

Review

Novel Aspects of Regulation of Nitrogen Responses in the Tea Plant (*Camellia sinensis* (L.))

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Abstract: Tea brewed from leaves of *Camellia sinensis* (L.) is one of the most popular worldwide non-alcoholic beverages, and nitrogen is an essential nutrient that affects the growth and development of the tea plant. Inorganic nitrogen and organic nitrogen are major forms of nitrogen that are absorbed by the tea plant and also play an important role as a vital signaling molecule, which also affects the nitrogen use efficiency (NUE) of *C. sinensis* in its growth and development period. In addition, improving the NUE of *C. sinensis* is therefore important for the economic and environmental sustainability of the tea plantation industry. In this review, we discuss recently identified tea plant genes that have an essential role in the responses of different nitrogen forms in the short-term period and in the long-term nitrogen effect. We also focus in particular on how nitrogen regulates the growth and development of the tea plant, mainly on the aspects of root system architecture and leaf metabolism that are important parts of root development and leaf quality. Finally, this review concentrates recent research that has expanded the outline of the mechanisms underlying nitrogen responses and regulation in plants, focusing in particular on tea plants.

Keywords: tea plant (*Camellia sinensis* (L.)); nitrogen form; nitrogen regulation; short-term nitrogen effect; long-term nitrogen effect; root development; leaf quality



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1. Introduction

The tea plant is the source of one of the worldwide's most popular beverages, consumed for both its pleasing flavor and its many beneficial health effects. Section *Thea* of genus *Camellia* contains 12 species and 6 varieties 2 of which are widely cultivated for tea production: *Camellia sinensis* (L.) O. Kuntze and *Camellia sinensis* var. *assamica* (Masters) Kitamura [1,2]. All species in section *Thea* are found in China, and almost all have been used by local people for consumption and/or tea brewing in areas where they naturally occur.

The productivity of crop plants—including tea—is strongly influenced by soil availability of nitrogen (N) [3–5], and changes in the supply of this essential macronutrient have profound effects on plant growth and development [6]. Roots of the tea plant can absorb inorganic nitrogen forms (such as nitrate and ammonium) and organic nitrogen forms (such as amino acids and peptides) [7], but supplies of both are typically limited in natural and agricultural ecosystems. As a result, crop yields are sustained only by annual application of thousands of tons of nitrogen fertilizers. Harvest of high-yield crops then removes N from the system, necessitating continued N applications to sustain productivity over time [8]. Furthermore, much of the applied N is not acquired by plants but is instead lost to leaching [9]. Because there have been no substantial improvements in crop N-use efficiency in the past 50 years [10], high levels of N fertilizer application not only exact a heavy economic cost but also lead to numerous environmental problems [1,11] including global warming and water pollution [12,13]. Tea plantations are not immune to these significant environmental consequences and economic costs, and understanding how tea

plants sense, acquire, respond to, and use various N forms is thus critical for sustainable tea cultivation.

Indeed, N is the most limiting factor for both tea plant growth and tea leaf quality. Application of N fertilizer rapidly increases new shoot production as well as leaf content of nitrogenous compounds, such as free amino acids some of which contribute directly to tea flavor and health benefits [14,15]. Some studies have reported that ammonium has a greater effect than nitrate on tea plant growth and tea quality [16]. Nonetheless, tea plant roots obtain the most N from the soil as nitrate, which is at least partially reduced in the roots before transport to the leaves [17], and nitrate concentrations in tea leaves are thus quite low ($<0.06 \text{ g NO}_3^- \text{ kg}^{-1} \text{ DW}$) [18]. Nitrate is also the predominant N form in aerobic soils [11] and functions as a molecular signal that mediates both short- (minutes to hours) and long-term (days) plant responses [6,19]. In addition to nitrate and ammonium, plants can also acquire urea and amino acids, another nitrogen forms from the soil [20], and the latter represent a substantial N pool in some soil types [21–23]. The quality of tea is largely dependent on the contents of polyphenols, theanine, and caffeine in the newest shoots or leaves [24,25], which are in turn related to amino-acid uptake from the soil, especially in organic plantations [25].

This review discusses several recently identified genes that have an essential role in the nitrogen response some of which are involved in short-term and long-term nitrogen effects (e.g., *CsAMTs*, *CsNRTs*, *CsNPFs*, *CsLHTs*, *CsCIPKs*). Finally, we focus on the importance of nitrogen uptake and perception, effects of nitrogen signaling, fine-tuning of transcriptional control, and events that connect nitrogen signals with developmental responses.

