The critical roles of three sugar-related proteins (HXK, SnRK1, TOR) in regulating plant growth and stress responses

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Abstract

Sugar signaling is one of the most critical regulatory signals in plants, and its metabolic network contains multiple regulatory factors. Sugar signal molecules regulate cellular activities and organism development by combining with other intrinsic regulatory factors and environmental inputs. HXK, SnRK1 and TOR are three fundamental proteins that have a pivotal role in the metabolism of sugars in plants. HXK, being the initial glucose sensor discovered in plants, is renowned for its multifaceted characteristics. Recent investigations have unveiled that HXK additionally assumes a significant role in plant hormonal signaling and abiotic stress. SnRK1 serves as a vital regulator of growth under energy-depleted circumstances, whereas TOR, a large protein, acts as a central integrator of signaling pathways that govern cell metabolism, organ development, and transcriptome reprogramming in response to diverse stimuli. Together, these two proteins work to sense upstream signals and modulate downstream signals to regulate cell growth and proliferation. In recent years, there has been an increasing amount of research on these three proteins, particularly on TOR and SnRK1. Furthermore, studies have found that these three proteins not only regulate sugar signaling but also exhibit certain signal crosstalk in regulating plant growth and development. This review provides a comprehensive overview and summary of the basic functions and regulatory networks of these three proteins. It aims to serve as a reference for further exploration of the interactions between these three proteins and their involvement in co-regulatory networks.

Keywords

2

Introduction

In plants, nutrient signaling mechanisms are complex and form part of regulatory networks with distinct physiological, metabolic, and functional regulation in different cells and tissues. Nutrient signals regulate cellular activities and organism development by integrating with other intrinsic regulatory factors and environmental inputs [1,2]. The sugar metabolic network is one of the most critical regulatory networks in nutrient signaling mechanisms and plays a vital role in important biological processes within plants [2]. As an essential energy source and signaling molecule, sugars play a crucial role in the sugar metabolic network [3]. Hexokinase (HXK), SNF1-related protein kinases 1 (SnRK1), and Target of rapamycin (TOR) serve as crucial sugar response signals that play a regulatory role in the growth of plants and respond to external nutrients and light [2,4-9].

Sucrose (Suc), the main carbohydrate produced through photosynthesis in higher plants, is transported through the phloem to different tissues. In these tissues, it is hydrolyzed by cytoplasmic invertases (CIN) into glucose and fructose (Fig. 1) [5,10-12]. Meanwhile, sucrose can be converted into UDP-Glc and Fru by the action of sucrose synthases (SuSy). Glc and Fru are converted into glucose-6-phosphate (Glc-6-P) and fru-6-phosphate (Fru-6-P) by HXKs [1,11]. UDP-Glc and Glc-6-P undergo enzymatic conversion mediated by trehalose-6-phosphate synthase (TPS), resulting in the formation of trehalose-6-phosphate (T6P). Subsequently, T6P is further transformed into trehalose (T) via the action of T6P phosphatase (TPP). Finally, the T can be hydrolyzed by trehalase (Ti) into two molecules of Glc. Fru-6-P and UDP-Glc are

3

converted into Suc-phosphate (Suc-P) by Suc-P synthase (SPS), and then Suc-P is converted into Suc by the action of Suc-P phosphatase (SPP) (Fig. 1) [11].
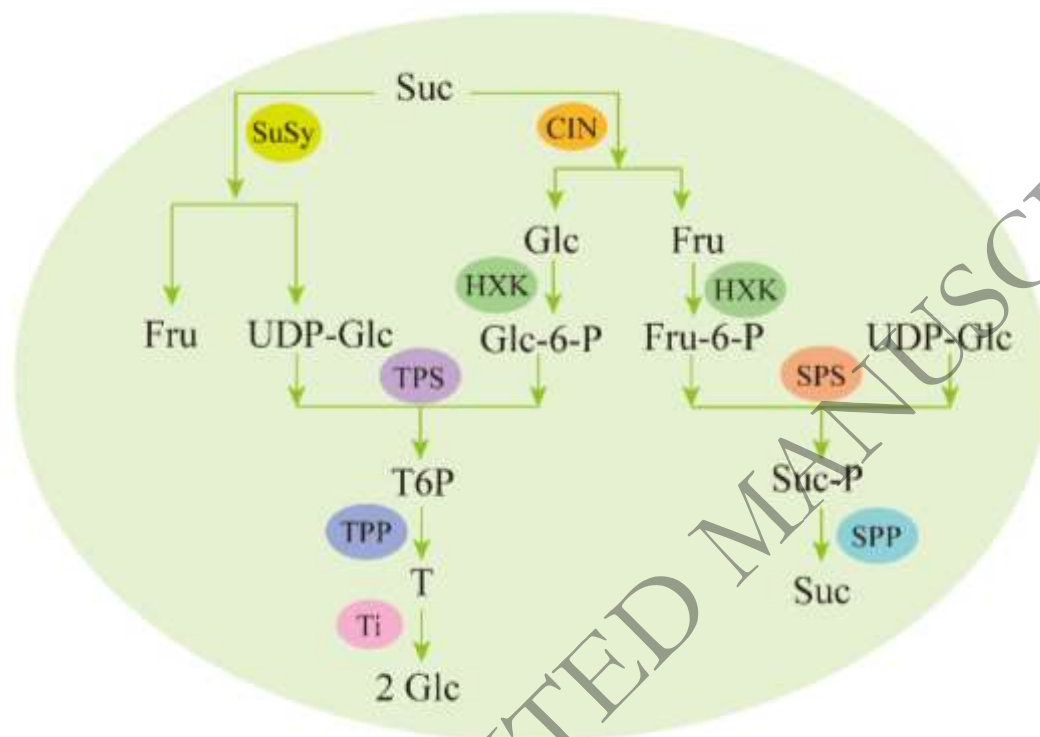
Fig 1. Sugar metabolism in plants

Sugar metabolism in plants. Suc, Sucrose; SuSy, sucrose synthases; Fru, Fructose; Glc, Glucose; HXK, Hexokinase; CIN, cytoplasmic invertases; T6P, trehalose-6-phosphate; TPS, trehalose-6-phosphate synthase; TPP, T6P phosphatase; Ti, trehalase; Suc-P, Suc-phosphate; SPS, Suc-P synthase; SPP, Suc-P phosphatase.

These above sugar molecules are able to regulate the receptors. For example, Glc-6-P and T6P inhibit SnRK1 [1,13,14]. Glc activates TOR and HXK1 proteins to regulate growth and development [1,3,15,16]. Apart from their participation in the modulation of sugar signaling, HXK, SnRK1 and TOR also serve as pivotal regulators of stress responses that mediate plant growth and development. HXKs are recognized

4

for their capacity to elicit responses in the face of salt and drought stress conditions [3].

SnRK1 participates in the signaling cascade of abscisic acid (ABA), contributing to

its regulatory role in plant physiological processes [17,18]. TOR is a well-known protein

that coordinates plant growth [19,20]. The regulatory network of sugar signaling

molecules is important and complex. In recent years, there has been increasing

research on these three proteins, revealing that they not only regulate sugar signaling

but also exhibit certain signal crosstalk in the regulation of plant growth and

development processes. Currently, most reviews focus on the two sugar proteins TOR

and SnRK1, and less information about HXK has been summarized. The potential

signal crosstalk among these three proteins has also been less explored. This article

provides an overview of the significant significance and relationships of these three

proteins in regulating plant sugar metabolism and stress responses, aiming to provide

valuable insights into understanding plant growth and development processes.

Hexokinases (HXKs)

Hexose phosphorylation is a crucial and irreversible reaction in the early stages

of sugar metabolism in plants [21]. Enzymes that facilitate this reaction and classified

into three categories based on their affinity for substrates: fructokinases (FXKs),

glucokinases (GLKs) and hexokinases (HXKs) [21]. Although both GLKs and FRKs

are participate in the metabolism of Glc and Fru, respectively, they exhibit specificity

towards their respective substrates. HXKs can phosphorylate a range of hexose sugars,

including Glc, Fru, mannose and galactose [21,22]. HXKs proteins family is widely

present in plants and plays a significant role [23-25]. Grape, for example, is known for

5

high sugar content, and HXKs proteins family is also been identified. Researchers

have identified six genes encoding VvHXKs proteins in *Vitis vinifera* by using a

comprehensive screening approach on the grape genome sequence [21,26]. The six

VvHXK genes were localized on four chromosomes [21]. All of the members within

VvHXK genes family are comprised of nine coding exons, which are interrupted by

eight introns, with the exception of *VvHXK5* that comprises ten exons and nine introns,

and *VvHXK2* that consists of four exons and three introns [21]. An investigation into

the cis-acting elements present in the promoter region of six *VvHXK* genes has

revealed a diverse range of cis-acting elements that can be regulated by various

factors, including light, sugar, plant hormones, and abiotic stress [21]. This implies that

the relationship between the HXKs family and plant growth and development requires

further exploration.

HXK signaling in plant stress responses

The function of HXK is vital in plant responses to different stress, such as biotic

stress resulting from pathogen infections [27]. The predominant fungal pathogen

responsible for infecting peach fruit is *Monilinia fructicola*, which leads to the

development of brown rot and postharvest decay [27]. The researchers discovered that

infection by *M. fructicola* caused a rise in the activity of HXK and gene expression of

HXK2, which in turn led to a faster breakdown of sucrose in peach fruit (*Prunus*

persica). Furthermore, a positive relation was found between the activity of HXK and

the expression of the *PpHXK2* gene, and there was a negative correlation between the

activity of HXK and the sucrose content within the fruit [27]. The presence of three

6

W-box cis-acting elements within *PpHXK2* gene promoter suggests that PpHXK2 potentially act as a sugar sensor, playing a role in the process of sugar signaling and metabolism in the context of immune responses to pathogen infections [27]. The expression of *Nicotiana benthamiana* HXK1 displayed an increase in expression levels in tobacco leaves when infected with *Pseudomonas syringae*. Moreover, it was observed that a high level of HXK significantly enhanced the plant's ability to resist the infection [28]. *BnHXK1*, *BnHXK3* and *BnHXK9* have been identified in *Brassica napus* as participating in the defense response against *Sclerotinia sclerotiorum* pathogen [29]. Several studies have demonstrated that the reduced activity of HXK can lead to decreased resistance against *Monilinia fructicola* infection by influencing sugar metabolism and the phenylpropanoid biosynthetic pathway [30].

