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Enhancing lutein content in yellow-fleshed watermelon through potassium-driven regulation of lycopene β-cyclase (LCYB) expression

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Watermelon (*Citrullus lanatus*) is notably rich in carotenoids, with yellow-fleshed varieties containing high levels of lutein. Lutein accumulation is influenced by genetic, environmental, and cultivation factors. Potassium, a critical macronutrient for photosynthesis and metabolism, plays an unclear role in regulating lutein accumulation in watermelon. To investigate this, foliar sprays of varying potassium chloride (KCl) concentrations were applied and agronomic trait changes during fruit development were monitored. Ultra-performance convergence chromatography (UPC^2) was used to quantify changes in lutein content, while RNA-seq was employed to analyze the regulatory mechanisms behind potassium-induced changes in carotenoids. It was found that foliar application of 50 mgL^{-1} KCl significantly increased fruit weight, soluble solid content, chroma, and lutein levels. qRT-PCR revealed that lycopene β-cyclase (LCYB) expression was upregulated with this treatment, which positively correlated with lutein accumulation. Transcriptome analysis suggested that potassium mediates lutein content through chloroplast-related pathways. In conclusion, optimal potassium concentrations enhance lutein biosynthesis and accumulation in watermelon by regulating key genes involved in carotenoid synthesis and activating chloroplast metabolic pathways.

Key words: Watermelon, potassium treatment, lutein, agronomic traits, chloroplast.

INTRODUCTION

Carotenoids are a significant class of natural pigments recognized for their C40 lipophilic isoprenoid structure. These compounds function as vital secondary metabolites in plants and are essential for the vibrant and diverse coloration observed across various plant species (Watkins and Pogson, 2020). They also play an important role in cardiovascular health, serving as precursors to vitamin A and possessing antioxidant properties, in particular, lutein has the function of protecting the retina and the skin (Martini et al., 2022). Watermelon (*Citrullus lanatus*), which originated in Africa, is an annual trailing herbaceous plant known for its sweet and juicy flesh, which has made it popular among consumers. This fruit is particularly rich in carotenoids, with its composition varying significantly and leading to a spectrum of flesh colors. For instance, red-fleshed varieties are high in lycopene, orange-fleshed types are rich in *β*-carotene, and yellow-fleshed ones contain primarily lutein (Yuan et al., 2021). Currently, a single red watermelon cannot meet consumer demand; yellow-fleshed watermelon is

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becoming increasingly popular.

The pathway for carotenoid synthesis is crucial in plant secondary metabolism. Recent advancements have improved the understanding of the genes and regulatory mechanisms involved in this process. The biosynthesis begins with the formation of isopentenyl diphosphate (IPP) via either the mevalonate (MVA) or methylerythritol phosphate (MEP) pathways. This is followed by enzymatic reactions that produce intermediates like phytoene and lycopene, eventually leading to end products such as *β*-carotene and lutein. Key enzymes like phytoene synthase (PSY) and lycopene *β*-cyclase (LCYB) are essential in this synthesis (Sun and Li, 2020). The accumulation of carotenoids is influenced by both genetic factors and environmental conditions, as well as cultivation practices. Potassium is a vital nutrient for plant growth, playing a crucial role in photosynthesis, sugar transport, enzyme activity regulation, and stress responses. It notably affects carotenoid content, as potassium ions participate in electron transfer processes within photosystem II (PSII), regulating photosynthetic efficiency and secondary metabolite distribution (Hassan et al., 2022). Some studies indicate that low potassium levels can enhance carotenoid content in crops like lamb's lettuce (Hernández et al., 2021), while treatments such as exogenous potassium chloride (KCl) can increase lycopene levels in tomatoes (Liu et al., 2014). However, excessive potassium can lead to a decrease in carotenoid content (Carol et al., 2021). Watermelon, classified as a potassium-loving crop, relies heavily on proper potassium fertilization to maintain fruit quality. While many studies have investigated potassium's effects on carotenoid levels in various crops, its specific influence on watermelon carotenoids is not well understood.

Recent advances in molecular biology have shed light on how exogenous substances, including hormones like indole-3-acetic acid (IAA) and abscisic acid (ABA), affect carotenoid synthesis (Weng et al., 2015; Su et al., 2015). However, there is still a lack of research on the molecular mechanisms through which potassium influences carotenoids. Current research predominantly focuses on lycopene in red-fleshed watermelons, leaving the regulatory mechanisms of lutein in yellow-fleshed varieties underexplored.

This study utilizes the yellow-fleshed watermelon variety 'lanxin', applying different concentrations of KCl to leaves during the vine extension stage. It measures agronomic traits such as soluble solids and fruit weight during ripening, analyzes lutein levels using ultra-performance convergence chromatography (UPC^2), and employs qRT-PCR to assess gene expression related to carotenoid synthesis. Additionally, transcriptome sequencing seeks to explore the regulatory effects of potassium on carotenoid synthesis, aiming to provide a theoretical basis for enhancing watermelon quality and implementing precise fertilization strategies.

MATERIALS AND METHODS

Plant and growth conditions

The watermelon variety 'lanxin', used in this study, is a small, yellow-fleshed type that has been carefully screened and cultivated by the Ningbo Academy of Agricultural Sciences in Zhejiang, China. The watermelon plants were grown in a plastic greenhouse during the autumn of 2024. The row and plant spacing for cultivation were set at 90 cm × 40 cm. The base fertilizers applied per 667 m^2 included 400 kg of commercial organic fertilizer, 25 kg of ternary compound fertilizer, 15 kg of potassium sulfate, and 1 kg of borax. During planting, vertical trellis cultivation techniques were employed, with each plant pruned to two vines. Female flowers after the second one were selected for pollination, and 1 to 2 watermelons were left on each plant.