2. Short-Term Nitrogen Effects: The Genes Involved in Nitrogen Response Process

The short-term nitrogen effect, also called the primary nitrogen response, describes the rapid regulation of numerous plant genes that occurs immediately after plant nitrogen exposure. In recent years, a number of the molecular components that participate in nitrogen signaling have been identified in model plants, such as *Arabidopsis* [26,27] and rice [28,29]. In *Arabidopsis*, nitrate transporter genes (*AtNRTs*) have been classified on the basis of their expression as nitrate inducible, repressible, or constitutive throughout the whole plant [26,30], and the roles of ammonium transporters (*AtAMTs*) in root ammonium uptake have been characterized [31]. *OsNRT1.1b*, homolog of *AtNRT1.1*, has also been identified in rice, and variations in *OsNRT1.1b* have been shown to affect nitrate absorption and transport [32]. Both *AMT* [33] and *NRT* genes [30] are known to regulate plant nitrogen requirements through their roles in N acquisition, capture, transport, and/or release.

In tea plants, a number of genes whose proteins are required for nitrogen assimilation and transport are upregulated rapidly upon N exposure [34–36] and are thus considered to participate in the primary nitrogen response. Researchers have characterized several of the key regulators that mediate this response using a combination of genetics and systems biology methods.

2.1. Nitrogen Transporters

Tea plants have been reported to utilize ammonium more efficiently than nitrate, resulting in better growth [37], and this finding has subsequently been confirmed by other researchers using ^{15}N labelling of hydroponically grown tea plants [38]. However, young shoots of plants fed with nitrate had a greater total catechin content and higher expression of genes encoding the flavonoid biosynthetic enzymes dihydroflavonol 4-reductase (DFR), chalcone synthase (CHS), and phenylalanine ammonia-lyase (PAL) compared with shoots from ammonium-fed plants [39]. As the main inorganic N forms absorbed by tea plants, ammonium and nitrate also act as signals to induce rapid expression of genes involved in the uptake and assimilation of inorganic N [40,41] and in nitrogen-carbon metabolic pathways [41]. *AMTs* act as sensors of ammonium, whereas *NRTs* act as sensors of nitrate, and perception of either stimulus results in N signal transduction [42].

Homologs of the *NRTs* and *AMTs* have been identified in *C. sinensis*. The Cheng laboratory reported contrasting expression patterns of the ammonium transporter genes *CsAMT1.1* and *CsAMT3.1* in response to N supply: *CsAMT1.1* was upregulated in tea leaves and buds by a short (2–6 h) N exposure, whereas *CsAMT3.1* was upregulated in leaves after a longer N exposure (72 h) [43]. A third ammonium transporter gene, *CsAMT1.2*, was highly expressed in roots and strongly induced by a shorter N (ammonium) exposure period. The latter gene may have an important role in ammonium absorption by tea plant roots [43]. In a separate study, *CsAMT1.4* was highly expressed in pollen [44] and also in flowers, suggesting that it may participate in ammonium transport to floral organs [45]. *CsAMTs* were also expressed in leaves and had light-responsive promoters [45], consistent with a previous study in which *CsAMTs* were suggested to regulate photorespiratory ammonium metabolism and assimilation of C and N [46].

A number of recent studies have also examined *NRT* genes in *C. sinensis*. Expression of the primary nitrate response genes *CsNRT1.1* and *CsNRT1.2* was strongly induced as the tea plants were cultured with NO_3^- starvation for 10 days under the hydroponic system and also showed a complementary expression pattern after nitrate resupply [47]; both of these genes also appear to affect absorption and transportation of nitrogen dioxide in leaves [48]. Zhang et al. examined the expression of *CsNRT2* and *CsNRT3* genes in tea plants and concluded that *CsNRT2.4* was mainly involved in root uptaking nitrate, whereas *CsNRT3.2* appeared to assist *CsNRT2* in nitrate sensing and transport [47]. Zhang et al. also found that overexpression of *CsNRT2.4* increased the rate of root nitrate uptake at a low nitrate concentration. Their results suggested that *CsNRT2.4* is sensitive to nitrate and encodes a high-affinity transporter (HAT) that could regulate nitrate transport in *C. sinensis* [47]. Recent work has further underscored the complexity of *NRT1*-mediated regulation, as *Arabidopsis NRT1.1* has been shown to activate at least four different signaling mechanisms [49].