HXK plays a crucial role in regulating plant drought resistance, and it has been found that GNC, which belongs to the GATA family of transcription factors, is involved in this process [31]. Studies have revealed that *PdGNC* activates *PdHXK1*, resulting in a substantial increase in hexokinase activity. This activation enhances the plant's ability to cope with water shortage by improving sugar metabolism and other related physiological processes [31]. Furthermore, HXK facilitates the generation of nitric oxide (NO) and hydrogen peroxide (H_2O_2) within guard cells, leading to a reduction in stomatal opening and ultimately enhancing the plant's resistance to drought [31]. The similar result was found in strawberry (*Fragaria pentaphylla*). The inhibition on the FpHXK1 kinase activity weakened the strawberry plant's responses to the drought stress [25]. Meanwhile, about HXK2, researchers found that *Glycine*

7

max HXK2 (*GmHXK2*) transgenic *Arabidopsis* plants improved the tolerance to salt stress [24]. Conversely, *GmHXK2*-slienced plants decrease the genes levels of salt tolerance, resulting in increased sensitivity to salt stress [24]. At same time, the study showed a positive correlation between *GmHXK15* gene and hexokinase (HXK) activity. Furthermore, when *GmHXK15* was overexpressed in soybean hairy roots, it led to increased tolerance to alkali stress [32].

By ectopically expressing the *Prunus HXK3* gene, an improvement in the tolerance of Arabidopsis to both salt and drought stress was observed under the conditions of growth chamber [33]. In addition, metabolomics analysis of these transgenic Arabidopsis plants indicated alterations in the levels of several metabolites, such as G6P (phosphorylated sugars), starch, and certain metabolites linked to the TCA (tricarboxylic acid) cycle [33]. By identifying specific metabolic changes associated with the transgenic Arabidopsis plants, it establishes a robust basis for subsequent investigations focused on understanding how the gene functions in imparting stress tolerance. This information could be useful in further studies aimed at understanding the mechanisms by which the Prunus *HXK3* gene confers salt and drought tolerance, as well as in identifying other genes and pathways that may be involved in these processes [33]. *HXKs* responded to cold stress in *Jatropha curcas* [34]. Specifically, *JcHXK1* and *JcHXK2* were found to be up-regulated in the leaves after being exposed to cold at a temperature of 12 °C for 12 and 24 hours [34]. In the root, *JcHXK1*, *JcHXK2* and *JcHKL1* (*HXK-like*) exhibited comparable down-regulation patterns following 12 and 24 hours of exposure to 12°C cold stress [34].

8

SNF1-related protein kinases 1 (SnRK1)

SnRK1 serves as a widely conserved key regulator of plant growth, playing a critical role in the maintenance of energy homeostasis during periods of limited energy availability. In mammals and yeast, its functional counterparts are represented by AMPK and Snf1 kinases, respectively [35]. SnRK1 is a prototypical heterotrimeric protein complex found in plants, consisting of an α kinase subunit and β and βγ regulatory subunits [1,35,36] (Fig. 2). Arabidopsis encodes the α catalytic subunit as SnRK1.1 (KIN10) or SnRK1.2 (KIN11) [37]. In yeast *snf1* mutant, SnRK1α subunit from different plants (Arabidopsis, tobacco, potato, rice and wheat) could functionally complement, which indicated a conserved functional role across eukaryotes [35,38-42].
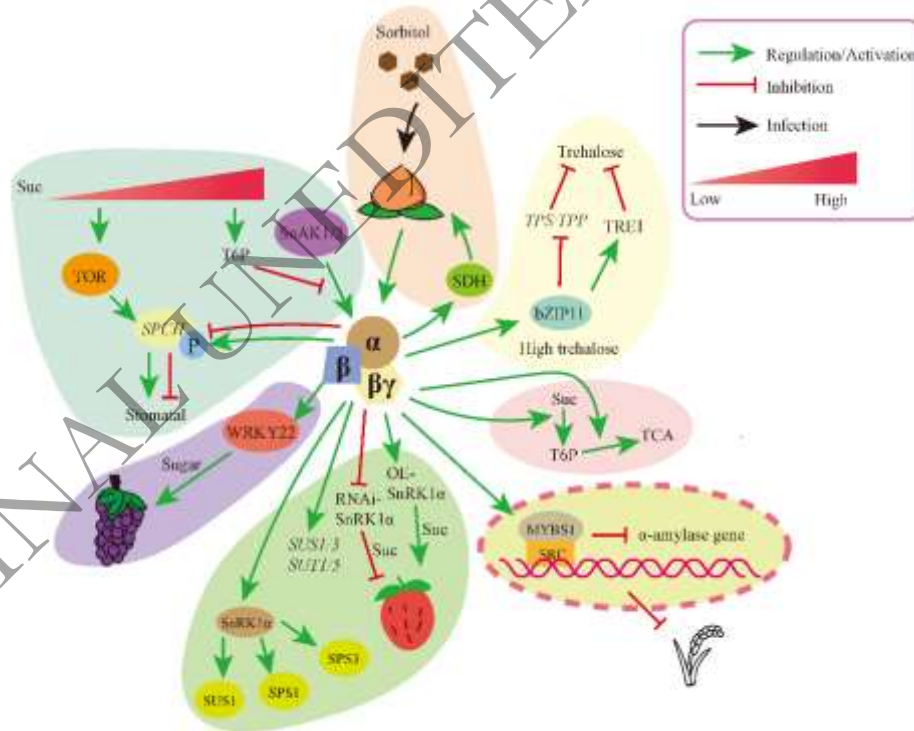

Fig 2. SnRK1 signaling in sugar metabolism

SnRK1 signaling regulates plant sugar metabolism. SnAK1/2, SnRK1 activate kinases 1/2. T6P,

9

Trehalose 6-phosphate. Suc, sucrose. TOR, target of rapamycin. SPCH, *SPEECHLESS.* P, phosphorylation. SDH, sorbitol dehydrogenase. TPS, trehalase phosphate synthases. TPP, trehalose phosphate phosphatase. TRE1, trehalose metabolism related gene expression. bZIP11, basic leucine zipper 11. TCA, tricarboxylic acid cycle. MYBS1, MYB transcription factor. SRC, sugar response complex. OE, overexpress. RNAi, RNA interference. SUS, sucrose, synthase. SUT, sucrose transporter. SPS, sucrose phosphate synthase. WRKY, transcription factor.

SnRK1 signaling in plant sugar metabolism

The application of sorbitol in peach fruits increased the activity of certain enzymes, such as SnRK1, sucrose synthase (SS), and sorbitol dehydrogenase (SDH), leading to an increase in sucrose content compared to the control group [43] (Fig. 2). Furthermore, the interaction between SnRK1α and SDH in peach indicated the activation of SDH by SnRK1, facilitating sorbitol metabolism and regulating the activity of SS. This, in turn, facilitated the accumulation of sucrose in peach fruit [43] (Fig. 2). In the presence of elevated trehalose levels, SnRK1 interacted with bZIP11 to inhibit the activity of genes related to trehalose synthesis (*TPS* and *TPP*) and activate genes expression related to trehalose metabolism. Consequently, there is a reduction in the trehalose content in peach [44]. In grape, SnRK1.1/1.2 interacted with WRKY22 transcription factor to regulate sugar accumulation [45]. In strawberry fruit, the overexpression of SnRK1α resulted in an elevation of sucrose content, while the suppression of SnRK1α expression via RNA interference resulted in a decrease in sucrose content [46]. Regarding the genes associated with sugar metabolism, SnRK1α increased the expression of *sucrose synthase 1* (*SUS1*) and *SUS3* [46]. Meanwhile, the

10

sucrose transporter genes expression levels, namely SUT1 and SUT5, was enhanced by SnRK1α. Moreover, SnRK1α interacted with proteins SUS1, SPS1 and SPS3 in strawberry by Y2H assay [46].

Through the analysis of metabolomics and transcriptomics in Arabidopsis SnRK1 gaining and losing function mutants, researchers have discovered that SnRK1 contributes to modifying the association between T6P and sucrose. This modification impacts the pathway responsible for converting sucrose into T6P accumulation, while also regulating the carbon flow towards the downstream of T6P signaling in the TCA cycle [47]. Scientists further explored the T6P-SnRK1 pathway and identified a new candidate gene, TPP-7A, which is specifically expressed in developing grains and significantly influences grain plumpness and size. This gene primarily regulates the breakdown, flux, and utilization of sucrose in the endosperm of grains through the T6P-SnRK1 pathway and the sugar-ABA interaction feedback mechanism [48].

SPCH (SPEECHLESS) acts as a central regulator governing the development of stomata [49,50]. Researchers have discovered that both TOR and SnRK1 play important roles in regulating the transcriptional activity and stability of the SPCH protein, thus, affecting the development of stomata in response to exogenous sucrose supply [49]. Under conditions of low sucrose level, sucrose triggers the activation of the TOR pathway, leading to the promotion of stomatal development through the induction of SPCH expression [49]. Additionally, the SnRK1 participates in this process by phosphorylating and stabilizing the SPCH protein. This phosphorylation event enhances the stability of the SPCH protein, leading to further promotion of stomatal

11

development [49]. When exposed to elevated sucrose levels, the increased concentration of T6P inhibits KIN10 (SnRK1.1) activity by diminishing the interaction between SnAKs and KIN10. As a result, this triggers the degradation of SPCH and hinders stomatal development [49] (Fig. 2). Several studies in Arabidopsis have indicated that, besides KIN10 activity, other mechanisms within the SnRK1 pathway also take part in the response of elongating hypocotyls to sucrose under photoperiod/daily light conditions. For example, about the circadian, the low-energy response can be mediated by bZIP63. In Arabidopsis, KIN10 activated the activity of bZIP63 to regulate the circadian clock in the low energy [51]. Meanwhile, the enhanced expression of KIN10 caused a postponement in the maximum expression of *GIGANTEA* (*GI*), an evening element of the circadian clock, under diurnal conditions. Furthermore, it extended the duration of the clock cycle, particularly in the condition of light [52]. In the case of rice germinating embryos and cell cultures, it has been observed by researchers that sugar functions as a suppressor of α-amylase expression [42]. This repression occurs through the involvement of a sugar response complex (SRC) located in the promoters of α-amylase genes, as well as its interacting MYBS1 [42]. The sugar signaling cascade involves SnRK1α as a critical intermediary, which operates upstream of the interaction between MYBS1 and the SRC promoter for αAmy3 (α-amylase gene) (Fig. 2).