Exogenous potassium treatment

During the vine-stretching stage of watermelons, different concentrations of KCl were sprayed on the leaves. The concentrations were 50, 100, 150, and 200 mgL^{-1}, with spraying water as the control. The spraying was carried out once every 7 days for a total of 3 times, a random block design was adopted and each treatment had 30 plants. Sampling started 10 days after pollination (DAP) and was carried out every 7 days, for a total of 4 times, that is, samples were taken 10, 17, 24, and 31 DAP. When sampling, 5 fruits with consistent growth and good development were selected from each treatment for measurement.

Measurement of agronomic traits

The fruit weight after different concentrations of KCl treatment was measured using a weighing instrument. The change in soluble solid content during fruit development after different concentrations of KCl treatment was measured using a sugar refractometer (PAL-BXIACID F5, ATAGO, and Japan). The fruit was cut transversely, and the central pulp was squeezed into juice and dropped on the sugar refractometer to record the value. The change in flesh color during fruit development after different concentrations of KCl treatment was measured using a colorimeter (LS175, Shenzhen, and China). The flesh color was characterized by CIELAB parameters (brightness index L^*, red-green index a^*, and yellow-blue index b^*). The fruit was cut transversely, and divided into two equal parts, and 3 points on the cut surface of the watermelon fruit were randomly measured. The lab values were recorded, and the average of the three points was calculated as the lab value of the watermelon fruit. The chroma (C) of the watermelon fruit was calculated according to Equation 1. The chroma indicates the purity of color; consequently, a higher C value corresponds to greater vividness:

$$C = \sqrt{(a^*)^2 + (b^*)^2} \quad (1)$$

Identification of carotenoid content using UPC^2

Take half of a watermelon fruit. After removing the seeds, squeeze the fruit into juice. Weigh 5 g (accurate to 0.01 g) of the watermelon homogenate and place it in a 50 mL centrifuge tube. Add 15 mL of tert-butyl methyl ether and then shake the tube for extraction for 30 min. After that, centrifuge the mixture at 5000 r/min for 3 min using a centrifuge. Pipette the supernatant, filter it through a 0.22 μm filter membrane, and use the filtrate as a sample for detection with UPC^2 (ACQUITY UPC2, Waters, America).

UPC^2 was equipped with a PDA detector and a chromatography workstation (Empower 3). The chromatographic column was an HSS C18 SB column (3.0 × 100 mm, 1.8 μm), the column temperature was 40°C, the mobile phase was CO_2: ethanol (50%:50%), the flow rate was 1.5 mL/min, the injection volume was 1 μL, and the detection wavelength was 440 nm. Standard samples of various carotenoids (lycopene, *β*-carotene, and lutein) were dissolved in the mobile phase respectively to prepare standard solutions of certain concentrations, which were injected under the aforementioned conditions. The composition of carotenoids in the samples was determined by comparing the retention times of carotenoids in the samples, and quantitative analysis was performed based on the peak areas. 5 fruits were tested for each group of samples, and the average value was calculated.

Quantitative RT-PCR and gene expression analysis

Watermelon flesh at different days after pollination and with different treatments was collected. Total RNA was extracted using the RNAiso Plus extraction kit (TaKaRa, Shiga, and Japan), and reverse transcription was performed using the PrimerScript RT reagent kit (TaKaRa, Shiga, and Japan) to generate the first strand of cDNA. qRT-PCR experiments were carried out on a QuantStudio™ 6 Flex (Applied Biosystems) using the PerfectStart® Green qPCR SuperMix (TransGen, China). ClACTIN was used as the internal control gene, and the gene-specific primers are shown in Table S1. For each sample, three biological replicates were performed, and the relative expression level of the gene was calculated using the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001).

RNA-seq analysis

Watermelon flesh was treated with 50 mgL^{-1} KCl and the control (water treatment) at 31 DAP was collected. Total RNA was extracted using the RNAiso Plus extraction kit (TaKaRa, Shiga, and Japan), and mRNA was enriched using the NEBNext Poly (A) mRNA Magnetic Isolation Module (NEB, E7490). Using mRNA as a template, an on-machine library was constructed using the NEBNext mRNA Library Prep Master Mix Set for Illumina (NEB, E6110) and NEBNext Multiplex Oligos for Illumina (NEB, E7500). Three biological replicates were performed for each treatment. The qualified libraries were sequenced on the Illumina HiSeq™ 2500 platform (Shen et al., 2019). The original fastq data were filtered by fastp to obtain valid data, and the quality of the filtered data was controlled using fastqc. The filtered transcriptome data were aligned with the reference genome (97103v2, http://cucurbitgenomics.org/). Differential expression analysis was performed using DESeq2, and significant differences were filtered using the p-value. The screening threshold was p-value < 0.05 and $|\log_2 FoldChange| > 1.0$. The KEGG database (https://www.kegg.jp) was utilized to conduct KEGG enrichment pathway analysis on the differentially expressed genes (DEGs) (Kanehisa et al., 2023). Gene set enrichment analysis (GSEA) was used to perform enrichment analysis on all genes, and the screening threshold was p.adj-value < 0.05 and |Normalized Enrichment Score (NES)| > 1.0.