Nitrate transporter 1/peptide transporter family (NPF) proteins are another type of nitrate and peptide transporter in plants [50,51] and have previously been characterized in *Arabidopsis* [52] and wheat [50]. Recent research revealed that both *CsNPF2.3* and *CsNPF6.1* are localized to the plasma membrane in *C. sinensis*, consistent with their hypothesized function as transmembrane nitrate transporters [53]. Transcription of *CsNPF4.1* and *CsNPF4.8* appeared to be suppressed under high-nitrate conditions [53] (Figure 1).

2.2. Transcription Factors

A number of key transcription factors are known to coordinate plant N responses. Among them are the plant-specific lateral organ boundaries domain (LBD) proteins, a major family of transcription factors that contain a zinc finger-like domain. The LBD proteins have crucial roles in lateral organ and pollen development, plant regeneration, and pathogen and hormone responses [54,55]. A total of 31 *CsLBD* genes were originally identified in the tea genome database [56], and that number has now increased to 54 [57]. Several *CsLBDs* have been functionally characterized. *CsLBD37* and *CsLBD39* were shown to be important nitrate-response regulators [58,59], and expression of *CsLBD37/39* is strongly induced by nitrate [58,59]. *CsLBD37*, a homolog of *Arabidopsis AtLBD37*, belongs to class II [58], the second of two LBD subfamilies [55]. Teng and colleagues revealed that *CsLBD37* overexpression downregulates nitrate transport genes, and it thus appears to function as a negative regulator in nitrate signaling [58]. *CsLBD39* also belongs to LBD class II [59]. Its overexpression in transgenic *Arabidopsis* led to reductions in nitrate content and downregulation of genes involved in nitrate transport and regulation, suggesting that *CsLBD39* may also act as a negative regulator during nitrate signal transduction in *C. sinensis* [59] (Figure 1).

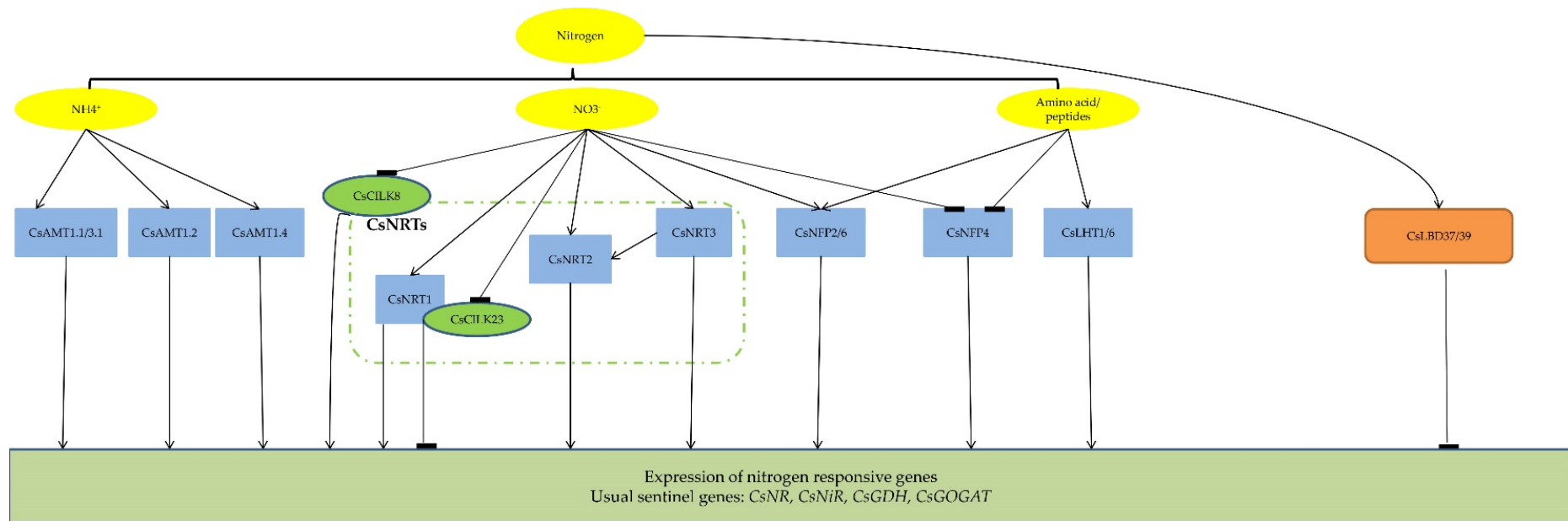


Figure 1. Schematic representation of some genes involved in the nitrogen response under different nitrogen forms (ammonium, nitrate, amino acid and peptides). The yellow box indicates nitrogen or a nitrogen form; the blue box indicates a nitrogen transporter factor; the orange box indicates protein kinases; the green box indicates a transcription factor; the light green dashed box indicates CsNRT genes family (*CsNRTs*). Arrow indicates positive regulation; blunted line indicates negative regulation.