Target of rapamycin (TOR)

TOR is a large protein (~280 kDa) that functions as an atypical Ser/Thr protein kinase, and which is highly conserved across organisms. It acts as a crucial signaling

12

integrator, governing various cellular processes such as organ growth, cell metabolism, and transcriptome reprogramming in response to nutrient, hormonal signals, and stress conditions [1,53-58]. In most plants, there is only one TOR protein [35]. The TOR complex 1 (TORC1) were formed by TOR, LST8 (LETHAL-WITH-SEC13-PROTEIN 8) and RAPTOR (REGULATORY-ASSOCIATED-PROTEIN-OF-MTOR) to regulate plant growth, dynamically [1,54] (Fig. 3). The TOR protein is formed by five domains, including HEAT (Huntington, EF3A, ATM, TOR) repeats, FAT (Focal adhesion target), FRB (FKBR12 and rapamycin binding), Kinase and FATC (C-terminal of FAT) [54,59-61]. In typical scenarios, the FKBP12 protein combines with TOR and rapamycin to create an inhibitory complex, which has the ability to control the functioning of the TOR. However, when the FKBP12 protein mutates, it is unable to form a stable inhibitory complex with TOR and rapamycin. This mutation hinders the normal inhibitory mechanism of the TOR pathway, resulting in the plant's insensitivity to rapamycin [62,63]. Based on the reasons mentioned above, scientists have developed the new generation inhibitors of TOR, including KU-63794, Torin1/2, PP242, WYE-132 and AZD8055. By competing with ATP, these TOR inhibitors have the ability to bind with the kinase domain of the TOR, leading to the inhibition of its activity [15,20,54,64].

TOR signaling in plant sugar metabolism

TOR can sense all kinds of upstream signals, like sugar, light, and hormone. It directly or indirectly regulates the downstream signals to modulate cell growth and cell proliferation in plants [1,19,65] (Fig. 3). The Glc-TOR signaling pathway holds a

13

pivotal position in plant growth, with glucose being a potent activator of TOR protein that governs the development of root hairs in plants [66]. Scientists have uncovered that glucose, originating from shoot photosynthesis, propels the relay of TOR signaling by means of glycolysis and mitochondrial bioenergetics, thereby regulating the activation of root meristem [15]. In Arabidopsis, glucose activates TOR protein, which then phosphorylates E2Fa to promote root hair cell proliferation [15]. Glc-TOR-E2Fa is a novel regulatory pathway of plant hair development [15] (Fig. 3).
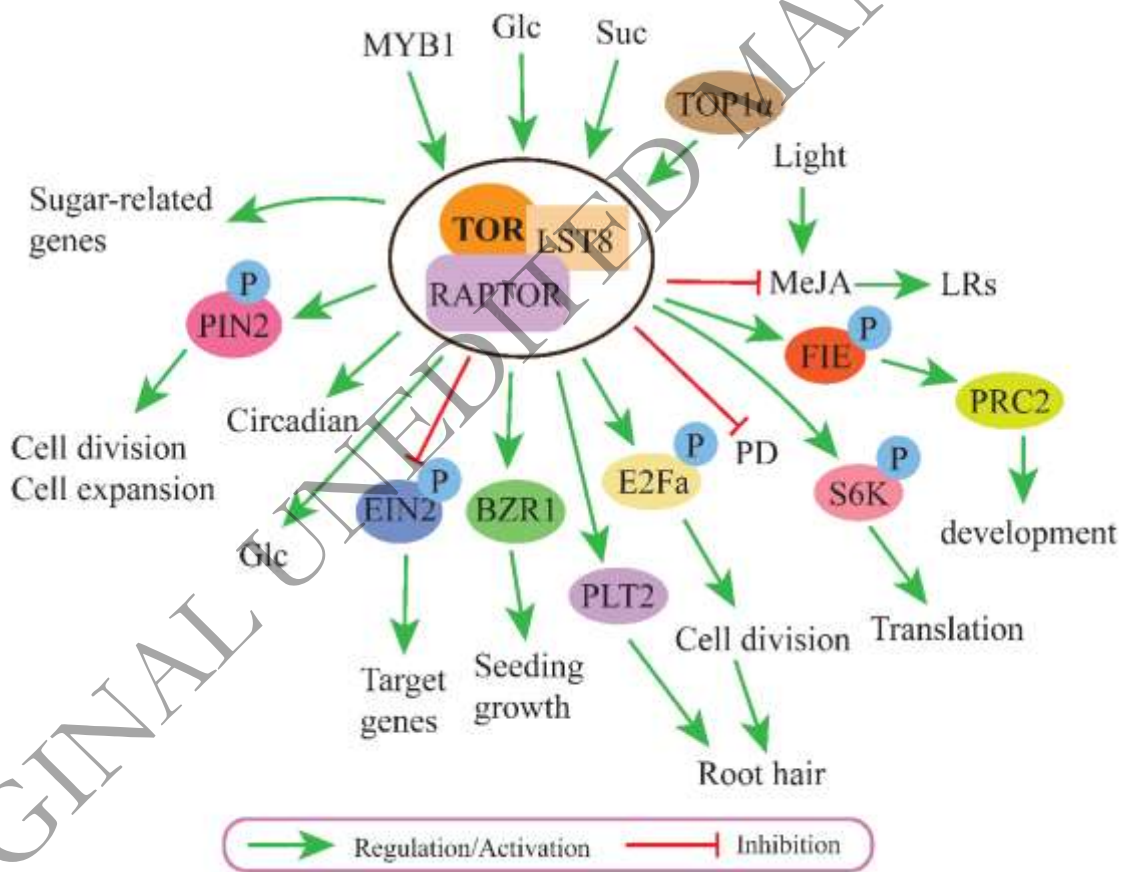
Fig 3. TOR signaling in sugar metabolism

Glc-TOR signaling regulates plant growth. MYB1, v-myb avian myeloblastosis viral oncogene homolog transcription factors. Glc, glucose. Suc, sucrose. MeJA, methyl jasmonate. LRs, lateral

14

roots. S6K, 40S ribosomal S6 protein kinase. P, phosphorylation. PD, plasmodesmata. E2Fa, transcription factor. BZR1, Brassinosteroid (BR) signaling transcription factor. EIN2, Ethylene-insensitive protein 2. PIN2, PIN-FORMED 2. PLT, PLETHORA. PRC2, Polycomb repressive complex 2. TOP1α, TOPOISOMERASE1α

EIN2 (ethylene insensitive protein 2) has recently been confirmed as a substrate of TOR, with the ability to shuttle between the cytoplasm and nucleus and can be directly phosphorylated by TOR, hindering its nuclear localization. EIN2 negatively regulates the expression of multiple target genes involved in the glc-TOR signaling pathway, including DNA replication, cell wall synthesis, and various secondary metabolic processes [20]. FIE (FERTILIZATION-INDEPENDENT ENDOSPERM), a crucial constituent of Polycomb repressive complex 2 (PRC2), is a target of TOR protein [67]. Glc-TOR-FIE-PRC2 signaling modulates plant development (Fig. 3) [67]. According to a recent study, glc-TOR signaling played a critical role in adjusting the circadian period [56,68]. When glucose was externally applied, it activated TOR and shortened the circadian period [68]. Conversely, the induction of TOR silencing by estradiol resulted in a significant lengthened of the circadian period, completely blocking the recovery of the circadian period by exogenous glucose [68].

Efficient transportation of sugar from mature "source" leaves to developing "sink" leaves requires a rigorous regulation of sugar transport between cells, which is facilitated by plasmodesmata (PD) [64]. Researchers revealed that glc-TOR metabolic network plays a crucial role in restricting PD transport in leaves [64]. Plant upgrowth is strongly influenced by the energy level within the cells [69]. By creating gradients, PLT

15

(PLETHORA) plays a crucial role in defining the characteristics of the root apical meristem (RAM). Researchers demonstrated that TOPOISOMERASE1α (TOP1α) controlled the TOR-PLT2 pathway, which is responsible for maintaining homeostasis and gravitropism in the root tip in response to sugars during development [69].

The transcription factor BZR1, participated in Brassinosteroid (BR) signaling, plays a crucial role in promoting growth in response to hormonal and environmental signals [70]. By regulating TOR, glucose signals stimulate the accumulation of BZR1 and promote seedling growth [70,71] (Fig. 3). However, the effects of sugars are abolished when TOR is inactivated, and the degradation of BZR1 due to TOR inactivation is prevented by inhibiting autophagy [70]. These findings suggest a sequential process where cellular starvation leads to TOR inactivation, followed by BZR1 degradation and autophagy [70,71]. Recent research has uncovered that glucose antagonize the methyl jasmonate response through TOR signaling and inhibit the erect root architecture, inducing wider branching angles [72]. Through a large-scale Arabidopsis mutant screening, scientists identified an auxin efflux facilitator called PIN2 (PIN-FORMED 2), which was a critical downstream regulator of glc-TOR signaling [65]. Glc-activated TOR phosphorylated and stabilized PIN2, which in turn affected the gradient distribution of PIN2 in the primary root of Arabidopsis, thereby regulating cell growth [65].

Meanwhile, recent researchers found that TOR also regulated sugar metabolism in grapes [57]. Through the use of Y1H and dual-luciferase reporter systems, researchers have discovered that MYB1 plays a role in regulating TOR expression by

16

controlling the TOR promoter, and is involved in glucose accumulation in grapes (Fig. 3) [73]. These findings indicate a potential interplay between MYB1, TOR, and glucose accumulation [73]. Except for glucose, sucrose increased the activity of TOR and promoted S6K (40S ribosomal S6 protein kinase) phosphorylation. S6K is an important direct substrate of TOR. We detect the phosphorylation level of S6K to monitor the activity of TOR protein [1] (Fig. 3). During the extensive process of evolution, plants have developed a highly sophisticated TOR signaling network in response to sugar signaling, enabling them to withstand various environmental pressures and stresses [54].

HXK, SnRK and TOR signaling networks in the plant growth and development

The HXK signaling network

The function of HXK in regulating sugar metabolism in horticultural crops is well known. Pear (*Pyrus × bretschneideri*) is a widely cultivated and economically significant fruit globally [5]. Transcriptome analysis was employed to construct HXKs expression patterns in various tissues. It was observed that *PbHXK1* exhibited preferential expression in fruits, while its expression levels were relatively lower in petals, sepals, ovaries, and buds [5]. *PbHXK1* overexpression in tomatoes led to in a significant enhancement of HXK activity and a reduction in the sugar content [5]. This study proposed a negative regulatory function of PbHXK1 in sugar content modulation [5]. Similar findings were obtained in grapes, where a higher HXK activity and protein level in the initial of phases of grape development correlated with lower hexose content. However, as the grapes matured, there was a sharp decline in the

17

activity and protein level of HXK accompanied by an increase in hexose levels [74].