RESULTS

Exogenous potassium treatment can improve the agronomic traits of watermelons

Cross-sections of watermelon fruits at various stages of development were photographed after treatment with different concentrations of KCl using an image acquisition platform designed to eliminate the influence of environmental factors on the images (Gu et al., 2025). At 10 DAP, the flesh of the yellow-fleshed watermelon variety 'lanxin' showed no noticeable color difference between the treatment and control groups. At 17 DAP, a color change began to appear near the carpels of the fruit. Watermelons treated with KCl at concentrations of 50 and 100 mgL^{-1} exhibited a more pronounced color change compared to the control group. At 31 DAP, when the fruits reached maturity, the flesh color of the watermelons treated with 50 and 100 mgL^{-1} KCl was notably brighter than that of the control group. In contrast, no significant difference in flesh color was observed between the fruits treated with 200 mgL^{-1} KCl and those in the control group (Figure 1).

The change in the flesh color of yellow-fleshed watermelons after treatment with KCl was evaluated using a colorimeter after 17 DAP. The L^* value, which indicates brightness, did not show significant differences between the treatment group and the control group, remaining consistent throughout the fruit's development. Both groups had negative a^* values during development, which suggests that the flesh color had a slight green hue. In contrast, the b^* value increased progressively as the fruit developed, indicating a gradual transition to yellow. Notably, there was a significant rise in the b^* value after treatment with 50 mgL^{-1} KCl (Figure S1). Chroma, a measure of color intensity, was calculated using a standard formula. As the fruit developed, chroma showed gradual improvement. Specifically, fruits treated with 50 mgL^{-1} KCl exhibited significantly higher chroma compared to the control group during the early stages of development (Figure 2a). This suggests that treatment with 50 mgL^{-1} KCl could enhance the color saturation of watermelon fruit and make the fruit more vivid.

The change in fruit weight following treatment with different concentrations of KCl was assessed. At 10 DAP, there were no significant differences observed between the treatment groups and the control group. However, at 17 DAP, the fruit weights of the groups treated with 50, 100, and 150 mgL^{-1} KCl showed a significant increase compared to the control group, with increases of 36.9, 40.8, and 29.7%, respectively. In contrast, the group treated with 200 mgL^{-1} KCl did not show a significant difference in fruit weight when compared to the control (Figure 2b).

The soluble solid content of fruits treated with various concentrations of KCl was measured using a sugar refractometer. At 10 DAP, no significant differences were observed between the treatment group and the control group. However, at 17 DAP, the soluble solid content in fruits treated with 50 and 100 mgL^{-1} KCl showed a significant increase compared to the control group. As the fruit developed, the soluble solid content continued to rise, with KCl-treated fruits demonstrating levels that were significantly higher than those in the control group,

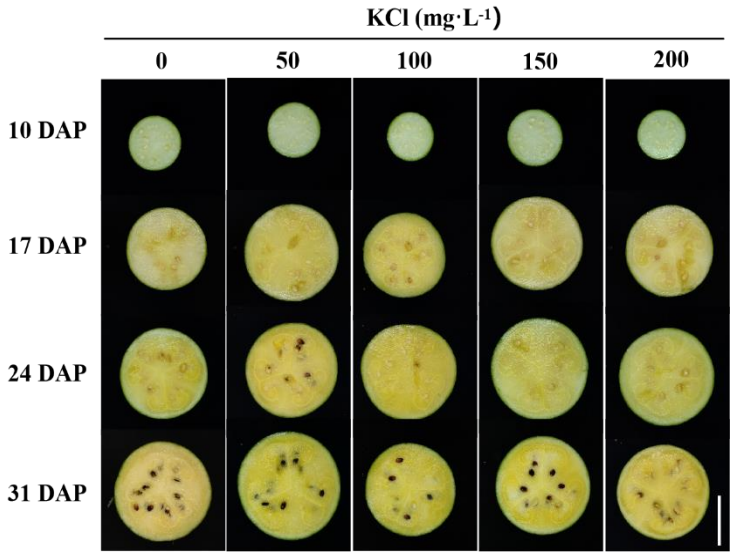


Figure 1. Development of watermelon fruit in different days after pollination after different concentrations of potassium treatment. Scale bars: 5 cm.