2.3. Genes Related to N Assimilation

Genes encoding the first major enzymes of primary nitrate assimilation, such as nitrate reductase (NR) and nitrite reductase (NiR), are also differentially regulated by different N forms [60]. When tea plants were fed with ^{15}N -labelled ammonium or nitrate, *CsNR* and *CsNiR* in roots showed similar expression patterns during the experimental course [61]. However, root expression of not only *CsNR* and *CsNiR*, but also *CsGDH* and *CsGOGAT* was affected more strongly by ammonium than by nitrate. The results suggested that nitrate assimilation was inefficient in tea roots, helping to explain why more N was absorbed from ammonium than nitrate [61] (Figure 1).

2.4. Protein Kinases

Protein kinases and their interaction partners are also involved in the primary nitrate response. These include the calcineurin B-like (CBL) Ca^{2+} -binding proteins and the CBL-interacting protein kinases (CIPKs), whose interactions play a central part in calcium signal transduction, thereby regulating growth, development, and environmental stress responses in the tea plant [62,63]. In total, 8 *CsCBLs* and 25 *CsCIPKs* have been identified in the tea plant genome [63]. *CsCIPK8* (GENE ID: TEA022816.1), also called *CsCIPK7* [64], is homologous to *AtCIPK8*. *AtCIPK8* controls nitrate-induced expression of *NRTs* under higher (but not lower) nitrate conditions and thus acts as a positive regulator of the primary nitrate response [65]. *CsCIPK23a* (GENE ID: TEA006044.1) and *CsCIPK23c* (GENE ID: TEA006064.1), also called *CsCIPK11* and *CsCIPK12* [64], are both homologous to *AtCIPK23*, whose encoded protein modulates the transport function of *NRT1.1* in response to nitrate supply. *AtCIPK23* phosphorylates *NRT1.1* under low nitrate concentrations, enabling it to function as a nitrate-HAT, but it dephosphorylates *NRT1.1* when nitrate is sufficient, switching it to a low-affinity nitrate transporter [66] (Figure 1).

2.5. Amino Acid Transporters *CsLHT1* and *CsLHT6*

Because the level of amino acid is much lower in soil than in root cells, amino acid uptake requires the presence of specific plasma membrane transporters [67] most of which belong to the amino acid permease (AAP), proton-dependent oligopeptide transporter (ProT), and lysine–histidine-like transporter (LHT) families in the amino acid/auxin permease (AAAP) superfamily [68–72]. In *Arabidopsis*, the LHT family members, *AtLHT1* and *AtLHT6*, are critical for root amino-acid uptake, particularly acidic and neutral types of amino acids, under soil concentrations [69].

Li et al. recently cloned seven *CsLHTs* from *C. sinensis* and grouped them into two clusters based on their phylogenetic relationships with the *Arabidopsis* *LHTs* [35]. Experiments in transgenic yeast demonstrated that *CsLHT1* and *CsLHT6* from cluster I of *C. sinensis* genome functioned as amino-acid transporters [35]; both genes encoded plasma membrane proteins, were in high expression in root part, and were upregulated in response to glutamate feeding, consistent with a function in amino-acid uptake from root soil [35]. The transport activity of *CsLHT1* and *CsLHT6* was higher at low pH but significantly lower at alkaline and/or neutral pH, and their glutamate uptake was nearly abolished by addition of the protonophore CCCP and the H^+ -ATPase inhibitor DES. These results are consistent with the function of *CsLHT1* and *CsLHT6* as amino acid-proton cotransporters [35]. *CsLHT1* was ultimately shown to be a HAT for a wide variety of amino acids ($K_m \sim 40 \mu\text{M}$ for Glu-N), whereas *CsLHT6* was characterized as a low-affinity transporter ($K_m \sim 2.5 \text{ mM}$ for Glu-N) with higher substrate specificity [35]. In field production, tea plantation soils typically have amino acid concentrations less than $30 \mu\text{M}$, and *CsLHT1* may therefore have a greater role than *CsLHT6* in amino acid uptake under such conditions [35] (Figure 1).