In addition to responding to sugar signal, HXK can also regulate a variety of metabolic processes in plants (Fig. 4). HXK1 signaling enhances shoot branching and interacts with the cytokinin and strigolactone pathways [75]. EIN3 (ETHYL-ENE-INSENSITIVE 3) is a crucial constituent of the ethylene/glucose signaling network [76]. Researchers found that HXK1 exerts a negative influence on the stability of EIN3, and that EIN3 acts upstream of SUC2 in the modulation of root sink growth through glucose signaling [76]. Consequently, these components together formed the HXK1-EIN3-SUC2 module, which is instrumental in facilitating sucrose phloem loading in sucrose tissues, ultimately leading to an increase in sucrose content in sink roots (Fig. 4) [76]. At the condition of elevated glucose levels, AtHXK1 formed a repressor complex composed of three subunits with the VHA-B1 (vacuolar H + -ATPase B1) and the RPT5B (26S regulatory particle of proteasome subunit 5B). The trimeric complex bound to the *CAB2* (chlorophyll *a/b* binding protein 2) promoter to inhibit the transcription of *CAB2* [23,77] (Fig. 4). The glucose insensitive phenotype observed in *vha-B1* and *rpt5b* mutants, even in the presence of AtHXK1, was a crucial finding that suggested the essential roles of all three proteins in the glucose sensing [23,77]. In apple (*Malus domesticus*), MdHXK1 participated in regulating both anthocyanin biosynthesis, and salt stress tolerance which was mediated by glucose [16,78]. Similarly, under high glucose concentration, MdHXK1 was shown to engage in an interaction with and subsequently phosphorylate the bHLH (basic helix-loop-helix) associated with anthocyanin biosynthesis, specifically at the Ser361 site. This

18

phosphorylation event serves to stabilize the aforementioned transcription factor, ultimately resulting in enhanced transcriptional activity of genes participated in the biosynthesis of anthocyanin, and consequently leading to increased production of anthocyanin [16,23] (Fig. 4). Researchers used immunoprecipitation coupled with mass spectrometry to demonstrate direct interactions between HXK1 and two catalytic subunits of the Polycomb Repressive Complex 2, SWINGER (SWN) and CURLY LEAF (CLF) (Fig. 4) [79]. These interactions were found to be instrumental in targeting shared glucose-responsive genes, thereby exerting regulatory control over glucose signaling pathways [79].
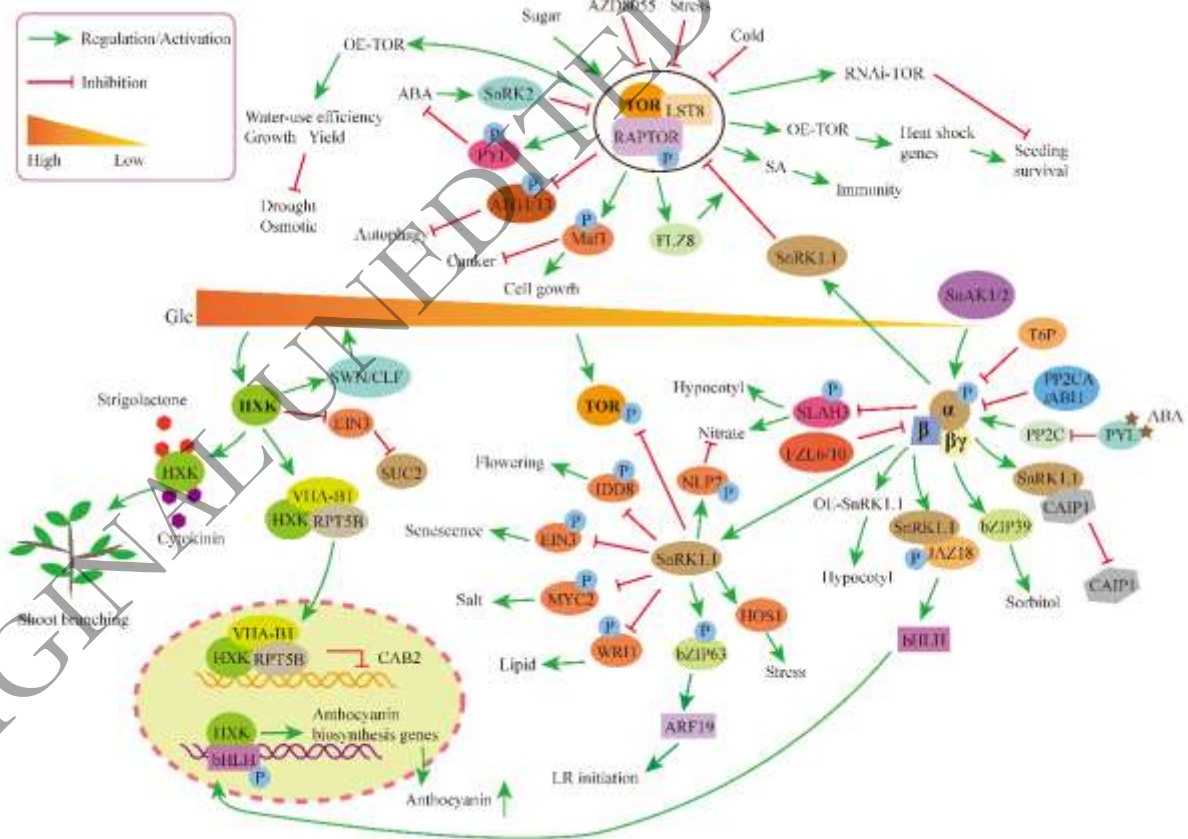

Fig 4. HXK, SnRK1 and TOR signaling networks in plant growth and

development

19

HXK, SnRK1 and TOR signaling networks regulate plant growth and development. HXK, Hexokinase. TOR, Target of rapamycin. SnRK1, SNF1-related protein kinases 1. VHA-B1, vacuolar H + - ATPase B1. RPT-5B, 26S regulatory particle of proteasome subunit 5B. CAB2, chlorophyll *a/b* binding protein 2. Two catalytic subunits of Polycomb Repressive Complex 2: SWN, SWINGER. CLF, CURLY LEAF. bHLH, basic helix-loop-helix. IDD8, INDETERMINATE DOMAIN 8. EIN3, Ethylene-insensitive protein 3. MYC2, a bHLH transcription factor. WRI1, WRINKLED1. bZIP63, basic leucine zipper 63. ARF19, AUXN RESPONSE FACTOR. LR, lateral root. SLAH3, SLAC1 homolog 3. FLZ6/10, FCS-like zinc finger. JAZ18, a repressor in the jasmonate (JA) signaling pathway. CAIP1, C2-domain ABA Insensitive Protein 1. ABI1, ABA insensitive protein 1. PP2C, protein phosphatases 2C. T6P, Trehalose 6-phosphate. SnAK1/2, SnRK1 activate kinases 1/2. Maf1, a global repressor of RNA polymerase III (Pol III). ATG1/13, autophagy-related 1/13 kinase complex. PYL, a receptor of ABA. SnRK2, SNF1-related protein kinases 2. OE, overexpression. AZD8055, an inhibitor of TOR. THADA, Thyroid Adenoma Associated. RNAi, RNA interference. SA, salicylic acid. P, phosphorylation. Glc, glucose. ABA, abscisic, acid. NLP7, NIN-LIKE PROTEIN 7. HOS1, High Expression of Osmotically Responsive Genes 1.

The SnRK1 signaling network

SnRK1 is a critical player in various metabolic networks, exerting regulatory functions in multiple pathways (Fig. 4). In plants, SnRK1 is accountable for triggering comprehensive alterations in transcriptome and growth adaptation to cope with energy deprivation [1]. SnAK1/2 (SnRK1 activate kinases 1/2) play a role upstream of SnRK1 [35]. T6P (Trehalose 6-phosphate), known as both a sugar molecule and a signaling

20

molecule, function as a key regulator in plants [54,80]. Notably, T6P was observed to directly bind KIN10, leading to reduced interaction with upstream SnAK1/2 and consequent inhibition of phosphorylation and activation in vitro [1,35,81]. This indicates a distinctive mechanism in plants that enables SnRK1 to perceive changes in cellular metabolic status through T6P [81]. When sufficient energy is present, both PP2CA (A type 2C protein phosphatases) and ABI1 (ABA insensitive protein 1) can interact with the catalytic subunit of SnRK1, leading to dephosphorylation and inactivation of SnRK1.1 and inhibition of the SnRK1 signaling pathway [82]. However, during energy deprivation, ABA can bind to PYL (Pyrabactin Resistance1/Pyrabactin Resistance1-Like (PYL)/Regulatory Components of ABA Receptors family of ABA receptors) proteins, inhibit PP2C protein, and activate SnRK1 signaling transduction [17,82,83]. There is a signal crosstalk occurring between SnRK1.1 and ABA pathways. In apple and Arabidopsis, CAIP1 (C2-domain ABA Insensitive Protein 1) reduced ABA sensitivity [84]. Concurrently, SnRK1.1 interacted with CAIP1 and promoted its degradation [84]. The aforementioned research suggests that SnRK1.1 serves to inhibit CAIP1-mediated ABA sensitivity, whereas overexpression of CAIP1 partially attenuated the SnRK1.1-mediated ABA sensitivity [84].

Nitrate is an important signaling molecule for plants to adapt to environmental changes. Under nitrate-depleted conditions, SnRK1.1 is activated and phosphorylates NLP7 (NIN-LIKE PROTEIN 7) at serine-125 and serine-306 sites, promoting the cytoplasmic retention and degradation of NLP7, thereby inhibiting nitrate-mediated gene expression and plant growth [85]. SnRK1.1 is also the negative regulator of

21

SLAC1 (slow anion channel) homolog 3 (SLAH3), playing a pivotal role in the modulating of the nitrate-dependent alleviation of ammonium toxicity by interacting with and phosphorylating the C terminal of SLAH3 [86]. The study also found that under dark conditions, SnRK1.1 relies on the SLAH3 protein to respond to sucrose signal and regulate hypocotyl growth [86]. The similar results that the energy signaling mediated by SnRK1 controls the elongation of hypocotyls in response to sucrose supplementation [87,88]. These results provide a new viewpoint for studying SnRK1 in plants (Fig. 4). FCS-like zinc finger (FLZ) proteins, as adaptor proteins, facilitate the association between SnRK1 and different protein partners [89]. Specifically, FLZ6 and FLZ10 act as inhibitors of SnRK1, and their interaction takes place within cytoplasmic foci, leading to the repression of SnRK1 activity (Fig. 4) [89]. There is relationship between SnRK1 and FLZs in regulating autophagy [90]. Recently, a study identified a clade of FLZ proteins as novel ATG8 (Autophagy related 8)-interacting partners in *Arabidopsis thaliana*. These AtFLZs inhibit SnRK1 signaling by repressing the α catalytic subunit (SnRK1.1), thereby negatively regulating autophagy. Under energy starvation, autophagy is activated to mediate the degradation of AtFLZs, thus relieving the repression of SnRK1.1 [90]. The ATG8-FLZs-SnRK1 regulatory axis form a feedback regulation in plant autophagy [90].

