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Review

Plant Iron Homeostasis: Regulatory Networks, Subcellular Trafficking, and Nutrient Crosstalk

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Abstract

Iron (Fe) is an essential plant micronutrient, acting as a cofactor in electron transfer, respiration, photosynthesis, and DNA synthesis. Despite its abundance in soil, Fe bioavailability is frequently limited, particularly in calcareous soils, causing Fe deficiency that restricts crop yield and quality worldwide. Plants have evolved two canonical Fe acquisition strategies: reduction-based Strategy I in non-graminaceous species and chelation-based Strategy II in graminaceous species. This review synthesizes the molecular mechanisms underlying these strategies, including key transporters and enzymes, and critically evaluates the emerging microbial siderophore-mediated iron acquisition. Furthermore, the hierarchical basic helix–loop–helix (bHLH) transcriptional regulatory network, negative regulation by BTS/BTSL E3 ligases, and systemic signaling by IRON MAN peptides are examined through a vertically integrated lens. Subcellular Fe trafficking and crosstalk with other nutrients (Zn, P, Cu, Mn, S, and N) are also discussed. Finally, this review identifies key knowledge gaps and proposes testable research directions to advance the field toward a predictive understanding of plant iron homeostasis.

Keywords: iron homeostasis; Fe acquisition strategies; regulatory networks; subcellular trafficking; nutrient crosstalk

1. Introduction

Iron (Fe) is indispensable to virtually all life, serving as a critical cofactor in numerous enzymes. Despite ranking as the fourth most abundant element in the Earth's crust, its bioavailability in well-oxygenated, alkaline soils is severely restricted, because Fe^{2+} is rapidly oxidized into sparingly soluble Fe^{3+} oxides and hydroxides [1,2]. This striking discrepancy between lithospheric abundance and scarcity at the root–soil interface renders iron deficiency one of the most prevalent micronutrient shortfalls in agriculture, leading to considerable reductions in both crop yield and nutritional quality [3]. In humans, iron deficiency affects over two billion individuals, making it the single most widespread micronutrient deficiency globally; consequently, biofortification of staple crops has emerged as a pivotal strategy to help alleviate this public health burden [4].

In plants, iron functions as an essential cofactor across diverse metabolic processes, from electron transport chains in chloroplasts and mitochondria to nitrogen fixation, phytohormone production, and DNA replication [2]. Notably, approximately 80% of the total iron within photosynthetic cells is sequestered in chloroplasts, where it is indispensable for the biosynthesis of heme, siroheme, and Fe–S clusters, all of which are incorporated into key photosynthetic complexes, including photosystem I (PSI), photosystem II (PSII), the cytochrome b_6f complex, and ferredoxin [5,6]. As a consequence, iron deficiency typically

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presents as interveinal chlorosis in young leaves, a hallmark symptom that directly signals both impaired chlorophyll biosynthesis and diminished photosynthetic performance.

However, excess iron is cytotoxic, as it can catalyze the formation of highly reactive hydroxyl radicals via the Fenton reaction [7]. To counteract this threat, plants have evolved diverse iron acquisition strategies and multilayered regulatory networks that tightly control iron influx and maintain systemic homeostasis. These networks operate at multiple levels, involving transcriptional regulation by bHLH transcription factors (TFs), peptide signals, and ubiquitin-mediated protein degradation. Unraveling these regulatory mechanisms is therefore critical for breeding crops with enhanced iron content or improved tolerance to iron-deficient soils.

Although plant iron nutrition has been extensively reviewed, covering isolated aspects like light-iron signaling [5], general molecular regulation [8–10], agricultural biofortification [11], and specific nutrient crosstalk [12], these topics are usually treated separately. This review aims to highlight the systemic regulatory network of iron homeostasis and its interactions with other nutrients by vertically integrating advances in the following four aspects: (1) expanded iron uptake strategies; (2) structural linkage of BTS/HRZ sensors to bHLH cascades and IMA (IRON MAN) or FEP (Fe Uptake-Inducing Peptide) signaling; (3) subcellular Fe trafficking among chloroplasts, mitochondria, and vacuoles; and (4) mechanistic crosstalk between iron and other nutrients. To ensure methodological transparency, this review was conducted as a structured narrative review. Literature was retrieved from PubMed, Web of Science, and Scopus (2010–present, with emphasis on the last five years) using combinations of terms related to iron uptake, regulation, subcellular trafficking, and nutrient crosstalk. Records were screened by title and abstract for relevance to plant iron homeostasis and its regulatory, trafficking, or crosstalk dimensions; original research articles and focused reviews were prioritized, and studies were selected based on mechanistic insight and experimental rigor rather than by a predefined quantitative protocol. Focusing primarily on *Arabidopsis thaliana* and rice (*Oryza sativa*), with supplementary evidence from other crops, this review bridges these layers to provide a cohesive mechanistic framework linking molecular biology to whole-plant physiology.

2. Plant Iron Acquisition Strategies

To secure iron from the rhizosphere, plants have evolved two canonical strategies [13]. Strategy I, adopted by non-graminaceous plants, reduces Fe^{3+} to Fe^{2+} before uptake, whereas Strategy II, characteristic of grasses, relies on the secretion of phytosiderophores that chelate Fe^{3+} (Figure 1). Both pathways share the same overarching objective, mobilizing sparingly soluble soil iron, and are subject to common regulatory principles. Nevertheless, accumulating evidence indicates that the distinction between these two strategies is less rigid than previously assumed [14–17]. For instance, Strategy I species are capable of secreting coumarin-type phenolics that chelate and transport Fe^{3+}, reminiscent of the function of Strategy II phytosiderophores [14]. In addition, microbial siderophores in the rhizosphere provide an alternative iron source, which plants may exploit through a recently proposed, emerging mechanism involving direct uptake of iron–siderophore complexes [15].

2.1. Strategy I: Reduction-Based Iron Acquisition

Strategy I proceeds via a reduction-centered mechanism that consists of three sequential biochemical steps (Figure 1). The initial step entails proton (H^+) extrusion into the rhizosphere by plasma membrane H^+-ATPases, which reduces apoplastic pH and consequently promotes Fe^{3+} solubility. In *Arabidopsis*, *AHA2* (H^+-ATPase 2) represents the principal isoform induced under iron deficiency, with *AHA1* playing a secondary role [18]. As members of the P-type ATPase family, H^+-ATPases link ATP hydrolysis to proton movement

across the plasma membrane, generating both a pH gradient and a membrane potential that are essential for nutrient acquisition [19]. The promoter of *AHA2* harbors iron deficiency-responsive cis-elements that are recognized by the FIT (FER-like Iron Deficiency-induced Transcription Factor) network, thus directly coupling proton release to the iron signaling cascade [18].

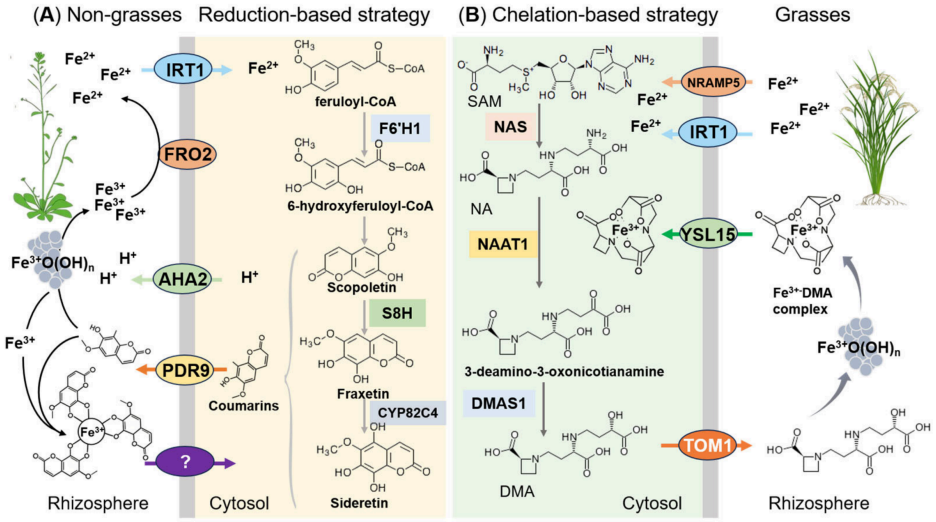


Figure 1. Comparative model of iron (Fe) acquisition strategies in non-grasses and grasses. (**A**) Non-grasses employ a reduction-based strategy. They acidify the rhizosphere via the proton pump AHA2 and secrete coumarins through the PDR9 transporter to mobilize insoluble Fe^{3+}. These coumarins are synthesized via a pathway involving F6′H1, S8H, and CYP82C4. Solubilized Fe^{3+} is then reduced to Fe^{2+} at the root surface by the ferric reductase FRO2, and Fe^{2+} is taken up into the cytosol by IRT1. (**B**) Grasses utilize a chelation-based strategy. They synthesize phytosiderophores, specifically deoxymugineic acid (DMA), in the cytosol through a pathway involving NAS, NAAT1, and DMAS1, and then DMA is secreted to rhizosphere via the TOM1 transporter. In the rhizosphere, DMA chelates Fe^{3+} to form Fe^{3+}-DMA complexes, which are taken up by the OsYSL15 transporter. Additionally, free Fe^{2+} can be directly absorbed by OsNRAMP5 and OsIRT1 in rice.

Upon solubilization, apoplastic Fe^{3+} must be reduced to the bioavailable Fe^{2+} form before root uptake. This essential step is catalyzed by FRO2 (Ferric Reduction Oxidase 2), a plasma membrane-anchored metalloreductase that utilizes FAD and heme groups to transfer electrons from cytosolic NADPH across the membrane [20,21]. *FRO2* is robustly and selectively upregulated in root epidermal cells under iron deficiency, and its activity constitutes the rate-limiting step for Fe acquisition in Strategy I species [21]. The inability of foliar iron application to rescue the severe chlorosis observed in the *fro2* mutant further highlights the importance of this reduction step [22].

The final step of Strategy I uptake relies on Iron-Regulated Transporter 1 (IRT1), a ZIP (ZRT/IRT-like Protein) family plasma membrane transporter responsible for moving Fe^{2+} from the rhizosphere into root epidermal cells [23]. Discovered via yeast mutant complementation, IRT1 is the main Fe^{2+} transporter in *Arabidopsis* [23]. Under iron deficiency, *IRT1* transcription is upregulated, whereas under iron-replete conditions, IRT1 undergoes ubiquitination at cytosolic lysine residues, which directs the transporter to the vacuole for degradation to avert toxic buildup [24,25]. IRT1 exhibits broad substrate selectivity, also transporting Mn^{2+}, Zn^{2+}, Co^{2+}, and Cd^{2+}, which has major implications for heavy metal accumulation during iron scarcity (Table 1) [23,26]. Beyond Fe^{2+} transport, IRT1 has also been implicated in regulating root-to-shoot iron partitioning in *Arabidopsis* [27]. Upon entry, Fe^{2+} is immediately chelated by nicotianamine (NA), a non-proteinogenic amino acid that serves as an intracellular shuttle to prevent redox-active iron from producing

reactive oxygen species (ROS) [28]. Notably, the core components of Strategy I (AHA2, FRO2, and IRT1) do not operate independently; rather, they are functionally coupled at the plasma membrane, and their coordinated action is thought to enhance uptake efficiency by minimizing diffusion losses between sequential steps [29]. However, whether these three proteins form a stable physical complex, and whether its stoichiometry is dynamically regulated, has not been directly demonstrated.

In addition to the primary IRT1-mediated pathway, NRAMP1 (Natural Resistance-Associated Macrophage Protein 1) provides a secondary Fe^{2+} uptake route at the root epidermis (Table 1). Localized to the plasma membrane, NRAMP1 ensures iron acquisition particularly when IRT1 is limiting or saturated. Its distinct kinetic properties and substrate range complement IRT1, providing functional redundancy that allows plants to fine-tune iron uptake across diverse environmental iron levels [30].

Beyond molecular machinery, Strategy I plants remodel their root architecture to maximize iron foraging, notably through enhanced lateral root formation, pronounced root hair elongation, and transfer cell differentiation with wall ingrowths [31]. In *Arabidopsis*, root hair elongation depends on the FIT transcription factor acting with ethylene signaling [32]. Similarly, in pepper (*Capsicum annuum*) and cucumber (*Cucumis sativus*), iron deficiency triggers transfer cells whose expanded membrane surfaces enhance apoplastic iron solubilization and uptake [31]. Furthermore, rhizosphere microorganisms play crucial roles in plant reduction-based Fe uptake. Specifically, the volatile pentadecane produced by *Bacillus velezensis* SQR9 mediates NO signaling and upregulates reduction-based Fe uptake genes in *Arabidopsis*, including *FIT*, *FRO2*, and *IRT1*, thereby enhancing plant Fe acquisition under Fe-limited conditions [33].

Accumulating evidence reveals that Strategy I species also possess a coumarin-mediated pathway that operates alongside, and sometimes independently of, the canonical reduction-based mechanism. At alkaline pH, FRO2 activity is negligible [34], thereby precluding effective Fe^{3+} reduction and constraining Fe uptake. To circumvent this limitation, Fe-mobilizing coumarins are exuded into the rhizosphere via the ABCG transporter PDR9 (Pleiotropic Drug Resistance 9) [35]. These metabolites are synthesized via F6′H1 (Feruloyl-CoA 6-Hydroxylase 1), which produces scopoletin; scopoletin is then hydroxylated by S8H (Scopoletin 8-Hydroxylase) to fraxetin (predominant at alkaline pH) and by CYP82C4 to sideretin (predominant at acidic pH), respectively [35,36]. While scopoletin itself lacks catechol groups and therefore cannot bind Fe [37], fraxetin and sideretin are capable of both reducing Fe^{3+} to Fe^{2+} and forming stable Fe^{3+} complexes. Interestingly, scopoletin can be converted to the iron-mobilizing catechol coumarin esculetin by a root fungal endophyte, *Macrophomina phaseolina* (F80), which then relieves plant iron deficiency by providing soluble Fe^{3+} for FRO2-mediated reduction and IRT1-dependent import [38]. Although the role of catechol coumarins in Fe reduction has been clearly demonstrated in acidic soils, their functions under alkaline conditions remain unclear. In high pH soils, Fe^{2+} uptake is unlikely because reduction by coumarins [39] or FRO2 [34] is negligible. Given that the root uptake of coumarins is widespread across the plant kingdom [40], it is hypothesized that fraxetin forms stable Fe^{3+} complexes that are taken up independently of IRT1 [14,30]. This is supported by the observation that *irt1* mutants retained the capacity to acquire iron when supplied with fraxetin, even in the presence of the Fe^{2+} chelator ferrozine [14]. Indeed, a recent study revealed that NRT1/PTR FAMILY 7.2 (NPF7.2) functions as an import transporter of coumarins (fraxetin and scopoletin) in roots, facilitating the cellular loading of coumarins from apoplastic spaces, which leads to the enhancement of plant Fe acquisition (Table 1) [41]. These findings challenge the classical paradigm and suggest a unified model where Strategy I plants deploy Fe^{3+}-chelating mechanisms similar to Strategy II, blurring the functional boundaries between them.

Table 1. Summary of major iron transporters with genetically defined substrate and direction in plants.

Transporter (Gene)	Species	Subcellular Localization	Substrate	Transport Direction	Primary Function	Evidence
AtIRT1	*Arabidopsis*	Plasma membrane	Fe^{2+}, Mn^{2+}, Zn^{2+}, Co^{2+}, Cd^{2+}	Import	Primary Strategy I Fe uptake	Mutants, yeast complementation
OsIRT1	Rice	Plasma membrane	Fe^{2+}	Import	Strategy I-like Fe uptake (flooded soils)	Mutants, yeast complementation
AtNRAMP1	*Arabidopsis*	Plasma membrane	Mn^{2+}, Fe^{2+}	Import	High-affinity Mn uptake; secondary Fe route	Mutants
AtNRAMP3/4	*Arabidopsis*	Vacuolar membrane	Fe^{2+}, Mn^{2+}	Export	Vacuolar Fe/Mn remobilization during germination	Mutants, electrophysiology
OsNRAMP5	Rice	Plasma membrane	Fe^{2+}, Mn^{2+}, Cd^{2+}	Import	Direct Fe^{2+} uptake in flooded soils	Mutants
OsYSL15	Rice	Plasma membrane	Fe^{3+}–DMA	Import	Primary Strategy II Fe uptake	Mutants, oocytes
OsYSL2	Rice	Plasma membrane (phloem)	Fe^{2+}–NA, Mn^{2+}–NA	Import (phloem loading)	Long-distance Fe/Mn transport to grains	Mutants
AtYSL4/6	*Arabidopsis*	Chloroplast inner envelope (localization debated; also reported at the tonoplast)	Fe^{2+}–NA	Export	Chloroplast Fe efflux under excess	Mutants
HvYS1	Barley	Plasma membrane (root epidermis)	Fe^{3+}–MA	Import	Selective uptake of Fe^{3+}–MA complexes	Oocytes
AtOPT3	*Arabidopsis*	Plasma membrane (phloem companion cells)	Fe, Cu (chelated)	Import (phloem loading)	Phloem loading; systemic Fe signaling to roots	Mutants, grafting
AtVIT1	*Arabidopsis*	Vacuolar membrane	Fe^{2+}, Mn^{2+}	Import	Vacuolar Fe sequestration in seeds	Structure resolved

Table 1. *Cont.*

Transporter (Gene)	Species	Subcellular Localization	Substrate	Transport Direction	Primary Function	Evidence
OsVIT1/2	Rice	Vacuolar membrane	Fe^{2+}, Zn^{2+}	Import	Vacuolar Fe/Zn sequestration in flag leaves	Mutants
AtFPN2	*Arabidopsis*	Vacuolar membrane	Fe^{2+}	Import (into vacuole)	Vacuolar Fe sequestration under excess	Mutants
AtFPN3 (IREG3)	*Arabidopsis*	Mitochondria & Chloroplast	Fe^{2+}, NA	Fe^{2+} (export); NA (import, proposed)	Dual-targeted export of excess Fe	Mutants, dual-targeting
AtPIC1	*Arabidopsis*	Chloroplast inner envelope	Fe^{3+} or Fe^{2+} (debated)	Import	Chloroplast Fe import	Mutants, GFP fusion
AtMIT1/2	*Arabidopsis*	Mitochondrial inner membrane	Fe^{2+}	Import	Mitochondrial Fe uptake; embryogenesis	Mutants, yeast complementation
AtNPF7.2	*Arabidopsis*	Plasma membrane	Coumarins (fraxetin, scopoletin)	Import	Re-import of apoplastic coumarins	Mutants
AtPDR9	*Arabidopsis*	Plasma membrane	Coumarins	Export	Secretion of coumarins into rhizosphere	Mutants

2.2. Strategy II: Chelation-Based Iron Acquisition

In contrast to Strategy I, which reduces ferric iron at the root surface, graminaceous plants utilize a fundamentally different approach based on high-affinity chelation. This Strategy II serves as the primary iron acquisition mechanism for graminaceous monocots, including rice, wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), and maize (*Zea mays*). Instead of reducing Fe^{3+}, these species synthesize and secrete high-affinity Fe^{3+} chelators known as phytosiderophores (PS), belonging to the mugineic acid (MA) family [13]. These Fe^{3+}–PS complexes are subsequently internalized as intact units via dedicated plasma membrane transporters, completing the cycle.

The biosynthesis of 2′-deoxymugineic acid (DMA), the common precursor of mugineic acid family phytosiderophores, involves three well-characterized steps converting S-adenosylmethionine (SAM) to the final Fe^{3+}-chelating product [42]. These steps are catalyzed by Nicotianamine synthase (NAS), Nicotianamine aminotransferase (NAAT), and Deoxymugineic acid synthase (DMAS). Specifically, NAS condenses three molecules of SAM to produce NA, a non-proteinogenic amino acid that binds metals across all plant species [43]. NA is subsequently transformed into 3′-deamino-3′-oxonicotianamine (3′-oxo-NA) by NAAT [44], before DMAS finally converts 3-DMA into DMA [45]. In rice roots, *OsNAS1/2/3*, *OsNAAT1*, and *OsDMAS1* are all induced by Fe deficiency [46–48]. DMA secretion into the rhizosphere is mediated by the Major Facilitator Superfamily (MFS) antiporter TOM1 (Transporter of MA1) [49]. Rice *ostom1* mutants cannot secrete DMA and show severe chlorosis [49]. TOM2, a paralog, also contributes to Fe homeostasis [50]. Root-secreted PSs mobilize Fe^{3+} from soil clay particles and chelate it to form Fe^{3+}–PS complexes. The intact Fe^{3+}–PS complex is absorbed by Yellow Stripe-Like (YSL) transporters (Table 1), named after the maize *yellow stripe1* (*ys1*) mutant [51]. OsYSL15 is required for Fe^{3+}–DMA uptake in rice roots (Table 1) [52]; HvYS1 mediates Fe^{3+}–MA uptake in the barley root epidermis [53], whereas HvYSL2, localized to the root endodermis, transports Fe^{3+}–DMA, Mn^{2+}–DMA and Fe^{2+}–NA [54]; similarly, maize *YSL* genes handle both Fe and Mn transport [55]. Notably, rice also possesses a Strategy I-like system, utilizing OsIRT1 [17,56] and OsNRAMP5 (Natural Resistance-Associated Macrophage Protein 5) [57,58] for Fe^{2+} uptake under flooded conditions, demonstrating adaptive plasticity and challenging the strict dichotomy between strategies.