3. Long-Term Nitrogen Effects

3.1. Nitrogen and Root System Architecture

Changes in root architecture growth and nutrient content in response to localized nutrient supply have been documented in numerous species, with greater lateral root density and elongation reported in nutrient-rich soil patches [73–77]. However, the extent of root proliferation in response to nutrient heterogeneity differs among species [78]. The highest N application rate produced the highest feeder root N content in clones UPASI-3 and UPASI-17, and the lowest N rate had a negative effect on feeder root N content of UPASI-3, suggesting that root N uptake increased with increasing N application [79]. Nonetheless, there was also evidence for a negative effect of applied nitrogen on tea root morphology and nitrogen uptake [79]. The timing of N usage influenced root growth, and application of ammonium sulfate in the pre-monsoon season had a positive influence on total nutrient content of feeder roots [79]. There was a significant genotype \times N rate interaction effect on root architecture growth, as some genotypes were highly responsive to the N application whereas others were not [79]. These differences may have been related to root cation exchange capacity (CEC): unlike nitrate, ammonium can bind to root cation exchange sites, and roots may therefore have had greater access to of ammonium-N than nitrate-N, particularly in heavily leached tea growing areas (Figure 2A).

Nitrogen efficiency of plants can be divided into two components: uptake efficiency and utilization efficiency [80]. Compared with the primary root, lateral roots have a greater surface area; their growth markedly increases the extent of the root system and enables the plant to absorb many more nutrients from soils [81–83]. Wu's group recently compared root growth and gene expression in two contrasting tea genotypes: Longjing43 (LJ-43, low-N tolerant) and Liyou002 (LY-002, high-N tolerant). They assessed plant growth phenotypes as well as free amino acids and N contents of the soil. Low-N tolerant LJ-43 produced more lateral roots than LY-002, suggesting that an enhanced capacity for lateral root production may support greater N capture in this genotype [84]. The expression of several genes involved in N transport and assimilation (such as *CsNRT2.5* and *CsGS2*) was upregulated in roots of LJ-43 sampled far from the site of fertilization, supporting the higher N transport ability and NUE of this genotype [84]. *CsAsPAT1*, *CsAsPAT3*, *CsAMT1-1*, *CsNR*, *CsGs(CsTS)1*, and *CsPDC2* were upregulated in both LJ-43 and LY-002 in response to fertilization, and this upregulation was greater in LY-002 than in LJ-43. By contrast, *CsNRT1.7*, *CsGAD1*, and *CsGAD2* were downregulated in LJ-43 but upregulated in LY-002, suggesting increased activity of glutamate decarboxylase in LY-002 but reduced activity in LJ-43 [84]. *CsGABA-T*, *CsNRT2.5*, *CsGS2*, and *CsAlaAT* were upregulated in LJ-43 but downregulated in LY-002 [84]. The glutamate decarboxylate *CsGAD1* and *CsGAD2* catalyze a crucial step in γ -aminobutyric acid (GABA) biosynthesis [85–87]. The subsequent conversion of GABA to alanine is catalyzed by γ -aminobutyric acid transaminase (GABA-T) [88], and a *GABA-T* knockdown mutant showed substantial GABA accumulation [89]. Alanine aminotransferase (*AlaAT*) transfers an amino group from alanine to 2-oxoglutarate, producing glutamic acid and pyruvate [90]. Both *CsGABA-T* and *CsAlaAT* were upregulated in LJ-43 whereas repressed in LY-002, suggesting that transformations of GABA to alanine and alanine to glutamic acid were promoted in LJ-43 but suppressed in LY-002. There was greater GABA and alanine accumulation in LY-002 than in LJ-43, whereas glutamic acid and theanine levels were higher in LJ-43 than in LY-002 under low-N conditions. Overall, genotype differences in free amino acid transformations appeared to reflect differential regulation of *CsGAD1*, *CsGAD2*, *CsGABA-T*, and *CsAlaAT* [84] (Figure 2A).

