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Research on Key Genes in Sugar Metabolism and Flavor Quality Improvement in Sweet Corn

Long Jiang[a], Baiming Yang[*]

Jilin Agricultural Science and Technology College, Jilin, Jilin 132101, P. R. China

[a]jianglong@jlnku.edu.cn, [*]yangbm660@nenu.edu.cn.

Abstract

Sweet corn is in high demand due to its rich nutrition and excellent taste, but it faces industry bottlenecks such as insufficient sweetness stability, monotonous flavor, and quality degradation under stress. Existing research lacks an understanding of the synergistic regulation of sugar metabolism and flavor synthesis, as well as the environmental impact mechanisms. This study used high-sweetness, fragrant, and soft-waxy sweet corn varieties as materials, and set up conventional, low-potassium, and high-temperature treatments. Quality indicators were measured at key growth stages. Combining transcriptomics, metabolomics, and WGCNA, core genes involved in the synergistic regulation of sugar and flavor were identified. A gene-trait-environment association model was established and validated by qPCR. The results showed significant differences in quality among different varieties. Ten hub genes, including SUS4, SPS2, and LOX3, were screened, and their expression was closely related to sucrose accumulation, aroma compound synthesis, and stress response. An integrated improvement system of "molecular breeding - cultivation optimization - postharvest preservation" was constructed to provide precise targets for sweet corn quality improvement. This study enriches the molecular mechanism of synergistic regulation of sugar and flavor in sweet corn, fills a gap in research on environmental responses, and contributes to the high-quality development of the industry.

Keywords

Sweet Corn, Sugar Metabolism, Flavor Synthesis, Multi-Omics, Hub Gene, Quality Improvement.

1. Introduction

Sweet corn, as an important crop for both fresh consumption and processing, is rich in dietary fiber, vitamins, and functional components, and has a sweet taste and excellent palatability, leading to continuously rising market demand and occupying an important position in the optimization of agricultural industrial structure. However, current sweet corn production and breeding still face core technological bottlenecks: sweetness is affected by both genetic background and environmental factors, resulting in insufficient stability; flavor components are mainly soluble sugars, with limited synergistic quality characteristics such as aroma and taste; under adverse conditions (such as high temperature and low potassium stress), sugar accumulation and flavor substance synthesis are easily imbalanced, leading to a significant decline in commercial quality and severely restricting the improvement of its industrial added value.

Sugar metabolism is the core physiological process determining the sweetness of sweet corn. Reported key genes mainly focus on classic metabolic pathways such as sucrose synthase (SUS), sucrose phosphate synthase (SPS), and starch branching enzyme (SBE). However, related studies mostly focus on functional verification of single genes, lacking a systematic analysis of

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the synergistic regulatory mechanisms between sugar metabolism and the synthesis of flavor compounds (such as volatile aldehydes, esters, and amino acid derivatives). Furthermore, current flavor quality improvement methods largely rely on traditional hybridization breeding, which suffers from long cycles and dispersed target traits [1]. Molecular breeding research also primarily focuses on marker development for single traits, failing to establish a synergistic improvement system for "sugar metabolism-flavor synthesis" and neglecting the influence of environmental factors on the regulatory network, resulting in insufficient targeting and practicality of improvement technologies.

This study used high-sweetness, fragrant, and soft-waxy sweet corn varieties as test materials [2]. Combining transcriptomics and metabolomics multi-omics technologies, and integrating weighted gene co-expression network analysis (WGCNA), this study systematically identified the core gene modules and hub genes regulating "sugar metabolism-flavor synthesis." By analyzing the environmental response characteristics of key genes under environmental stress, a three-in-one correlation model of "gene-trait-environment" was established. The research results will enrich the molecular mechanisms of the synergistic regulation of sugar content and flavor quality in sweet corn, fill the gap in research on the function of related genes under environmental responses, and provide precise targets for molecular marker-assisted breeding, cultivation optimization, and post-harvest preservation technology improvement [3]. This will contribute to the construction of an integrated quality improvement system, promoting high-quality and standardized production of sweet corn and driving high-quality development of the industry.