2.3. Microbial Siderophore-Mediated Iron Acquisition: An Emerging Mechanism

Although the classical view holds that plant-intrinsic Strategies I and II are sufficient to secure iron nutrition in so-called 'Fe-efficient' species, this premise is increasingly questioned by evidence highlighting the important role of rhizosphere microorganisms. Sunflower (*Helianthus annuus*) grown in sterile soil suffers from chlorosis, growth retardation, and reduced Fe content compared to non-sterile controls, and similar growth impairments in rape (*Brassica napus*) and red clover (*Trifolium pratense*) are rapidly rescued by Fe-EDDHA or Fe-EDTA [59,60]. These observations establish that optimal plant Fe nutrition depends on microbial activity, a conclusion further supported by studies showing that inoculation with *Trichoderma asperellum* T34 improves Fe acquisition in wheat, white lupin, and cucumber in calcareous media [61–63].

Accumulating evidence indicates that siderophores—low-molecular-weight (500–1500 Da), high-affinity Fe^{3+}-chelating compounds secreted by soil bacteria and fungi—are key microbial effectors that enhance plant Fe acquisition [64,65]. Under iron limitation, these molecules scavenge sparingly soluble Fe^{3+} from mineral phases with exceptional affinity, forming stable complexes that can be utilized by plant roots. This mechanism has been validated in specific strains: siderophores from *Chryseobacterium* C138 are capable of supplying Fe to iron-starved tomato (*Solanum lycopersicum*) plants via the root system, irrespective of

the presence of the bacteria [66]. Similarly, under iron-deficient conditions, *Pseudomonas* sp. strain SP3 effectively promotes apple rootstock growth and improves plant iron nutrition by secreting siderophores that enhance Fe availability [67]. Moreover, pyoverdine, a siderophore from *Pseudomonas fluorescens*, significantly increases Fe concentrations in *Arabidopsis*; this process does not rely on either reductase activity or the major IRT1 transporter, suggesting that Strategy I does not mediate this incorporation [68].

Plants acquire siderophore-bound iron via two mechanisms. In the indirect pathway, Strategy I plants reduce Fe^{3+} from Fe^{3+}-microbial siderophore complexes via root ferric reductases, and subsequently take up the resulting Fe^{2+} into cells through IRT1. The reduction efficiency depends on the stability constant of the Fe^{3+} bound to the microbial siderophore. For instance, cucumber can effectively reduce Fe^{3+} bound to low-affinity siderophores such as rhodotorulic acid and rhizoferrin (Kf = 10^{19}), but exhibits significantly lower efficacy against high-affinity siderophores like ferrioxamine B (Kf = 10^{31}) [69]. Conversely, Strategy II plants acquire microbial siderophore-bound Fe^{3+} via ligand exchange with phytosiderophores, forming Fe^{3+}-PS complexes that are subsequently internalized through YSL transporters [70]. The efficiency of this ligand exchange may also rely on the relatively low stability constant of the phytosiderophore.

In the direct pathway, plants have been hypothesized to absorb intact ferric-siderophore complexes across the plasma membrane via YS1/YSL transporters, akin to Strategy II but utilizing microbial chelators [71,72]. Under iron-limited conditions, iron nutrition can be substantially enhanced through the exogenous application of bacillibactin–Fe^{3+} complexes derived from *Bacillus* spp.; notably, this treatment coincided with the increased expression of *OsYSL15*, which, along with *OsYSL18*, mediates the translocation of phytosiderophore–Fe^{3+} complexes [71]. Molecular docking analyses suggested that OsYSL15 and OsYSL18 may possess a higher binding affinity for bacillibactin–Fe^{3+} than for phytosiderophore–Fe^{3+} [72]. Thus, rice may take up bacillibactin-Fe^{3+} via YS1/YSL, but direct transport of intact complexes has not been shown in vitro or in planta. Similarly, because *Arabidopsis* absorbs Fe from pyoverdine–Fe^{3+} independently of reductase activity and IRT1 [68], and soybean can take up aerobactin–Fe^{3+} complexes [73], it has been proposed that Strategy I plants may take up siderophore–Fe^{3+} either through unknown specific transporters or via endocytosis [15]. However, the transporter identity and the chemical form absorbed remain unresolved.

Microbial siderophore-mediated iron acquisition in plants encompasses a continuum of mechanisms—ranging from indirect pathways that interface with the classical Strategies I and II, to the direct uptake of intact ferric–siderophore complexes, now conceptualized as an emerging and still insufficiently resolved extension of plant iron acquisition [15]. While the specific plant transporters and regulatory mechanisms remain to be fully defined, this emerging framework broadens our understanding of plant iron nutrition, highlighting the rhizosphere microbiome as a central determinant of host metal homeostasis. Beyond its fundamental implications for plant–microbe co-evolution, this discovery opens new avenues for sustainable agricultural practices that harness siderophore-producing microbes to enhance crop iron nutrition under challenging soil conditions.

3. Transcriptional Regulatory Networks and Systemic Signaling

A tiered architecture of bHLH TFs controls the Fe deficiency response through dimerization, transcriptional activation of downstream targets, and ubiquitin-dependent protein degradation (Figure 2). While this regulatory framework has been comprehensively mapped in *Arabidopsis*, comparable mechanisms are now being uncovered in rice and related grasses [16,17].

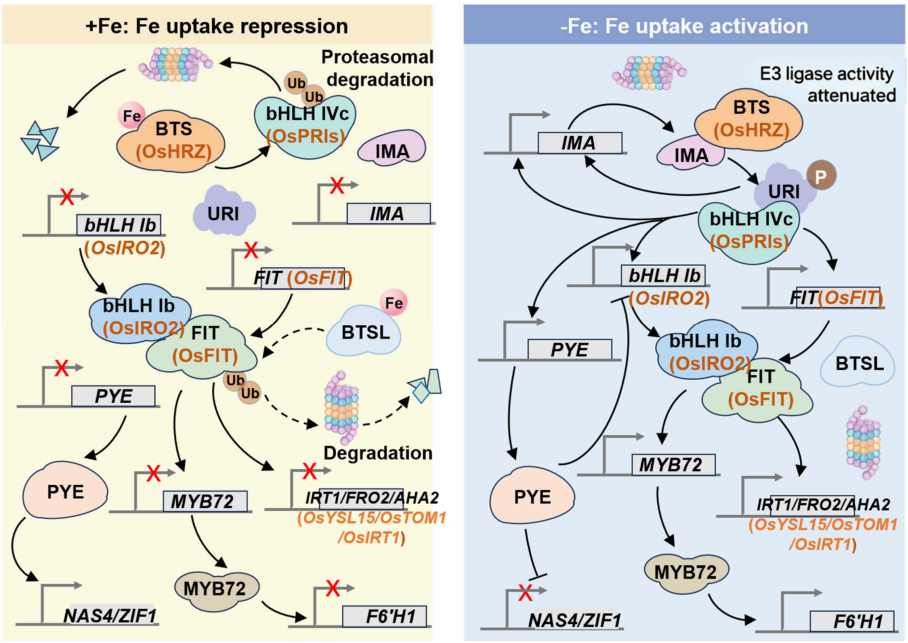


Figure 2. Regulatory network of Fe deficiency responses in *Arabidopsis* and rice. The two species share the overall bHLH cascade architecture, but differ in the upstream ubiquitin-ligase modules and some downstream relationships. In *Arabidopsis*, under Fe sufficiency, active BTS mediates the ubiquitination and degradation of bHLH IVc (bHLH34/104/105/115), and BTSL1/2 target FIT (bHLH29) for degradation. The loss of these factors prevents the activation of downstream bHLH Ib (bHLH38/39/100/101) and PYE, thereby repressing Fe acquisition and transport genes (e.g., *IRT1*, *FRO2*, *AHA2*, and *F6′H1*; red crosses). Conversely, under Fe deficiency, induced IMA peptides bind to BTS/BTSL and inhibit their E3 ligase activity, stabilizing bHLH IVc; the accumulated bHLH IVc then activates bHLH Ib, FIT, and PYE. bHLH IVc (bHLH105/115) and bHLH121 also positively regulate *IMA* expression, forming a positive feedback loop. Finally, the bHLH Ib–FIT heterodimer activates Fe uptake genes and *MYB72* (which further activates *F6′H1*), while PYE negatively regulates transport genes such as *NAS4* and *ZIF1*. In rice, the corresponding negative regulation is mediated by OsHRZ1/2, which ubiquitinate and degrade OsPRI1–4; whether a BTSL-like module targets OsFIT (OsbHLH156) has not been established. OsPRI1–4 activate OsIRO2, and OsIRO2, together with OsFIT, promotes the expression of Strategy II genes (e.g., *OsYSL15* and *OsTOM1*) and *OsIRT1*. Dashed arrows indicate proposed or inferred relationships (e.g., a potential BTSL–OsFIT interaction), whereas solid arrows denote experimentally supported pathways.

3.1. FIT Network: The Master Regulator of Both Strategy I and II

FIT, alternatively designated as bHLH29 or FRU (FER-like regulator of uptake), belongs to subgroup IIIa of the bHLH family and orchestrates the Strategy I iron acquisition program in *Arabidopsis* [74]. Fe scarcity triggers *FIT* expression selectively in root epidermal cells, while its protein accumulation is strictly controlled via 26S proteasome-mediated degradation depending on the plant's iron status [75]. FIT functions as a heterodimer with subgroup Ib bHLH partners (bHLH38, bHLH39, bHLH100, and bHLH101) (Table 2) to assemble a transcriptionally competent complex that recognizes E-box motifs within the *FRO2* and *IRT1* promoters [75–77]. Co-overexpression of *FIT* with subgroup Ib bHLH genes is sufficient for constitutive activation of downstream targets, independent of Fe status [75–77]. Loss-of-function *fit* mutants are unable to upregulate *FRO2* or *IRT1* and suffer lethal chlorosis from Fe deprivation [74]. Similarly, the quadruple mutant (*bhlh4x*) of subgroup Ib bHLH genes phenocopies the Fe deficiency symptoms of *fit* [78]. Furthermore, the bHLH IVa subgroup members (bHLH18, bHLH19, bHLH20, and bHLH25) suppress these heterodimers by promoting jasmonate-dependent, 26S proteasome-mediated degradation of FIT [79].

Table 2. Key regulators (transcription factors, E3 ligases and peptide signals) of plant iron homeostasis.

Regulator	Family/Clade	Species	Upstream Regulators	Interacting Proteins/Targets	Function	Key Evidence
AtBTS and AtBTSL1/2	RING-type E3 ubiquitin ligase; HHE domain	*Arabidopsis*	Fe status (direct Fe binding); IMA/FEP peptides inhibit activity under Fe deficiency	bHLH IVc (bHLH105/ILR3, bHLH115); FIT (BTSL1/2)	Negative Fe sensors/regulators; promote 26S proteasomal degradation	*bts*, *btsl1 btsl2*, *bts btsl1 btsl2* mutants; in vitro ubiquitination; Fe-binding assays; Y2H
AtbHLH34/ 104/105/115	bHLH IVc	*Arabidopsis*	AtBTS (direct targets: bHLH105/115)	*AtbHLH Ib*, *AtPYE*, *AtIMA3*	Upstream positive hub	Mutants, Y2H
AtURI (AtbHLH121)	bHLH IVb	*Arabidopsis*	Fe deficiency (phosphorylation)	*AtFIT*, *AtbHLH Ib*, *AtMYB72*, *AtIMA1/2*	Direct molecular bridge linking IVc factors to FIT activation	Mutants, ChIP-qPCR, Y2H, phosphorylation assays
AtFIT (AtbHLH29)	bHLH IIIa	*Arabidopsis*	AtbHLH IVc, AtURI (AtbHLH121)	*AtIRT1*, *AtFRO2*, *AtMYB72*	Master activator of Strategy I	Mutants, ChIP-qPCR, EMSA
AtbHLH38/ 39/100/101	bHLH Ib	*Arabidopsis*	AtbHLH IVc, AtURI (AtbHLH121)	*AtIRT1*, *AtFRO2*, *AtMYB72*	Obligate heterodimeric partners of FIT for activating Strategy I genes	Mutants (*bhlh4x*), Y2H, ChIP
AtPYE (bHLH47)	bHLH IVb	*Arabidopsis*	AtbHLH IVc	e.g., *AtbHLH Ib*, *AtFRO3*, *AtNAS4*, *AtZIF1*	Negative regulator of Fe distribution	Mutants, ChIP-seq
AtMYB72	R2R3-MYB	*Arabidopsis*	AtFIT-AtbHLH Ib, AtURI (AtbHLH121)	*AtF6′H1* (coumarin pathway)	Key regulator of coumarin synthesis and rhizosphere microbiome assembly	Mutants (*myb72*), ChIP-qPCR
IMA/FEP	Small peptide	*Arabidopsis* (AtIMA1–8); Rice (OsIMA1/2)	Fe deficiency; AtbHLH105/115 (for AtIMA3), AtURI (for AtIMA1/2)	AtBTS/AtBTSL OsHRZ1/2	Mobile phloem signal; inhibits BTS-mediated degradation of bHLH IVc to amplify Fe uptake	Overexpression, mutants, peptide-protein interaction

Table 2. *Cont.*

Regulator	Family/Clade	Species	Upstream Regulators	Interacting Proteins/Targets	Function	Key Evidence
OsHRZ1/2	Hemerythrin RING E3 ligase	Rice	Fe status (direct Fe binding)	OsPRI1/2/3, OsbZIP83, OsGRX6/9	Negative regulators; mediate ubiquitination and degradation of target TFs under Fe sufficiency	Mutants, yeast complementation, in vitro ubiquitination
OsPRI1-4	bHLH IVc	Rice	OsHRZ1/2 (E3 ligases)	*OsIRO2*, *OsIRO3*	Positive regulators of Strategy II	Mutants, Complementation
OsFIT (OsbHLH156)	bHLH IIIa	Rice	OsPRI1-4	OsIRO2 (interaction)	Functional homolog of AtFIT	Mutants, Complementation
OsIRO2	bHLH Ib	Rice	OsPRI1-4, OsbHLH156	e.g., *OsYSL15*, *OsNAS*, *OsTOM1*	Master activator of Strategy II	Mutants, ChIP-qPCR

In addition to the FRO2/IRT1 pathway, coumarin biosynthesis is governed by the FIT–bHLH Ib module [80]. Central to this process is MYB72, which is required for optimal growth under alkaline conditions and serves as a primary determinant of coumarin production [81,82]. MYB72 directly binds the *F6′H1* promoter, leading to a near-total depletion of scopoletin in *myb72* mutants [82]. Conversely, scopoletin accumulation remains intact in *fit* mutants, corroborating the partial dependence of MYB72 on FIT [83]. While *MYB72* transcript levels are elevated upon *FIT/bHLH Ib* dual-overexpression, its inducibility is retained in *fit* mutants, revealing a distinct FIT-independent regulatory pathway. Recent studies have shown that bHLH Ib and MYB72 are directly regulated by the subgroup IVb bHLH transcription factor bHLH121 (also known as URI, Upstream Regulator of IRT1), and that mutation of *bHLH121* significantly reduces the levels of fraxetin and sideretin glycosides [84,85]. Intriguingly, *CYP82C4* is not induced at elevated pH—unlike *MYB72* and *S8H*—indicating its expression is uncoupled from MYB72 regulation. Collectively, the FIT–bHLH Ib module and MYB72 act in concert to fine-tune coumarin synthesis in response to Fe availability and ambient pH.

Interestingly, OsbHLH156 (OsFIT) was concurrently identified as the functional ortholog of FIT in rice [86,87]. OsFIT encodes a subgroup bHLH IIIa protein that forms heterodimers with a subgroup Ib protein, OsIRO2 (OsbHLH56) [86–88]. Mutations in *OsFIT* impair the expression of several key genes involved in phytosiderophore synthesis and transport, such as *OsYSL15/16*, *OsNAAT1*, *OsENA1/2*, *OsNAS1/2/3*, *OsDMAS1*, *OsTOM1*, underscoring its important role in Strategy II [86,87]. Notably, *OsFIT* disruption also downregulates *OsIRT1*, a key Strategy I transporter facilitating Fe^{2+} acquisition under reducing conditions prevalent in waterlogged soils [86,87]. Thus, OsFIT reveals a conserved regulatory layer governing iron homeostasis across angiosperms, reinforcing the parallels between rice and *Arabidopsis*.

The FIT-interacting network has recently expanded. Dof3.6/OBP3 directly associates with *bHLH Ib* promoters to modulate their expression during Fe homeostasis [89]. Additionally, GRF-Interacting Factor 1 (GIF1) directly interacts with FIT; however, this interaction is competitively repressed by SOD7 (suppressor of da1-1), thereby influencing iron uptake and downstream responses [90]. Furthermore, the Cu-Deficiency Induced Transcription Factor 1 (CITF1, also known as bHLH160) physically interacts with FIT during Cu scarcity to induce COPT2 and regulates Fe uptake by modulating FIT activity [91]. CITF1 modulates FIT activity via three distinct mechanisms: (i) disrupting the interaction between BTSL1/2 and FIT; (ii) promoting the cytoplasmic retention of FIT; and (iii) trapping FIT in a FIT-CITF1 dimer to block its transcriptional activation of Fe uptake genes [91].

3.2. POPEYE (PYE): The Negative Regulatory Network

POPEYE (PYE, bHLH47), a subgroup IVb bHLH transcription factor, acts as a central suppressor of iron deficiency responses in *Arabidopsis* [92]. Despite being prominently induced in the pericycle and vascular tissues, the PYE protein localizes to nuclei across all root cell types, linking pericycle signaling to the FIT-dependent network [92,93]. When PYE is absent, plants fail to efficiently mobilize internal Fe and develop chlorosis even when external Fe is abundant [92].

PYE directly represses subgroup Ib bHLH genes (*bHLH38*, *bHLH39*, *bHLH100*, and *bHLH101*), dampening the FIT-dependent activation cascade for root Fe uptake [93]. In *Arabidopsis*, it also downregulates a suite of Fe transport genes (*FRO3*, *NAS4*, *ZIF1*, *FRD3*, *NPF5.9*, *YSL2/3*, and *OPT3*) involved in Fe distribution, mitochondrial homeostasis, vacuolar sequestration, and intercellular transport [92,94]. Additionally, it fine-tunes Fe storage by modulating *FER1*, *FER3*, and *FER4* [92,94]. Although PYE contains an EAR motif, it does

not interact with TPL/TPRs; instead, its nuclear export signal (NES) mediates cytoplasmic retention, and *NES* mutation enhances its repressive function [93].

The repressive activity of PYE is integrated into the larger bHLH cascade. The subgroup bHLH IVc, including bHLH34/IDT1 (Iron Deficiency Tolerant 1), bHLH104, bHLH105/ILR3 (IAA-Leucine Resistant 3), and bHLH115, sit at the top of this hierarchy, where they activate *PYE* expression and promote its nuclear accumulation [93,95]. PYE then forms a repressive complex with bHLH105/ILR3, which not only prevents the over-induction of Fe-related genes but also represses its own transcription via a negative feedback loop [92,93]. Furthermore, PYE can act as a transcriptional activator through its interaction with bHLH105/ILR3, and it coordinates posttranslational stability with transcriptional control by engaging BTS-like E3 ligases [92].

Beyond Fe distribution, PYE and bHLH105/ILR3 are required for photoprotection [96]. Mutations in either gene induce leaf bleaching, with singlet oxygen accumulating as the primary ROS [96]. Under Fe deficiency, *Arabidopsis ilr3-4* and *pye* mutants preserve normal chloroplast ultrastructure and avoid the PSII D1 destabilization seen in wild-type plants, suggesting that PYE and bHLH105/ILR3 promote PSII repair and constrain excitation to prevent ROS accumulation [96].

Recent studies have expanded the PYE network in *Arabidopsis*. The small Fe-deficiency-induced protein OLIVIA (OLV) interacts with PYE and exerts a mild influence on plant growth and Fe deficiency responses involving *NAS4*, although its precise mode of action remains undefined [97]. Additionally, the light-signaling basic leucine zipper (bZIP) transcription factor HY5 (Elongated Hypocotyl 5) physically associates with PYE and directly binds to overlapping regions within the PYE and NAS4 promoters [94]. Furthermore, HY5 directly targets a suite of intercellular Fe transport genes, including *OPT3*, *FRD3*, *NPF5.9*, *YSL2*, *YSL3*, and *NAS4*, thereby establishing a molecular link between light signaling and PYE-dependent regulatory control [94]. Notably, this mechanism is coordinated with blue light, which promotes iron accumulation via cryptochromes (CRY1 and CRY2) and HY5, offering a novel light-mediated pathway for modulating iron homeostasis [98].

Taken together, PYE serves as a regulatory hub by directly repressing the Ib subgroup and its own locus, downregulating Fe distribution and storage genes, and ensuring internal Fe mobilization and photoprotection.