SnRK1 has been identified as a crucial participant in the biosynthesis of both anthocyanins and proanthocyanidins (PA) [91-93]. Specifically, within the jasmonate (JA) signaling, SnRK1.1 has been shown to interact with JAZ18 protein, ultimately phosphorylating JAZ18 and promoting its subsequent degradation via the 26S

22

proteasome. This process then leads to the release of bHLH3, which in turn activates the expression of genes involved in the promotion of anthocyanins and PA biosynthesis (Fig. 4) [91]. Meanwhile, SnRK1 down-regulates the biosynthesis of anthocyanin induced by high light [93]. Researchers have observed that SnRK1.1 (also known as KIN10) exerts direct phosphorylation effects on various transcription factors, thereby exerting regulatory control over a range of biological processes. Notably, SnRK1.1 has been found to reduce the protein stability of EIN3 (Ethylene-insensitive protein 3) during senescence and MYC2 in response to salt. Additionally, it diminishes the transcriptional activity of IDD8 (INDETERMINATE DOMAIN 8) during flowering. Furthermore, SnRK1.1 phosphorylates WRI1 (WRINKLED1), leading to its subsequent proteasomal degradation. SnRK1.1 can also interact with HOS1 (High Expression of Osmotically Responsive Genes 1) to regulate plant responses to cold, heat, and salinity stress [94]. This multifaceted regulation by SnRK1.1 establishes energy balance in plants [95-98]. In Arabidopsis, it has been observed that unforeseen darkness and short-term low light exposure disrupt energy homeostasis and diminish sugar availability in the roots, subsequently resulting in the initiation of lateral root (LR) formation [99]. ARF19 (AUXN RESPONSE FACTOR) has been identified as a pivotal regulator of LR growth [99]. SnRK1 has been found to phosphorylate the bZIP6, which in turn directly binds to and activates the promoter region of ARF19 [99] (Fig. 4). SnRK1 mediated the phosphorylation of bZIP39 to regulate sorbitol metabolism in apple [100]. In rice, overexpression *OsSnRK1α* improved leaf photosynthetic activity and contributed to

23

grain filling and panicle development [101]. *OsSnRK1α* also regulates plant immunity

against pathogens [102].

The TOR signaling network

The powerful functions of the TOR signaling pathway are gradually becoming

well-known. TOR functions as a pivotal regulator in controlling root branching by

integrating local auxin-dependent pathways with systemic metabolic signals that

modulate the translation of genes induced by auxin [19,103]. In *Arabidopsis thaliana*,

the process of lateral root formation is characterized by the auxin-mediated activation

of specific genes, namely ARF7, ARF9, and LBD16 [19]. The inhibition of TOR

activity has been shown to diminish the translation of ARF19, ARF7, and LBD16,

thereby affecting the expression of these key regulatory factors [19]. The interplay

between TOR and ABA pathways is crucial for preserving a delicate balance between

plant growth and stress responses [83]. RAPTOR is an essential component of the TOR

complex. Under stressful conditions, ABA activates SnRK2s, which subsequently

phosphorylate and inhibit TOR activity, leading to suppress growth. Moreover, PYLs,

the receptors of ABA, are involved in this regulatory mechanism. In conditions of

high nutrient availability, TOR represses ABA signaling and responds to stress stimuli

by phosphorylating PYLs, thereby promoting plant growth (Fig. 4) [83].

TOR can also negatively regulate plant immunity [104]. About tomato, the

inhibition of TOR has been shown to stimulate the activation of immune responses

and confer a decreased susceptibility to multiple pathogens through a salicylic acid

(SA)-dependent mechanism [104]. Maf1 is a highly conserved RNA polymerase III

24

(Pol Ⅲ) repressor, playing an important role in regulating protein translation [105]. In citrus plants, Maf1 has been identified as a canker elicitor-binding protein and it inhibits cell growth associated with canker development. Research has found that TOR can regulate Maf1 in plants, and treatment with TOR inhibitors induces dephosphorylation of Maf1, thereby suppressing canker development [105] (Fig. 4). TOR has been identified as the main negative regulator of autophagy [106]. Autophagy has been shown to promote plant resistance to various stressors such as nutrient deficiency, oxidative stress, salt and drought stress. These stresses activate autophagy via TOR, and TOR overexpression under these stresses has been found to significantly reduce stress-induced autophagy [107]. In plants, ATG1/13 (autophagy-related 1/13 kinase complex) were the substrates of TOR, which were phosphorylated by TOR protein kinase. Conversely, the dephosphorylation of ATG1/13 enhances autophagy in plants [108,109] (Fig. 4).

Temperature impacts the activity of TOR too. Under the cold stress, the TOR kinase activity undergoes transient inhibition, indicating that TOR inhibition represents a significant network for plants to resist to cold stress [110]. Moreover, hypersensitivity to cold conditions has been observed in TOR-RNAi lines [111]. Furthermore, high temperatures also exert an influence on TOR. Decreased seedling survival has been associated with both the down-regulation of TOR and treatment with the TOR inhibitor AZD8055. Researchers found that overexpression of TOR has been found to improve the expression of heat shock genes and seedling survival rates following recovery from heat stress treatments [112]. Additionally, TOR have a positive

25

regulatory role in response to drought and osmotic stresses. When the Arabidopsis

TOR gene was expressed in rice, it led to improved water-use efficiency, growth, and

yield under conditions of limited water availability [113]. These findings collectively

display that TOR can mitigate the adverse effects of drought or osmotic stress on plant

[55] (Fig. 4).

Conclusion and Outlook

HXK, SnRK1 and TOR are all pivotal proteins involved in sugar signaling and

growth regulation. Ongoing research is being conducted to investigate the roles and

functions of these three proteins. Moreover, intricate interconnections have been

observed between HXK, SnRK1, and TOR. It is widely acknowledged that TOR and

SnRK1 closely interact and maintain a delicate balance in coordinating various

metabolic processes (Fig. 4). SnRK1.1 interacted and phosphorylated RAPTOR1B to

inhibit TOR activity [114]. Additionally, in Arabidopsis, an interaction has been

observed between TOR and SnRK1α1, which was found to be enhanced twofold upon

treatment with ABA [17]. Notably, investigations in grape have revealed that TOR

interacts with SnRK1.1 to regulate the genes expression, which are involved in sugar

metabolism [115]. SnRK1 forms a complex with SnRK2 and PP2C, resulting in the

dissociation of TOR and subsequent activation of early developmental processes.

Conversely, during stress conditions, PP2C associates with PYR/PYL, leading to the

liberation of SnRK1 and SnRK2, which subsequently activate stress response

mechanisms. Additionally, SnRK1.1 has been found to interact with the TOR protein,

thereby exerting inhibitory effects on TOR [17,115]. Simultaneously, under stress

26

conditions, SnRK2 phosphorylates RAPTOR, impeding growth by suppressing TOR activity [83].

SnRK1 and FLZ8 both are critical proteins in the negative feedback regulation. TOR-FLZ8-SnRK1 signaling axis helps plants adapt to environmental changes continuously [116]. Recent study revealed that TOR and SnRK1 both are involved in controlling light-regulated splicing events [117]. Concurring activities of these two energy sensors are indispensable for proper regulation of gene expression and seeding development [117]. TOR and SnRK1 both regulated LR formation. T6P regulates LR at the center of a regulatory hub linking with energy homeostasis through TOR and SnRK1 [103]. Within the plant system, TOR serves as a pivotal sensing component that integrates cues related to nutrients, energy availability, and environmental factors to finely orchestrate growth and development [1]. In contrast, SnRK1 assumes a pivotal role in perceiving nutrient deprivation and stress signals, leading to the promotion of catabolic processes while concurrently inhibiting anabolic process and growth [1]. SnRK1 and TOR function synergistically to govern the dynamic equilibrium of plant energy homeostasis [17,51,83,115].

In recent years, some studies have revealed the relationship between HXK and SnRK1. In *Setaria viridis*, the expression patterns of HXK and SnRK1 were found to be distinctly influenced by high and low light conditions [118]. Additionally, it was observed that low light and sugar depletion effects on the expression of pivotal target genes regulated by HXK and SnRK1, whereas high light and substantial sugar accumulation resulted in the inhibitor of SnRK1 pathway [118]. ACT DOMAIN

27

REPEAT (ACR) proteins have been reported to serve as a repressor in Glc signaling pathway [119]. The *acr9-1* mutant was hypersensitive to Glc during seeding growth and anthocyanin accumulation [119]. However, the *acr9-1/hxk1-3* and *acr9-1/snrk1* double mutants were no longer sensitivity to Glc, which indicated that HXK1 and SnRK1 were necessary for the *acr9-1* mutant to be sensitive to Glc. The result suggests that ACR9 may act upstream of the HXK1-SnRK1 signaling module [119]. In *Nicotiana tabacum*, sucrose synergistically regulates the activities of HXK and SnRK1 to regulate the senescence of leaves [120].

Although we have gained considerable knowledge about the regulatory functions of these three proteins individually and made significant research progress and discoveries in terms of energy and stress signaling regulatory factors, there are still many unanswered questions. The interaction between HXK and TOR is currently not well understood, which suggests potential avenues for future research. Exploring the relationship between HXK and TOR could provide valuable insights into the intricate regulatory mechanisms underlying plant physiology. Numerous unresolved questions surrounding HXK, SnRK1 and TOR warrant further investigation. How do these three proteins collaboratively maintain a delicate balance and regulate sugar metabolism alongside stress response in plants? Is it possible to identify additional substrates of TOR, SnRK1, or HXK, and elucidate their functions within plant signaling pathways? Beyond their involvement in sugar metabolism and stress response, are there other shared roles that these three proteins play?

TOR, SnRK1, and HXK are three genes that play important roles in plant growth,

28

metabolic regulation, and responses to environmental stress. Therefore, the application and regulation of these genes in horticultural plants hold the potential to improve crop quality, increase yield, and enhance plant resistance to various adversities, providing important theoretical and practical foundations for the improvement and breeding of horticultural plants. Especially exploring the balanced and coordinated network between TOR and SnRK1 can contribute to future molecular-level regulation of fruit size and quality in horticultural crops, improving the quality characteristics of horticultural plants, such as fruit texture, color, and flavor. Addressing these inquiries concerning TOR, SnRK1, and HXK will undoubtedly contribute to the advancement of plant science. It is plausible that future advancements in manipulating the expression levels of these three proteins may offer a means to regulate horticultural crops.

Data Availability Statement

Not applicable.

Conflicts of Interest

The authors declare no conflicts of interest.

Authors contributions

Ying Zhao wrote and approved the manuscript. Guangshuo Li contributed to the revision of this review.

29

References

1. Li, L., Liu, K.H. & Sheen, J. Dynamic Nutrient Signaling Networks in Plants. *Annu Rev Cell Dev Biol* **37**, 341-367 http://dx.doi.org/10.1146/annurev-cellbio-010521-015047 (2021).

2. Choudhary, A., Kumar, A., Kaur, N. & Kaur, H. Molecular cues of sugar signaling in plants. *Physiologia Plantarum* **174**, http://dx.doi.org/10.1111/ppl.13630 (2022).

3. Aguilera-Alvarado, G.P. & Sanchez-Nieto, S. Plant Hexokinases are Multifaceted Proteins. *Plant Cell Physiol* **58**, 1151-1160 http://dx.doi.org/10.1093/pcp/pcx062 (2017).