2. Research Content, Technical Route, and Differential Characteristic Analysis

2.1. Core Research Content

This study focuses on the synergistic improvement of sugar and flavor in sweet corn, centering on four main directions: First, systematically screening variety-specific differences in sugar composition, volatile aroma compounds, and taste parameters among high-sweetness, fragrant, and soft-waxy sweet corn varieties; second, integrating transcriptomics and metabolomics multi-omics technologies, combined with weighted gene co-expression network analysis (WGCNA), to identify key gene modules regulating sugar metabolism and flavor synthesis; third, verifying the association between key genes and quality traits through stress treatment, clarifying the gene-trait-environment interaction patterns; and fourth, constructing an integrated flavor and quality improvement strategy based on the research results, combining molecular marker screening and cultivation regulation, to enhance the targetedness and practicality of the improvement [4].

2.2. Technical Route

Using representative sweet corn varieties as test materials, three treatment groups were set up: conventional cultivation, low potassium stress, and high temperature stress. Ear samples were collected at three key growth stages: grain-filling, milk-ripe, and harvest [5]. High-performance liquid chromatography (HPLC) was used to determine sugar content indicators such as soluble sugars, sucrose, and fructose; gas chromatography-mass spectrometry (GC-MS) was used to analyze the composition of volatile flavor compounds; and a texture analyzer was used to determine taste parameters such as hardness and crispness. Transcriptome and metabolome sequencing were performed on samples with significant differences. Hub genes for sugar-flavor synergistic regulation were screened using WGCNA. The expression characteristics of candidate genes were verified using qPCR, and a correlation model was established based on

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environmental response data. Finally, a quality improvement scheme combining molecular breeding markers and cultivation optimization was proposed.

2.3. Experimental Materials and Measurement Methods

Three representative sweet corn varieties widely used in production were selected for testing: the high-sweetness variety "Yuetian 9," the fragrant variety "Aofelan," and the soft and glutinous variety "Dongtiannuo 100." The experiment included a conventional treatment group (normal fertilization and suitable temperature), a low potassium stress group (soil potassium content halved), and a high temperature stress group (average daily temperature of 35℃ during the grain-filling period), with each group replicated three times. Sugar content was determined using an Agilent Zorbax carbohydrate column (4.6mm × 250mm, 5μm), with 75% acetonitrile as the mobile phase, column temperature 25℃, and flow rate 1mL/min, detecting fructose, glucose, sucrose, and total soluble sugars [6]. Flavor compounds were determined using headspace solid-phase extraction combined with GC-MS, focusing on key aroma components such as aldehydes and esters. Texture parameters (hardness, crispness, cohesiveness, and chewiness) were measured using a texture analyzer.

2.4. Differences in Sugar Content and Flavor Compounds

Significant genotypic differences in quality indicators were observed among different sweet corn varieties under conventional cultivation conditions. Table 1 shows that the high-sweetness variety 'Yue Tian 9' had the highest total soluble sugar content at 18.62%, with sucrose accounting for 62.3%, significantly higher than other varieties, consistent with its high sweetness characteristics. The aromatic variety 'Ao Fu Lan' had a total soluble sugar content of 14.35%, but also had the most types of volatile flavor compounds detected, with ethyl palmitate reaching 12.87 μg/g, a key component of the aromatic flavor of sweet corn [7]. The soft and glutinous variety 'Dong Tian Nuo 100' had the lowest total soluble sugar content (10.28%), but amylopectin accounted for 99.0%, and its cohesiveness and chewiness indicators were significantly better than the other two varieties, reflecting its soft and glutinous texture.

Table 1. Differences in core quality indicators among different sweet corn varieties under conventional treatment (harvest period)

variety	Total soluble sugars (%)	Sugar content (%)	Ethyl palmitate (μg/g)	Hardness (N)	Cohesiveness	Branched-chain starch percentage (%)
Yuetian No. 9	18.62±0.53a	62.3±1.2a	8.45±0.32b	28.6±1.4b	0.18±0.01c	78.5±1.8c
Aofelan	14.35±0.41b	51.7±1.5b	12.87±0.46a	23.4±1.1c	0.21±0.02b	82.3±2.1b
Dongtian Nuo 100	10.28±0.37c	43.5±1.8c	9.12±0.38b	35.2±1.7a	0.27±0.03a	99.0±0.5a

Abiotic stress significantly affected the quality indicators of sweet corn, with differences among varieties (Table 2). Under low potassium stress, the total soluble sugar content of all three varieties decreased significantly, with "Yuetian 9" showing the largest decrease (23.6%), confirming the sensitivity of soluble sugars to low potassium stress [8]. High temperature stress mainly affected the synthesis of flavor compounds; the ethyl palmitate content of "Aofran" decreased by 31.2%, while the hardness index of "Dongtiannuo 100" increased significantly, resulting in a harder texture. Overall, the soft and glutinous "Dongtiannuo 100" showed relatively strong tolerance to both abiotic stresses, with its quality indicators decreasing less than those of the high-sweetness and light-aroma varieties, providing a reference for screening stress-resistant varieties.