3.3. The IVc bHLH Subgroup: Essential for the Upstream Regulatory Network

The bHLH IVc subgroup occupies the apex of the Fe-deficiency regulatory hierarchy and is widely recognized as a central hub of the upstream network [93,95]. In *Arabidopsis*, four IVc bHLH TFs, including bHLH34, bHLH104, bHLH105/ILR3, and bHLH115, function as the primary activators of the Fe-deficiency response [95,99,100]. These factors form homo- and heterodimers, exhibiting partially redundant, synergistic transcriptional activities [95,99,100]. Their direct targets are well characterized: on the one hand, they induce the subgroup Ib bHLH genes [95,99,100]; on the other hand, they activate PYE, thereby balancing the activating and repressive arms of the cascade [93,95].

A critical function of the subgroup bHLH IVc is its regulation of FIT, the central regulator of root Fe uptake in *Arabidopsis*. While FIT is indirectly activated by bHLH IVc TFs, the missing link was long unresolved until the discovery that bHLH121 acts as the direct bridge [84,85,101,102]. bHLH121 interacts with bHLH IVc TFs and activates FIT and subgroup *bHLH Ib* gene expression to stimulate Fe acquisition [84,85,101,102]. Functioning downstream of bHLH IVc TFs, *bHLH121* expression is induced by Fe deficiency in a bHLH IVc-dependent manner. Genetic analyses reveal that *bhlh121* combined with individual subgroup bHLH IVc mutations exacerbates Fe-deficiency-associated growth defects, indicating synergistic cooperation and the involvement of distinct bHLH121/bHLH

IVc and bHLH IVc/bHLH IVc complexes [84,85,101,102]. Under iron-deficient conditions, bHLH121 accumulates in its phosphorylated form, which enhances its ability to bind the promoter regions of its target genes, predominantly those belonging to subgroup Ib [84]. In addition to bHLH121, bHLH IVc TFs are inhibited by bHLH11, a subgroup IVb transcription factor (similar to bHLH121 and PYE), which represses the expression of subgroup *bHLH Ib* genes by recruiting TOPLESS/TOPLESS-RELATED (TPL/TPRs) corepressors [103].

Interestingly, PYE is not only a target of bHLH IVc but also a direct interacting partner of these TFs in *Arabidopsis*. Specifically, bHLH104 and ILR3 can directly bind to the promoters of subgroup Ib bHLH genes and PYE, thereby functioning in the regulation of Fe deficiency responses [95]. PYE interacts with the bHLH IVc proteins bHLH104, ILR3/bHLH105, and bHLH115 to form a repressive complex that downregulates FERRITIN and genes involved in Fe distribution [104].

In rice, four bHLH IVc members, OsPRI1/OsbHLH060, OsPRI2/OsbHLH058, OsPRI3/OsbHLH059, and OsPRI4/OsbHLH057 (POSITIVE REGULATOR OF IRON HOMEOSTASIS 1, 2, 3, and 4), directly bind and regulate the expression of *OsIRO2* and *OsIRO3*/*OsbHLH063*, thereby playing a positive role in mediating the Fe deficiency response [105–108]. By contrast, bHLH IVb members, such as OsbHLH062, OsIRO3/OsbHLH063, and OsbHLH064, act as negative regulators of OsIRO2 and inhibit the transcriptional activation by OsPRI proteins [109–112]. Specifically, OsIRO3 interacts with OsPRI1 and OsPRI2, thereby antagonizing their transcriptional activation of downstream target genes including *OsIRO2*, thus forming a negative feedback loop that fine-tunes the Fe deficiency response [110,111]. Furthermore, OsbHLH062 directly associates with the *OsIRO2* promoter and represses its transcription by recruiting the OsTPL/OsTPRs corepressor complex [112]. Additionally, OsbHLH064 heterodimerizes with subgroup IVc factors to facilitate nuclear import, and represses *OsIRO2* and *OsIRO3* by competitively sequestering bHLH IVc activators at shared promoters [109].

Post-translationally, bHLH IVc protein abundance is strictly governed by hemerythrin-type E3 ubiquitin ligases, such as BRUTUS (BTS) in *Arabidopsis* and OsHRZ1 (Hemerythrin Motif-Containing Really Interesting New Gene and Zinc-Finger Protein 1) in rice, which target these factors for proteasomal degradation [113,114]. Collectively, the bHLH IVc TFs constitute a central upstream hub of the plant Fe-homeostasis network, orchestrating both activating (bHLH Ib/FIT) and repressive (PYE) signals while being fine-tuned by BTS-mediated degradation and the bHLH121 link.

3.4. BTS and IMA: Fe Sensing in Plants

BTS and its paralogs BTS-LIKE1 (BTSL1) and BTS-LIKE2 (BTSL2), as well as the rice orthologs OsHRZ1 and OsHRZ2 are RING-type E3 ubiquitin ligases that function as negative regulators of Fe deficiency responses [113,114]. These proteins contain putative Fe-binding haemerythrin (HHE) domains, a conserved feature shared with the human Fe sensor FBXL5 [115,116].

Biochemical evidence indicates that BTS/BTSLs and OsHRZs bind Fe in a redox-dependent manner via diiron centers located within their unique triple HHE-like domains [117,118]. However, whether this binding is the in vivo Fe-sensing event remains unresolved. While this Fe binding affects BTS protein stability, precisely how the Fe-binding signal is transmitted to the RING E3 ligase domain to modulate enzymatic activity remains to be fully clarified. Notably, the Fe-binding-induced instability of BTS is not necessarily in conflict with the 26S proteasome-mediated degradation observed for OsHRZ1 and OsHRZ2 [113].

Under Fe-sufficient conditions, BTS and OsHRZ facilitate substrate recognition and subsequent ubiquitination, leading to the 26S proteasome-mediated degradation of key

transcription factors. Specifically, BTS targets bHLH IVc proteins (e.g., bHLH105/ILR3 and bHLH115) to block their heterodimerization with PYE [118,119], whereas BTSL1/2 polyubiquitinate FIT [114] and may also promote bHLH IVc degradation [120]. In rice, OsHRZ1 interacts with and degrades OsPRI1/2/3 [107,108]; this ubiquitination is enhanced by OsIRO3 and OsbHLH062, which stabilize the OsHRZ1–OsPRI3 interaction [112]. OsHRZ1 also targets other Fe homeostasis proteins, such as OsbZIP83 and OsGRX6/9 [121]. Interestingly, this regulation exhibits spatial division: BTS functions in both shoots and roots (localized to the stele to limit xylem loading), whereas BTSL1/2 have been reported to function primarily in roots (localized to the epidermis/cortex to confine radial transport) [114,120]. Accordingly, the *btsl1 btsl2* double mutant accumulates Fe and is more tolerant to Fe deficiency, while the *bts btsl1 btsl2* triple mutant exhibits an enhanced phenotype, indicating functional redundancy [122]. However, clear BTSL homologs have not been reported in graminaceous species to date.

Conversely, under Fe deficiency, the E3 ligase activities of BTS and OsHRZ are suppressed, although the proteins themselves remain stable. This allows bHLH IVc proteins to accumulate and interact with one another, with bHLH121 (URI), or with PYE (Figure 2) [85,96,102]. Notably, bHLH121 (URI) undergoes phosphorylation under Fe deficiency, a modification that facilitates its interaction with bHLH IVc proteins to activate a downstream signaling cascade, ultimately inducing root Fe uptake [84]. The functional relevance of this module has now been demonstrated in crops; in wheat, CRISPR-Cas9-mediated editing of TaHRZ1 enhanced Fe loading in the grains, particularly in the scutellum, and coincided with upregulation of *TaFIT* and *TaIRO3* and downregulation of *IDEF1*, supporting a key regulatory role for TaHRZ1 in Fe-homeostasis signaling [123].

In addition to Fe, the activities of BTS/BTSL and OsHRZ are also controlled by small peptides named IMA or FEP, which act as systemic signals in Fe regulation [124–126]. The *IMA* genes are robustly upregulated by Fe deficiency in various plant species, including rice and *Arabidopsis* [124–126]. Plants overexpressing *IMA* overaccumulate Fe, upregulate Fe-deficiency-responsive genes, and exhibit enhanced tolerance to Fe deficiency, whereas loss-of-function mutations in *IMA* genes cause the opposite phenotypes [119,124–126]. These results imply that IMA functions upstream of Fe-deficiency response signaling.

IMA peptides bind to the BTS ubiquitin ligase and are subsequently ubiquitinated and degraded [119]. However, under Fe deficiency, IMA peptides outcompete subgroup IVc bHLH TFs for BTS/BTSL binding, protecting these factors and sustaining the Fe-deficiency response [119,127,128]. In turn, bHLH105 and bHLH115 directly bind the *IMA3* promoter to induce its transcription [119], while bHLH121 positively regulates *IMA1* and *IMA2* [85]. This mutual regulation forms a positive feedback loop: bHLH105 and bHLH115 induce *IMA3*, while *IMA3* stabilizes these factors by inhibiting BTS. Similarly, OsPRI2 and OsPRI3 positively regulate *OsIMA1*/*OsIMA2* transcription in rice [126]. However, whether OsIMA peptides stabilize the OsPRI2/OsPRI3 proteins remains unknown. In the model legume *Lotus japonicus*, *LjIMA1* and *LjIMA2* orchestrate both systemic and local Fe partitioning toward nodules during symbiotic nitrogen fixation, underscoring the conserved role of IMA peptides in integrating nitrogen–Fe homeostasis [129].

3.5. The Hierarchical Transcription Factor Cascade Model

A dominant model of Fe deficiency regulation proposes a hierarchical cascade in which regulatory signals flow from upstream Fe sensors to downstream transcription factors:

(1) Hemerythrin domain-containing proteins (BTS/OsHRZ) functioning as E3 ligases sense intracellular Fe status. Under Fe-replete conditions, these proteins are active and promote the degradation of downstream transcription factors.

(2) When Fe becomes deficient, BTS/OsHRZ-mediated degradation diminishes, permitting the accumulation of bHLH IVc TFs, which then activate the transcription of subgroup Ib bHLHs and IMA peptides.
(3) Subgroup Ib bHLHs dimerize with FIT to directly activate *FRO2*, *IRT1*, and additional Strategy I genes. IMA peptides generated through this cascade further amplify Fe acquisition by suppressing BTS/BTSL activity, thus creating a positive feedback loop.
(4) The negative regulator PYE is concurrently induced to modulate the response and prevent Fe overaccumulation by repressing subgroup Ib genes and Fe allocation genes.

3.6. Systemic Signaling Coordination

To maintain Fe homeostasis, root Fe uptake must be continuously coordinated with the physiological demand of the shoot. This systemic coordination relies on a strict division of labor between Fe transport and long-distance signaling, integrating local soil sensing with shoot-derived cues.

Iron transport across organs is primarily mediated by specific chelators and transporters. In the xylem, Fe is largely transported as Fe–citrate complexes, whose loading is mediated by the Ferric Reductase Defective 3 (FRD3) transporter in the root vasculature [130]. In the phloem, NA, a low-molecular-weight, nitrogen-containing metal-binding ligand, serves as a key intracellular and intercellular shuttle, chelating Fe to prevent precipitation and facilitate long-distance movement [28,131]. Additionally, OPT3 is a phloem companion cell-localized Fe/Cu transporter that loads Fe (and Cu) into companion cells, facilitating the redistribution of these metals from mature source leaves to sink tissues and developing seeds [132–134].

Distinct from these transport mechanisms, long-distance signaling transmits systemic information about shoot Fe status back to the roots. The IMA/FEP family of small peptides acts as mobile signals. Under Fe deficiency, IMA genes are upregulated in the shoot vasculature, and the resulting peptides are transported through the phloem to the roots, where they bind to BTS/BTSL and inhibit the degradation of bHLH IVc transcription factors, thereby activating root Fe uptake [119,124–126]. Similarly, OPT3 plays a dual signaling role; *opt3* mutants show a constitutive Fe-deficiency response in roots despite adequate shoot Fe, implying that OPT3 or an OPT3-dependent phloem-mobile signal is essential for transmitting shoot Fe status to the roots [132,133]. Importantly, both IMA and OPT3 systemic signaling influence reductive Fe uptake and coumarin secretion in *Arabidopsis* [135,136].

Beyond internal peptide and protein signals, environmental cues perceived by the shoot are integrated into this systemic coordination via light-activated mobile signals. The transcription factor HY5 is a central node in this process. Acting as a light-activated shoot-to-root mobile signal [5,137], HY5 directly represses *BTS* and *PYE* and positively regulates numerous genes involved in iron uptake (*FIT*, *IRT1*, *FRO2*), phloem loading (*OPT3*, *FRD3*, *NPF5.9*, *YSL2*, and *YSL3*), and coumarin biosynthesis (*CYP82C4*, *S8H*, *F6′H1* and *BGLU42*) [94,138]. This ensures efficient iron uptake and long-distance transport. Consequently, loss of HY5 disrupts this systemic signal, causing deregulated iron signaling and altered expression of root acquisition genes [94,98]. Furthermore, HY5 interacts with the negative regulator PYE at the overlapping *PYE* and *NAS4* promoters, integrating light signaling into the core transcriptional network [98]. Thus, HY5 links shoot-perceived light to systemic iron cues, calibrating root uptake capacity. Supporting this, in tomato, phytochrome B-mediated red light induces SlHY5, which travels from shoot to root to activate *FER* expression and promote Fe uptake transcripts [137].

Finally, local sensing interacts with these long-distance signals. Roots directly sense rhizosphere Fe availability via local transcription factors (e.g., FIT) and sensors (e.g., BTS) to mount immediate, cell-autonomous uptake adjustments [24,75]. The integration of

these local cues with systemic signals (such as IMA peptides and OPT3-dependent signals) ensures that root Fe acquisition is precisely scaled to whole-plant demand, preventing both toxic overaccumulation and growth-limiting deficiency.

4. Subcellular Iron Trafficking and Homeostasis

Upon entering the symplast, Fe must be precisely trafficked to chloroplasts and mitochondria, while simultaneously being safely stored in vacuoles to avoid oxidative stress (Figure 3). Recent advances have revealed a complex network of transporters, chaperones, and regulatory pathways that mediate this subcellular iron sorting [6].

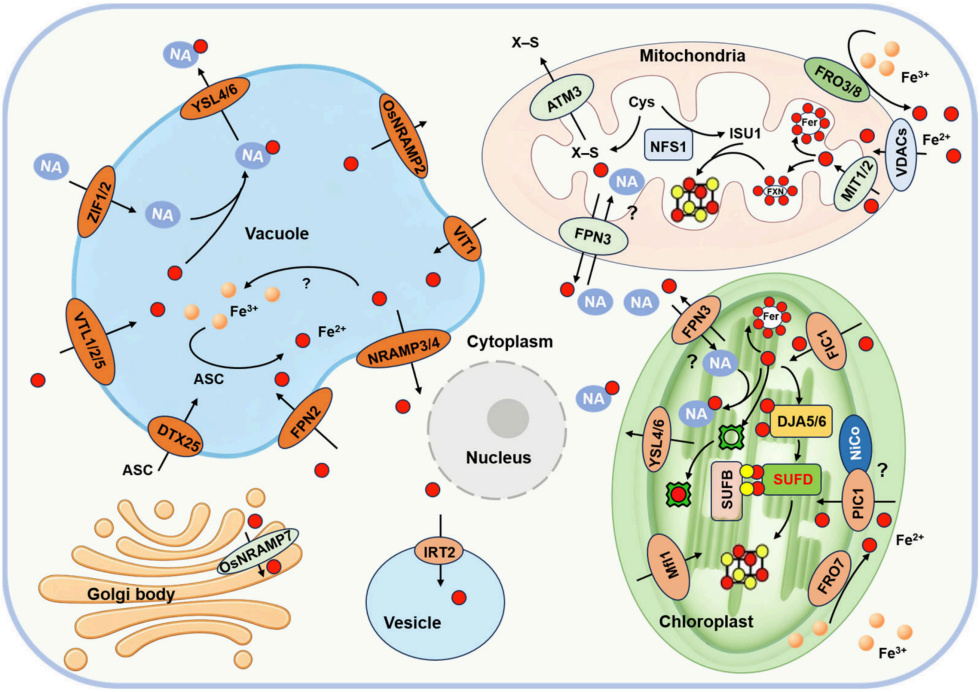


Figure 3. Schematic model of iron transport, trafficking, and homeostasis across plant cell organelles. In the vacuole, VIT1, VTL1/2/5, and FPN2 mediate Fe^{2+} influx, while NRAMP3/4 mediate Fe^{2+} efflux from the vacuole into the cytosol. DTX25 transports ascorbate (ASC) into the vacuole to reduce Fe^{3+} to Fe^{2+}. ZIF1/2 imports nicotianamine (NA), whereas YSL4/6 have been proposed to export Fe^{2+}–NA complexes. The question mark (?) indicates unknown steps. Fe^{3+} is reduced to Fe^{2+} by FRO3/8 at the outer mitochondrial membrane, and Fe^{2+} then enters the mitochondria via VDACs and MIT1/2, while FPN3 mediates Fe^{2+} efflux and has been proposed to import NA, although this activity remains speculative. ATM3 exports sulfur-containing compounds (X-S) for cytosolic Fe–S cluster assembly, whereas NFS1 and ISU1 facilitate mitochondrial Fe–S cluster biogenesis. In the chloroplast, Fe^{3+} is reduced to Fe^{2+} by FRO7, and then imported by PIC1, FIC1, and Mfl1, where Fe^{2+} is incorporated into Fe–S clusters by the SUF machinery. FPN3 mediates the export of Fe^{2+}, and its proposed NA import (as in mitochondria) remains speculative; the export of Fe^{2+}–NA by YSL4/6 is proposed but not yet conclusively established. Moreover, OsNRAMP7 localizes to the Golgi apparatus, and IRT2 localizes to vesicles, contributing to intracellular Fe trafficking and detoxification.

4.1. Chloroplast Iron Transport and Homeostasis

Chloroplasts represent the primary Fe sink in photosynthetic tissues, harboring approximately 80% of total cellular Fe [5]. Iron crosses the chloroplast outer envelope as Fe^{3+}-citrate [139,140] and is subsequently reduced to Fe^{2+} at the inner membrane by FRO7 [141], before being translocated into the stroma via inner membrane transporters. Although specific outer membrane transporters remain unidentified, the mechanism at the inner membrane is well-characterized.

PIC1 (Permease in Chloroplasts 1), also named Chloroplast Import Apparatus 5 (CIA5) or Translocon at The Inner Envelope Membrane of Chloroplasts 21 (TIC21), is an evolutionarily conserved permease-like protein in the chloroplast inner envelope that mediates Fe import (Table 1) [142,143]. *PIC1* overexpression leads to 2.5-fold higher chloroplast Fe levels, whereas *pic1* mutants display a severe dwarf albino phenotype indicative of Fe deficiency, confirming its essential role in chloroplast Fe acquisition [142,144]. RNA interference-mediated knockdown of *NtPIC1* caused albinism, dwarfism, and iron-deficient chloroplasts with distinct ultrastructural abnormalities. In contrast, *NtPIC1* overexpression resulted in dark-green leaves, increased chlorophyll content, denser chloroplast packing, and enhanced accumulation of iron and starch grains within the chloroplasts [145].

The NiCo (Nickel-Cobalt) transporter family has likewise attracted attention. While an earlier model proposed that NiCo proteins form an obligate complex with PIC1 [142,144], detailed expression analyses in rape have revealed markedly divergent expression patterns between *PIC1* and *NiCo* genes across developmental stages and iron nutritional states [146]. This argues against an exclusive, interdependent collaboration and instead suggests that the two families operate in distinct pathways.

The recently identified FIC1 (Fe-Deficiency-Induced Chlorosis 1), also known as DLDG1 (Day-Length-Dependent Delayed-Greening 1), defines a distinct class of chloroplast inner membrane iron importers with distinct regulation [147]. The *fic1* mutant shows chlorosis in newly emerging leaves under iron deficiency, with reduced iron content, lower photosynthetic complex levels, and excessive ROS accumulation [147]. Notably, expressing *PIC1* under the FIC1 promoter rescues the *fic1* phenotype, indicating that both transporters can transport iron across the chloroplast envelope but operate in different physiological contexts, with FIC1 prioritizing iron allocation to young, photosynthetically demanding tissues [147].

Mitoferrin-like 1 (Mfl1), an *Arabidopsis* mitochondrial carrier family protein, localizes to the inner chloroplast envelope and may mediate Fe transport [148]. *Mfl1* transcripts accumulate strongly under Fe excess, moderately under Fe sufficiency, and weakly under Fe deficiency. Both *Mfl1* knockout lines, *mfl1-1* and *mfl1-2*, show reduced vegetative growth. Under Fe excess, these mutants (seedlings and rosette leaves) contain less total Fe than wild type and display reduced expression of the iron-storage ferritin *FER1* [148].

The ATP binding cassette (ABC) transporters may contribute to chloroplast iron uptake [149–151]. In *Arabidopsis*, three ABCI proteins, ABCI10, ABCI11/NAP14 (non-intrinsic ABC transporter protein 14), and ABCI12, localize to chloroplast-intrinsic membranes and play important roles in plastid transition metal homeostasis [149,150]. Disruption of *ABCI10* and *ABCI11/NAP14* causes severe growth defects, over-accumulation of transition metals including iron, and aberrant chloroplast structures [149,150]. ABCI12 acts as a potential interaction partner of ABCI10 in the inner envelope [150]. In rice, OsABCI8 is involved in Fe and Ni uptake by chloroplasts; its loss leads to elevated leaf Fe accumulation, likely activating Fe-deficiency responses due to impaired chloroplastic Fe loading [151].