4. Kim, H.B. *et al.* Role of rice cytosolic hexokinase OsHXK7 in sugar signaling and metabolism. *J Integr Plant Biol* **58**, 127-35 http://dx.doi.org/10.1111/jipb.12366 (2016).

5. Zhao, B. *et al.* Identification of hexokinase family members in pear (*Pyrus* x *bretschneideri*) and functional exploration of *PbHXK1* in modulating sugar content and plant growth. *Gene* **711**, 143932 http://dx.doi.org/10.1016/j.gene.2019.06.022 (2019).

6. Moore, B. *et al.* Role of the Arabidopsis glucose sensor HXK1 in nutrient, light, and hormonal signaling. *Science* **300**, 332-6 http://dx.doi.org/10.1126/science.1080585 (2003).

7. Granot, D., David-Schwartz, R. & Kelly, G. Hexose kinases and their role in sugar-sensing and plant development. *Front Plant Sci* **4**, 44 http://dx.doi.org/10.3389/fpls.2013.00044 (2013).

8. Granot, D., Kelly, G., Stein, O. & David-Schwartz, R. Substantial roles of hexokinase and fructokinase in the effects of sugars on plant physiology and development. *J Exp*

Bot **65**, 809-19 http://dx.doi.org/10.1093/jxb/ert400 (2014).

9. Li, L. & Sheen, J. Dynamic and diverse sugar signaling. *Curr Opin Plant Biol* **33**, 116-125 http://dx.doi.org/10.1016/j.pbi.2016.06.018 (2016).

10. Li, M., Feng, F. & Cheng, L. Expression patterns of genes involved in sugar metabolism and accumulation during apple fruit development. *PLoS One* **7**, e33055 http://dx.doi.org/10.1371/journal.pone.0033055 (2012).

11. Zhang, C. *et al.* Transcriptome Analysis of Sucrose Metabolism during Bulb Swelling and Development in Onion (*Allium cepa* L.). *Front Plant Sci* **7**, 1425 http://dx.doi.org/10.3389/fpls.2016.01425 (2016).

12. Ruan & Yong-Ling. Sucrose metabolism: gateway to diverse carbon use and sugar signaling. *Annu Rev Plant Biol* **65**, 33-67 http://dx.doi.org/10.1146/annurev-arplant-050213-040251 (2014).

13. Baena-Gonzalez, E. & Lunn, J.E. SnRK1 and trehalose 6-phosphate - two ancient pathways converge to regulate plant metabolism and growth. *Curr Opin Plant Biol* **55**, 52-59 http://dx.doi.org/10.1016/j.pbi.2020.01.010 (2020).

14. Zhang, Y. *et al.* Inhibition of SNF1-related protein kinase1 activity and regulation of metabolic pathways by trehalose-6-phosphate. *Plant Physiol* **149**, 1860-71 http://dx.doi.org/10.1104/pp.108.133934 (2009).

15. Xiong, Y. *et al.* Glucose-TOR signalling reprograms the transcriptome and activates meristems. *Nature* **496**, 181-6 http://dx.doi.org/10.1038/nature12030 (2013).

16. Hu, D.G. *et al.* Glucose Sensor MdHXK1 Phosphorylates and Stabilizes MdbHLH3 to Promote Anthocyanin Biosynthesis in Apple. *PLoS Genet* **12**, e1006273

31

http://dx.doi.org/10.1371/journal.pgen.1006273 (2016).

17.   Belda-Palazon, B. *et al.* A dual function of SnRK2 kinases in the regulation of SnRK1

and plant growth. *Nat Plants* **6**, 1345-1353

http://dx.doi.org/10.1038/s41477-020-00778-w (2020).

18.   Guo, D. *et al.* Legume-specific SnRK1 promotes malate supply to bacteroids for

symbiotic nitrogen fixation. *Molecular Plant* **16**, 1396-1412

http://dx.doi.org/10.1016/j.molp.2023.08.009 (2023).

19.   Stitz, M. *et al.* TOR acts as a metabolic gatekeeper for auxin-dependent lateral root

initiation in Arabidopsis thaliana. *EMBO J* **42**, e111273

http://dx.doi.org/10.15252/embj.2022111273 (2023).

20.   Fu, L. *et al.* The TOR-EIN2 axis mediates nuclear signalling to modulate plant growth.

Nature **591**, 288-292 http://dx.doi.org/10.1038/s41586-021-03310-y (2021).

21.   Çakir, B. Identification and structure of six members of the hexokinase gene family

inVitis vinifera: Cloning, expression, and functional analysis of a putative chloroplast

stromal-type hexokinase. *J Hortic Sci Biotech* **89**, 663-673

http://dx.doi.org/10.1080/14620316.2014.11513135 (2015).

22.   Hayes, M.A., Davies, C. & Dry, I.B. Isolation, functional characterization, and

expression analysis of grapevine (Vitis vinifera L.) hexose transporters: differential

roles in sink and source tissues. *J Exp Bot* **58**, 1985-97

http://dx.doi.org/10.1093/jxb/erm061 (2007).

23.   Rodriguez-Saavedra, C. *et al.* Moonlighting Proteins: The Case of the Hexokinases.

Front Mol Biosci **8**, 701975 http://dx.doi.org/10.3389/fmolb.2021.701975 (2021).

24. Chen, S., Tian, Z. & Guo, Y. Characterization of hexokinase gene family members in Glycine max and functional analysis of GmHXK2 under salt stress. *Frontiers in Genetics* **14**, http://dx.doi.org/10.3389/fgene.2023.1135290 (2023).

25. Wu, R. *et al.* Hexokinase1: A glucose sensor involved in drought stress response and sugar metabolism depending on its kinase activity in strawberry. *Frontiers in Plant Science* **14**, http://dx.doi.org/10.3389/fpls.2023.1069830 (2023).

26. Jaillon, O. *et al.* The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature* **449**, 463-7 http://dx.doi.org/10.1038/nature06148 (2007).

27. Xu, W.J. *et al.* Molecular cloning and expression analysis of hexokinase genes in peach fruit under postharvest disease stress. *Postharvest Biol Technol* **172**, 111377 http://dx.doi.org/10.1016/j.postharvbio.2020.111377 (2021).

28. Sarowar, S., Lee, J.Y., Ahn, E.R. & Pai, H.S. A Role of Hexokinases in Plant Resistance to Oxidative Stress and Pathogen Infection. *J Plant Biol* **51**, 341-346 http://dx.doi.org/10.1007/Bf03036136 (2008).

29. Wang, J. *et al.* Genome-wide identification of hexokinase gene family in Brassica napus: structure, phylogenetic analysis, expression, and functional characterization. *Planta* **248**, 171-182 http://dx.doi.org/10.1007/s00425-018-2888-8 (2018).

30. Han, P. *et al.* N-Acetyl-d-glucosamine Inhibition of Hexokinase Results in Downregulation of the Phenylpropanoid Metabolic Pathway and Decreased Resistance to Brown Rot in Peach Fruit. *J Agric Food Chem* **70**, 3917-3928 http://dx.doi.org/10.1021/acs.jafc.1c06573 (2022).

33

31.   Shen, C. *et al.* PdGNC confers drought tolerance by mediating stomatal closure

      resulting from NO and H2 O2 production via the direct regulation of PdHXK1

      expression in Populus. *New Phytol* **230**, 1868-1882

      http://dx.doi.org/10.1111/nph.17301 (2021).

32.   Jiao, F., Chen, Y., Zhang, D. & Wu, J. Genome-Wide Characterization of Soybean

      Hexokinase Genes Reveals a Positive Role of GmHXK15 in Alkali Stress Response.

      Plants **12**, 3121 http://dx.doi.org/10.3390/plants12173121 (2023).

33.   Perez-Diaz, J. *et al.* Prunus Hexokinase 3 genes alter primary C-metabolism and

      promote drought and salt stress tolerance in Arabidopsis transgenic plants. *Sci Rep*

      11, 7098 http://dx.doi.org/10.1038/s41598-021-86535-1 (2021).

34.   Wang, H. *et al.* Genome-wide screening of hexokinase gene family and functional

      elucidation of HXK2 response to cold stress in Jatropha curcas. *Mol Biol Rep* **46**,

      1649-1660 http://dx.doi.org/10.1007/s11033-019-04613-0 (2019).

35.   Jamsheer, K.M., Jindal, S. & Laxmi, A. Evolution of TOR-SnRK dynamics in green

      plants and its integration with phytohormone signaling networks. *J Exp Bot* **70**,

      2239-2259 http://dx.doi.org/10.1093/jxb/erz107 (2019).

36.   Broeckx, T., Hulsmans, S. & Rolland, F. The plant energy sensor: evolutionary

      conservation and divergence of SnRK1 structure, regulation, and function. *J Exp Bot*

      67, 6215-6252 http://dx.doi.org/10.1093/jxb/erw416 (2016).

37.   Baena-Gonzalez, E., Rolland, F., Thevelein, J.M. & Sheen, J. A central integrator of

      transcription networks in plant stress and energy signalling. *Nature* **448**, 938-42

      http://dx.doi.org/10.1038/nature06069 (2007).

38.   Bhalerao, R.P. *et al.* Regulatory interaction of PRL1 WD protein with Arabidopsis

SNF1-like protein kinases. *Proc Natl Acad Sci U S A* **96**, 5322-7

http://dx.doi.org/10.1073/pnas.96.9.5322 (1999).

39.   Muranaka, T., Banno, H. & Machida, Y. Characterization of tobacco protein kinase

NPK5, a homolog of Saccharomyces cerevisiae SNF1 that constitutively activates

expression of the glucose-repressible SUC2 gene for a secreted invertase of S.

cerevisiae. *Mol Cell Biol* **14**, 2958-2965

http://dx.doi.org/10.1128/mcb.14.5.2958-2965.1994 (1994).

40.   Alderson, A. *et al.* Complementation of snf1, a mutation affecting global regulation of

carbon metabolism in yeast, by a plant protein kinase cDNA. *Proc Natl Acad Sci U S A*

88, 8602-5 http://dx.doi.org/10.1073/pnas.88.19.8602 (1991).

41.   Lovas, A., Sos-Hegedus, A., Bimbo, A. & Banfalvi, Z. Functional diversity of potato

SNF1-related kinases tested in Saccharomyces cerevisiae. *Gene* **321**, 123-9

http://dx.doi.org/10.1016/j.gene.2003.08.001 (2003).

42.   Lu, C.A. *et al.* The SnRK1A protein kinase plays a key role in sugar signaling during

germination and seedling growth of rice. *Plant Cell* **19**, 2484-99

http://dx.doi.org/10.1105/tpc.105.037887 (2007).