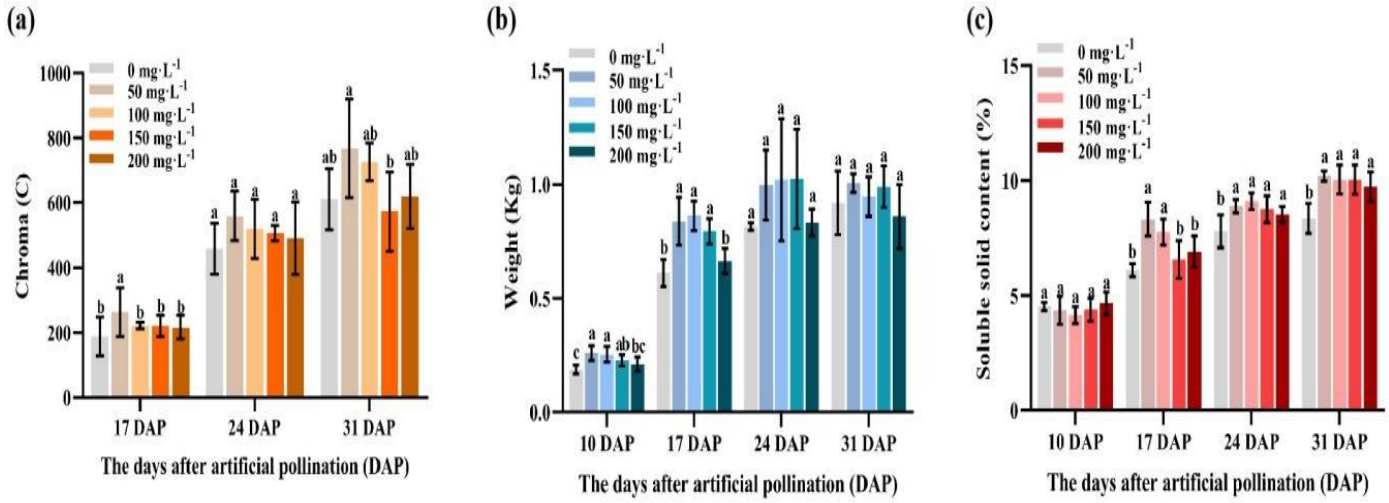


Figure 2. Statistical analysis of the agronomic traits of watermelon fruits at different stages after pollination following treatments with different concentrations of KCl. (a) The changes in chroma, (b) The changes in weight, and (c) The changes in soluble solid content. Different lowercase letters on the column indicated the significant difference between KCl treatment and control ($p < 0.05$).

increasing by approximately 22.0, 20.1, 20.1, and 16.5%, respectively (Figure 2c).

Exogenous potassium treatment can increase the lutein content of yellow-fleshed watermelons

The accumulation and variation of carotenoids during fruit development were assessed following different concentrations of KCl treatment using UPC[2]. In the case of the yellow-fleshed watermelon 'lanxin', only a minimal amount of lutein was detected during the early developmental stages, with noticeable accumulation beginning at 17 DAP. At this time point, the lutein levels in fruits treated with 50 and 100 mgL^{-1} KCl were significantly higher than those observed in the control group, increasing by approximately 110.1 and 134.9%, respectively. At 24 DAP, the lutein content in fruits subjected to 50 mgL^{-1} KCl remained significantly elevated compared to the control, increasing by about 49.2%.

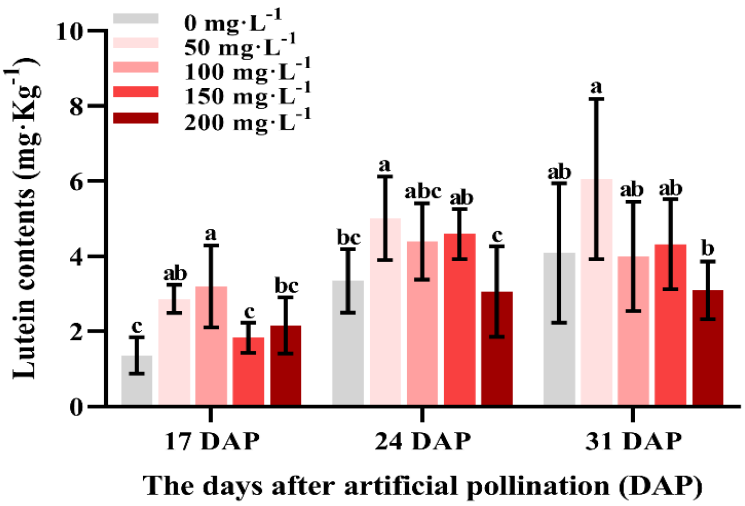


Figure 3. Statistical analysis of lutein contents in yellow-fleshed watermelon fruits at different stages after pollination following treatments with different concentrations of KCl. Different lowercase letters on the column indicated the significant difference between KCl treatment and control ($p < 0.05$).

During the fruit ripening stage, the accumulation of lutein in fruits treated with 50 mgL^{-1} KCl continued to surpass that found in the control group. Notably, throughout fruit development, no significant changes were observed in lutein accumulation following high-concentration KCl treatment compared to controls (Figure 3).

Exogenous potassium treatment increases the expression level of LCYB

Key genes involved in carotenoid metabolism were analyzed using qRT-PCR. PSY is recognized as the most critical rate-limiting enzyme in the carotenoid metabolic pathway (Luo et al., 2021). Following the KCl treatment, the expression level of PSY in watermelon fruits significantly increased at 17 DAP. At 24 DAP, there was a notable rise in PSY expression levels in fruits treated with 50, 100, and 150 mgL^{-1} KCl treatments. However, during the fruit-ripening stage, no significant difference was observed in PSY expression between the KCl-treated group and the control (Figure 4a).

LCYB functions as an essential branching enzyme that catalyzes the cyclization of lycopene (Sun and Li, 2020). At 17 DAP, LCYB expression levels significantly increased in fruits treated with both 50 and 100 mgL^{-1} KCl. However, no significant differences were noted for fruits treated with either 150 or 200 mgL^{-1} KCl compared to controls. At 24 DAP, a significant increase in LCYB expression was again observed in fruits treated with 50 mgL^{-1} KCl. During the fruit-ripening stage, no significant differences were detected between LCYB expression levels of the control and treatment groups (Figure 4c).

Pearson correlation analysis was conducted to investigate the relationships between key carotenoid-synthesizing genes and lutein content. The results indicated that while there was no significant correlation between lutein content and PSY expression levels, a substantial positive correlation existed between LCYB expression and lutein content at both 17 and 24 DAP (Figure 4b and d). Therefore, it was hypothesized that the increase in lutein content following KCl treatment can be attributed to the elevated expression of LCYB.

