CHI genes. Additionally, studying gene expression under different stress conditions, such as drought, salt stress, and pathogen infection, helps identify CHI genes that contribute to stress tolerance. These findings have potential applications in improving sweet potato resilience through genetic engineering or selective breeding. Regulatory elements within the promoter regions of CHI genes also play a significant role in controlling their expression. Bioinformatics tools enable the identification of cis-regulatory elements that interact with transcription factors to regulate gene expression. Understanding these regulatory mechanisms provides deeper insights into how CHI genes respond to environmental stimuli and developmental cues. This knowledge is essential for designing strategies to enhance flavonoid biosynthesis in sweet potato, which could improve its nutritional value and stress tolerance [4,5].

Conclusion

Functional characterization of CHI genes can be further validated using experimental approaches such as gene overexpression and RNA interference in transgenic plants. Overexpressing specific CHI genes may lead to increased flavonoid production, while silencing these genes can reveal their precise roles in metabolic pathways. Additionally, biochemical assays can confirm the enzymatic activity of CHI proteins and their involvement in flavonoid biosynthesis. These experimental validations complement bioinformatics findings, providing a comprehensive understanding of CHI gene functions. The application of bioinformatics in CHI gene research has significantly accelerated the discovery and characterization of genes involved in flavonoid biosynthesis in sweet potato. High-throughput sequencing technologies, combined with computational tools, allow researchers to analyse large datasets efficiently, leading to new insights into gene function and regulation. Machine learning approaches are also emerging as valuable tools for predicting gene functions based on sequence features and expression patterns. Integrating these advanced techniques will further enhance our understanding of the CHI gene family.

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Conflict of Interest

None.

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