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Summary

Sterols have long been associated with diverse fields, such as cancer treatment, drug development, and plant growth; however, their underlying mechanisms and functions remain enigmatic. Here, we unveil a critical role played by a GmNF-YC9-mediated CCAAT-box transcription complex in modulating the steroid metabolism pathway within soybeans. Specifically, this complex directly activates squalene monooxygenase (GmSQE1), which is a rate-limiting enzyme in steroid synthesis. Our findings demonstrate that overexpression of either *GmNF-YC9* or *GmSQE1* significantly enhances soybean stress tolerance, while the inhibition of SQE weakens this tolerance. Field experiments conducted over two seasons further reveal increased yields per plant in both *GmNF-YC9* and *GmSQE1* overexpressing plants under drought stress conditions. This enhanced stress tolerance is attributed to the reduction of abiotic stress-induced cell oxidative damage. Transcriptome and metabolome analyses shed light on the upregulation of multiple sterol compounds, including fucosterol and soyasaponin II, in *GmNF-YC9* and *GmSQE1* overexpressing soybean plants under stress conditions. Intriguingly, the application of soybean steroids, including fucosterol and soyasaponin II, significantly improves drought tolerance in soybean, wheat, foxtail millet, and maize. These findings underscore the pivotal role of soybean steroids in countering oxidative stress in plants and offer a new research strategy for enhancing crop stress tolerance and quality from gene regulation to chemical intervention.

Introduction

With the advent of climate change, abiotic stresses such as drought, salt, heat and cold are exerting increasingly severe influences on plant growth, leading to a reduction in grain production. However, being sessile organisms, plants have evolved a series of defence mechanisms to adapt to environmental stressors. For instance, extensive research has been conducted on the role of abscisic acid (ABA) in enhancing tolerance to abiotic stress conditions, such as drought (Zhang *et al.*, 2022; Zhu, 2016). Cold stress triggers a Ca^{2+}-signal-activated MAP-kinase cascade that activates the expression of cold-responsive genes in plants and can also modulate *HSP* gene expressions to enhance plant tolerance towards heat stress (Sangwan *et al.*, 2002; Zhang *et al.*, 2022; Zhu, 2016). Nevertheless, with advancements in metabolomics technology, several small molecular compounds have been discovered to play crucial roles in promoting plant stress tolerance. For example, recent studies have revealed that high levels of putrescine are induced during cold stress, and its exogenous application improves cold-acclimated freezing tolerance in potato after acclimation to low temperatures (Kou *et al.*, 2018). Additionally, flavonoid accumulation has been found beneficial for enhancing UV tolerance in rice (Liu *et al.*, 2020). However, due to the inherent challenges associated with small metabolite techniques used for their characterisation and quantification purposes, our understanding of their precise roles under abiotic stress conditions remains limited.

One notable family of small metabolites is sterols. While extensive research has been conducted on these compounds in animal systems, progress regarding plant sterols has remained limited. Nonetheless, sterols have been implicated in numerous vital plant processes, encompassing cell division, elongation and polarity (He *et al.*, 2018; Men *et al.*, 2008; Schrick *et al.*, 2000; Willemsen *et al.*, 2003). They also play a crucial role in regulating