43.   Yu, W. *et al.* SnRK1 phosphorylation of SDH positively regulates sorbitol metabolism

and promotes sugar accumulation in peach fruit. *Tree Physiol* **41**, 1077-1086

http://dx.doi.org/10.1093/treephys/tpaa163 (2021).

44.   Zhang, S. *et al.* Peach PpSnRK1alpha interacts with bZIP11 and maintains trehalose

balance in plants. *Plant Physiol Biochem* **160**, 377-385

35

http://dx.doi.org/10.1016/j.plaphy.2021.01.036 (2021).

45. Huang, T., Yu, D. & Wang, X. VvWRKY22 transcription factor interacts with VvSnRK1.1/VvSnRK1.2 and regulates sugar accumulation in grape. *Biochem Biophys Res Commun* **554**, 193-198 http://dx.doi.org/10.1016/j.bbrc.2021.03.092 (2021).

46. Luo, J., Peng, F., Zhang, S., Xiao, Y. & Zhang, Y. The protein kinase FaSnRK1alpha regulates sucrose accumulation in strawberry fruits. *Plant Physiol Biochem* **151**, 369-377 http://dx.doi.org/10.1016/j.plaphy.2020.03.044 (2020).

47. Peixoto, B. *et al.* Impact of the SnRK1 protein kinase on sucrose homeostasis and the transcriptome during the diel cycle. *Plant Physiol* **187**, 1357-1373 http://dx.doi.org/10.1093/plphys/kiab350 (2021).

48. Liu, H. *et al.* TaTPP-7A positively feedback regulates grain filling and wheat grain yield through T6P-SnRK1 signalling pathway and sugar–ABA interaction. *Plant Biotechnology Journal* **21**, 1159-1175 http://dx.doi.org/10.1111/pbi.14025 (2023).

49. Han, C. *et al.* TOR and SnRK1 fine tune SPEECHLESS transcription and protein stability to optimize stomatal development in response to exogenously supplied sugar. *New Phytol* **234**, 107-121 http://dx.doi.org/10.1111/nph.17984 (2022).

50. Shi, W. *et al.* Spatially patterned hydrogen peroxide orchestrates stomatal development in Arabidopsis. *Nature Communications* **13**, http://dx.doi.org/10.1038/s41467-022-32770-7 (2022).

51. Viana, A.J.C. *et al.* The sugar-responsive circadian clock regulator bZIP63 modulates plant growth. *New Phytol* **231**, 1875-1889 http://dx.doi.org/10.1111/nph.17518 (2021).

52. Shin, J. *et al.* The metabolic sensor AKIN10 modulates the Arabidopsis circadian clock

in a light-dependent manner. *Plant Cell Environ* **40**, 997-1008

http://dx.doi.org/10.1111/pce.12903 (2017).

53. Zhu, T., Li, L., Feng, L., Mo, H. & Ren, M. Target of Rapamycin Regulates Genome

Methylation Reprogramming to Control Plant Growth in Arabidopsis. *Front Genet* **11**,

186 http://dx.doi.org/10.3389/fgene.2020.00186 (2020).

54. Zhao, Y. & Wang, X.Q. The hot issue: TOR signalling network in plants. *Funct Plant*

Biol **48**, 1-7 http://dx.doi.org/10.1071/FP20071 (2020).

55. Fu, L., Wang, P. & Xiong, Y. Target of Rapamycin Signaling in Plant Stress

Responses. *Plant Physiol* **182**, 1613-1623 http://dx.doi.org/10.1104/pp.19.01214

(2020).

56. Zhao, Y. & Wang, X.Q. In Silico analysis of Vitis vinifera Cabernet Sauvignon TOR

and its responses to sugar and abscisic acid signaling. *Acta Bot Bras* **36**,

e2020abb0482 http://dx.doi.org/10.1590/0102-33062020abb0482 (2022).

57. Zhao, Y. & Wang, X.Q. VvTOR Responds to ABA Signal and Affects Sugar Related

Genes Expression in Grape. *Russ J Plant Physl+* **69**, 1-8

http://dx.doi.org/10.1134/S1021443722020236 (2022).

58. Li, D. *et al.* Target of rapamycin (TOR) regulates the response to low nitrogen stress

via autophagy and hormone pathways in Malus hupehensis. *Hortic Res* **9**, uhac143

http://dx.doi.org/10.1093/hr/uhac143 (2022).

59. Lamming, D.W., Ye, L., Sabatini, D.M. & Baur, J.A. Rapalogs and mTOR inhibitors as

anti-aging therapeutics. *J Clin Invest* **123**, 980-9 http://dx.doi.org/10.1172/JCI64099

(2013).

60. Xiong, F. *et al.* Tomato FK506 Binding Protein 12KD (FKBP12) Mediates the

    Interaction between Rapamycin and Target of Rapamycin (TOR). *Front Plant Sci* **7**,

    1746 http://dx.doi.org/10.3389/fpls.2016.01746 (2016).

61. Schepetilnikov, M. *et al.* Viral factor TAV recruits TOR/S6K1 signalling to activate

    reinitiation after long ORF translation. *EMBO J* **30**, 1343-56

    http://dx.doi.org/10.1038/emboj.2011.39 (2011).

62. Ren, M. *et al.* Target of rapamycin signaling regulates metabolism, growth, and life

    span in Arabidopsis. *Plant Cell* **24**, 4850-74 http://dx.doi.org/10.1105/tpc.112.107144

    (2012).

63. Ren, M. *et al.* Target of rapamycin regulates development and ribosomal RNA

    expression through kinase domain in Arabidopsis. *Plant Physiol* **155**, 1367-82

    http://dx.doi.org/10.1104/pp.110.169045 (2011).

64. Brunkard, J.O. *et al.* TOR dynamically regulates plant cell-cell transport. *Proc Natl*

    Acad Sci U S A **117**, 5049-5058 http://dx.doi.org/10.1073/pnas.1919196117 (2020).

65. Yuan, X., Xu, P., Yu, Y. & Xiong, Y. Glucose-TOR signaling regulates PIN2 stability to

    orchestrate auxin gradient and cell expansion in *Arabidopsis* root. *Proc Natl Acad Sci*

    U S A **117**, 32223-32225 http://dx.doi.org/10.1073/pnas.2015400117 (2020).

66. Xiong, Y. & Sheen, J. Rapamycin and glucose-target of rapamycin (TOR) protein

    signaling in plants. *J Biol Chem* **287**, 2836-42

    http://dx.doi.org/10.1074/jbc.M111.300749 (2012).

67. Ye, R. *et al.* Glucose-driven TOR–FIE–PRC2 signalling controls plant development.

    Nature **609**, 986-993 http://dx.doi.org/10.1038/s41586-022-05171-5 (2022).

68. Zhang, N. *et al.* Metabolite-mediated TOR signaling regulates the circadian clock in

Arabidopsis. *Proc Natl Acad Sci U S A* **116**, 25395-25397

http://dx.doi.org/10.1073/pnas.1913095116 (2019).

69. Zhang, H. *et al.* TOP1alpha fine-tunes TOR-PLT2 to maintain root tip homeostasis in

response to sugars. *Nat Plants* **8**, 792-801

http://dx.doi.org/10.1038/s41477-022-01179-x (2022).

70. Zhang, Z. *et al.* TOR Signaling Promotes Accumulation of BZR1 to Balance Growth

with Carbon Availability in Arabidopsis. *Curr Biol* **26**, 1854-60

http://dx.doi.org/10.1016/j.cub.2016.05.005 (2016).

71. Zhang, W. *et al.* Unveiling the significance of Target of Rapamycin (TOR) signalling in

grafting. *Vegetable Research* **4**, e004 http://dx.doi.org/10.48130/vegres-0024-0003

(2024).

72. Sharma, M., Sharma, M., Jamsheer, K.M. & Laxmi, A. Jasmonic acid coordinates with

light, glucose and auxin signalling in regulating branching angle of Arabidopsis lateral

roots. *Plant Cell Environ* **45**, 1554-1572 http://dx.doi.org/10.1111/pce.14290 (2022).

73. Zhao, Y. & Wang, X.Q. VvMYB1 potentially affects *VvTOR* gene expression by

regulating *VvTOR* promoter and participates in glucose accumulation. *J Plant Physiol*

272, 153668 http://dx.doi.org/10.1016/j.jplph.2022.153668 (2022).

74. Wang, X.Q., Li, L.M., Yang, P.P. & Gong, C.L. The role of hexokinases from grape

berries (Vitis vinifera L.) in regulating the expression of cell wall invertase and sucrose

synthase genes. *Plant Cell Rep* **33**, 337-47

http://dx.doi.org/10.1007/s00299-013-1533-z (2014).

75. Barbier, F.F. *et al.* HEXOKINASE1 signalling promotes shoot branching and interacts with cytokinin and strigolactone pathways. *New Phytol* **231**, 1088-1104 http://dx.doi.org/10.1111/nph.17427 (2021).

76. Tong, C. *et al.* Long-distance transport of sucrose in source leaves promotes sink root growth by the EIN3-SUC2 module. *PLoS Genet* **18**, e1010424 http://dx.doi.org/10.1371/journal.pgen.1010424 (2022).

77. Cho, Y.H., Yoo, S.D. & Sheen, J. Regulatory functions of nuclear hexokinase1 complex in glucose signaling. *Cell* **127**, 579-89 http://dx.doi.org/10.1016/j.cell.2006.09.028 (2006).

78. Sun, M.H. *et al.* The Glucose Sensor MdHXK1 Phosphorylates a Tonoplast Na(+)/H(+) Exchanger to Improve Salt Tolerance. *Plant Physiol* **176**, 2977-2990 http://dx.doi.org/10.1104/pp.17.01472 (2018).

79. Liu, Y. *et al.* HEXOKINASE1 forms a nuclear complex with the PRC2 subunits CURLY LEAF and SWINGER to regulate glucose signaling. *J Integr Plant Biol* **64**, 1168-1180 http://dx.doi.org/10.1111/jipb.13261 (2022).

80. Hanson, J. & Smeekens, S. Sugar perception and signaling--an update. *Curr Opin Plant Biol* **12**, 562-7 http://dx.doi.org/10.1016/j.pbi.2009.07.014 (2009).

81. Zhai, Z. *et al.* Trehalose 6-Phosphate Positively Regulates Fatty Acid Synthesis by Stabilizing WRINKLED1. *Plant Cell* **30**, 2616-2627 http://dx.doi.org/10.1105/tpc.18.00521 (2018).

82. Rodrigues, A. *et al.* ABI1 and PP2CA phosphatases are negative regulators of Snf1-related protein kinase1 signaling in Arabidopsis. *Plant Cell* **25**, 3871-84

40

http://dx.doi.org/10.1105/tpc.113.114066 (2013).

83. Wang, P. *et al.* Reciprocal Regulation of the TOR Kinase and ABA Receptor Balances

Plant Growth and Stress Response. *Mol Cell* **69**, 100-112 e6

http://dx.doi.org/10.1016/j.molcel.2017.12.002 (2018).