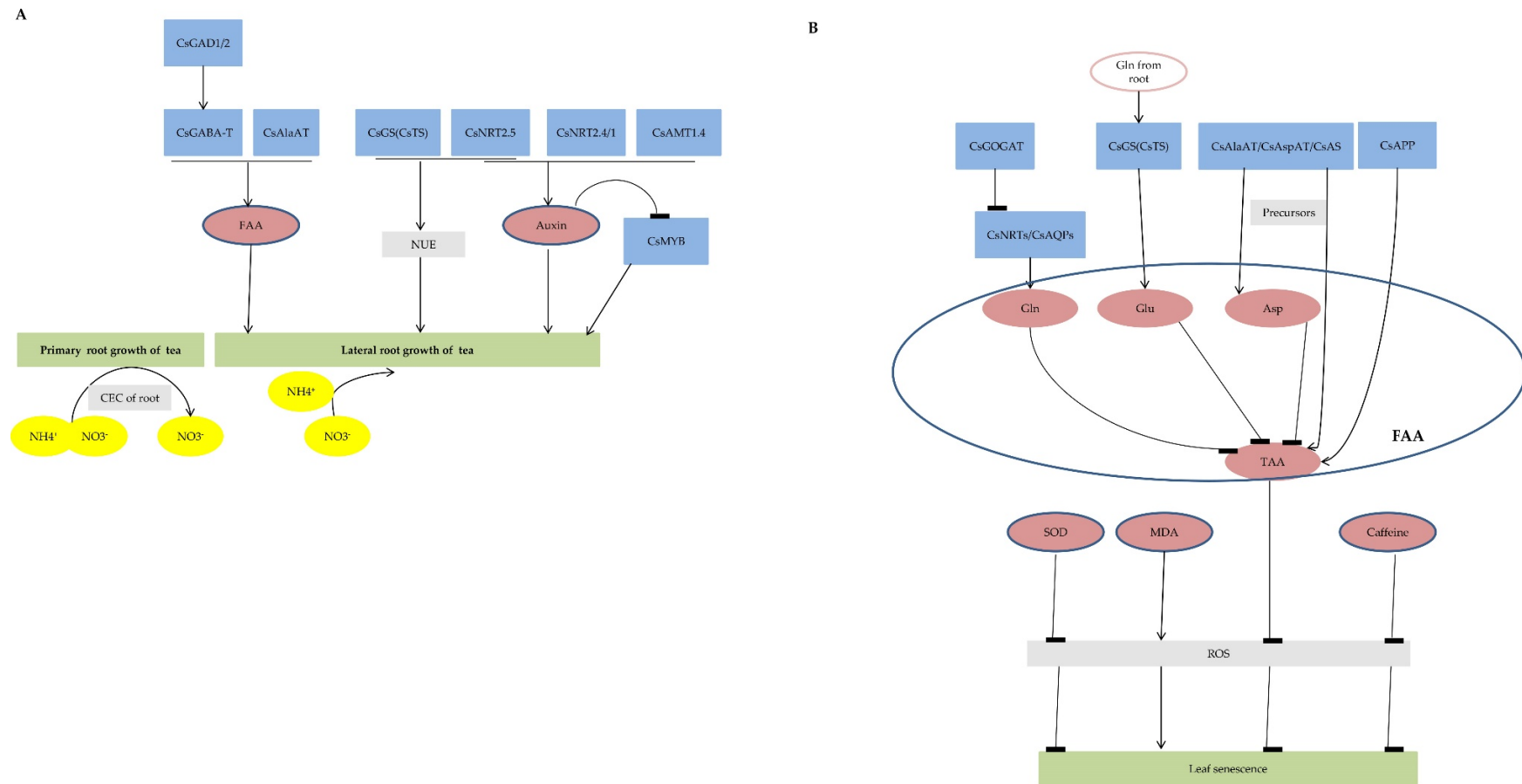


Figure 2. Schematic representation of nitrogen regulation on root system architecture and leaf metabolism. **(A)** The schematic for nitrogen regulation on primary and lateral root growth of tea plant. **(B)** The schematic for nitrogen regulation on leaf metabolism. The yellow box indicates nitrogen or a nitrogen form; the blue box indicates genes involved in the nitrogen response; light red boxes indicate metabolites of tea plant; light gray indicates biological response. Arrows indicate positive regulation. Blunted lines indicate negative regulation. *CsGAD1/2*, glutamic acid decarboxylase 1/2 in *Camellia sinensis*; *CsGABA-T*, γ -aminobutyric acid in *Camellia sinensis*; *CsAlaAT*, alanine aminotransferase in *Camellia sinensis*; *CsGS(CsTS)*, glutamine synthetase (theanine synthetase) in *Camellia sinensis*; *CsNRT2.5*, nitrate transporter 2.5 in *Camellia sinensis*; *CsNRT2.4/1*, nitrate transporter 2.4/1 in *Camellia sinensis*; *CsAMT1.4*, ammonium nitrogen transporter 1.4 in *Camellia sinensis*; *CsMYB*, MYB transcription factors in *Camellia sinensis*; *GsGOGAT*, glutamate synthase in *Camellia sinensis*; *CsAAP*, amino acid permeases in *Camellia sinensis*.