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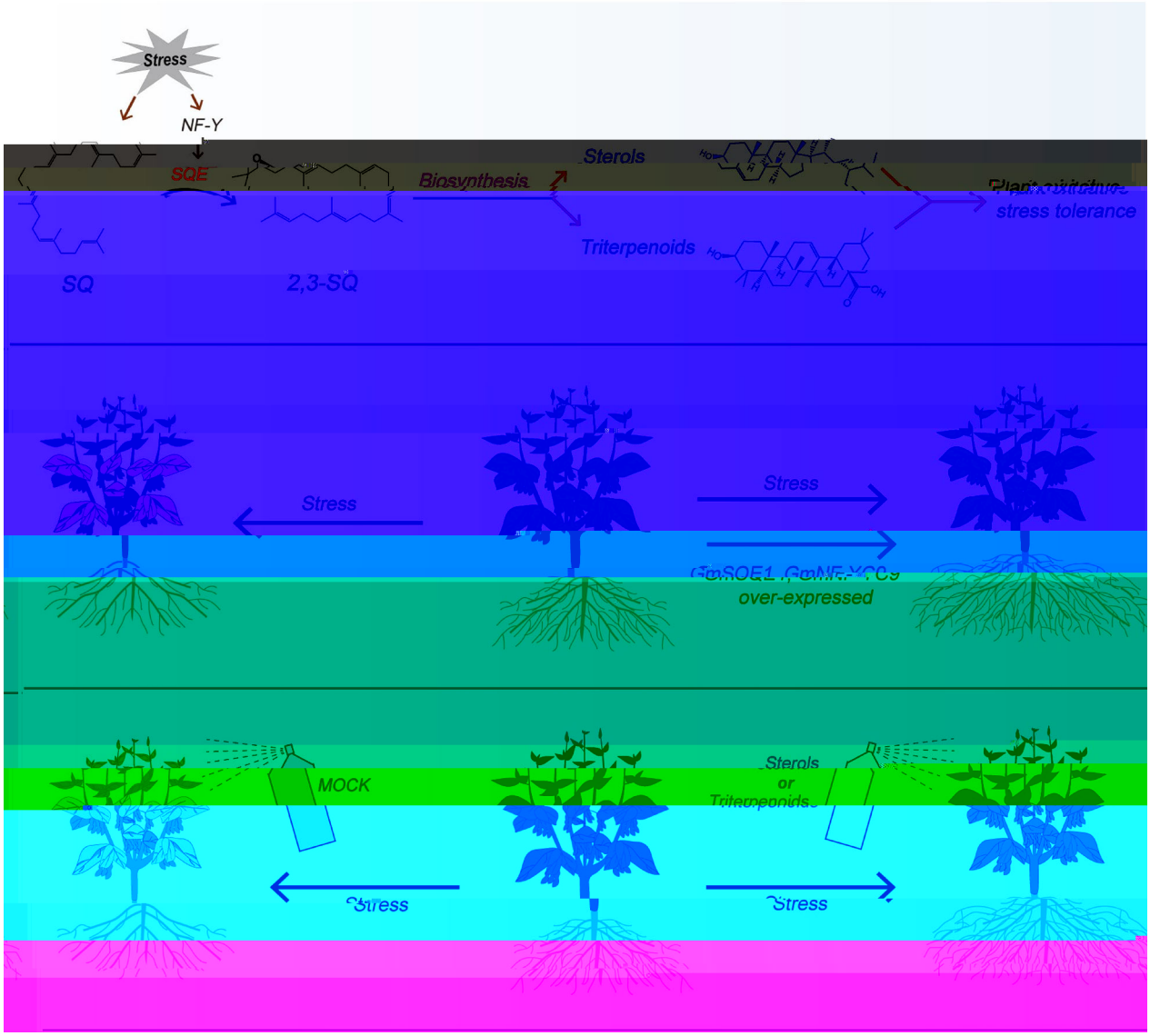

Figure 7 The model of NF-Y-SQE module and soybean steroids improving plant stress tolerance. NF-Y-SQE module participates in regulating plant stress tolerance by enhancing SQE-mediated squalene metabolic pathways. Application of plant steroids or triterpenoids in crops enhanced their tolerance to drought stress.

In vitro GST pull-down assay

The open reading frames (ORFs) of bait protein and candidate protein genes were cloned into the pCold™ TF vector (TaKaRa, Bio) and pGEX-4T-1 vector (GE Healthcare, Chicago, IL), respectively. Subsequently, the recombinant plasmids were introduced into the *E. coli* strain transetta (TransGen, Biotech). Expressions of the corresponding proteins were induced overnight using 0.5 mM isopropyl β-D-thiogalactoside (IPTG) (Inalco SPA, San Luis Obispo, CA) at 16 °C, and then a pull-down assay was performed. The experimental details were described by Yu *et al*. (2021).

In vitro EMSA binding assay

The genes encoding three subunit proteins of the NF-Y transcription factor were cloned into expression vectors harbouring the tag proteins (His, GST, and MBP), respectively, and subsequently transferred into competent cells of the *E. coli* strain *Rosetta*. These recombinant proteins were employed for an EMSA using a biotin end-labelled duplex DNA probe. The method was previously described by Yu *et al*. (2021).

Effect of fucosterol and soyasaponin II on crop growth under different treatments

Three-week-old of soybean, wheat, foxtail millet, and maize seedlings grown under normal conditions were subjected to controlled water treatment. During the treatment, the seedlings were sprayed with aqueous solutions of mock (40 mL distilled water containing 200 μL of 40 mM fatty alcohol polyoxyethylene ether (APE), which was a leaf surfactant), fucosterol (20 μL of fucosterol at a concentration of 600 mg/L was added into 40 mL distilled water containing 200 μL of 40 mM APE), and soyasaponin II (20 μL of soyasaponin II at a concentration of 600 mg/L was added into 40 mL distilled water containing 200 μL of 40 mM APE). The sprays were applied four times each week, with at least 1 day between each spraying. The changes in crop phenotypes

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were observed and recorded during controlled water treatment. The leaf samples of crops were collected at the onset of phenotypic variations in order to quantify physiological and biochemical alterations.

Five-week-old of soybean, wheat, foxtail millet, and maize seedlings cultivated under normal conditions were subjected to osmotic stress treatment by irrigating them with 200 mM mannitol aqueous solutions. During osmotic stress treatment, the seedlings were sprayed with mock (mock, 40 mL distilled water containing 200 μL of 40 mM APE), fucosterol (fucosterol aqueous solutions, 20 μL fucosterol (600 mg/L) into 40 mL distilled water containing 200 μL of 40 mM APE), and soyasaponin II aqueous solutions (soyasaponin II aqueous solutions, 20 μL soyasaponin II (600 mg/L) into 40 mL distilled water containing 200 μL of 40 mM APE). The sprays were applied four times each week, with at least 1 day between each spraying. The phenotype changes of the crops were observed and recorded during controlled water treatment. Leaf samples of the crops were taken when differences in the leave phenotype began to appear in order to measure physiological and biochemical changes.