Ferroportin 3 (FPN3), also known as IREG3 (Iron Regulated 3) or MAR1 (Multiple Antibiotic Resistance 1), is an opportunistic entry point for antibiotics and has been speculated to participate in NA uptake into plastids (Table 1) [152]. FPN3 has also been shown to function as a dual-targeted iron exporter localized to both mitochondria and chloroplasts [153]. Under iron deficiency, *fpn3* mutants grow poorly and accumulate less shoot iron than the wild type, whereas mitochondrial and chloroplastic iron levels are elevated [153]. Notably, iron-deficient *fpn3* mutants exhibit abnormal mitochondrial ultrastructure but normal chloroplast ultrastructure, implying a critical role for FPN3 in mitochondria [153].

Additionally, YSL4 and YSL6 have also been proposed to mediate the efflux of Fe^{2+}–NA complexes from chloroplasts (Table 1) [154], although this activity has not been directly

demonstrated and their localization is debated (see Section 4.3). Knockout of both *YSL4* and *YSL6* severely impairs the plant's ability to tolerate excess iron. In *ysl4 ysl6* double mutants, iron is trapped in chloroplasts, accompanied by ferritin accumulation. Moreover, ubiquitous expression of *YSL4* or *YSL6* markedly reduces tolerance to iron deficiency and lowers chloroplast iron content [154].

Once inside the chloroplast, iron is directly incorporated into hemes, siroheme, and Fe–S clusters, which collectively represent the major metabolic sinks for organellar iron [2,139,155]. The assembly of plastidial Fe–S clusters via the sulfur mobilization (SUF) machinery and the synthesis of hemes/siroheme via the tetrapyrrole pathway exert a strong demand on the chloroplastic Fe pool [156,157]. Consequently, the activity of these biosynthetic pathways directly reflects and modulates the availability of free iron within the organelle.

Although iron is essential for chloroplasts, its overload is detrimental because it generates ROS that cause oxidative damage. Excess or liberated Fe is therefore stored in plastids in the form of ferritin [158,159]. Ferritins are conserved eukaryotic proteins that assemble into a 24-subunit homo-oligomer with a hollow core capable of holding up to 4000 Fe^{3+} ions [160]. *Arabidopsis* has four ferritin genes, *FER1*, *FER3*, and *FER4*, which encode chloroplast-targeted proteins in various vegetative organs, and *FER2*, which encodes a seed plastid-targeted protein [161]. Furthermore, *FER4* can also be localized to mitochondria [162]. Although less abundant in mature leaf chloroplasts than in seeds, ferritins serve as transient iron buffers, sequestering excess iron under high availability and releasing it upon increased demand, thus supplying iron for recycling during developmental senescence [163].

4.2. Mitochondrial Iron Transport and Fe–S Cluster Assembly

Mitochondria are the primary site of Fe–S cluster biosynthesis, a process essential for numerous enzymes involved in respiration and central metabolism. The mitochondrial Fe–S assembly machinery is homologous to the bacterial ISC system and comprises key components such as the cysteine desulfurase NFS1, the scaffold protein ISU1, and frataxin (FXN), which serves as the iron donor [164,165]. This assembly machinery represents a major mitochondrial iron sink, and its activity directly reflects the availability of iron within the organelle.

Iron transport into and out of mitochondria is also critical for Fe–S cluster assembly and overall iron homeostasis. A reduction-based mechanism may mediate mitochondrial iron import and export, as the ferric chelate reductases FRO3 and FRO8 localize to mitochondria in *Arabidopsis* [20]. These two mitochondrial FROs likely have non-overlapping functions: *FRO3* is induced by iron deficiency, whereas *FRO8* is not iron-regulated [166].

Iron is thought to enter mitochondria through the outer membrane via Voltage-Dependent Anion Channels (VDACs) [167] and then reach the matrix via Mitochondrial Carrier Family (MCF) transporters such as Mitochondrial Iron Transporter 1/2 (AtMIT1/2) in *Arabidopsis* and the mitoferrin ortholog OsMIT in rice [168]. OsMIT, the first mitochondrial iron transporter identified in plants, is required for normal rice growth and development [169]. OsMIT localizes to mitochondria and complements the growth of Δ*mrs3*Δ*mrs4* yeast defective in mitochondrial Fe transport. While *mit* knockout mutants are embryo lethal, knockdown of OsMIT reduces mitochondrial iron and aconitase activity, an iron-sulfur enzyme [169]. In *Arabidopsis*, MIT1 and MIT2 localize to mitochondria, and combined loss of *MIT1* and *MIT2* reduces mitochondrial iron and impairs mitochondrial biochemical function (Table 1) [170].

On the efflux side, the dual-targeted mitochondrial/chloroplast iron exporter FPN3 plays a critical role in exporting excess iron from the mitochondrial matrix (Table 1) [153]. The *fpn3* mutant accumulates iron in mitochondria and exhibits abnormal mitochondrial

ultrastructure under iron deficiency, confirming that FPN3-mediated iron export is critical for maintaining mitochondrial iron homeostasis and preventing iron toxicity in this organelle [153].

Additionally, ABC Transporter of the Mitochondrion 3 (ATM3) has been shown to export persulfides, rather than iron, from the mitochondrial matrix to the cytosol; these persulfides are required for cytosolic CIA Fe–S cluster biosynthesis [171,172]. Loss of *OsATM3* function is lethal in rice at the four-leaf stage, with reduced cytosolic Fe–S protein activity, altered iron metabolism gene expression, impaired glutathione metabolism, and elevated ROS, especially superoxide [171]. In *Arabidopsis*, *ATM3* mutations cause cytosolic Fe–S protein deficiency without dramatic iron homeostasis defects or mitochondrial iron accumulation [172]. ATM3 also exports GSSG and molybdenum cofactor in addition to persulfides [172–174].

4.3. Vacuolar Iron Storage and Mobilization

Beyond mitochondria and chloroplasts, vacuoles play a central role in cytosolic Fe homeostasis in plants by mediating Fe sequestration, storage, and remobilization (efflux) through multiple transporters. Among these, the Vacuolar Iron Transporter (VIT) and VIT-Like (VTL) proteins are of particular importance. *VIT1* is highly expressed in developing seeds, where it functions as a H^+-dependent antiporter for Fe^{2+} and mediates Fe^{2+} sequestration into vacuoles within the embryo provascular strands (Table 1) [175,176]. In contrast to wild-type seeds, in which iron is concentrated in cells surrounding the embryo provasculature, iron in *vit1* loss-of-function mutants is found in the subepidermal cell layer [175]. In *Arabidopsis*, the VTL family comprises five additional members (VTL1–VTL5). VTL1, VTL2 or VTL5 participate in vacuolar iron sequestration with partially overlapping functions and distinct expression profiles [177]. Another VIT family member, Membrane Protein of ER Body 3 (MEB3), functions as a vacuolar metal transporter involved in iron distribution in *Arabidopsis*. Iron levels are reduced in *meb3* knockout mutant roots, suggesting that *MEB3* contributes to root iron storage capacity [178]. In rice, OsVIT1 and OsVIT2 localize to the vacuolar membrane and are highly expressed in flag leaves, where they function to transport Fe and Zn into vacuoles across the tonoplast (Table 1) [179]. In wheat, TaVTL5 localizes to the vacuolar membrane and facilitates Fe and Zn accumulation specifically in the vacuoles of the grain endosperm [180].

In addition to the VIT family proteins, FERROPORTIN 2 (FPN2) has also been identified as a vacuolar localized metal transporter in several plant species (Table 1) [181–183]. *FPN2* is expressed in the two outermost cell layers of *Arabidopsis* roots, where it mediates iron influx into the vacuole, particularly under iron-excess conditions [181]. Consistent with this function, *fpn2* mutants exhibit a diminished iron-deficiency response [181].

The remobilization of vacuolar Fe stores during germination and under iron-deficient conditions is redundantly mediated by NRAMP3 and NRAMP4, tonoplast transporters that release Fe from the vacuole into the cytosol (Table 1) [184]. The *nramp3 nramp4* double mutant cannot mobilize Fe stores and fails to germinate properly in the absence of external Fe [184,185]. In rice, the tonoplast-localized transporter OsNRAMP2 fulfills an analogous function; knockdown of *OsNRAMP2* alters Fe distribution in the scutellum and reduces germination rates [186]. In addition, unlike those previously mentioned [154], YSL4 and YSL6 have also been suggested to localize to vacuolar membranes and to mediate the export of metal–NA complexes from vacuoles into the cytosol, including Fe^{2+}–NA [187].

Interestingly, VIT1 and NRAMP3/4 form a functional import/export module for iron storage in endodermal cells, as a *VIT1* mutation causing Fe mislocalization rescues the Fe-deficiency-sensitive phenotype of *nramp3 nramp4* mutants [188]. Thus, coordinated vacuolar import and export allows the vacuole to act as a dynamic iron buffer, rapidly

adjusting its content to cellular demand while protecting the cytosol from iron toxicity and maintaining a reserve for scarcity. Current evidence indicates that iron is transported into and out of vacuoles as Fe^{2+} but stored as Fe^{3+} [189]. DTX25, a vacuolar membrane Multidrug and Toxic Compound Efflux (MATE) protein, mediates this Fe redox regulation by transporting ascorbate into vacuoles. Ascorbate is a potent Fe^{3+}-reducing compound that reduces phytate-bound Fe^{3+} to generate Fe^{2+}, thereby enabling efflux by NRAMP3 and NRAMP4 [189].

Additionally, OsNRAMP7, an Fe transporter localized to the Golgi and trans-Golgi network (TGN), is required for Fe distribution and accumulation in rice grains. Knockdown of *OsNRAMP7* by RNAi increased Fe accumulation in the flag leaf blade but decreased Fe concentration in node I and rice grains, whereas overexpression of *OsNRAMP7* significantly promoted Fe accumulation in grains [190]. The *Arabidopsis* IRT2 protein, which localizes to intracellular vesicles, likely prevents toxicity caused by IRT1-dependent iron fluxes in epidermal cells via compartmentalization [191].

5. Cross-Talk Between Iron and Other Nutrients

Iron homeostasis is intricately interconnected with the metabolism of other essential nutrients (Table 3). This crosstalk operates at four distinct mechanistic levels: (1) soil chemistry, which alters nutrient bioavailability; (2) competition at shared transporters; (3) intracellular partitioning; and (4) convergent regulatory signaling networks.

Table 3. Summary of crosstalk mechanisms between iron and other essential nutrients in plants.

Interacting Nutrient	Crosstalk Level	Plant Species/Context	Key Regulators/Transporters	Effect on Fe Response	References
Zn	Transporter competition	*Arabidopsis*	IRT1	↓ Fe uptake (competitive)	[26,192,193]
Zn	Intracellular partitioning	*Arabidopsis*	ZIF1, NAS4, NA	↓ Intercellular Fe movement	[131,194,195]
P	Soil chemistry	All plants	Fe^{3+} + phosphate precipitation	↓ Bioavailability	[196]
P	Regulatory signaling	*Arabidopsis*	PHR1–FER1; LPR1-STOP1	↓ Fe storage; ↑ Fe deposition	[197,198]
Cu	Regulatory signaling	*Arabidopsis*	CITF1-FIT, IMA/FEP	↑ Fe uptake under Cu deficiency	[78,91,199]
Mn	Transporter competition	*Arabidopsis*	IRT1, NRAMP1	↓ Fe uptake	[24,200,201]
Mn	Intracellular partitioning	*Arabidopsis*	VIT1, NRAMP3/4, MTP8	Alters seed Fe/Mn allocation	[175,202–204]
S	Regulatory signaling	Tomato (Strategy I)	SlST1.1, SlST1.2, SlST2.1, SlST4.1	↑ S uptake; ↓ Fe uptake	[205]
S	Regulatory signaling	Barley (Strategy II)	PS synthesis, HvYS1	↓ PS release; ↓ Fe uptake	[206–208]
N	Soil chemistry/Signaling	Rice vs. Arabidopsis	NLP4, NO_3^-/NH_4^+ forms	Context-dependent (↑ or ↓)	[12,209,210]

Note: ↑ and ↓ indicate an increase and decrease, respectively.

5.1. Iron–Zinc Interactions

IRT1 is the best-characterized polyvalent cation transporter and the first node in iron–zinc crosstalk. It has low substrate selectivity, transporting Fe^{2+} as well as Zn^{2+}, Mn^{2+}, Co^{2+},

and Cd^{2+} [24,26]. This explains iron–zinc competition: excess Zn^{2+} competes with Fe^{2+} for IRT1 binding, inhibiting Fe uptake and causing physiological Fe deficiency [192,193]. Beyond passive transport, IRT1 also acts as a transceptor. Under high Zn^{2+}, IRT1 directly binds Zn^{2+} via a histidine-rich motif in its cytosolic loop, triggering CIPK23-mediated phosphorylation. This phosphorylation recruits the IDF1 E3 ligase, which extends K63-linked polyubiquitin chains on IRT1. K63 polyubiquitination, rather than multi-monoubiquitination alone, is required for the subsequent vacuolar sorting and degradation of IRT1 [24]. This negative feedback reduces plasma membrane IRT1 to prevent toxic metal overload. Evolutionarily, this is an imperfect trade-off: broad specificity allows efficient Fe acquisition under Fe deficiency but risks Zn uptake under Zn excess.

NA chelates various metals, including Fe and Zn, within cells, facilitating their sequestration and translocation and thus acting as a key node of Fe–Zn crosstalk [28,131]. In the form of NA–metal complexes, NA is important not only for iron remobilization [211] but also for zinc tolerance in *Arabidopsis* [131]. Consistent with these functions, T-DNA insertion mutants of *NAS4* (*nas4*) show reduced NA levels in both roots and shoots, accompanied by reduced Fe uptake and root-to-shoot transport, as well as increased sensitivity to excess Zn [81]. Moreover, silencing *AhNAS2* by RNA interference in *A. halleri* decreases root NA content and root-to-shoot Zn translocation [212]. In a transgenic *Arabidopsis* line (K1) overexpressing *TcNAS1* from *Noccaea caerulescens*, NA overaccumulated (100-fold higher than in the wild type), resulting in decreased Fe content and increased Zn content in Fe-sufficient roots [213]. Collectively, these findings indicate that NA is involved in the distribution and balance of Fe and Zn homeostasis in plants.

In addition to NAS, the tonoplast-localized NA transporters ZINC-INDUCED FACILITATOR 1 (ZIF1), ZIFL1/2, and ZIF2 redundantly mediate the vacuolar localization of NA–Zn^{2+} and thereby affect intercellular Fe movement by controlling the vacuolar storage of NA [131,194,195]. Overexpression of *ZIF1* enhances NA transport into root vacuoles, causing enhanced root Zn sequestration, impaired leaf intercellular Fe movement, and constitutive Fe deficiency symptoms that phenocopy NA biosynthesis mutants [131]. Conversely, the *zif1* and *zifl1* mutants are hypersensitive to Fe deficiency and excess Zn [131,195]. ZIF1-mediated sequestration of NA–Zn^{2+} in the root vacuole may depend on the assistance of other vacuole Zn transporters such as metal tolerance protein 1 (MTP1) and MTP3 [214].

Besides NA, citrate is also essential for inter- and intracellular Zn and Fe transport, because both metals are transported to shoots via the xylem predominantly as metal–citrate complexes [215]. Citrate efflux into the xylem is mediated by Ferric Reductase Defective 3 (FRD3), which is responsible for efficient iron translocation to the leaves and acts as an important control point in Fe–Zn crosstalk in *Arabidopsis* [130,215,216]. In the Zn-sensitive accession Shahdara, expression of *FRD3* is drastically reduced, which is associated with reduced Fe and Zn in root exudates and decreased root-to-shoot translocation of Fe and Zn when Zn is in excess [215]. Consistent with this, *frd3* mutants show impaired root-to-shoot Fe transport, overexpress the Fe uptake machinery, and accumulate high levels of Zn and Fe in tissues [130,217].

Another key node of Fe–Zn crosstalk is FIT [192,214]. Acting as a heterodimer with bHLH Ib proteins, FIT upregulates genes involved in Fe uptake (e.g., *FRO2*, *IRT1*) and translocation (e.g., *IRT2*), vacuolar Zn transport (e.g., *MTPA2*, *IREG2*), as well as NA synthesis (e.g., *NAS1*, *NAS2*) [80,218]. As mentioned above, these FIT-regulated genes extensively participate in the uptake, transport, and subcellular sequestration of metals including Fe and Zn, suggesting an essential role of FIT in Fe–Zn crosstalk. Notably, FIT activity is regulated by other regulators such as FIT-binding protein (FBP), BTS, and BTSLs. FBP, an antagonistic partner expressed in the root stele, binds to the bHLH domain of FIT, abolishing its DNA-binding capacity. Knockout of *FBP* results in enhanced expression of

NAS genes and increased NA content, accompanied by higher Zn accumulation in roots and increased Fe translocation to shoots [214].

Additionally, BTS(L) and HRZ also act as important regulators of Fe–Zn crosstalk. The *btsl1 btsl2* mutation increased the expression of FIT-regulated genes involved in Fe uptake (*IRT1*, *FRO2*, *NAS*) and Zn storage (*MTP3*, *ZIF1*), while Zn accumulation remained unchanged and excess Fe accumulation in roots was suppressed under high-Zn conditions [193]. Similarly, the *bts-1* mutant exhibited higher expression of key Fe nutrition-related genes, including *FIT*, *bHLH38*, *bHLH39*, *bHLH100*, *IRT1*, *FRO2*, *FRD3*, and *MYB10*, than the wild type, along with higher Zn and Fe concentrations in roots and shoots and a higher Fe/Zn ratio in shoots under Zn stress [219]. In rice, the stability and function of OsHRZs are affected by Fe nutritional conditions via the binding of Zn or Fe to multiple domains within the OsHRZ proteins [220].

5.2. Iron–Phosphorus Interactions

Iron and phosphorus interact via multiple interconnected mechanisms. In soil, Fe^{3+} and phosphate form insoluble ferric phosphate precipitates, mutually limiting their bioavailability [196]. In plants, P and Fe act antagonistically in multiple processes: (1) P deficiency increases Fe accumulation, while Fe deficiency promotes P uptake [221]; (2) P deficiency reduces primary root (PR) elongation and increases root hair density, a response that is alleviated by reducing Fe availability [222,223]; (3) P deficiency negatively modulates metabolites induced by Fe deficiency, such as amino acids, organic acids, and coumarins, a process controlled by both Fe- and P-deficiency response regulators [83,224]; and (4) P deficiency upregulated Fe-excess-responsive genes and downregulated Fe-deficiency-responsive genes [225].

Low-P-induced inhibition of PR growth is primarily attributed to Fe deposition and toxicity [223], with several genes involved, including *LPR1* (Low Phosphate Root 1), *PDR2* (Phosphate Deficiency Response 2), *ALMT1* (Aluminum-Activated Malate Transporter 1), and *STOP1* (Sensitive To Proton Rhizotoxicity 1). Among these factors, the *STOP1–ALMT1* module functions in a signaling pathway that inhibits cell elongation under low-P availability [198]. *ALMT1*, which encodes a plasma membrane transporter that exudes malate, mediates Fe deposition in the apoplast of the elongation zone in a malate-dependent manner, whereas the C2H2 zinc finger transcription factor STOP1 regulates *ALMT1* expression [198,226,227]. The STOP1–ALMT1 pathway is inhibited by the tonoplast-localized Aluminum Sensitive 3 (ALS3)/Sensitive To Aluminum Rhizotoxicity 1 (STAR1) transporter complex, which transports an unknown substrate and suppresses *ALMT1* transcription by repressing the nuclear accumulation of STOP1 [227,228]. In addition, SIZ1, a SUMO E3 ligase, SUMOylates STOP1, thereby altering *ALMT1* expression and the accumulation of Fe and ROS in roots under P deficiency [229,230]. Furthermore, the transcription factor WRKY33 negatively regulates Fe^{3+} accumulation in root tips and inhibits root growth by controlling *ALMT1* transcription under P deficiency [231].

LPR1 is a ferroxidase that catalyzes the oxidation of Fe^{2+} to Fe^{3+} in the extracellular space, a process critical for Fe transport and homeostasis in plants [232], whereas *PDR2* encodes an ER-localized P5-type ATPase and restrains secretion of LPR or its associated ferroxidase activity [233,234]. The LPR1–PDR2 module facilitates cell-specific apoplastic Fe and callose deposition in the meristem and elongation zone of primary roots under Pi limitation [234]. Upon P deficiency, LPR1 promotes the aggregation of apoplastic Fe in the meristematic and elongation zones of the PR, resulting in ROS formation and callose deposition, which promotes cell wall stiffening in the elongation zone [234]. In addition, *LPR1* transcription is also activated by HY5 in P deficient *Arabidopsis* roots, resulting in the accumulation of apo-Fe [235]. Moreover, the chromatin remodeler BRAHMA (BRM), a Switch defective/sucrose non-fermentable (SWI/SNF) ATPase, recruits Histone Deacetylase

6 (HDA6) to interact with Histone Deacetylase Complex 1 (HDC1), facilitating histone H3 deacetylation at the LPR1 locus and thereby negatively regulating local Pi deficiency responses [236]. Similarly, in wheat, the plasma membrane-localized ferroxidase TaMCO3 (Multicopper3) generates Fe^{3+} to mobilize Fe to shoots [237].