N affects lateral root development via N signaling and regulates biosynthesis and transport of hormones, such as ABA, GA, and IAA. Xinghui Li's lab identified 296 differentially expressed genes (DEGs) in lateral roots of tea plants exposed to different N concentrations and auxin treatments. These genes were enriched in functions related to N metabolism, hormone signaling, and glutathione metabolism and encoded a number of transcription factors [91]. DEGs related to N metabolism included those encoding ammonium transporters (*CsAMTs*), high-affinity nitrate transporters (*CsNRTs*), and NRT1/PTR family proteins (*CsNPFs*). DEGs related to hormone signaling included auxin-related genes, such as *Aux/IAAs*, auxin response factor 2 (*CsARF2*), and *GH3* (IAA-amidosynthetase); cytokinin-related genes encoding cytokinin dehydrogenases, cytokinin hydroxylases, and adenylate isopentenyltransferase; and a number of genes involved in ethylene biosynthesis and metabolism. Differentially expressed transcription factor genes (DEGs) encoded members of MADS-box, NAC, WRKY, and MYB families. DEGs also included glutathione S-transferase genes (*CsGSTs*) and F-box/kelch genes, whose products participate in ubiquitin/26S proteasomal protein degradation [91] (Figure 2A).

CsNRT2.4 and *CsNRT2.5* were upregulated in lateral roots of tea seedlings under low-N conditions; because *NRT1/2* also transport auxin under such conditions, these results suggest that low N levels can increase *CsNRT* expression and thus support auxin production and accumulation, contributing to tea plant lateral root formation [91]. Although previous studies reported that ammonia improved tea root nitrate uptake, a separate study reported that *CsAMT* and *CsNRT* genes had opposite expression patterns under low-N and high-N conditions [92]. Although *AtAMT1.4* is expressed in pollen of *Arabidopsis* [44], *CsAMT1.4* (CSA018499) was expressed in lateral roots of the tea plant [91]. Expression of *CsAMT*, *CsNRT*, and *CsNPF* genes revealed a synergistic effect of auxin and N signaling on lateral root development. Low-N treatment induced auxin biosynthesis and levels of related transcripts and also affected cytokinin metabolism and ethylene biosynthesis, thereby enhancing lateral root formation [91]. Transcription factors from the NAC, MADS-box, MYB and WRKY families also promoted lateral root growth in tea plants through their effects on secondary cell wall biosynthesis [91]. N deficiency and auxin inhibited secondary wall formation by suppressing *CsMYB* expression to facilitate lateral root production. N deficiency and auxin also synergistically modulated the GSH/GSSG ratio through their effects on glutathione metabolism. *CsMADS*, *CsNAC*, and *CsWRKY* gene expression was also influenced by auxin and N treatments, as was the expression of early auxin response genes, such as *GH3* and *Aux/IAAs* [91], indicating that auxin content is increased under low-N conditions in lateral roots of *C. sinensis* [93–96] (Figure 2A).

A recent study examined the effects of N nutrition on flavonoid metabolism in tea plant roots [97]. They reported upregulation of multiple flavonoid biosynthesis genes (e.g., *CsANSs*, *CsANRs*, *CsCHSs*, *CsDFR*, and *CsPALs*), which likely contributed to greater flavonoid content in roots under low-N conditions [97]. Proanthocyanidin (PA) contents in tea plant roots may also be affected by N availability; in contrast to tea leaves, which contain abundant catechins, tea roots typically contain more PAs. PA precursors are synthesized in ER, but the PAs themselves are stored in the vacuole [98], and a number of proteins are involved in these polymerization and subcellular transport processes: ABC transporters, glutathione transferases (GSTs), and UDP glycosyltransferases (UGTs) [99]. A recent study reported that four UGTs were induced at the transcriptional or translational level under low-N conditions three of which were also ubiquitinated. Transcript and protein levels of numerous *CsABCs* and *CsGSTs* also changed significantly, and their proteins showed differential ubiquitination [97] (Figure 2A).

3.2. Nitrogen and Leaf Metabolism

Leaf senescence, which is thought to reflect a balance between generation and scavenging of intracellular reactive oxygen species (ROS) and accumulation of ROS-related cellular damage [100], may also be influenced by N nutrition in tea. For example, a recent study by Xiao et al. indicated that activity of SOD, an important ROS scavenging enzyme [101],

increased in response to N treatment in leaves of ‘Wuniuzao’ tea, although it declined again at the very highest N level [102]. Likewise, the content of MDA, a peroxidation product indicative of ROS damage [101], decreased as N fertilization increased, although it declined slightly at the highest N level [102]. These results were consistent with a previous study in which excess N affected the balance of plant C and N metabolism and inhibited enzyme activity [103]. Nonetheless, the findings of Xiao et al. suggest that moderate N fertilization can increase SOD activity, enhancing ROS scavenging capacity and delaying leaf senescence. They also found that N fertilization increased free amino acid and caffeine content [102], consistent with previous studies that showed similar increases in caffeine [104] and tea polyphenols [105] (Figure 2B).