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Table 2. Effects of Abiotic Stress Treatment on Core Quality Indicators of Sweet Corn (Harvest Time, Compared with Conventional Treatment)

variety	Processing type	Decrease in total soluble sugars (%)	Ethyl palmitate price decrease (%)	Hardness increase (%)
Yue Tian No. 9	Low potassium stress	23.6±1.8a	15.3±1.1b	8.7±0.6c
	High temperature stress	12.4±1.3b	22.5±1.5a	15.2±1.1b
Overland	Low potassium stress	18.7±1.5b	18.6±1.3b	10.3±0.8c
	High temperature stress	9.8±1.1c	31.2±1.8a	18.5±1.3a
Dongtian Glutinous Rice 100	Low potassium stress	11.5±1.2c	10.7±0.9c	6.4±0.5d
	High temperature stress	7.3±0.9d	14.8±1.0b	12.1±0.9c

3. Discovery and Validation of Key Genes in Sugar Metabolism

3.1. Multi-omics Data Integration and Analysis

Transcriptomic and metabolomic sequencing were performed on sweet corn samples from different varieties and treatment groups, yielding 68.4 Gb of effective transcriptomic data. After filtering, the Unigene annotation rate reached 82.7%. 187 differentially expressed metabolites were detected, including 23 related to sugar metabolism and 31 related to volatile flavor compounds. Differential expression analysis identified 3246 differentially expressed genes (DEGs) among varieties and 2189 differentially expressed genes between the stress-treated and control groups, primarily enriched in pathways related to sucrose synthesis, starch metabolism, and fatty acid derivative synthesis [9].

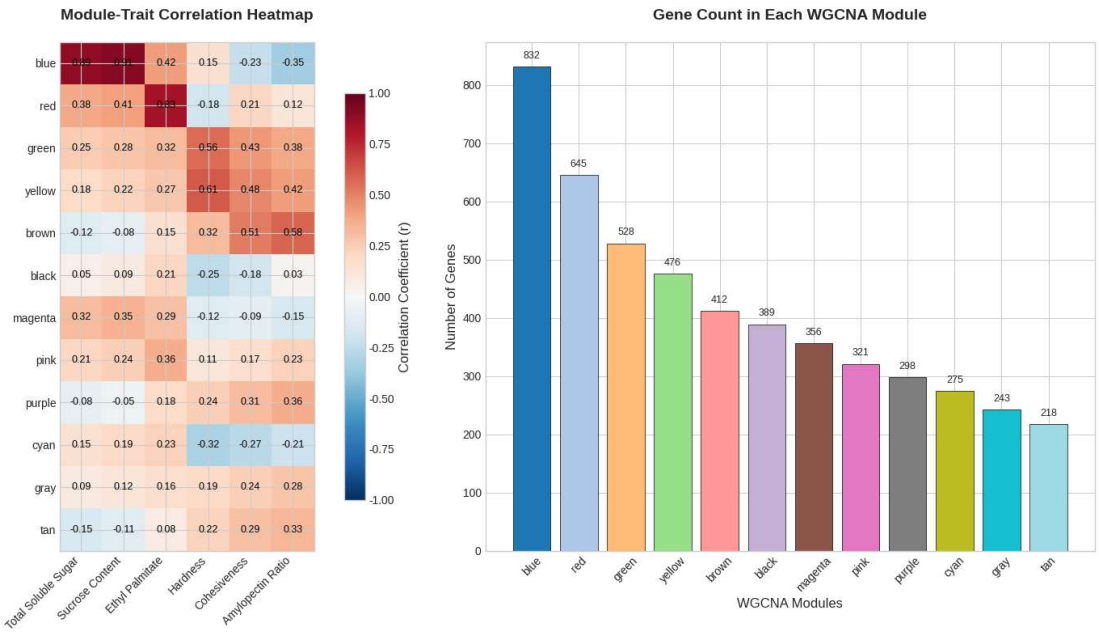

Fig. 1 Heatmap of WGCNA module division and trait association in sweet maize gene co-expression network