In addition to the regulators described above, two CYBDOM proteins, Cytosolic Root Reduction (CRR) and Hypersensitive to Low P 1 (HYP1), catalyze the reduction of Fe^{3+} to Fe^{2+} in an ascorbate-dependent manner and control apoplastic Fe deposition in the root meristem under low-P conditions [238,239]. In contrast, Phosphate-Deficiency Sensitive 1 (PDE1), which encodes a hydroxyphenylpyruvate reductase, is repressed by P deficiency, concurrently enhancing Fe and ROS accumulation in primary roots [240].

PHR1 (Phosphate Starvation Response 1) in *Arabidopsis* and PHR2 in rice function as well-established master regulators of Pi homeostasis and positively regulate Pi deficiency-induced root hair elongation [197,241,242]. PHR1 and PHL1 (PHR1-LIKE 1) bind to the P1BS cis-regulatory element in the *FER1* promoter independently of Fe availability, thereby mediating Pi-starvation-induced *FER1* expression and controlling Fe storage in *Arabidopsis* [197]. In *phr1 phl1* double mutants, the response of *FER1* to phosphate starvation was completely lost, and Fe distribution around the vessels was abnormal [197]. Furthermore, PHR1 binds to the promoter of *RSL2* (Root Hair Defective 6-Like 2) to activate its expression; RSL2 in turn targets cell wall remodeling genes such as *XTH26* (Xyloglucan Endotransglucosylase/Hydrolase 26), thereby regulating root hair elongation [241]. In rice, PHR2 and HRZ proteins form a reciprocal inhibitory module that coordinates Pi and Fe signaling and homeostasis. Fe deficiency can attenuate Pi starvation signaling by inducing *HRZ* expression, which in turn triggers ubiquitination and degradation of PHR2. Conversely, PHRs negatively regulate *HRZ* expression to modulate iron deficiency responses [243].

5.3. Iron–Copper Crosstalk

Iron and copper share similar redox chemistry and partially overlapping uptake and transport machinery, resulting in extensive crosstalk between their homeostatic networks. A hallmark of this crosstalk is enhanced Cu uptake under Fe deficiency and enhanced Fe uptake under Cu deficiency [91,132,244]. Consistent with the increased Cu uptake, the expression of Cu-deficiency-regulated genes is upregulated under Fe deficiency [78,245,246]. Conversely, Fe overaccumulation can also decrease Cu uptake in *Arabidopsis* [247].

At the systemic level, shoot-to-root signaling of Cu–Fe crosstalk is mediated by OPT3 and IMA/FEP [132,199,248]. OPT3 loads Cu and Fe into phloem companion cells, facilitating their long-distance transport and thereby influencing root responses to Cu and Fe deficiencies [132–134]. The *opt3* mutant has lower concentrations of both Cu and Fe in the phloem, and feeding either Cu or Fe via the phloem regulates the expression of both Cu- and Fe-deficiency-responsive genes in roots of Fe- or Cu-deficient plants. This suggests that Fe and Cu in the phloem can, in part, substitute for each other's signaling functions in regulating the expression of Cu and Fe uptake genes in roots, thereby fine-tuning the uptake of these minerals in response to plant needs [132].

IMAs can bind both Fe and Cu ions, mediating their homeostasis in *Arabidopsis* [119,124,199]. Transcriptional regulation of Cu uptake relies on two transcription factors, CITF1 and Squamosa Promoter Binding Protein-Like 7 (SPL7), a homolog of the algal Cu sensor Copper Response Regulator 1 (CRR1). *CITF1* is upregulated by Cu deficiency but downregulated by Fe deficiency in *Arabidopsis* roots [246]. SPL7 partially controls *CITF1* expression; together, they regulate Cu-deficiency-responsive genes and Cu uptake into roots and delivery to flowers [199,246,249]. In contrast to their role in Fe deficiency, IMAs act as negative regulators of Cu homeostasis. Under Cu sufficiency, IMAs interact with CITF1, reducing its DNA binding and repressing its transcriptional activation activity, thereby

downregulating Cu uptake genes [199]. Conversely, when Cu is limited, *IMA* genes are downregulated by SPL7, allowing CITF1 to induce Cu uptake genes [199]. Consistently, *Arabidopsis* mutants lacking all IMA peptides (*ima8x*) exhibit increased tolerance to Cu deficiency due to increased expression of *COPT2*, *FRO4*, and *FRO5*, whereas overexpression of *IMA1* or *IMA3* reduces Cu uptake gene expression and limits root growth under Cu-deficient conditions [199].

Locally, FIT plays a crucial role in modulating iron–copper crosstalk in *Arabidopsis* [78,91]. The FIT–bHLH Ib heterodimer directly binds to the promoters of *COPT2*, *FRO4*, and *FRO5* and upregulates their expression under Fe deficiency [78]. Fe-deficiency-induced expression of *COPT2*, *FRO4*, and *FRO5*, independent of SPL7, is suppressed in *fit-2* and *bhlh4x* mutants and activated by co-overexpression of *bHLH38* (or *bHLH39*) and *FIT* [78]. FIT also interacts with CITF1, which acts as a Cu-deficiency-induced transcription factor to activate Cu uptake genes (e.g., *COPT2*) and, concurrently, modulates FIT activity by promoting its cytoplasmic retention and preventing its interaction with bHLH Ib partners. This negative regulation of FIT by CITF1 limits Fe acquisition under Cu deficiency. Conversely, under Fe deficiency, reduced *CITF1* expression alleviates this constraint, allowing FIT to interact with subgroup Ib bHLHs to promote Fe acquisition genes [91]. In rice, Fe deficiency led to significant increases in shoot Cu concentrations, but these increases were significantly suppressed in *osbhlh156* and *osiro2* mutants, suggesting that the OsFIT/OsbHLH156–OsIRO2 complex plays a role in Cu uptake and transport [250].

5.4. Iron–Manganese Crosstalk

An antagonistic relationship exists between Fe and Mn. In soils with high extractable iron, Fe can interfere with root Mn uptake, and vice versa [1]. Mn^{3+} is reduced by Fe^{2+}, and Fe^{2+} is oxidized to Fe^{3+}, resulting in Fe deficiency and chlorosis in plant leaves. Meanwhile, high Mn inhibits the uptake of Fe and Mg from soil into plants [251]. In plants, the most fundamental basis of Fe–Mn crosstalk lies in the sharing of uptake transporters such as IRT1 and NRAMP1. As mentioned above, IRT1 is primarily responsible for Fe uptake, but it also transports Mn and Zn [23,26,252]. When present in excess, Mn binds to histidine-rich domains in the cytosolic portion of IRT1, triggering its K63-linked polyubiquitination and subsequent degradation, as detailed above [24]. This post-translational regulation represents a critical checkpoint that prevents excessive Mn accumulation via IRT1.

NRAMP1 is required for high-affinity Mn uptake into *Arabidopsis* root cells and can also transport Fe with low affinity [201], preferentially taking up whichever substrate is more abundant [200]. NRAMP1 cooperates with IRT1 to take up Fe and Mn in roots under replete conditions [200]. The dynamic cycling of NRAMP1 in response to Mn availability involves phosphorylation-mediated endocytosis from the plasma membrane, which tightly controls the level of NRAMP1 on the root cell surface [253]. The overlapping substrate specificity of IRT1 and NRAMP1 means that Fe and Mn inevitably compete during root uptake: when soil Mn concentration increases, Mn^{2+} competitively occupies the transport sites of IRT1 and NRAMP1, inhibiting Fe uptake; conversely, under Fe-deficient conditions, upregulation of *IRT1* and *NRAMP1* increases inadvertent Mn uptake, potentially leading to excessive Mn accumulation [251].

Following uptake by roots, Fe and Mn are trafficked within cells or translocated to shoots. In *Arabidopsis*, both NRAMP3 and NRAMP4 localize to the vacuolar membrane and play redundant roles in Fe–Mn crosstalk by mediating the remobilization of these metals for proper plant growth during seed germination and the early seedling stage under Fe- or Mn-deficient conditions [184,254]. Mn accumulation is increased in *nramp3* knockout mutants but reduced in *35S::AtNRAMP3 Arabidopsis* lines under Fe deficiency [184]. Under Mn deficiency, the export of Mn from mesophyll vacuoles is reduced, while FER1

accumulation and Fe concentration increase in leaves of *nramp3 nramp4* plants [254]. The vacuolar membrane transporter VIT1 is required not only for iron localization in *Arabidopsis* seeds [175,204] but also for Mn transport in embryos [255]. Similarly, TaVIT2 facilitates the transport of iron and manganese; overexpression of *TaVIT2* in the endosperm of wheat and barley results in more than twice the iron content in white flour fractions. Barley grains also contain twice as much manganese, whereas manganese levels are not increased in wheat [202].

MTP8, a tonoplast-localized Mn transporter that interacts with VIT1, is responsible for detoxifying Mn and also transports Fe, thereby mediating Mn homeostasis and Fe reallocation during seed development and germination [203,255,256]. When Mn was present in the medium, *mtp8* mutants not only translocated more Mn to the shoot than wild-type plants but also exhibited critically low Fe concentrations and, consequently, Fe chlorosis, even though the transcriptional Fe-deficiency response was more strongly upregulated in *mtp8* [256]. CPK5/CPK11-mediated MTP8 affects Mn storage in seeds and is important for MTP8 function in high-Mn stress tolerance under Fe-deficient conditions [257]. These findings suggest that complex crosstalk regulates Mn and Fe homeostasis in cells.

Mn and Fe are also interconnected in their long-distance transport processes. The *Arabidopsis* phloem-specific iron transporter OPT3 plays a key role in systemic Fe signaling, Fe redistribution, and Fe movement to developing seeds, as well as metal homeostasis including Mn [134,184]. In addition to Fe, Mn is also overaccumulated in leaves, flowers, siliques, and seeds of the *opt3-2* mutant; this is unlikely due to the *opt3-2* mutation per se, but rather a consequence of deregulated metal transport via IRT1 in mutant roots [184]. Rice *OsYSL2* is localized to the plasma membrane and mainly expressed in the phloem companion cells of Fe-deficient leaves; it is responsible for loading Fe^{2+}–NA and Mn^{2+}–NA complexes into the phloem and participates in the long-distance transport of iron and manganese to grains [258,259]. Maize ZmYS1 functions as a proton-coupled symporter for DMA- and NA-chelated metals, including Fe^{3+}/Fe^{2+}/Mn^{2+}–DMA complexes and Fe^{3+}/Fe^{2+}–NA [260]. Barley HvYSL2, localized to the root endodermis, has broader substrate specificity and is able to transport Fe^{3+}/Mn^{2+}–DMA and Fe^{2+}–NA [54].

5.5. Iron–Sulfur Interactions

Iron and sulfur are metabolically intertwined through their joint assembly into Fe–S clusters, which serve as essential cofactors for proteins involved in photosynthesis, respiration, and DNA repair [172,261]. The biogenesis of Fe–S clusters requires the coordinated provision of both Fe and S, and deficiency in either nutrient disrupts cluster assembly, with cascading effects on cellular metabolism. Thus, the uptake systems for S and Fe appear to be more tightly coordinated than those of other nutrients [206,262,263].

Nutrient uptake is coordinately regulated by Fe and S availability. S deficiency reduces Fe concentration in shoots or leaves across various plant species, including *Arabidopsis*, tomato, maize, durum wheat, rice, and barley, consistent with a decline in root Fe-uptake activity triggered by S starvation [207,264–268]. In grasses (Strategy II plants), the S deficiency-induced reduction in Fe accumulation in plant tissues could be attributed to decreased production and release of PS [206–208], whereas in tomato (a Strategy I plant), the effect was instead attributable to impaired ethylene and NA production [264]. Conversely, Fe scarcity increases S uptake and perturbs its homeostasis [262,268–270]; this response may, in turn, satisfy the increased demand for methionine and its derivatives, thereby helping plants cope with Fe starvation.

In *Arabidopsis*, S assimilation and transport genes are co-expressed with Fe-deficiency-responsive genes; for example, Fe deficiency markedly downregulates the high-affinity sulfate transporter gene *SULTR1.1*, while S limitation represses *IRT1*-dependent Fe up-

take [265]. Fe deficiency reduces sulfate uptake, likely matching the lower S demand for Fe–S clusters; similarly, S deficiency downregulates IRT1 [265]. However, in tomato, most sulfate transporter genes, including two high-affinity sulfate transporter genes (*SlST1.1* and *SlST1.2*) and two low-affinity sulfate transporter genes (*SlST2.1* and *SlST4.1*), were significantly upregulated in roots under Fe deficiency. This upregulation was accompanied by substantial accumulation of total sulfur and thiols in shoots of Fe-starved plants, likely supporting increased uptake and root-to-shoot translocation of sulfate [205]. These opposing strategies are likely driven by species-specific metabolic priorities and experimental contexts, such as variations in growth systems, treatment duration, and the specific demand for S-containing signaling molecules required for Fe acquisition.

In graminaceous plants, S starvation decreases PS synthesis and release, resulting in reduced Fe uptake [206–208]. Consistently, S resupply to S-deprived barley restores root PS exudation and *HvST1*/*HvYS1* transcript levels, alongside the recovery of leaf ATPS and OASTL activities, demonstrating the tight link between Fe-starvation tolerance and S status [206]. In durum wheat, most S assimilation genes and enzyme activities (APS reductase, ATP sulfurylase, sulfite reductase, and serine acetyltransferase) are upregulated under Fe-deficient/S-sufficient conditions, resembling S starvation. However, *SULTR1.1* is strongly induced by S deficiency but unaffected by Fe starvation [268]. Although interactions between Fe and S metabolism have begun to be described at the molecular level, limited information is available regarding the mechanisms that regulate these cross-talks.

5.6. Iron–Nitrogen Interactions

Nitrogen (N) and Fe interact at multiple levels in plants. N can modify Fe deficiency symptoms depending on soil type, plant species, and N form [12]. Increasing NO_3^- availability from low to sufficient levels resulted in a threefold increase in shoot Fe content in durum wheat [271], whereas NO_3^- supply induces Fe deficiency in rice and apple [272,273]. The effect of NH_4^+ also varies among species: NH_4^+-fed *Brachypodium distachyon* exhibited greater sensitivity to Fe deficiency [274], whereas NH_4^+ alleviates Fe deficiency in rice and *Arabidopsis* [275,276]. OsNLP4 (NIN-LIKE PROTEIN 4), a NO_3^- sensor/transcription factor, regulates nitrogen use efficiency [277] and mediates N–Fe crosstalk by promoting N/Fe uptake and ROS scavenging while inhibiting strigolactone signaling [210]. Notably, low Fe elevates H_2O_2 levels, reducing OsNLP4 nuclear localization and causing growth defects; in contrast, balanced N–Fe sufficiency reduces H_2O_2 levels, promoting OsNLP4 nuclear localization and reinforcing its regulatory activity [210].

The interaction between NH_4^+ and Fe is mediated by multiple mechanisms. In *Arabidopsis*, altered Fe management is an important cause of ammonium sensitivity, with MYB28 and MYB29 playing key roles in the interaction between ammonium nutrition and Fe homeostasis [278]. The ferroxidase LPR2 mediates NH_4^+-induced root growth inhibition in an Fe-dependent manner [279]. LPR2 is induced by NH_4^+ and oxidizes Fe^{2+} to Fe^{3+} at the cell walls of root phloem sieve elements, causing ROS burst, callose accumulation, reduced assimilate unloading to the root growth zone, and arrested root development. This effect is abolished when Fe is low or when NO_3^- is the main N source [279]. High NH_4^+ combined with Fe accumulation promotes NH_4^+ efflux, whereas low Fe improves NH_4^+ use efficiency by enhancing protein N-glycosylation via a vitamin C1-independent pathway [209]. Dolomite reduces Fe toxicity and NH_4^+ efflux by lowering *LPR2* expression, thereby improving NH_4^+ use efficiency [209].

Jasmonate (JA) acts as an inhibitor that fine-tunes Fe deficiency responses and is also involved in NH_4^+–Fe interaction in *Arabidopsis* [280,281]. The JA signaling transcription factor MYC2 directly binds and represses NRT1.1 (Nitrate Transporter 1.1), a NO_3^- dual-affinity transceptor that positively affects NH_4^+ uptake and modulates NH_4^+–Fe balance of

the plants [280,282]. JA suppression of early Fe deficiency responses via MYC2 and JAR1, and MYC2 represses Fe-responsive genes including *FIT* and bHLHs [79]. Thus, MYC2-dependent JA signaling decreases both NH_4^+ and Fe accumulation, thereby alleviating root growth inhibition and regulating the NH_4^+/Fe balance [280]. In addition, as mentioned above, *LjIMA1* and *LjIMA2* in *L. japonicus* direct both systemic and local Fe distribution to nodules during symbiotic nitrogen fixation, emphasizing their conserved contribution to nitrogen–Fe homeostasis [129].

6. Final Remarks

Over the past two decades, the molecular framework of plant Fe homeostasis has been substantially elucidated. Rather than isolated pathways, this system functions as a vertically integrated network spanning distinct regulatory layers. (i) At the root–soil interface, iron chemical speciation and bioavailability are modulated by plant roots through the exudation of H^+, coumarins, and phytosiderophores. This exudation is governed by a suite of genes, including *AHA2*, *F6′H1*, *S8H*, *CYP82C4*, *PDR9*, *NAS*, *NAAT1*, *DMAS1*, and *TOM1*. Furthermore, microbial siderophores also chelate iron, thereby enhancing its availability for root uptake. (ii) At the plasma membrane, Fe uptake is facilitated by distinct transporters with varying substrate specificities, such as NRAMP5 and IRT1 for Fe^{2+}, and YSL15 for Fe^{3+}–DMA and potentially bacillibactin–Fe^{3+}. (iii) Intracellularly, subcellular trafficking precisely orchestrates iron distribution, thereby ensuring efficient metal utilization while simultaneously preventing iron deficiency and toxicity. This sophisticated sorting is mediated by a suite of organelle-specific transporters, including VIT1, NRAMP3/4, and FPN2 for vacuolar flux; PIC1, FIC1, and YSL4/6 for chloroplast homeostasis; and MIT1/2 and FPN3 for mitochondrial iron handling.

These distinct spatial layers are globally coordinated by three overarching regulatory mechanisms. First, the hierarchical bHLH transcriptional cascade, comprising the central regulators FIT, bHLH IVc (e.g., ILR3 and bHLH115), and downstream bHLH Ib factors, directly controls the expression of key genes across these layers, from root exudation (*AHA2*, *PDR9*) to membrane uptake (*IRT1*, *FRO2*) [74,82,100]. Second, systemic IMA/FEP peptides act as long-distance mobile signals, transmitting shoot iron status to the roots. By competitively binding to BTS/BTSL E3 ligases, IMA peptides stabilize the bHLH IVc factors, thereby amplifying root uptake in response to whole-plant demand [119,126]. Third, HY5-dependent light signaling integrates environmental cues with iron regulatory networks; HY5 not only directly targets multiple intercellular transport genes (e.g., *OPT3*, *YSL2*/*3*) but also interacts with the negative regulator PYE, ensuring that iron acquisition is synchronized with the plant's photosynthetic capacity [94]. Together, these three regulatory tiers ensure that local iron sensing is effectively translated into whole-plant physiological adjustments.

Recent breakthroughs have further reshaped our understanding. The identification of microbial siderophore utilization represents an emerging—though still mechanistically unresolved—extension of classical Fe acquisition [15]. Additionally, coumarin-based Fe mobilization has blurred the boundaries between Strategies I and II [14,36], while multi-nutrient crosstalk positions Fe as a central hub coordinating responses to Zn, P, Cu, Mn, S, and N [12,192,197,263]. Moreover, the linkage of systemic signaling to root transcriptional networks by IMA/FEP and HY5 highlights the crucial role of shoot iron status in regulating root uptake. Collectively, these findings depict a far more interconnected and dynamic system than previously recognized.

Despite these advances, critical gaps remain. It is still unknown whether plants possess specific transporters for microbial siderophore–Fe and coumarin–Fe complexes, and how Fe binding is translated into E3 ligase activity. Resolving these will require heterologous transport assays and proximity-labeling proteomics. Similarly, whether chloroplasts

and mitochondria possess independent Fe-sensing mechanisms, and whether IMA/FEP phloem mobility is conserved across species, demands investigation using tissue-specific manipulation combined with stable isotope tracing. Crucially, extrapolating laboratory findings to complex field environments remains a major challenge, requiring in situ tracing within the rhizosphere microbiome. Ultimately, the grand challenge is to manipulate this network to concurrently achieve high yield, stress tolerance, and grain iron biofortification. Bridging molecular biology with field-based validation will be key to advancing sustainable agriculture.