Characteristic nitrogenous secondary metabolites of tea (e.g., theanine and caffeine) not only contribute important flavors and aromas but also affect leaf metabolism. A 2020 study by Zhang et al. reported that genes related to theanine synthesis, including *CsGOGAT*, *CsGS(TS)*, *CsAlaAT*, *CsAspAT*, *CsAS*, and *CsAAP*, showed coordinated regulation and were more highly expressed in the high-theanine variety ZM [106]. *GOGAT1* and *GOGAT2* are involved in leaf ammonium assimilation [107], and Liu et al. found that *CsGOGAT* expression correlated with theanine content of tea leaves exposed to different temperatures and shading levels [108]. Likewise, Liu’s group also reported positive correlations between *CsGOGAT* activity and theanine content in multiple tissues of the tea plant [109], consistent with the findings of Zhang et al. [106]. *AlaAT*, *AspAT*, and *AS* catalyze the reversible interconversions of multiple amino acids, including *Asp*, *Ala*, *Asn*, *Glu*, and *Gln*, which also serve as precursors for theanine biosynthesis [109]. Cheng et al. reported that glutamine synthetase (*GS*) and theanine synthetase (*TS*) of tea are highly homologous (>97%) with similar enzymatic activities [110]. Negative correlations of *Asp*, *Glu*, and *Gln* contents with theanine-related gene expression were also observed in the ZM variety [106], suggesting that *Asp*, *Glu*, and *Gln* in ZM serve as substrates for synthesis of other nitrogenous compounds, such as theanine. Both *CsGS(CsTS)1* and *CsGS(CsTS)2* showed greater expression in older leaves of ZM, but *CsGS(CsTS)* expression and theanine content were not correlated [106]. Expression of *CsAAPs*, whose protein products transport theanine between plant organs [111], was greater in ZM and was in positive correlation with theanine content, suggesting more active theanine could transport from older leaves to younger leaves in this variety (Figure 2B).

N assimilation into amino acids in the leaves of the different varieties was greater after N fertilizer input, consistent with significantly greater expression of the N uptake genes *AQP*, *AMT*, and *NRT* in leaves. Ammonium taken up by the roots is assimilated into *Gln* by *GS* through the root *Gln-Glu* cycle, then transported to leaves [112], and *GS* expression is induced in response to ammonium [113]. Li revealed a significant correlation between *CsGS* expression and *Glu* content in leaves [34], suggesting that leaf *CsGS* expression may play a crucial part in mediating *Glu* levels in tea leaves. *CsGOGAT* expression was negatively correlated with that of *CsNRT* and *CsAQP* in leaves, suggesting feedback repression of *CsGOGAT* by high ammonium levels which also serves to release ammonium from *Gln* [34]. Greater expression of *CsGS* and *CsAMT* was accompanied by a greater capacity for ammonium uptake and increased N assimilation [34]. After N application, *Glu* content increased in the high-amino-acid HJ variety but decreased in the commonly planted FD variety [34], suggesting a balance between production of *Glu* and its consumption as a substrate in other metabolic processes, including theanine synthesis [113]. Thus, contents of *Glu* and theanine in tea are regulated by both N transporter genes and assimilation-related genes such as *CsGS* and *CsGOGAT* (Figure 2B).

4. Conclusions

There are many studies on the absorption and transfer of nitrogen in tea plants at present, as well as how nitrogen levels and nitrogen forms affect the growth and development of tea plants. However, there are few in-depth studies on how nitrogen regulates the physiological metabolism of tea plants as a whole and how nitrogen affects the genetic

changes of tea plants. In the future, the use of omics technology to explore the effects of nitrogen on the whole tea plant (such as metabolomics, proteomics, epigenomics, long non-coding RNA analysis, etc.) is an important direction for tea plant scientific research. In addition, in-depth study of the effect of nitrogen on the key genes of tea plant by molecular techniques will also be an important part of revealing the mechanism of nitrogen affecting tea plant. Thirdly, the picking of tea trees is mainly based on new shoots, and nitrogen is the most needed nutrient element for tea trees, but the utilization efficiency of tea trees for nitrogen is very low. At present, the utilization efficiency of nitrogen is mainly improved by reasonable cultivation measures combined with fertilization methods in tea garden production. In the future, it will be an important research direction to study the nitrogen absorption and utilization of tea trees to excavate the related genes that improve the nitrogen utilization efficiency of tea trees and screen tea varieties with high nitrogen utilization efficiency.

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