Potassium may influence chloroplasts to participate in lutein synthesis

To clarify how potassium regulates lutein content, a total RNA from watermelon fruits was extracted and treated with 50 mg/L KCl and from a control group 31 days after pollination, using the Trizol method for transcriptome sequencing. A total of 22960 uniquely expressed genes were identified. To investigate the differences between the treatment and control groups, principal component analysis (PCA) and clustering analysis on the samples were conducted. The results showed a clear distinction between the treatment and control groups, with PC1 and PC2 together accounting for over 62% of the total variance (Figure S2). This indicates a high degree of consistency among the three biological replicates in both groups, highlighting the reproducibility and reliability of the data.

According to the established criteria, a total of 563 differentially expressed genes (DEGs) between the treatment group and the control group was identified.

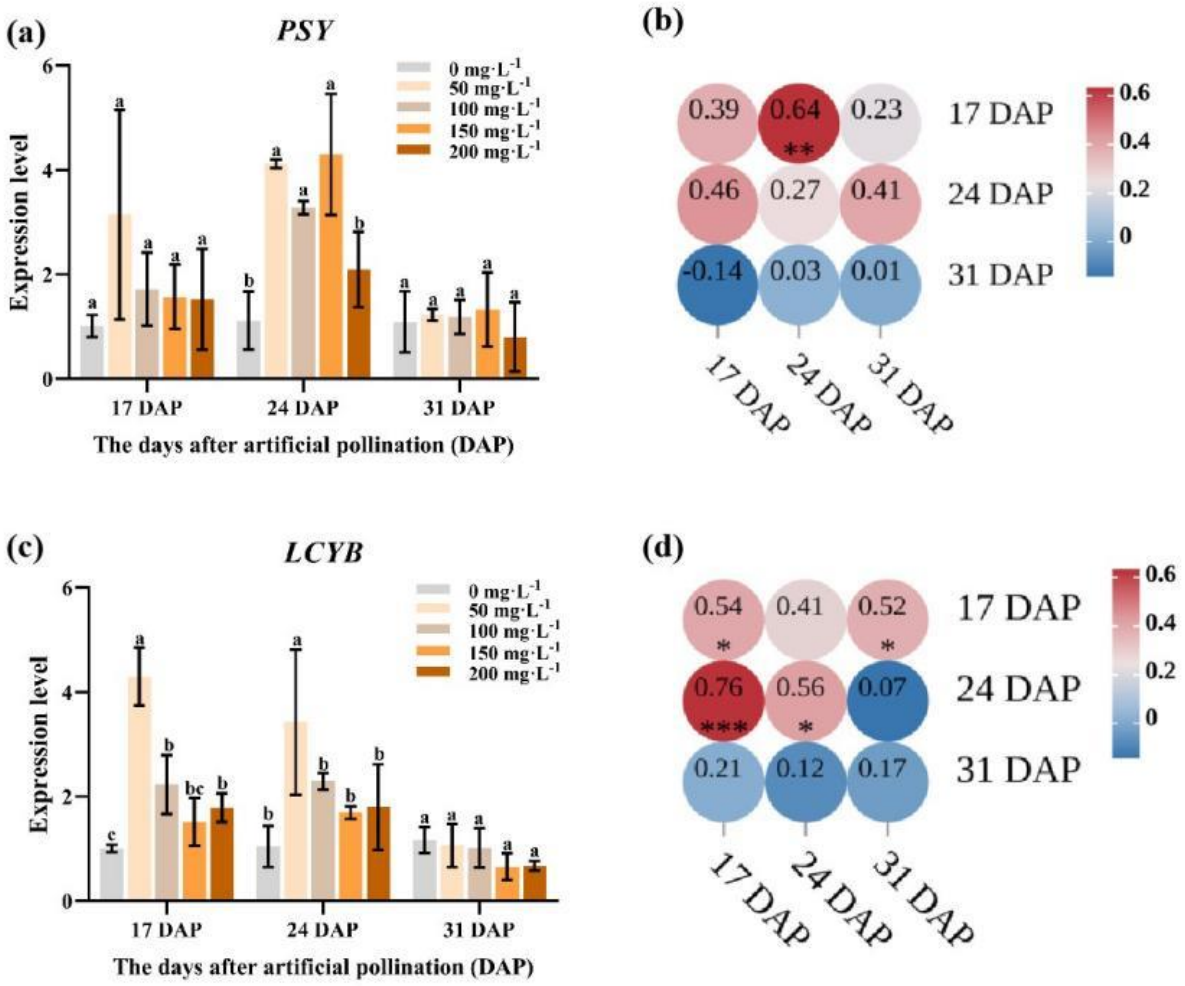


Figure 4. The changes in gene expression at different stages after pollination following treatments with different concentrations of KCl. (**a** and **c**) The changes in the expression of PSY (a) and LCYB (**c**), (b and d) Correlation analysis between PSY (b) and LCYB (d) expression levels and lutein content at different days after pollination following treatments with different concentrations of KCl. Different lowercase letters on the column indicated the significant difference between KCl treatment and control ($p < 0.05$), *Indicates $p < 0.05$, ***Indicates $p < 0.001$.

This included 236 up-regulated genes and 337 down-regulated genes (Figure 5a). KEGG enrichment analysis on these DEGs was then performed, which showed that a significant majority were enriched in pathways related to secondary metabolite synthesis (Figure 5b). To further investigate the role of potassium in lutein synthesis, a GSEA on all genes was conducted, focusing specifically on gene ontology (GO) terms. This analysis revealed two pathways with significant enrichment, one of which was the chloroplast thylakoid membrane (Figure 5c). The gene expression within this pathway was analyzed and based on findings from differentially expressed genes (DEGs), identified two specific DEGs: Cla97C11G219570, which encodes Chlorophyll a-b binding protein, and Cla97C11G220240, which encodes Ascorbate peroxidase 3 (Figure 5d).