Metabolites extraction, UHPLC–MS–MS analysis, and data processing

The samples of stress induced WT and transgenic soybean seedlings (*GmSQE1*-OE6 and *GmNF-YC9*-OE8 plants) were freeze-dried, and then crushed with a mixer mill. A 50 mg aliquot of each individual samples were precisely weighed and transferred to Eppendorf tubes, which were used for metabolites extraction and UHPLC–MS analysis (Allwegene Technology Co., Ltd, Beijing, China). The methods of plant metabolites extraction were described in detail by Vos *et al*. (2007).

The UHPLC separation was performed using an EXIONLC System (Sciex). The mobile phase A was 0.1% formic acid in water, while mobile phase B was acetonitrile. The column temperature was set at 40 °C, and the auto-sampler temperature was set at 4 °C with an injection volume was 2 μL. A Sciex QTrap 6500+ (Sciex Technologies) was applied for assay development. Typical ion source parameters were as follows: IonSpray Voltage, +5500/−4500 V; Curtain Gas, 35 psi; Temperature, 400 °C; Ion Source Gas, 1:60 psi; Ion Source Gas 2, 60 psi; DP, ± 100 V (Allwegene Technology Co., Ltd, Beijing, China).

SCIEX Analyst Work Station Software (Version 1.6.3) was employed for MRM data acquisition and processing. MS raw data (.wiff) files were converted to the TXT format using MSconventer. An in-house R program and database were applied to peak detection and annotation (Allwegene Technology Co., Ltd, Beijing, China).

Measurement of squalene, cycloartenol, and beta-amyrin by LC–MS

The samples of untreated, 25 mM terbinafine treated, and 100 mM mannitol induced soybean seedlings were freeze-dried, and then crushed with a mixer mill. A 50 mg aliquot of each sample was accurately weighed and transferred to Eppendorf tubes for metabolites extraction. The extracted metabolites were used for squalene, cycloartenol, and beta-amyrin content measurement by UHPLC–MS analysis. The method of extracting plant metabolites was described in detail by Vos *et al*. (2007).

Squalene (5 mg/mL) (Sigma, USA), cycloartenol (5 mg/mL) (Sigma, USA), and beta-amyrin (5 mg/mL) (Sigma, USA) were used in appropriate amounts to form standard solutions. These solutions were then diluted with methyl alcohol to create a suitable standard series of standards at concentrations of 5, 10, 20, 50, 100, 200, and 500 ng/mL. The peak areas of the standard substances at different concentrations were used to draw the standard curves that exhibited a good linear relationship with an R^2 value >0.99. The standard curves were drawn based on the peak areas of the standard substance at different concentrations and their corresponding concentrations. With an R^2 value >0.99, it indicated that the standard curves exhibit a strong linear relationship and could be utilised for calculating the concentrations of squalene, cycloartenol, and beta-amyrin in the samples.

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Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure S1 Generation and stress tolerance identification of *GmNF-YC9*-OE soybean plants.

Figure S2 Functional analysis of GmNF-YB24 and GmNF-YA2 candidate proteins.

Figure S3 Differentially expressed genes of *GmNF-YC9*-OE soybean plants by transcriptome sequencing.

Figure S4 Interaction analysis between the NF-Y transcription factor and the potential target gene *GmSQE1*.

Figure S5 Effect of terbinafine on soybean plant growth and content analysis of squalene, cycloartenol, and β-amyrin under different treatments by LS-MS.

Figure S6 Identification and stress tolerance identification of *GmSQE1* overexpressing soybean plants.

Figure S7 Agronomic trait analysis of *GmNF-YC9*- and *GmSQE1*-OE soybean plants under normal conditions.

Figure S8 Agronomic trait analysis of *GmSQE1*- and *GmNF-YC9*-OE soybean plants under drought conditions.

Figure S9 Oxidative stress tolerance analysis of *GmNF-YC9*- and *GmSQE1*-OE soybean plants.

Figure S10 Effect of terbinafine on soybean oxidative stress tolerance.

Figure S11 Effect of fucosterol and soyasaponin II on crop stress tolerance.

Figure S12 Effect of cycloartenol and beta-amyrin on crop stress tolerance.

Figure S13 Expression level analysis of the genes related with response to ROS in *GmNF-YC9*-OE and WT soybean plants.

Figure S14 Difference analysis of SQE-mediated catalytic pathway in humans and higher plants.

Figure S15 Stress tolerance of soybean materials by application of rain-proof installations in the experimental field.

Table S1 Differentially expressed genes in four groups (Up/Down-regulated)

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