To discover genes that synergistically regulate sugar and flavor, a co-expression network was constructed using WGCNA, dividing all DEGs into 12 modules (Fig. 1). The blue module

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(containing 832 genes) showed a highly significant positive correlation with the content of total soluble sugar and sucrose (r=0.89), while the red module (containing 645 genes) showed a significant correlation with the content of aroma compounds such as ethyl palmitate (r=0.83). The two modules shared 47 overlapping genes, presumably representing core genes for synergistic regulation. Further connectivity analysis within the modules identified 10 hub genes, including SUS4 (sucrose synthase gene), SPS2 (sucrose phosphate synthase gene), and LOX3 (lipoxygenase gene). These genes exhibited the highest connectivity in the network, and their annotation functions were directly related to sugar metabolism or flavor compound synthesis.

3.2. Validation of Key Gene Expression

Five core hub genes-SUS4, SPS2, LOX3, ADH2 (alcohol dehydrogenase gene), and UGT74E2 (glycosyltransferase gene)-were selected, and their expression characteristics in different varieties and treatment groups were validated using qPCR. The results showed that the expression trends of the candidate genes were consistent with the transcriptome sequencing results (R^2 = 0.87–0.93), validating the reliability of the sequencing data [10].

As shown in Fig. 2, among the varieties, the expression levels of SUS4 and SPS2 in the high-sweetness variety "Yue Tian 9" were significantly higher than in other varieties, being 3.2 times and 2.8 times higher than in "Dong Tian Nuo 100," respectively, consistent with the high sucrose content phenotype of this variety. LOX3 was expressed most abundantly in the light-aroma variety "Ao Fu Lan," 2.5 times higher than in "Yue Tian 9," and LOX3 is a key gene catalyzing the synthesis of aroma precursors from fatty acids. Under stress treatment, low potassium and high temperature significantly inhibited the expression of all five genes [11]. Among them, the expression level of SUS4 in the low-potassium treatment group of "Yue Tian 9" decreased by 67.3% compared to the conventional group, which was positively correlated with the decrease in the total soluble sugar content of this variety (23.6%), confirming its regulatory role in sugar accumulation.

Homologous sequence alignment and GO/KEGG enrichment analysis revealed that SUS4 and SPS2 are primarily involved in key steps of sucrose synthesis, and their high expression can promote sucrose accumulation. LOX3 and ADH2 are involved in fatty acid metabolism pathways, regulating the formation of volatile aldehydes and esters, and UGT74E2 may affect the stability of flavor compounds through glycosylation modification. These results demonstrate that the selected hub genes do indeed play a core regulatory role in the formation of the "sugar-flavor" quality of sweet corn.

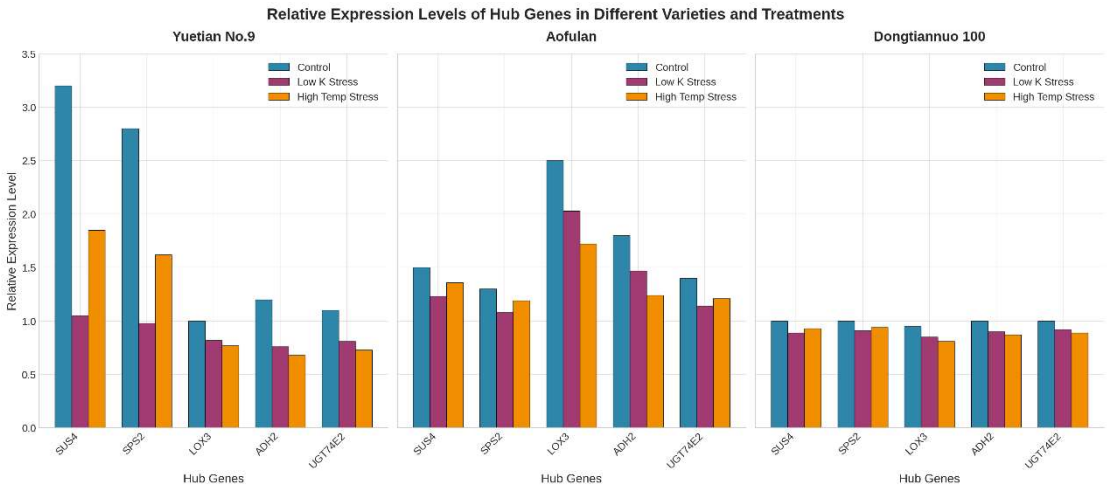

Fig. 2 QPCR expression analysis of 5 hub genes in different varieties and treatment groups