DISCUSSION

Carotenoids are primarily synthesized through the isoprenoid pathway within plastids (Sun et al., 2018). In fruits, these compounds are mostly stored in chromoplasts, which develop from chloroplasts, leucoplasts, amyloplasts, and other types of plastids (Sandmann, 2021; Tzuri et al., 2015). Key metabolic enzyme genes involved in the carotenoid synthesis pathway include PSY and LCYB. In tomatoes, the transcription level of PSY1 significantly increases during fruit ripening, which correlates with a substantial accumulation of lycopene. However, mutations in PSY1 result in a marked decrease in total carotenoid content (Gady et al., 2012; Fantini et al., 2013). LCYB is an important branching enzyme that catalyzes the

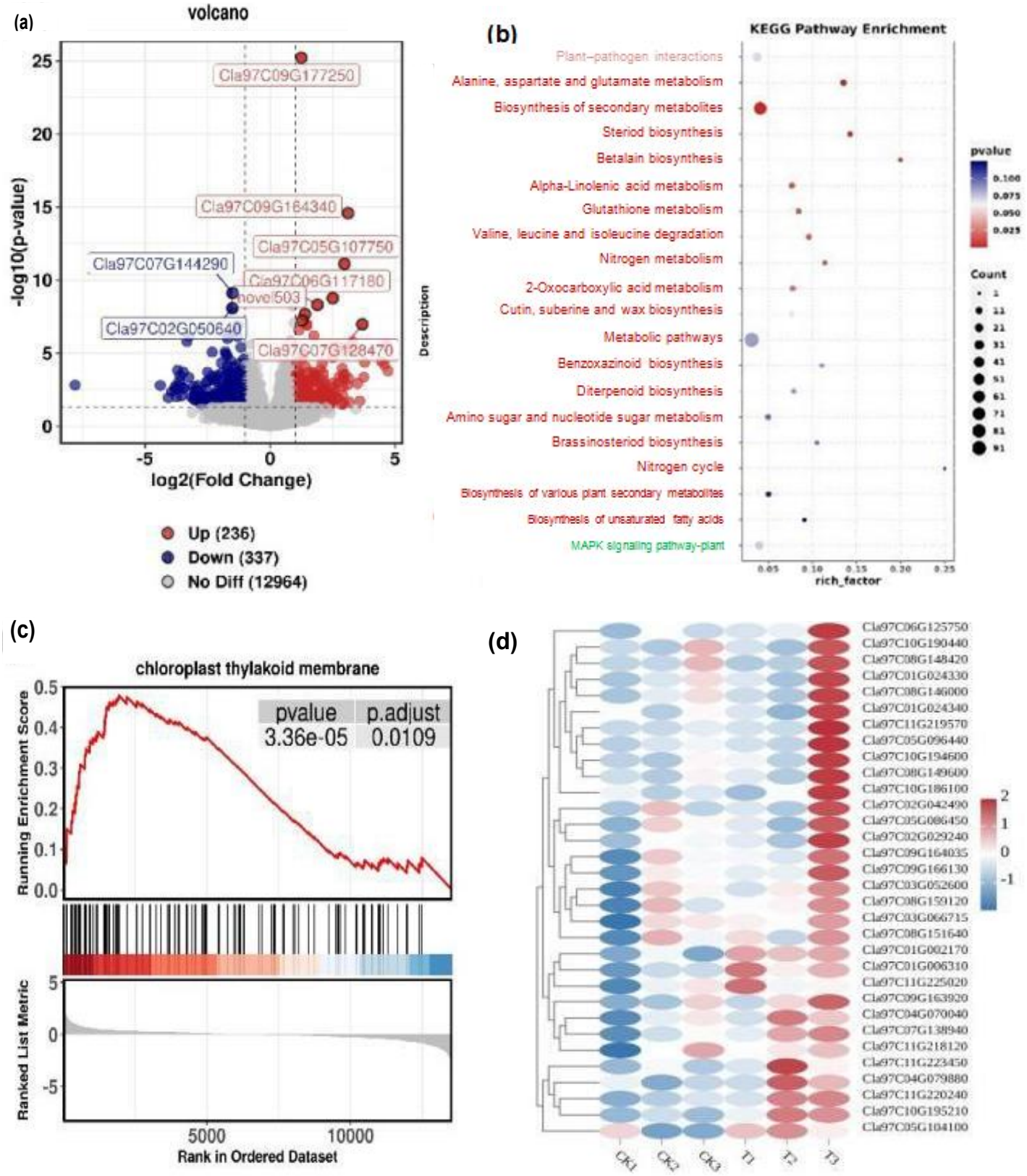


Figure 5. Comparison of transcriptomic changes in watermelon fruits after 50 mgL^{-1} KCl treatment. (a) Volcano plots of DEGs in 50 mgL^{-1} KCl treatment, compared to the untreated control, the red dots represent the up-regulated DEGs, and the blue dots represent the down-regulated DEGs; (b) KEGG enrichment analysis diagram of DEGs; (c) The resulting diagram of GSEA to the chloroplast thylakoid membrane; and (d) Heatmap of gene expression in the chloroplast thylakoid membrane.

cyclization of lycopene, playing a crucial role in determining both the content and composition of carotenoids within plant tissues (Sun and Li, 2020). By comparing full-length cDNA sequences of LCYB from red-fleshed and bright, yellow-fleshed watermelons, researchers identified three single nucleotide polymorphism (SNP) sites within its coding region. Molecular markers developed based on these SNP sites can accurately differentiate between populations of red-fleshed and yellow-fleshed watermelons. Thus, LCYB may serve as a genetic factor responsible for the vibrant yellow or red coloration seen in watermelon flesh (Bang et al., 2007).