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References

1. Marschner, P. *Mineral Nutrition of Higher Plants*; Academic Press: Amsterdam, The Netherlands, 2011; p. 340, ISBN 978-0-12-384905-2.
2. Vigani, G.; Solti, Á.; Thomine, S.; Philippar, K. Essential and Detrimental—An Update on Intracellular Iron Trafficking and Homeostasis. *Plant Cell Physiol.* **2019**, *60*, 1420–1439. [CrossRef] [PubMed]
3. Kobayashi, T.; Nishizawa, N.K. Iron Uptake, Translocation, and Regulation in Higher Plants. *Annu. Rev. Plant Biol.* **2012**, *63*, 131–152. [CrossRef] [PubMed]
4. Bashir, T.; Rashid, R.; Malik, A.R.; Sundouri, A.S. Reframing Fruit Biofortification for Sustainable Micronutrient Security: From Crop Innovation to Nutritional Impact. *Front. Plant Sci.* **2026**, *17*, 1853898. [CrossRef] [PubMed]
5. Trofimov, K.; Mankotia, S.; Ngigi, M.; Baby, D.; Satbhai, S.B.; Bauer, P. Shedding Light on Iron Nutrition: Exploring Intersections of Transcription Factor Cascades in Light and Iron Deficiency Signaling. *J. Exp. Bot.* **2025**, *76*, 787–802. [CrossRef] [PubMed]
6. López-Millán, A.F.; Duy, D.; Philippar, K. Chloroplast Iron Transport Proteins—Function and Impact on Plant Physiology. *Front. Plant Sci.* **2016**, *7*, 178. [CrossRef] [PubMed]
7. Dixon, S.J.; Stockwell, B.R. The Role of Iron and Reactive Oxygen Species in Cell Death. *Nat. Chem. Biol.* **2014**, *10*, 9–17. [CrossRef] [PubMed]
8. Li, R.; Ma, L.; Li, M.; Zhu, X.; Zhai, Y.; Liu, J.; Wang, D.; Yang, L. Iron Need Attention: A Review on the Role of Iron in Plants. *Front. Plant Sci.* **2026**, *17*, 1876801. [CrossRef] [PubMed]
9. Berger, N.; Marin, A.J.; Stassen, M.J.J.; Lourenço, T.; Li, M.; Watanabe, S.; Azevedo, H.; Castro, P.H.; Stringlis, I.A.; Marino, D.; et al. Molecular Regulation of Iron Homeostasis in Plants. In *Progress in Botany Vol. 85*; Lüttge, U., Cánovas, F.M., Risueño Almeida, M.C., Leuschner, C., Pretzsch, H., Eds.; Springer Nature: Cham, Switzerland, 2023; Volume 85, pp. 75–103, ISBN 978-3-031-77342-6.
10. Li, M.; Watanabe, S.; Gao, F.; Dubos, C. Iron Nutrition in Plants: Towards a New Paradigm? *Plants* **2023**, *12*, 384. [CrossRef] [PubMed]
11. Khan, S.; Kaur, K.; Kumar, V.; Tiwari, S. Iron Transport and Homeostasis in Plants: Current Updates and Applications for Improving Human Nutrition Values and Sustainable Agriculture. *Plant Growth Regul.* **2023**, *100*, 373–390. [CrossRef]
12. Wairich, A.; Lima-Melo, Y.; Menguer, P.K.; Ortolan, F.; Ricachenevsky, F.K. Iron, Cold Iron, Is Master of Them All: Iron Crosstalk with Zinc, Copper, Phosphorus, and Nitrogen Homeostasis. *J. Exp. Bot.* **2025**, *76*, 4787–4803. [CrossRef] [PubMed]
13. Römheld, V.; Marschner, H. Evidence for a Specific Uptake System for Iron Phytosiderophores in Roots of Grasses. *Plant Physiol.* **1986**, *80*, 175–180. [CrossRef] [PubMed]
14. Robe, K.; Stassen, M.J.J.; Watanabe, S.; Espadas, J.; Gonzalez, P.; Rossille, A.; Li, M.; Hem, S.; Roux, A.; Santoni, V.; et al. Coumarin-Facilitated Iron Transport: An IRT1-Independent Strategy for Iron Acquisition in *Arabidopsis thaliana*. *Plant Commun.* **2025**, *6*, 101431. [CrossRef] [PubMed]
15. Gu, S.; Wang, N.; Zheng, Y.; Wang, T.; Shen, Q.; Zhang, F.; Kümmerli, R.; Wei, Z.; Zuo, Y. Integrating Microbial Siderophores into Concepts of Plant Iron Nutrition. *Nat. Plants* **2026**, *12*, 26–36. [CrossRef] [PubMed]
16. Martín-Barranco, A.; Thomine, S.; Vert, G.; Zelazny, E. A Quick Journey into the Diversity of Iron Uptake Strategies in Photosynthetic Organisms. *Plant Signal. Behav.* **2021**, *16*, 1975088. [CrossRef] [PubMed]
17. Ishimaru, Y.; Suzuki, M.; Tsukamoto, T.; Suzuki, K.; Nakazono, M.; Kobayashi, T.; Wada, Y.; Watanabe, S.; Matsuhashi, S.; Takahashi, M.; et al. Rice Plants Take up Iron as an Fe^{3+}-Phytosiderophore and as Fe^{2+}. *Plant J.* **2006**, *45*, 335–346. [CrossRef] [PubMed]

18. Santi, S.; Schmidt, W. Dissecting Iron Deficiency-Induced Proton Extrusion in *Arabidopsis* Roots. *New Phytol.* **2009**, *183*, 1072–1084. [CrossRef] [PubMed]
19. Palmgren, M.G. Plant Plasma Membrane H+-ATPases: Powerhouses for Nutrient Uptake. *Annu. Rev. Plant Biol.* **2001**, *52*, 817–845. [CrossRef] [PubMed]
20. Jain, A.; Wilson, G.T.; Connolly, E.L. The Diverse Roles of FRO Family Metalloreductases in Iron and Copper Homeostasis. *Front. Plant Sci.* **2014**, *5*, 100. [CrossRef] [PubMed]
21. Robinson, N.J.; Procter, C.M.; Connolly, E.L.; Guerinot, M.L. A Ferric-Chelate Reductase for Iron Uptake from Soils. *Nature* **1999**, *397*, 694–697. [CrossRef] [PubMed]
22. Yi, Y.; Guerinot, M.L. Genetic Evidence That Induction of Root Fe(III) Chelate Reductase Activity Is Necessary for Iron Uptake under Iron Deficiency. *Plant J.* **1996**, *10*, 835–844. [CrossRef] [PubMed]
23. Eide, D.; Broderius, M.; Fett, J.; Guerinot, M.L. A Novel Iron-Regulated Metal Transporter from Plants Identified by Functional Expression in Yeast. *Proc. Natl. Acad. Sci. USA* **1996**, *93*, 5624–5628. [CrossRef] [PubMed]
24. Dubeaux, G.; Neveu, J.; Zelazny, E.; Vert, G. Metal Sensing by the IRT1 Transporter-Receptor Orchestrates Its Own Degradation and Plant Metal Nutrition. *Mol. Cell* **2018**, *69*, 953–964.e5. [CrossRef] [PubMed]
25. Barberon, M.; Zelazny, E.; Robert, S.; Conéjéro, G.; Curie, C.; Friml, J.; Vert, G. Monoubiquitin-Dependent Endocytosis of the IRON-REGULATED TRANSPORTER 1 (IRT1) Transporter Controls Iron Uptake in Plants. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, E450–E458. [CrossRef] [PubMed]
26. Korshunova, Y.O.; Eide, D.; Clark, W.G.; Guerinot, M.L.; Pakrasi, H.B. The IRT1 Protein from *Arabidopsis thaliana* Is a Metal Transporter with Broad Substrate Range. *Plant Mol. Biol.* **1999**, *40*, 37–44. [CrossRef] [PubMed]
27. Quintana, J.; Bernal, M.; Scholle, M.; Holländer-Czytko, H.; Nguyen, N.T.; Piotrowski, M.; Mendoza-Cózatl, D.G.; Haydon, M.J.; Krämer, U. Root-to-Shoot Iron Partitioning in *Arabidopsis* Requires IRON-REGULATED TRANSPORTER1 (IRT1) Protein but Not Its Iron(II) Transport Function. *Plant J.* **2022**, *109*, 992–1013. [CrossRef] [PubMed]
28. von Wirén, N.; Klair, S.; Bansal, S.; Briat, J.-F.; Khodr, H.; Shioiri, T.; Leigh, R.A.; Hider, R.C. Nicotianamine Chelates Both FeIII and FeII: Implications for Metal Transport in Plants. *Plant Physiol.* **1999**, *119*, 1107–1114. [CrossRef] [PubMed]
29. Martín-Barranco, A.; Spielmann, J.; Dubeaux, G.; Vert, G.; Zelazny, E. Dynamic Control of the High-Affinity Iron Uptake Complex in Root Epidermal Cells. *Plant Physiol.* **2020**, *184*, 1236–1250. [CrossRef] [PubMed]
30. Chao, Z.-F.; Chao, D.-Y. Similarities and Differences in Iron Homeostasis Strategies between Graminaceous and Non-Graminaceous Plants. *New Phytol.* **2022**, *236*, 1655–1660. [CrossRef] [PubMed]
31. Schmidt, W.; Tittel, J.; Schikora, A. Role of Hormones in the Induction of Iron Deficiency Responses in *Arabidopsis* Roots. *Plant Physiol.* **2000**, *122*, 1109–1118. [CrossRef] [PubMed]
32. Lingam, S.; Mohrbacher, J.; Brumbarova, T.; Potuschak, T.; Fink-Straube, C.; Blondet, E.; Genschik, P.; Bauer, P. Interaction between the bHLH Transcription Factor FIT and ETHYLENE INSENSITIVE3/ETHYLENE INSENSITIVE3-LIKE1 Reveals Molecular Linkage between the Regulation of Iron Acquisition and Ethylene Signaling in *Arabidopsis*. *Plant Cell* **2011**, *23*, 1815–1829. [CrossRef] [PubMed]
33. Tan, T.; Tao, L.; Zhang, Y.; Beauregard, P.B.; Sun, X.; Miao, Y.; Zhang, N.; Xun, W.; Ran, W.; Jia, B.; et al. The Volatile Pentadecane From Bacillus Alleviates Plant Iron Deficiency Through Activating the Reduction-Based Fe Uptake System. *Plant Biotechnol. J.* **2026**, *24*, 1564–1577. [CrossRef] [PubMed]
34. Terés, J.; Busoms, S.; Perez Martín, L.; Luís-Villarroya, A.; Flis, P.; Álvarez-Fernández, A.; Tolrà, R.; Salt, D.E.; Poschenrieder, C. Soil Carbonate Drives Local Adaptation in *Arabidopsis thaliana*. *Plant Cell Environ.* **2019**, *42*, 2384–2398. [CrossRef] [PubMed]
35. Fourcroy, P.; Sisó-Terraza, P.; Sudre, D.; Savirón, M.; Reyt, G.; Gaymard, F.; Abadía, A.; Abadia, J.; Álvarez-Fernández, A.; Briat, J.-F. Involvement of the ABCG37 Transporter in Secretion of Scopoletin and Derivatives by *Arabidopsis* Roots in Response to Iron Deficiency. *New Phytol.* **2014**, *201*, 155–167. [CrossRef] [PubMed]
36. Robe, K.; Izquierdo, E.; Vignols, F.; Rouached, H.; Dubos, C. The Coumarins: Secondary Metabolites Playing a Primary Role in Plant Nutrition and Health. *Trends Plant Sci.* **2021**, *26*, 248–259. [CrossRef] [PubMed]
37. Rajniak, J.; Giehl, R.F.H.; Chang, E.; Murgia, I.; von Wirén, N.; Sattely, E.S. Biosynthesis of Redox-Active Metabolites in Response to Iron Deficiency in Plants. *Nat. Chem. Biol.* **2018**, *14*, 442–450. [CrossRef] [PubMed]
38. Van Dijck, L.; Esposto, D.; Huelsmann, C.; Malisic, M.; Piro, A.; Giehl, R.F.H.; Balcke, G.U.; Tissier, A.; Parker, J.E. Cooperation between a Root Fungal Endophyte and Host-Derived Coumarin Scopoletin Mediates Arabidopsis Iron Nutrition. *New Phytol.* **2025**, *248*, 857–871. [CrossRef] [PubMed]
39. Paffrath, V.; Tandron Moya, Y.A.; Weber, G.; von Wirén, N.; Giehl, R.F.H. A Major Role of Coumarin-Dependent Ferric Iron Reduction in Strategy I-Type Iron Acquisition in *Arabidopsis*. *Plant Cell* **2024**, *36*, 642–664. [CrossRef] [PubMed]
40. Robe, K.; Conejero, G.; Gao, F.; Lefebvre-Legendre, L.; Sylvestre-Gonon, E.; Rofidal, V.; Hem, S.; Rouhier, N.; Barberon, M.; Hecker, A.; et al. Coumarin Accumulation and Trafficking in *Arabidopsis thaliana*: A Complex and Dynamic Process. *New Phytol.* **2021**, *229*, 2062–2079. [CrossRef] [PubMed]

41. Watanabe, S.; Li, M.; Rossille, A.; Boustani, C.; Robe, K.; Kanno, Y.; Seo, M.; Dubos, C. The Arabidopsis NPF7.2 Mediates Coumarin Uptake for Root Iron Acquisition. *New Phytol.* **2026**, *250*, 1619–1633. [CrossRef] [PubMed]
42. Mori, S.; Nishizawa, N. Methionine as a Dominant Precursor of Phytosiderophores in Graminaceae Plants. *Plant Cell Physiol.* **1987**, *28*, 1081–1092. [CrossRef]
43. Higuchi, K.; Suzuki, K.; Nakanishi, H.; Yamaguchi, H.; Nishizawa, N.K.; Mori, S. Cloning of Nicotianamine Synthase Genes, Novel Genes Involved in the Biosynthesis of Phytosiderophores. *Plant Physiol.* **1999**, *119*, 471–480. [CrossRef] [PubMed]
44. Takahashi, M.; Yamaguchi, H.; Nakanishi, H.; Shioiri, T.; Nishizawa, N.K.; Mori, S. Cloning Two Genes for Nicotianamine Aminotransferase, a Critical Enzyme in Iron Acquisition (Strategy II) in Graminaceous Plants. *Plant Physiol.* **1999**, *121*, 947–956. [CrossRef] [PubMed]
45. Bashir, K.; Inoue, H.; Nagasaka, S.; Takahashi, M.; Nakanishi, H.; Mori, S.; Nishizawa, N.K. Cloning and Characterization of Deoxymugineic Acid Synthase Genes from Graminaceous Plants. *J. Biol. Chem.* **2006**, *281*, 32395–32402. [CrossRef] [PubMed]
46. Inoue, H.; Higuchi, K.; Takahashi, M.; Nakanishi, H.; Mori, S.; Nishizawa, N.K. Three Rice Nicotianamine Synthase Genes, *OsNAS1*, *OsNAS2*, and *OsNAS3*, Are Expressed in Cells Involved in Long-Distance Transport of Iron and Differentially Regulated by Iron. *Plant J.* **2003**, *36*, 366–381. [CrossRef] [PubMed]
47. Inoue, H.; Takahashi, M.; Kobayashi, T.; Suzuki, M.; Nakanishi, H.; Mori, S.; Nishizawa, N.K. Identification and Localisation of the Rice Nicotianamine Aminotransferase Gene *OsNAAT1* Expression Suggests the Site of Phytosiderophore Synthesis in Rice. *Plant Mol. Biol.* **2008**, *66*, 193–203. [CrossRef] [PubMed]
48. Bashir, K.; Hanada, K.; Shimizu, M.; Seki, M.; Nakanishi, H.; Nishizawa, N.K. Transcriptomic Analysis of Rice in Response to Iron Deficiency and Excess. *Rice* **2014**, *7*, 18. [CrossRef] [PubMed]
49. Nozoye, T.; Nagasaka, S.; Kobayashi, T.; Takahashi, M.; Sato, Y.; Uozumi, N.; Nakanishi, H.; Nishizawa, N.K. Phytosiderophore Efflux Transporters Are Crucial for Iron Acquisition in Graminaceous Plants. *J. Biol. Chem.* **2011**, *286*, 5446–5454. [CrossRef] [PubMed]
50. Nozoye, T.; Nagasaka, S.; Kobayashi, T.; Sato, Y.; Uozumi, N.; Nakanishi, H.; Nishizawa, N.K. The Phytosiderophore Efflux Transporter TOM2 Is Involved in Metal Transport in Rice. *J. Biol. Chem.* **2015**, *290*, 27688–27699. [CrossRef] [PubMed]
51. Curie, C.; Panaviene, Z.; Loulergue, C.; Dellaporta, S.L.; Briat, J.-F.; Walker, E.L. Maize Yellow Stripe1 Encodes a Membrane Protein Directly Involved in Fe(III) Uptake. *Nature* **2001**, *409*, 346–349. [CrossRef] [PubMed]
52. Inoue, H.; Kobayashi, T.; Nozoye, T.; Takahashi, M.; Kakei, Y.; Suzuki, K.; Nakazono, M.; Nakanishi, H.; Mori, S.; Nishizawa, N.K. Rice OsYSL15 Is an Iron-Regulated Iron(III)-Deoxymugineic Acid Transporter Expressed in the Roots and Is Essential for Iron Uptake in Early Growth of the Seedlings. *J. Biol. Chem.* **2009**, *284*, 3470–3479. [CrossRef] [PubMed]
53. Murata, Y.; Ma, J.F.; Yamaji, N.; Ueno, D.; Nomoto, K.; Iwashita, T. A Specific Transporter for Iron(III)–Phytosiderophore in Barley Roots. *Plant J.* **2006**, *46*, 563–572. [CrossRef] [PubMed]
54. Araki, R.; Murata, J.; Murata, Y. A Novel Barley Yellow Stripe 1-like Transporter (HvYSL2) Localized to the Root Endodermis Transports Metal-Phytosiderophore Complexes. *Plant Cell Physiol.* **2011**, *52*, 1931–1940. [CrossRef] [PubMed]
55. Song, Z.; Li, S.; Li, Y.; Zhou, X.; Liu, X.; Yang, W.; Chen, R. Identification and Characterization of *Yellow Stripe-like* Genes in Maize Suggest Their Roles in the Uptake and Transport of Zinc and Iron. *BMC Plant Biol.* **2024**, *24*, 3. [CrossRef] [PubMed]
56. Bughio, N.; Yamaguchi, H.; Nishizawa, N.K.; Nakanishi, H.; Mori, S. Cloning an Iron-Regulated Metal Transporter from Rice. *J. Exp. Bot.* **2002**, *53*, 1677–1682. [CrossRef] [PubMed]
57. Ishimaru, Y.; Takahashi, R.; Bashir, K.; Shimo, H.; Senoura, T.; Sugimoto, K.; Ono, K.; Yano, M.; Ishikawa, S.; Arao, T.; et al. Characterizing the Role of Rice NRAMP5 in Manganese, Iron and Cadmium Transport. *Sci. Rep.* **2012**, *2*, 286. [CrossRef] [PubMed]
58. Ishimaru, Y.; Bashir, K.; Nakanishi, H.; Nishizawa, N.K. OsNRAMP5, a Major Player for Constitutive Iron and Manganese Uptake in Rice. *Plant Signal. Behav.* **2012**, *7*, 763–766. [CrossRef] [PubMed]
59. Rroco, E.; Kosegarten, H.; Harizaj, F.; Imani, J.; Mengel, K. The Importance of Soil Microbial Activity for the Supply of Iron to Sorghum and Rape. *Eur. J. Agron.* **2003**, *19*, 487–493. [CrossRef]
60. Jin, C.W.; He, Y.F.; Tang, C.X.; Wu, P.; Zheng, S.J. Mechanisms of Microbially Enhanced Iron Uptake in Red Clover (*Trifolium pratense* L.). *Plant Cell Environ.* **2006**, *29*, 888–897. [CrossRef] [PubMed]
61. de Santiago, A.; Quintero, J.M.; Aviles, M.; Delgado, A. Effect of Trichoderma Asperellum Strain T34 on Iron Nutrition in White Lupin. *Soil Biol. Biochem.* **2009**, *41*, 2453–2459. [CrossRef]
62. de Santiago, A.; Quintero, J.M.; Aviles, M.; Delgado, A. Effect of Trichoderma Asperellum Strain T34 on Iron, Copper, Manganese, and Zinc Uptake by Wheat Grown on a Calcareous Medium. *Plant Soil* **2011**, *342*, 97–104. [CrossRef]
63. de Santiago, A.; García-López, A.M.; Quintero, J.M.; Avilés, M.; Delgado, A. Effect of *Trichoderma asperellum* Strain T34 and Glucose Addition on Iron Nutrition in Cucumber Grown on Calcareous Soils. *Soil Biol. Biochem.* **2013**, *57*, 598–605. [CrossRef]
64. Neilands, J.B. Siderophores: Structure and Function of Microbial Iron Transport Compounds. *J. Biol. Chem.* **1995**, *270*, 26723–26726. [CrossRef] [PubMed]