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4. Sweet Corn Flavor and Quality Improvement Strategies

4.1. Molecular Marker-Assisted Breeding

Specific SSR or SNP molecular markers were developed to construct a dual-target trait screening system of "high sugar + superior flavor" based on the screened core hub genes such as SUS4, SPS2, and LOX3. Marker detection was used to rapidly identify the dominant genotypes of key genes in breeding materials, shortening the screening cycle and replacing traditional time-consuming quality determination methods [12]. A multi-gene aggregation breeding scheme was proposed, precisely aggregating sucrose synthesis-related genes (SUS4, SPS2) with flavor compound synthesis genes (LOX3, ADH2), while simultaneously introducing stress resistance-related gene loci to cultivate new sweet corn varieties with high sweetness, superior flavor, and environmental adaptability.

4.2. Cultivation and Postharvest Regulation

Cultivation measures were optimized: A potassium-boron fertilization ratio (K_2O:B_2O_3=10:1) was adopted to promote the expression of SUS4 and SPS2 genes and increase sugar accumulation based on the environmental response patterns of key genes. The optimal harvest time was determined to be 7-10 days after the milk stage, balancing sweetness and aroma based on gene expression and peak quality indicators. Postharvest preservation employed low-temperature (4℃) treatment combined with 1-MCP preservative to inhibit the attenuation of UGT74E2 gene expression, delay flavor degradation, extend shelf life by 3-5 days, and reduce quality loss [13].

4.3. Highlights of the Integrated Improvement System

A three-pronged improvement model integrating "genes, traits, and environment" is constructed, overcoming the limitations of traditional breeding and cultivation that are disconnected. Molecular marker breeding provides a high-quality genetic foundation, cultivation regulation adapts to gene expression needs, and environmental response mechanisms are tailored to different ecological regions, achieving synergy across the entire chain of "genetic improvement - cultivation optimization - post-harvest preservation." This system targets key genes as core targets, specifically addressing industry pain points such as unstable sweetness and monotonous flavor, balancing theoretical support with field applicability, and significantly improving the efficiency and conversion rate of sweet corn quality improvement.

5. Conclusion

This study used high-sweetness, fragrant, and soft-glutinous sweet corn as test materials to systematically explore the synergistic regulatory mechanism of "sugar metabolism-flavor synthesis" and its environmental response patterns. The results are as follows: Genotypic differences in sugar composition, flavor compounds, and taste parameters among different types of sweet corn were clarified. The high-sweetness variety "Yuetian 9" had the highest sucrose content, the fragrant variety "Aofelan" was rich in volatile aroma compounds, and the soft-glutinous variety "Dongtiannuo 100" had a high amylopectin content and strong stress resistance. Through transcriptomic and metabolomic integration analysis and WGCNA, core hub genes such as SUS4, SPS2, and LOX3 were screened, elucidating their key roles in sucrose synthesis, flavor compound generation, and stress response, and establishing a "gene-trait-environment" three-in-one correlation model. An integrated quality improvement system combining molecular marker-assisted breeding based on gene function and environmental response characteristics, cultivation optimization, and post-harvest preservation was constructed, effectively addressing industry pain points such as unstable sweetness and

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monotonous flavor. However, this study also has certain limitations: only three varieties were tested, failing to cover more ecotypes and genetic backgrounds, and the generalizability of the conclusions needs further verification; the multi-omics analysis focused on key growth stages, with insufficient analysis of the dynamic regulatory processes of sugar and flavor compound synthesis; gene function verification mainly relied on expression characteristic analysis, lacking direct functional verification such as in vitro enzyme activity assays and transgenic methods. Future research could expand the range of tested varieties and ecological regions, deepen the analysis of the interaction networks between core genes; combine gene editing and transgenic technologies to conduct precise functional verification, revealing the molecular mechanisms of regulatory pathways; further optimize the adaptability of cultivation measures and post-harvest preservation technologies, expand the application scenarios of the system under different stress conditions, and continuously improve the accuracy and practicality of sweet corn quality improvement.

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