Environmental factors play a significant role in influencing carotenoid content. In the case of watermelons, research indicates that environmental differences have a more pronounced effect on lycopene content than genetic variation among different varieties (Dia et al., 2016). Additionally, external substances can influence carotenoid levels. While watermelon is recognized as a crop that thrives on potassium, there is currently a lack of research regarding the impact of potassium on carotenoid concentrations in this fruit.

This study's findings indicate that low concentrations of KCl can increase the lutein content in these watermelons. However, high concentrations of KCl appear to have little effect on lutein levels (Figure 5). This suggests a dose-dependent relationship between potassium application and lutein content in yellow-fleshed watermelons, which is consistent with previous research findings (Carol et al., 2021). Potassium is a vital macronutrient for plant growth, significantly contributing to the accumulation of sugars by enhancing the expression of genes involved in sucrose metabolism. This process importantly provides the carbon skeleton necessary for carotenoid synthesis (Wu et al., 2024). However, an excessive concentration of potassium can lead to increased potassium levels in the cytoplasm, which inhibits mitochondrial oxidative phosphorylation. In response to this situation, the glycolytic pathway is activated to maintain the energy supply. However, as carbon flow shifts toward glycolysis, the substrates needed for isoprenoid synthesis decrease, ultimately resulting in a reduction of carotenoid content (Armengaud et al., 2009). Consistent with previous findings, foliar application of KCl significantly enhances the soluble solid content in watermelon fruits. Notably, the application of 50 mgL^{-1} KCl demonstrated the most pronounced effect on soluble solid content (Figure 2c). Additionally, KCl treatment contributed to an increase in fruit weight (Figure 2b). Previous research conducted by the authors established a correlation between watermelon fruit color and carotenoid levels, especially highlighting the positive relationship between lutein concentration and chroma (Hu et al., 2025). After applying 50 mgL^{-1} KCl, the saturation levels of watermelon fruits were significantly higher than those observed in the control group throughout their development, resulting in a more vibrant coloration of the fruits (Figures 1 and 2a). Therefore, it can be concluded that administering 50 mgL^{-1} KCl not only increases lutein levels in yellow-fleshed watermelons but also enhances their agronomic traits simultaneously.

To clarify the regulatory role of potassium in carotenoid synthesis, the expression levels of PSY and LCYB during fruit development following treatment with different concentrations of KCl can be investigated. Treatment with 50 mgL^{-1} KCl led to a significant increase in the expression levels of both LCYB and PSY throughout fruit development. However, at the fruit ripening stage, no significant differences in the expression levels of PSY and LCYB between the treatment group and the control group were observed. Additionally, Pearson correlation analysis indicated a significant positive correlation between LCYB expression levels and lutein content during fruit development. In contrast, no such correlation was found for PSY expression levels (Figure 4). Previous studies have shown that increasing the expression of the LCYB gene in chloroplasts and chromoplasts can boost lutein concentration by 6-8 times (Zhu et al., 2014). Based on this, it was hypothesized that low concentrations of potassium may enhance LCYB expression, leading to an increase in lutein accumulation. Additionally, transcriptome sequencing on watermelon fruits from both the 50 mgL^{-1} KCl treatment group and the control group was performed. The results of the KEGG enrichment analysis showed that most of the differentially expressed genes were linked to pathways involved in the synthesis of secondary metabolites. Since carotenoids are important secondary metabolites in plants (Nisar et al., 2015), it was hypothesized that potassium treatment may affect carotenoid metabolism.

The GSEA enrichment analysis revealed a significant enrichment of the gene set associated with the chloroplast thylakoid membrane. Chloroplasts play a crucial role in providing the necessary enzymatic system and metabolic environment for carotenoid synthesis (Jiménez-Francisco et al., 2016), while potassium is essential for maintaining the structure, function, and photosynthesis of chloroplasts (Weng et al., 2007). Based on these results, it was hypothesized that applying low concentrations of potassium is beneficial for maintaining the stability of chloroplast structures in watermelons, which may influence carotenoid accumulation. This study provides a theoretical foundation and practical guidance for improving the quality and functionality of horticultural crops, such as watermelons, through the precise application of potassium fertilizers.