65. Madan, A.; Garg, R.; Rani, M.; Dev, S.; Singh, S.; Singh, N.K.; Barwant, M.M.; Saini, R.; Sharma, H.; Wu, Y.S. Microbial Siderophores in Sustainable Agriculture: Molecular Insights, Smart Delivery Systems, and Biotechnological Applications. *Prog. Microb. Mol. Biol.* **2026**, *9*, a0000478. [CrossRef]
66. Radzki, W.; Gutierrez Mañero, F.J.; Algar, E.; Lucas García, J.A.; García-Villaraco, A.; Ramos Solano, B. Bacterial Siderophores Efficiently Provide Iron to Iron-Starved Tomato Plants in Hydroponics Culture. *Antonie Van Leeuwenhoek* **2013**, *104*, 321–330. [CrossRef] [PubMed]
67. Gao, B.; Chai, X.; Huang, Y.; Wang, X.; Han, Z.; Xu, X.; Wu, T.; Zhang, X.; Wang, Y. Siderophore Production in *Pseudomonas* sp. Strain SP3 Enhances Iron Acquisition in Apple Rootstock. *J. Appl. Microbiol.* **2022**, *133*, 720–732. [CrossRef] [PubMed]
68. Vansuyt, G.; Robin, A.; Briat, J.F.; Curie, C.; Lemanceau, P. Iron Acquisition from Fe-Pyoverdine by *Arabidopsis thaliana*. *Mol. Plant-Microbe Interact.* **2007**, *20*, 441–447. [CrossRef] [PubMed]
69. Johnson, G.V.; Lopez, A.; La Valle Foster, N. Reduction and Transport of Fe from Siderophores. *Plant Soil* **2002**, *241*, 27–33. [CrossRef]
70. Yehuda, Z.; Shenker, M.; Römheld, V.; Marschner, H.; Hadar, Y.; Chen, Y. The Role of Ligand Exchange in the Uptake of Iron from Microbial Siderophores by Gramineous Plants. *Plant Physiol.* **1996**, *112*, 1273–1280. [CrossRef] [PubMed]
71. Singh, P.; Kumar, R.; Khan, A.; Singh, A.; Srivastava, A. *Bacillibactin* Siderophore Induces Iron Mobilisation Responses inside Aerobic Rice Variety through YSL15 Transporter. *Rhizosphere* **2023**, *27*, 100724. [CrossRef]
72. Singh, P.; Khan, A.; Kumar, R.; Ojha, K.K.; Singh, V.K.; Srivastava, A. In Silico Analysis of Comparative Affinity of Phytosiderophore and Bacillibactin for Iron Uptake by YSL15 and YSL18 Receptors of *Oryza sativa*. *J. Biomol. Struct. Dyn.* **2023**, *41*, 2733–2746. [CrossRef] [PubMed]
73. Chen, L.; Dick, W.A.; Streeter, J.G. Production of Aerobactin by Microorganisms from a Compost Enrichment Culture and Soybean Utilization. *J. Plant Nutr.* **2000**, *23*, 2047–2060. [CrossRef]
74. Colangelo, E.P.; Guerinot, M.L. The Essential Basic Helix-Loop-Helix Protein FIT1 Is Required for the Iron Deficiency Response. *Plant Cell* **2004**, *16*, 3400–3412. [CrossRef] [PubMed]
75. Sivitz, A.; Grinvalds, C.; Barberon, M.; Curie, C.; Vert, G. Proteasome-Mediated Turnover of the Transcriptional Activator FIT Is Required for Plant Iron-Deficiency Responses. *Plant J.* **2011**, *66*, 1044–1052. [CrossRef] [PubMed]
76. Yuan, Y.; Wu, H.; Wang, N.; Li, J.; Zhao, W.; Du, J.; Wang, D.; Ling, H.-Q. FIT Interacts with AtbHLH38 and AtbHLH39 in Regulating Iron Uptake Gene Expression for Iron Homeostasis in *Arabidopsis*. *Cell Res.* **2008**, *18*, 385–397. [CrossRef] [PubMed]
77. Wang, N.; Cui, Y.; Liu, Y.; Fan, H.; Du, J.; Huang, Z.; Yuan, Y.; Wu, H.; Ling, H.-Q. Requirement and Functional Redundancy of Ib Subgroup bHLH Proteins for Iron Deficiency Responses and Uptake in *Arabidopsis thaliana*. *Mol. Plant* **2013**, *6*, 503–513. [CrossRef] [PubMed]
78. Cai, Y.; Li, Y.; Liang, G. FIT and bHLH Ib Transcription Factors Modulate Iron and Copper Crosstalk in *Arabidopsis*. *Plant Cell Environ.* **2021**, *44*, 1679–1691. [CrossRef] [PubMed]
79. Cui, Y.; Chen, C.-L.; Cui, M.; Zhou, W.-J.; Wu, H.-L.; Ling, H.-Q. Four IVa bHLH Transcription Factors Are Novel Interactors of FIT and Mediate JA Inhibition of Iron Uptake in *Arabidopsis*. *Mol. Plant* **2018**, *11*, 1166–1183. [CrossRef] [PubMed]
80. Schwarz, B.; Bauer, P. FIT, a Regulatory Hub for Iron Deficiency and Stress Signaling in Roots, and FIT-Dependent and -Independent Gene Signatures. *J. Exp. Bot.* **2020**, *71*, 1694–1705. [CrossRef] [PubMed]
81. Palmer, C.M.; Hindt, M.N.; Schmidt, H.; Clemens, S.; Guerinot, M.L. MYB10 and MYB72 Are Required for Growth under Iron-Limiting Conditions. *PLoS Genet.* **2013**, *9*, e1003953. [CrossRef] [PubMed]
82. Stringlis, I.A.; Yu, K.; Feussner, K.; de Jonge, R.; Van Bentum, S.; Van Verk, M.C.; Berendsen, R.L.; Bakker, P.A.H.M.; Feussner, I.; Pieterse, C.M.J. MYB72-Dependent Coumarin Exudation Shapes Root Microbiome Assembly to Promote Plant Health. *Proc. Natl. Acad. Sci. USA* **2018**, *115*, E5213–E5222. [CrossRef] [PubMed]
83. Chutia, R.; Abel, S.; Ziegler, J. Iron and Phosphate Deficiency Regulators Concertedly Control Coumarin Profiles in *Arabidopsis thaliana* Roots During Iron, Phosphate, and Combined Deficiencies. *Front. Plant Sci.* **2019**, *10*, 113. [CrossRef] [PubMed]
84. Kim, S.A.; LaCroix, I.S.; Gerber, S.A.; Guerinot, M.L. The Iron Deficiency Response in *Arabidopsis thaliana* Requires the Phosphorylated Transcription Factor URI. *Proc. Natl. Acad. Sci. USA* **2019**, *116*, 24933–24942. [CrossRef] [PubMed]
85. Gao, F.; Robe, K.; Bettembourg, M.; Navarro, N.; Rofidal, V.; Santoni, V.; Gaymard, F.; Vignols, F.; Roschzttardtz, H.; Izquierdo, E.; et al. The Transcription Factor bHLH121 Interacts with bHLH105 (ILR3) and Its Closest Homologs to Regulate Iron Homeostasis in *Arabidopsis*. *Plant Cell* **2020**, *32*, 508–524. [CrossRef] [PubMed]
86. Liang, G.; Zhang, H.; Li, Y.; Pu, M.; Yang, Y.; Li, C.; Lu, C.; Xu, P.; Yu, D. *Oryza sativa* FER-LIKE Fe DEFICIENCY-INDUCED TRANSCRIPTION FACTOR (OsFIT/OsbHLH156) Interacts with OsIRO2 to Regulate Iron Homeostasis. *J. Integr. Plant Biol.* **2020**, *62*, 668–689. [CrossRef] [PubMed]
87. Wang, S.; Li, L.; Ying, Y.; Wang, J.; Shao, J.F.; Yamaji, N.; Whelan, J.; Ma, J.F.; Shou, H. A Transcription Factor OsbHLH156 Regulates Strategy II Iron Acquisition through Localising IRO2 to the Nucleus in Rice. *New Phytol.* **2020**, *225*, 1247–1260. [CrossRef] [PubMed]

88. Ogo, Y.; Itai, R.N.; Nakanishi, H.; Inoue, H.; Kobayashi, T.; Suzuki, M.; Takahashi, M.; Mori, S.; Nishizawa, N.K. Isolation and Characterization of IRO2, a Novel Iron-Regulated bHLH Transcription Factor in Graminaceous Plants. *J. Exp. Bot.* **2006**, *57*, 2867–2878. [CrossRef] [PubMed]
89. Xu, P.; Yang, Y.; Zhao, Z.; Hu, J.; Xie, J.; Wang, L.; Zheng, H.; Cai, W. The Transcription Factor Dof3.6/OBP3 Regulates Iron Homeostasis in *Arabidopsis*. *EMBO J.* **2025**, *44*, 251–268. [CrossRef] [PubMed]
90. Zheng, L.; Wu, H.; Wang, A.; Zhang, Y.; Liu, Z.; Ling, H.-Q.; Song, X.-J.; Li, Y. The SOD7/DPA4–GIF1 Module Coordinates Organ Growth and Iron Uptake in *Arabidopsis*. *Nat. Plants* **2023**, *9*, 1318–1332. [CrossRef] [PubMed]
91. Chia, J.C.; Liu, X.; Dey, S.; Yan, J.; Niu, Y.; Vatamaniuk, O.K. CITF1 Interacts with FIT and Regulates Copper–Iron Crosstalk in *Arabidopsis*. *Plant Cell* **2026**, *38*, koag114. [CrossRef] [PubMed]
92. Long, T.A.; Tsukagoshi, H.; Busch, W.; Lahner, B.; Salt, D.E.; Benfey, P.N. The bHLH Transcription Factor POPEYE Regulates Response to Iron Deficiency in *Arabidopsis* Roots. *Plant Cell* **2010**, *22*, 2219–2236. [CrossRef] [PubMed]
93. Pu, M.; Liang, G. The Transcription Factor POPEYE Negatively Regulates the Expression of *bHLH Ib* Genes to Maintain Iron Homeostasis. *J. Exp. Bot.* **2023**, *74*, 2754–2767. [CrossRef] [PubMed]
94. Mankotia, S.; Dubey, A.; Jakhar, P.; Satbhai, S.B. ELONGATED HYPOCOTYL 5 (HY5) and POPEYE (PYE) Regulate Inter-Cellular Iron Transport in Plants. *Plant Cell Environ.* **2025**, *48*, 2647–2661. [CrossRef] [PubMed]
95. Zhang, J.; Liu, B.; Li, M.; Feng, D.; Jin, H.; Wang, P.; Liu, J.; Xiong, F.; Wang, J.; Wang, H.-B. The bHLH Transcription Factor bHLH104 Interacts with IAA-LEUCINE RESISTANT3 and Modulates Iron Homeostasis in *Arabidopsis*. *Plant Cell* **2015**, *27*, 787–805. [CrossRef] [PubMed]
96. Akmakjian, G.Z.; Riaz, N.; Guerinot, M.L. Photoprotection during Iron Deficiency Is Mediated by the bHLH Transcription Factors PYE and ILR3. *Proc. Natl. Acad. Sci. USA* **2021**, *118*, e2024918118. [CrossRef] [PubMed]
97. Lichtblau, D.M.; Baby, D.; Khan, M.; Trofimov, K.; Ari, Y.; Schwarz, B.; Bauer, P. The Small Iron-Deficiency-Induced Protein OLIVIA and Its Relation to the bHLH Transcription Factor POPEYE. *PLoS ONE* **2024**, *19*, e0295732. [CrossRef] [PubMed]
98. Jakhar, P.; Mankotia, S.; Koolath, V.; Ladhwal, S.; Bodh, N.; Dhanawat, K.; Pandey, A.K.; Satbhai, S.B. Blue Light Promotes Root Iron Acquisition via a Shoot CRY–HY5 Signaling Module in *Arabidopsis*. *Plant Physiol.* **2026**, *201*, kiag366. [CrossRef] [PubMed]
99. Li, X.; Zhang, H.; Ai, Q.; Liang, G.; Yu, D. Two bHLH Transcription Factors, bHLH34 and bHLH104, Regulate Iron Homeostasis in *Arabidopsis thaliana*. *Plant Physiol.* **2016**, *170*, 2478–2493. [CrossRef] [PubMed]
100. Liang, G.; Zhang, H.; Li, X.; Ai, Q.; Yu, D. bHLH Transcription Factor bHLH115 Regulates Iron Homeostasis in *Arabidopsis thaliana*. *J. Exp. Bot.* **2017**, *68*, 1743–1755. [CrossRef] [PubMed]
101. Lei, R.; Li, Y.; Cai, Y.; Li, C.; Pu, M.; Lu, C.; Yang, Y.; Liang, G. bHLH121 Functions as a Direct Link That Facilitates the Activation of FIT by bHLH IVc Transcription Factors for Maintaining Fe Homeostasis in *Arabidopsis*. *Mol. Plant* **2020**, *13*, 634–649. [CrossRef] [PubMed]
102. Gao, F.; Li, M.; Dubos, C. bHLH121 and Clade IVc bHLH Transcription Factors Synergistically Function to Regulate Iron Homeostasis in *Arabidopsis thaliana*. *J. Exp. Bot.* **2024**, *75*, 2933–2950. [CrossRef] [PubMed]
103. Li, Y.; Lei, R.; Pu, M.; Cai, Y.; Lu, C.; Li, Z.; Liang, G. bHLH11 Inhibits bHLH IVc Proteins by Recruiting the TOPLESS/TOPLESS-RELATED Corepressors. *Plant Physiol.* **2022**, *188*, 1335–1349. [CrossRef] [PubMed]
104. Tissot, N.; Robe, K.; Gao, F.; Grant-Grant, S.; Boucherez, J.; Bellegarde, F.; Maghiaoui, A.; Marcelin, R.; Izquierdo, E.; Benhamed, M.; et al. Transcriptional Integration of the Responses to Iron Availability in *Arabidopsis* by the bHLH Factor ILR3. *New Phytol.* **2019**, *223*, 1433–1446. [CrossRef] [PubMed]
105. Wang, W.; Shinwari, K.I.; Zhang, H.; Zhang, H.; Dong, L.; He, F.; Zheng, L. The bHLH Transcription Factor OsbHLH057 Regulates Iron Homeostasis in Rice. *Int. J. Mol. Sci.* **2022**, *23*, 14869. [CrossRef] [PubMed]
106. Kobayashi, T.; Ozu, A.; Kobayashi, S.; An, G.; Jeon, J.-S.; Nishizawa, N.K. OsbHLH058 and OsbHLH059 Transcription Factors Positively Regulate Iron Deficiency Responses in Rice. *Plant Mol. Biol.* **2019**, *101*, 471–486. [CrossRef] [PubMed]
107. Zhang, H.; Li, Y.; Yao, X.; Liang, G.; Yu, D. POSITIVE REGULATOR OF IRON HOMEOSTASIS1, OsPRI1, Facilitates Iron Homeostasis. *Plant Physiol.* **2017**, *175*, 543–554. [CrossRef] [PubMed]
108. Zhang, H.; Li, Y.; Pu, M.; Xu, P.; Liang, G.; Yu, D. *Oryza sativa* POSITIVE REGULATOR OF IRON DEFICIENCY RESPONSE 2 (OsPRI2) and OsPRI3 Are Involved in the Maintenance of Fe Homeostasis. *Plant Cell Environ.* **2020**, *43*, 261–274. [CrossRef] [PubMed]
109. Gao, F.; Zhu, Z.; Xue, K.; Fu, Z.; Yue, J.; Zhang, N.; Zhou, H.; Deng, Y.; Zhou, J.; Kuang, L.; et al. *OsbHLH064*, an IVb bHLH Transcription Factor, Regulates Iron Homeostasis and Enhances Grain Fe Accumulation in Rice. *Plant Biotechnol. J.* **2026**, *24*, 3754–3776. [CrossRef] [PubMed]
110. Li, C.; Li, Y.; Xu, P.; Liang, G. OsIRO3 Negatively Regulates Fe Homeostasis by Repressing the Expression of *OsIRO2*. *Plant J.* **2022**, *111*, 966–978. [CrossRef] [PubMed]
111. Wang, W.; Ye, J.; Ma, Y.; Wang, T.; Shou, H.; Zheng, L. OsIRO3 Plays an Essential Role in Iron Deficiency Responses and Regulates Iron Homeostasis in Rice. *Plants* **2020**, *9*, 1095. [CrossRef] [PubMed]

112. Li, C.; Zhao, J.; Ping, H.; Li, Y.; Lei, R.; Pan, B.; Liang, G. OsbHLH062 Negatively Regulates Fe Homeostasis by Enhancing OsHRZ1 Targeting OsPRIs for Degradation. *New Phytol.* **2025**, *247*, 160–177. [CrossRef] [PubMed]
113. Kobayashi, T.; Nagasaka, S.; Senoura, T.; Itai, R.N.; Nakanishi, H.; Nishizawa, N.K. Iron-Binding Haemerythrin RING Ubiquitin Ligases Regulate Plant Iron Responses and Accumulation. *Nat. Commun.* **2013**, *4*, 2792. [CrossRef] [PubMed]
114. Rodríguez-Celma, J.; Connorton, J.M.; Kruse, I.; Green, R.T.; Franceschetti, M.; Chen, Y.-T.; Cui, Y.; Ling, H.-Q.; Yeh, K.-C.; Balk, J. *Arabidopsis* BRUTUS-LIKE E3 Ligases Negatively Regulate Iron Uptake by Targeting Transcription Factor FIT for Recycling. *Proc. Natl. Acad. Sci. USA* **2019**, *116*, 17584–17591. [CrossRef] [PubMed]
115. Vashisht, A.A.; Zumbrennen, K.B.; Huang, X.; Powers, D.N.; Durazo, A.; Sun, D.; Bhaskaran, N.; Persson, A.; Uhlen, M.; Sangfelt, O.; et al. Control of Iron Homeostasis by an Iron-Regulated Ubiquitin Ligase. *Science* **2009**, *326*, 718–721. [CrossRef] [PubMed]
116. Salahudeen, A.A.; Thompson, J.W.; Ruiz, J.C.; Ma, H.-W.; Kinch, L.N.; Li, Q.; Grishin, N.V.; Bruick, R.K. An E3 Ligase Possessing an Iron-Responsive Hemerythrin Domain Is a Regulator of Iron Homeostasis. *Science* **2009**, *326*, 722–726. [CrossRef] [PubMed]
117. Pullin, J.; Rodríguez-Celma, J.; Franceschetti, M.; Mundy, J.E.A.; Svistunenko, D.A.; Bradley, J.M.; Le Brun, N.E.; Balk, J. Iron-Sensing and Redox Properties of the Hemerythrin-Like Domains of *Arabidopsis* BRUTUS and BRUTUS-LIKE2 Proteins. *Nat. Commun.* **2025**, *16*, 3865. [CrossRef] [PubMed]
118. Selote, D.; Samira, R.; Matthiadis, A.; Gillikin, J.W.; Long, T.A. Iron-Binding E3 Ligase Mediates Iron Response in Plants by Targeting Basic Helix-Loop-Helix Transcription Factors. *Plant Physiol.* **2015**, *167*, 273–286. [CrossRef] [PubMed]
119. Li, Y.; Lu, C.K.; Li, C.Y.; Lei, R.H.; Pu, M.N.; Zhao, J.H.; Peng, F.; Ping, H.Q.; Wang, D.; Liang, G. IRON MAN Interacts with BRUTUS to Maintain Iron Homeostasis in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* **2021**, *118*, e2109063118. [CrossRef] [PubMed]
120. Zhao, J.; Li, Y.; Ping, H.; Lei, R.; Pan, B.; Liang, G. Arabidopsis BRUTUS, BRUTUS-LIKE, and bHLH IVc Subgroup Proteins Coordinate Iron Homeostasis in the Root and Shoot. *Plant Cell* **2026**, *38*, koag006. [CrossRef] [PubMed]
121. Kobayashi, T.; Shinkawa, H.; Nagano, A.J.; Nishizawa, N.K. The Basic Leucine Zipper Transcription Factor OsbZIP83 and the Glutaredoxins OsGRX6 and OsGRX9 Facilitate Rice Iron Utilization under the Control of OsHRZ Ubiquitin Ligases. *Plant J.* **2022**, *110*, 1731–1750. [CrossRef] [PubMed]
122. Ren, Z.; Zhang, L.; Li, H.; Yang, M.; Wu, X.; Hu, R.; Lu, J.; Wang, H.; Wu, X.; Wang, Z.; et al. The BRUTUS Iron Sensor and E3 Ligase Facilitates Soybean Root Nodulation by Monoubiquitination of NSP1. *Nat. Plants* **2025**, *11*, 595–611. [CrossRef] [PubMed]
123. Tyagi, D.S.; Banoo, H.; Jha, D.K.; Meena, V.; Joon, R.; Agrwal, K.; Yadav, P.; Kumar, A.; Satbhai, S.B.; Long, T.; et al. CRISPR/Cas9 Editing of the Wheat Iron Sensor TaHRZ1 Confirms Its Conserved Role in Iron Homeostasis and Allocation in Grains. *Plant Cell Environ.* **2026**, *49*, 4975–4991. [CrossRef] [PubMed]
124. Grillet, L.; Lan, P.; Li, W.; Mokkapati, G.; Schmidt, W. IRON MAN Is a Ubiquitous Family of Peptides That Control Iron Transport in Plants. *Nat. Plants* **2018**, *4*, 953–963. [CrossRef] [PubMed]
125. Hirayama, T.; Lei, G.J.; Yamaji, N.; Nakagawa, N.; Ma, J.F. The Putative Peptide Gene *FEP1* Regulates Iron Deficiency Response in *Arabidopsis*. *Plant Cell Physiol.* **2018**, *59*, 1739–1752. [CrossRef] [PubMed]
126. Kobayashi, T.; Nagano, A.J.; Nishizawa, N.K. Iron Deficiency-Inducible Peptide-Coding Genes *OsIMA1* and *OsIMA2* Positively Regulate a Major Pathway of Iron Uptake and Translocation in Rice. *J. Exp. Bot.* **2021**, *72*, 2196–2211. [CrossRef] [PubMed]
127. Lichtblau, D.M.; Schwarz, B.; Baby, D.; Endres, C.; Sieberg, C.; Bauer, P. The Iron Deficiency-Regulated Small Protein Effector FEP3/IRON MAN1 Modulates Interaction of BRUTUS-LIKE1 With bHLH Subgroup IVc and POPEYE Transcription Factors. *Front. Plant Sci.* **2022**, *13*, 930049. [CrossRef] [PubMed]
128. Vélez-Bermúdez, I.C.; Schmidt, W. How Plants Recalibrate Cellular Iron Homeostasis. *Plant Cell Physiol.* **2022**, *63*, 154–162. [CrossRef] [PubMed]
129. Ito, M.; Tajima, Y.; Ogawa-Ohnishi, M.; Nishida, H.; Nosaki, S.; Noda, M.; Sotta, N.; Kawade, K.; Kamiya, T.; Fujiwara, T.; et al. IMA Peptides Regulate Root Nodulation and Nitrogen Homeostasis by Providing Iron According to Internal Nitrogen Status. *Nat. Commun.* **2024**, *15*, 733. [CrossRef] [PubMed]
130. Durrett, T.P.; Gassmann, W.; Rogers, E.E. The FRD3-Mediated Efflux of Citrate into the Root Vasculature Is Necessary for Efficient Iron Translocation. *Plant Physiol.* **2007**, *144*, 197–205. [CrossRef] [PubMed]
131. Haydon, M.J.; Kawachi, M.; Wirtz, M.; Hillmer, S.; Hell, R.; Krämer, U. Vacuolar Nicotianamine Has Critical and Distinct Roles under Iron Deficiency and for Zinc Sequestration in *Arabidopsis*. *Plant Cell* **2012**, *24*, 724–737. [CrossRef] [PubMed]
132. Chia, J.-C.; Yan, J.; Rahmati Ishka, M.; Faulkner, M.M.; Simons, E.; Huang, R.; Smieska, L.; Woll, A.; Tappero, R.; Kiss, A.; et al. Loss of OPT3 Function Decreases Phloem Copper Levels and Impairs Crosstalk between Copper and Iron Homeostasis and Shoot-to-Root Signaling in *Arabidopsis thaliana*. *Plant Cell* **2023**, *35*, 2157–2185. [CrossRef] [PubMed]
133. Mendoza-Cózatl, D.G.; Xie, Q.; Akmakjian, G.Z.; Jobe, T.O.; Patel, A.; Stacey, M.G.; Song, L.; Demoin, D.W.; Jurisson, S.S.; Stacey, G.; et al. OPT3 Is a Component of the Iron-Signaling Network between Leaves and Roots and Misregulation of OPT3 Leads to an over-Accumulation of Cadmium in Seeds. *Mol. Plant* **2014**, *7*, 1455–1469. [CrossRef] [PubMed]
134. Zhai, Z.; Gayomba, S.R.; Jung, H.-I.; Vimalakumari, N.K.; Piñeros, M.; Craft, E.; Rutzke, M.A.; Danku, J.; Lahner, B.; Punshon, T.; et al. OPT3 Is a Phloem-Specific Iron Transporter That Is Essential for Systemic Iron Signaling and Redistribution of Iron and Cadmium in *Arabidopsis*. *Plant Cell* **2014**, *26*, 2249–2264. [CrossRef] [PubMed]