84. Liu, X.J. *et al.* An Apple Protein Kinase MdSnRK1.1 Interacts with MdCAIP1 to

Regulate ABA Sensitivity. *Plant Cell Physiol* **58**, 1631-1641

http://dx.doi.org/10.1093/pcp/pcx096 (2017).

85. Wang, H. *et al.* Regulatory functions of cellular energy sensor SnRK1 for nitrate

signalling through NLP7 repression. *Nature Plants* **8**, 1094-1107

http://dx.doi.org/10.1038/s41477-022-01236-5 (2022).

86. Sun, D. *et al.* Kinase SnRK1.1 regulates nitrate channel SLAH3 engaged in

nitrate-dependent alleviation of ammonium toxicity. *Plant Physiol* **186**, 731-749

http://dx.doi.org/10.1093/plphys/kiab057 (2021).

87. Simon, N.M.L. *et al.* The Energy-Signaling Hub SnRK1 Is Important for

Sucrose-Induced Hypocotyl Elongation. *Plant Physiol* **176**, 1299-1310

http://dx.doi.org/10.1104/pp.17.01395 (2018).

88. Simon, N.M.L., Sawkins, E. & Dodd, A.N. Involvement of the SnRK1 subunit KIN10 in

sucrose-induced hypocotyl elongation. *Plant Signal Behav* **13**, e1457913

http://dx.doi.org/10.1080/15592324.2018.1457913 (2018).

89. Jamsheer, K.M. *et al.* FCS-like zinc finger 6 and 10 repress SnRK1 signalling in

Arabidopsis. *Plant J* **94**, 232-245 http://dx.doi.org/10.1111/tpj.13854 (2018).

90. Yang, C., Li, X., Zhou, J. & Gao, C. Autophagy contributes to positive feedback

regulation of SnRK1 signaling in plants. *Autophagy* **19**, 3248-3250

http://dx.doi.org/10.1080/15548627.2023.2247741 (2023).

91. Liu, X.J. *et al.* MdSnRK1.1 interacts with MdJAZ18 to regulate sucrose-induced

anthocyanin and proanthocyanidin accumulation in apple. *J Exp Bot* **68**, 2977-2990

http://dx.doi.org/10.1093/jxb/erx150 (2017).

92. Broucke, E. *et al.* SnRK1 inhibits anthocyanin biosynthesis through both

transcriptional regulation and direct phosphorylation and dissociation of the

MYB/bHLH/TTG1 MBW complex. *The Plant Journal* **115**, 1193-1213

http://dx.doi.org/10.1111/tpj.16312 (2023).

93. Zirngibl, M.-E. *et al.* Triose phosphate export from chloroplasts and cellular sugar

content regulate anthocyanin biosynthesis during high light acclimation. *Plant*

Communications **4**, 100423 http://dx.doi.org/10.1016/j.xplc.2022.100423 (2023).

94. Margalha, L. *et al.* HOS1 promotes plant tolerance to low-energy stress via the SnRK1

protein kinase. *The Plant Journal* **115**, 627-641 http://dx.doi.org/10.1111/tpj.16250

(2023).

95. Zhai, Z., Liu, H. & Shanklin, J. Phosphorylation of WRINKLED1 by KIN10 Results in Its

Proteasomal Degradation, Providing a Link between Energy Homeostasis and Lipid

Biosynthesis. *Plant Cell* **29**, 871-889 http://dx.doi.org/10.1105/tpc.17.00019 (2017).

96. Kim, G.D., Cho, Y.H. & Yoo, S.D. Regulatory Functions of Cellular Energy Sensor

SNF1-Related Kinase1 for Leaf Senescence Delay through ETHYLENE-

INSENSITIVE3 Repression. *Sci Rep* **7**, 3193

http://dx.doi.org/10.1038/s41598-017-03506-1 (2017).

42

97.   Jeong, E.Y., Seo, P.J., Woo, J.C. & Park, C.M. AKIN10 delays flowering by

        inactivating IDD8 transcription factor through protein phosphorylation in Arabidopsis.

        BMC Plant Biol **15**, 110 http://dx.doi.org/10.1186/s12870-015-0503-8 (2015).

98.   Im, J.H. *et al.* Inverse modulation of the energy sensor Snf1-related protein kinase 1

        on hypoxia adaptation and salt stress tolerance in Arabidopsis thaliana. *Plant Cell*

        Environ **37**, 2303-12 http://dx.doi.org/10.1111/pce.12375 (2014).

99.   Muralidhara, P. *et al.* Perturbations in plant energy homeostasis prime lateral root

        initiation via SnRK1-bZIP63-ARF19 signaling. *Proc Natl Acad Sci U S A* **118**,

        e2106961118 http://dx.doi.org/10.1073/pnas.2106961118 (2021).

100.   Meng, D. *et al.* SnRK1 kinase-mediated phosphorylation of transcription factor bZIP39

        regulates sorbitol metabolism in apple. *Plant Physiol* **192**, 2123-2142

        http://dx.doi.org/10.1093/plphys/kiad226/7126682 (2023).

101.   Hu, Y. *et al.* Overexpression of OsSnRK1a through a green tissue-specific promoter

        improves rice yield by accelerating sheath-to-panicle transport of nonstructural

        carbohydrates and increasing leaf photosynthesis. *Plant Physiology and Biochemistry*

        203, 108048 http://dx.doi.org/10.1016/j.plaphy.2023.108048 (2023).

102.   Liu, J. *et al.* Rice ubiquitin-conjugating enzyme OsUbc13 negatively regulates

        immunity against pathogens by enhancing the activity of OsSnRK1a. *Plant*

        Biotechnology Journal **21**, 1590-1610 http://dx.doi.org/10.1111/pbi.14059 (2023).

103.   Stefania Morales-Herrera *et al.* Trehalose- 6- phosphate signaling regulates lateral

        root formation in Arabidopsis thaliana. *Proceedings of the National Academy of*

        Sciences http://dx.doi.org/10.1073/pnas (2023).

43

104.   Marash, I., Leibman-Markus, M., Gupta, R., Avni, A. & Bar, M. TOR inhibition primes

immunity and pathogen resistance in tomato in a salicylic acid-dependent manner.

Mol Plant Pathol **23**, 1035-1047 http://dx.doi.org/10.1111/mpp.13207 (2022).

105.   Ahn, C.S., Lee, D.H. & Pai, H.S. Characterization of Maf1 in Arabidopsis: function

under stress conditions and regulation by the TOR signaling pathway. *Planta* **249**,

527-542 http://dx.doi.org/10.1007/s00425-018-3024-5 (2019).

106.   Liu, Y. & Bassham, D.C. TOR is a negative regulator of autophagy in Arabidopsis

thaliana. *PLoS One* **5**, e11883 http://dx.doi.org/10.1371/journal.pone.0011883 (2010).

107.   Pu, Y., Luo, X. & Bassham, D.C. TOR-Dependent and -Independent Pathways

Regulate Autophagy in Arabidopsis thaliana. *Front Plant Sci* **8**, 1204

http://dx.doi.org/10.3389/fpls.2017.01204 (2017).

108.   Suttangkakul, A., Li, F., Chung, T. & Vierstra, R.D. The ATG1/ATG13 protein kinase

complex is both a regulator and a target of autophagic recycling in Arabidopsis. *Plant

Cell* **23**, 3761-79 http://dx.doi.org/10.1105/tpc.111.090993 (2011).

109.   Song, Y. *et al.* Target of Rapamycin (TOR) Regulates the Expression of lncRNAs in

Response to Abiotic Stresses in Cotton. *Front Genet* **9**, 690

http://dx.doi.org/10.3389/fgene.2018.00690 (2018).

110.   Wang, L. *et al.* The inhibition of protein translation mediated by AtGCN1 is essential

for cold tolerance in Arabidopsis thaliana. *Plant Cell Environ* **40**, 56-68

http://dx.doi.org/10.1111/pce.12826 (2017).

111.   Dong, Y., Teleman, A.A., Jedmowski, C., Wirtz, M. & Hell, R. The Arabidopsis THADA

homologue modulates TOR activity and cold acclimation. *Plant Biol (Stuttg)* **21 Suppl**

1, 77-83 http://dx.doi.org/10.1111/plb.12893 (2019).

112. Sharma, M., Banday, Z.Z., Shukla, B.N. & Laxmi, A. Glucose-Regulated HLP1 Acts as a Key Molecule in Governing Thermomemory. *Plant Physiol* **180**, 1081-1100 http://dx.doi.org/10.1104/pp.18.01371 (2019).

113. Bakshi, A. *et al.* Ectopic expression of Arabidopsis Target of Rapamycin (AtTOR) improves water-use efficiency and yield potential in rice. *Sci Rep* **7**, 42835 http://dx.doi.org/10.1038/srep42835 (2017).

114. Rodriguez, M., Parola, R., Andreola, S., Pereyra, C. & Martinez-Noel, G. TOR and SnRK1 signaling pathways in plant response to abiotic stresses: Do they always act according to the "yin-yang" model? *Plant Sci* **288**, 110220 http://dx.doi.org/10.1016/j.plantsci.2019.110220 (2019).

115. Zhao, Y. & Wang, X.Q. VvTOR interacts with VvSnRK1.1 and regulates sugar metabolism in grape. *Planta* **256**, 56 http://dx.doi.org/10.1007/s00425-022-03969-1 (2022).

116. Jamsheer, K.M. *et al.* A negative feedback loop of TOR signaling balances growth and stress-response trade-offs in plants. *Cell Rep* **39**, 110631 http://dx.doi.org/10.1016/j.celrep.2022.110631 (2022).

117. Saile, J. *et al.* SNF1-RELATED KINASE 1 and TARGET OF RAPAMYCIN control light-responsive splicing events and developmental characteristics in etiolated Arabidopsis seedlings. *The Plant Cell* **35**, 3413-3428 http://dx.doi.org/10.1093/plcell/koad168/7203678 (2023).

118. Henry, C. *et al.* Sugar sensing responses to low and high light in leaves of the C4

model grass Setaria viridis. *J Exp Bot* **71**, 1039-1052

http://dx.doi.org/10.1093/jxb/erz495 (2020).

119.   Liao, H.-S., Chen, Y.-J., Hsieh, W.-Y., Li, Y.-C. & Hsieh, M.-H. Arabidopsis ACT

DOMAIN REPEAT9 represses glucose signaling pathways. *Plant Physiology* **192**,

1532-1547 http://dx.doi.org/10.1093/plphys/kiad127 (2023).

120.   Asim, M. *et al.* Investigation of sugar signaling behaviors involved in sucrose-induced

senescence initiation and progression in N. tabacum. *Plant Physiology and*

Biochemistry **184**, 112-125 http://dx.doi.org/10.1016/j.plaphy.2022.05.024 (2022).