Conclusion

This study examined the effects of potassium fertilizer on carotenoid synthesis and the fruit quality of yellow-flesh

watermelon. The results demonstrated that 50 mgL^{-1} KCl significantly enhanced lutein content, soluble solids, and single-fruit weight in the flesh, exhibiting a dose-dependent effect. Genetic analysis revealed a significant positive correlation between lutein accumulation and LCYB expression, identifying LCYB as a key target for potassium regulation. Transcriptome analysis highlighted differential gene enrichment in secondary metabolic pathways and chloroplast thylakoid membrane-related processes. The findings confirm that optimal potassium concentrations improve fruit quality and commercial value by modulating LCYB expression and chloroplast functionality, providing insights into potassium-driven metabolic regulation in watermelon.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Supplementary data

Table S1. Primer sequence for qRT-PCR

Primer name	Sequences
ClLCYB-F	TTCAGAGGCAGGGCTTTCAGT
ClLCYB-R	GAACACGACAGCACCAGACCA
ClPSY-F	TATGAAACAGGCGGCTTTGGTAA
ClPSY-R	CTTTTGCCTCTCAGGAGTCATCA
ClACTIN-F	CCATCCAGGCCGTTCTATCT
ClACTIN-R	CAGTTAGATCACGACCAGCA

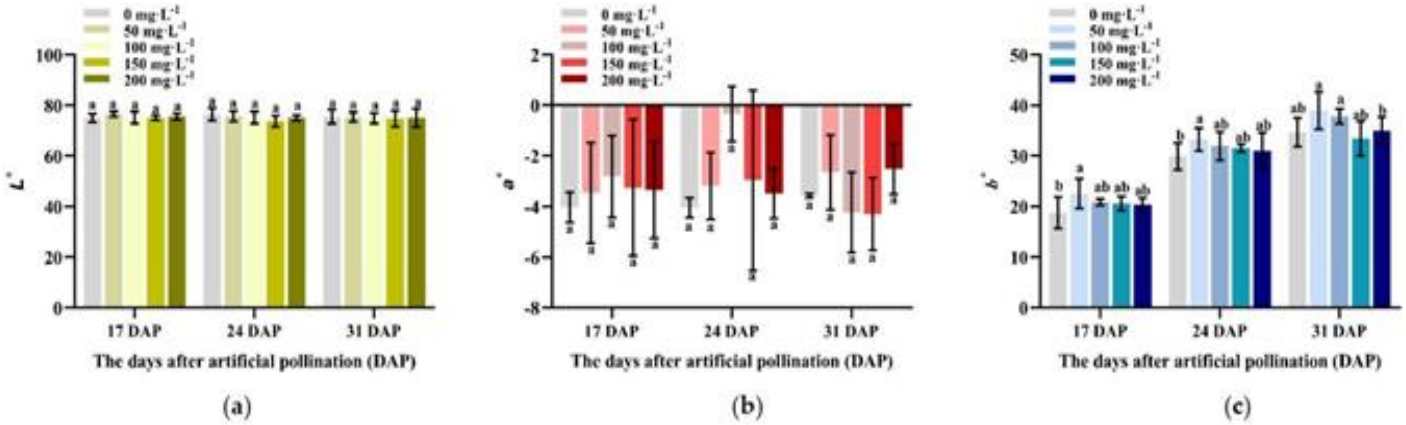


Figure S1. The changes in Lab-value of the fruits at different days after pollination following treatments with different concentrations of KCl. (**a**) The changes in L^* value. (**b**) The changes in a^* value. (**c**) The changes in b^* value. Lowercase letters indicate significant differences at the 0.05 level.

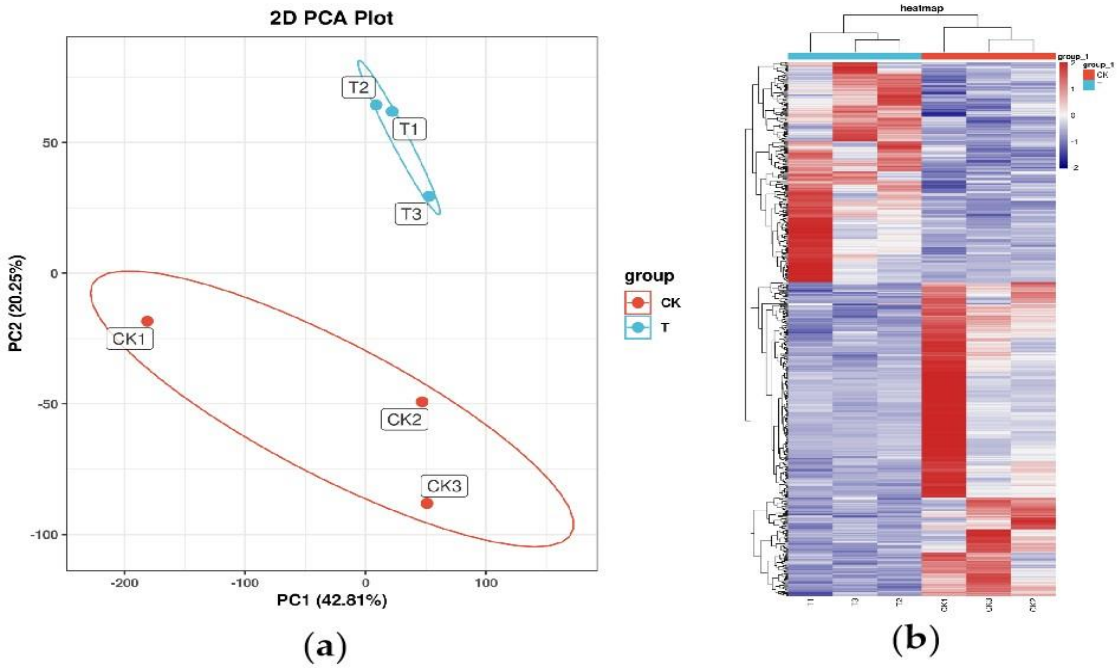


Figure S2. Consistency analysis of transcriptome samples. The results of principal component analysis (a) and cluster analysis (b) of the treatment with 50 mg·L^{-1} KCl and the control group. CK indicates control group, T indicates the treatment with 50 mg·L^{-1} KCl.