135. Gautam, C.K. Systemic Iron Signaling via OPT3 Influences Reductive Uptake and Coumarin Secretion in *Arabidopsis*. *J. Plant Biochem. Biotechnol.* **2026**, *35*, 1263–1268. [CrossRef]
136. Gautam, C.K.; Tsai, H.-H.; Schmidt, W. IRONMAN Tunes Responses to Iron Deficiency in Concert with Environmental pH. *Plant Physiol.* **2021**, *187*, 1728–1745. [CrossRef] [PubMed]
137. Guo, Z.; Xu, J.; Wang, Y.; Hu, C.; Shi, K.; Zhou, J.; Xia, X.; Zhou, Y.; Foyer, C.H.; Yu, J. The phyB-Dependent Induction of HY5 Promotes Iron Uptake by Systemically Activating *FER* Expression. *EMBO Rep.* **2021**, *22*, EMBR202051944. [CrossRef] [PubMed]
138. Mankotia, S.; Singh, D.; Monika, K.; Kalra, M.; Meena, H.; Meena, V.; Yadav, R.K.; Pandey, A.K.; Satbhai, S.B. ELONGATED HYPOCOTYL 5 Regulates BRUTUS and Affects Iron Acquisition and Homeostasis in *Arabidopsis thaliana*. *Plant J.* **2023**, *114*, 1267–1284. [CrossRef] [PubMed]
139. Solti, Á.; Kovács, K.; Basa, B.; Vértes, A.; Sárvári, É.; Fodor, F. Uptake and Incorporation of Iron in Sugar Beet Chloroplasts. *Plant Physiol. Biochem.* **2012**, *52*, 91–97. [CrossRef] [PubMed]
140. Müller, B.; Kovács, K.; Pham, H.-D.; Kavak, Y.; Pechoušek, J.; Machala, L.; Zbořil, R.; Szenthe, K.; Abadía, J.; Fodor, F.; et al. Chloroplasts Preferentially Take up Ferric–Citrate over Iron–Nicotianamine Complexes in *Brassica napus*. *Planta* **2019**, *249*, 751–763. [CrossRef] [PubMed]
141. Jeong, J.; Cohu, C.; Kerkeb, L.; Pilon, M.; Connolly, E.L.; Guerinot, M.L. Chloroplast Fe(III) Chelate Reductase Activity Is Essential for Seedling Viability under Iron Limiting Conditions. *Proc. Natl. Acad. Sci. USA* **2008**, *105*, 10619–10624. [CrossRef] [PubMed]
142. Duy, D.; Wanner, G.; Meda, A.R.; Von Wirén, N.; Soll, J.; Philippar, K. PIC1, an Ancient Permease in *Arabidopsis* Chloroplasts, Mediates Iron Transport. *Plant Cell* **2007**, *19*, 986–1006. [CrossRef] [PubMed]
143. Teng, Y.-S.; Su, Y.; Chen, L.-J.; Lee, Y.J.; Hwang, I.; Li, H. Tic21 Is an Essential Translocon Component for Protein Translocation across the Chloroplast Inner Envelope Membrane. *Plant Cell* **2006**, *18*, 2247–2257. [CrossRef] [PubMed]
144. Duy, D.; Stübe, R.; Wanner, G.; Philippar, K. The Chloroplast Permease PIC1 Regulates Plant Growth and Development by Directing Homeostasis and Transport of Iron. *Plant Physiol.* **2011**, *155*, 1709–1722. [CrossRef] [PubMed]
145. Gong, X.; Guo, C.; Terachi, T.; Cai, H.; Yu, D. Tobacco PIC1 Mediates Iron Transport and Regulates Chloroplast Development. *Plant Mol. Biol. Rep.* **2015**, *33*, 401–413. [CrossRef]
146. Pham, H.D.; Pólya, S.; Müller, B.; Szenthe, K.; Sági-Kazár, M.; Bánkúti, B.; Bánáti, F.; Sárvári, É.; Fodor, F.; Tamás, L.; et al. The Developmental and Iron Nutritional Pattern of PIC1 and NiCo Does Not Support Their Interdependent and Exclusive Collaboration in Chloroplast Iron Transport in *Brassica napus*. *Planta* **2020**, *251*, 96. [CrossRef] [PubMed]
147. Zhang, J.; You, L.; Liu, H.; Luo, S.; Li, R.; Xue, S.; Lai, X.; Hu, H. Fe-Deficiency-Induced Chlorosis 1 Is Essential for Chloroplast Iron Transport and Homeostasis under Continuous Light Conditions in *Arabidopsis*. *Cell Rep.* **2025**, *44*, 115942. [CrossRef] [PubMed]
148. Tarantino, D.; Morandini, P.; Ramirez, L.; Soave, C.; Murgia, I. Identification of an *Arabidopsis* Mitoferrinlike Carrier Protein Involved in Fe Metabolism. *Plant Physiol. Biochem.* **2011**, *49*, 520–529. [CrossRef] [PubMed]
149. Shimoni-Shor, E.; Hassidim, M.; Yuval-Naeh, N.; Keren, N. Disruption of Nap14, a Plastid-localized Non-intrinsic ABC Protein in *Arabidopsis thaliana* Results in the Over-accumulation of Transition Metals and in Aberrant Chloroplast Structures. *Plant Cell Environ.* **2010**, *33*, 1029–1038. [CrossRef] [PubMed]
150. Voith Von Voithenberg, L.; Park, J.; Stübe, R.; Lux, C.; Lee, Y.; Philippar, K. A Novel Prokaryote-Type ECF/ABC Transporter Module in Chloroplast Metal Homeostasis. *Front. Plant Sci.* **2019**, *10*, 1264. [CrossRef] [PubMed]
151. Zeng, X.; Tang, R.; Guo, H.; Ke, S.; Teng, B.; Hung, Y.-H.; Xu, Z.; Xie, X.-M.; Hsieh, T.-F.; Zhang, X.-Q. A Naturally Occurring Conditional Albino Mutant in Rice Caused by Defects in the Plastid-Localized OsABCI8 Transporter. *Plant Mol. Biol.* **2017**, *94*, 137–148. [CrossRef] [PubMed]
152. Conte, S.S.; Lloyd, A.M. The MAR1 Transporter Is an Opportunistic Entry Point for Antibiotics. *Plant Signal. Behav.* **2010**, *5*, 49–52. [CrossRef] [PubMed]
153. Kim, L.J.; Tsuyuki, K.M.; Hu, F.; Park, E.Y.; Zhang, J.; Iraheta, J.G.; Chia, J.-C.; Huang, R.; Tucker, A.E.; Clyne, M.; et al. Ferroportin 3 Is a Dual-targeted Mitochondrial/Chloroplast Iron Exporter Necessary for Iron Homeostasis in *Arabidopsis*. *Plant J.* **2021**, *107*, 215–236. [CrossRef] [PubMed]
154. Divol, F.; Couch, D.; Conéjéro, G.; Roschzttardtz, H.; Mari, S.; Curie, C. The *Arabidopsis* YELLOW STRIPE LIKE4 and 6 Transporters Control Iron Release from the Chloroplast. *Plant Cell* **2013**, *25*, 1040–1055. [CrossRef] [PubMed]
155. Sági-Kazár, M.; Solymosi, K.; Solti, Á. Iron in Leaves: Chemical Forms, Signalling, and in-Cell Distribution. *J. Exp. Bot.* **2022**, *73*, 1717–1734. [CrossRef] [PubMed]
156. Hedtke, B.; Sträter, S.M.; Pulido, A.C.C.; Grimm, B. Two Isoforms of *Arabidopsis* Protoporphyrinogen Oxidase Localize in Different Plastidal Membranes. *Plant Physiol.* **2023**, *192*, 871–885. [CrossRef] [PubMed]
157. Kairis, A.; Neves, B.D.; Couturier, J.; Remacle, C.; Rouhier, N. Iron-sulfur Cluster Synthesis in Plastids by the SUF System: A Mechanistic and Structural Perspective. *Biochim. Biophys. Acta Mol. Cell Res.* **2024**, *1871*, 119797. [CrossRef] [PubMed]
158. Ravet, K.; Touraine, B.; Boucherez, J.; Briat, J.; Gaymard, F.; Cellier, F. Ferritins Control Interaction between Iron Homeostasis and Oxidative Stress in *Arabidopsis*. *Plant J.* **2009**, *57*, 400–412. [CrossRef] [PubMed]

159. Reyt, G.; Boudouf, S.; Boucherez, J.; Gaymard, F.; Briat, J.-F. Iron- and Ferritin-Dependent Reactive Oxygen Species Distribution: Impact on *Arabidopsis* Root System Architecture. *Mol. Plant* **2015**, *8*, 439–453. [CrossRef] [PubMed]
160. Briat, J.-F.; Duc, C.; Ravet, K.; Gaymard, F. Ferritins and Iron Storage in Plants. *Biochim. Biophys. Acta (BBA) Gen. Subj.* **2010**, *1800*, 806–814. [CrossRef] [PubMed]
161. Petit, J.-M.; Briat, J.-F.; Lobréaux, S. Structure and Differential Expression of the Four Members of the *Arabidopsis thaliana Ferritin* Gene Family. *Biochem. J.* **2001**, *359*, 575–582. [CrossRef]
162. Murgia, I.; Vigani, G. Analysis of *Arabidopsis thaliana Atfer4-1*, *Atfh* and *Atfer4-1/Atfh* Mutants Uncovers Frataxin and Ferritin Contributions to Leaf Ionome Homeostasis. *Plant Physiol. Biochem.* **2015**, *94*, 65–72. [CrossRef] [PubMed]
163. Gracheva, M.; Sági-Kazár, M.; Farkas, S.Z.; Cseh, B.; Koszti, S.; Bonanni, V.; Žižić, M.; Enkhbileg, E.; Vogel-Mikuš, K.; Péter, L.; et al. Ferritin-Mediated Transient Iron Sequestration Facilitates Chloroplast Iron Recycling during Leaf Senescence. *Plant Physiol. Biochem.* **2026**, *232*, 111124. [CrossRef] [PubMed]
164. Feng, X.; Hu, Y.; Xie, T.; Han, H.; Bonea, D.; Zeng, L.; Liu, J.; Ying, W.; Mu, B.; Cai, Y.; et al. Plant-Specific Cochaperone SSR1 Affects Root Elongation by Modulating the Mitochondrial Iron-Sulfur Cluster Assembly Machinery. *PLoS Genet.* **2025**, *21*, e1011597. [CrossRef] [PubMed]
165. Song, Z.; Lin, S.; Fu, J.; Chen, Y.; Zhang, H.; Li, J.; Liang, M. Heterologous Expression of *ISU1* Gene from Fragaria Vesca Enhances Plant Tolerance to Fe Depletion in *Arabidopsis*. *Plant Physiol. Biochem.* **2022**, *184*, 65–74. [CrossRef] [PubMed]
166. Mukherjee, I.; Campbell, N.H.; Ash, J.S.; Connolly, E.L. Expression Profiling of the *Arabidopsis Ferric Chelate Reductase* (*FRO*) Gene Family Reveals Differential Regulation by Iron and Copper. *Planta* **2006**, *223*, 1178–1190. [CrossRef] [PubMed]
167. Colombini, M. VDAC Structure, Selectivity, and Dynamics. *Biochim. Biophys. Acta (BBA) Biomembr.* **2012**, *1818*, 1457–1465. [CrossRef] [PubMed]
168. Vargas, J.; Gómez, I.; Vidal, E.A.; Lee, C.P.; Millar, A.H.; Jordana, X.; Roschzttardtz, H. Growth Developmental Defects of *Mitochondrial Iron Transporter 1* and *2* Mutants in *Arabidopsis* in Iron Sufficient Conditions. *Plants* **2023**, *12*, 1176. [CrossRef] [PubMed]
169. Bashir, K.; Ishimaru, Y.; Shimo, H.; Nagasaka, S.; Fujimoto, M.; Takanashi, H.; Tsutsumi, N.; An, G.; Nakanishi, H.; Nishizawa, N.K. The Rice Mitochondrial Iron Transporter Is Essential for Plant Growth. *Nat. Commun.* **2011**, *2*, 322. [CrossRef] [PubMed]
170. Jain, A.; Dashner, Z.S.; Connolly, E.L. Mitochondrial Iron Transporters (MIT1 and MIT2) Are Essential for Iron Homeostasis and Embryogenesis in *Arabidopsis thaliana*. *Front. Plant Sci.* **2019**, *10*, 1449. [CrossRef] [PubMed]
171. Zuo, J.; Wu, Z.; Li, Y.; Shen, Z.; Feng, X.; Zhang, M.; Ye, H. Mitochondrial ABC Transporter ATM3 Is Essential for Cytosolic Iron-Sulfur Cluster Assembly. *Plant Physiol.* **2017**, *173*, 2096–2109. [CrossRef] [PubMed]
172. Bernard, D.G.; Cheng, Y.; Zhao, Y.; Balk, J. An Allelic Mutant Series of *ATM3* Reveals Its Key Role in the Biogenesis of Cytosolic Iron-Sulfur Proteins in *Arabidopsis*. *Plant Physiol.* **2009**, *151*, 590–602. [CrossRef] [PubMed]
173. Teschner, J.; Lachmann, N.; Schulze, J.; Geisler, M.; Selbach, K.; Santamaria-Araujo, J.; Balk, J.; Mendel, R.R.; Bittner, F. A Novel Role for *Arabidopsis* Mitochondrial ABC Transporter ATM3 in Molybdenum Cofactor Biosynthesis. *Plant Cell* **2010**, *22*, 468–480. [CrossRef] [PubMed]
174. Marty, L.; Bausewein, D.; Müller, C.; Bangash, S.A.K.; Moseler, A.; Schwarzländer, M.; Müller-Schüssele, S.J.; Zechmann, B.; Riondet, C.; Balk, J.; et al. *Arabidopsis* Glutathione Reductase 2 Is Indispensable in Plastids, While Mitochondrial Glutathione Is Safeguarded by Additional Reduction and Transport Systems. *New Phytol.* **2019**, *224*, 1569–1584. [CrossRef] [PubMed]
175. Kim, S.A.; Punshon, T.; Lanzirotti, A.; Li, L.; Alonso, J.M.; Ecker, J.R.; Kaplan, J.; Guerinot, M.L. Localization of Iron in *Arabidopsis* Seed Requires the Vacuolar Membrane Transporter VIT1. *Science* **2006**, *314*, 1295–1298. [CrossRef] [PubMed]
176. Kato, T.; Kumazaki, K.; Wada, M.; Taniguchi, R.; Nakane, T.; Yamashita, K.; Hirata, K.; Ishitani, R.; Ito, K.; Nishizawa, T.; et al. Crystal Structure of Plant Vacuolar Iron Transporter VIT1. *Nat. Plants* **2019**, *5*, 308–315. [CrossRef] [PubMed]
177. Gollhofer, J.; Timofeev, R.; Lan, P.; Schmidt, W.; Buckhout, T.J. Vacuolar-Iron-Transporter1-Like Proteins Mediate Iron Homeostasis in *Arabidopsis*. *PLoS ONE* **2014**, *9*, e110468. [CrossRef] [PubMed]
178. Endo, K.; Basak, A.K.; Wilkens, A.; Mirzaei, M.; Kopriva, S.; Yamada, K. *Arabidopsis* MEB3 Functions as a Vacuolar Metal Transporter to Regulate Iron Accumulation in Roots. *Front. Plant Sci.* **2025**, *16*, 1517144. [CrossRef] [PubMed]
179. Zhang, Y.; Xu, Y.-H.; Yi, H.-Y.; Gong, J.-M. Vacuolar Membrane Transporters OsVIT1 and OsVIT2 Modulate Iron Translocation between Flag Leaves and Seeds in Rice. *Plant J.* **2012**, *72*, 400–410. [CrossRef] [PubMed]
180. Agrwal, K.; Veena, P.; Singhal, N.; Pandey, A.K. Vacuolar Iron Transporter-like Protein VTL5 Enhances Iron and Zinc Accumulation in Wheat Grain Endosperm. *Plant Biotechnol. J.* **2025**, *23*, 4503–4505. [CrossRef] [PubMed]
181. Morrissey, J.; Baxter, I.R.; Lee, J.; Li, L.; Lahner, B.; Grotz, N.; Kaplan, J.; Salt, D.E.; Guerinot, M.L. The Ferroportin Metal Efflux Proteins Function in Iron and Cobalt Homeostasis in *Arabidopsis*. *Plant Cell* **2009**, *21*, 3326–3338. [CrossRef] [PubMed]
182. Cai, X.; Hu, Z.; Sun, D.; Li, X.; Feng, H.; Wang, S.; Jin, C.; Tang, Y.; Morel, J.-L.; Aarts, M.G.M.; et al. Ferroportin Transporters Contribute to Nickel Hyperaccumulation in *Odontarrhena chalcidica*. *Bioresour. Technol.* **2026**, *452*, 134571. [CrossRef] [PubMed]
183. González, D.A.; De La Torre, V.S.G.; Fernández, R.R.; Barreau, L.; Merlot, S. Divergent Roles of IREG/Ferroportin Transporters from the Nickel Hyperaccumulator *Leucocroton havanensis*. *Physiol. Plant.* **2024**, *176*, e14261. [CrossRef] [PubMed]

184. Lanquar, V.; Lelièvre, F.; Bolte, S.; Hamès, C.; Alcon, C.; Neumann, D.; Vansuyt, G.; Curie, C.; Schröder, A.; Krämer, U.; et al. Mobilization of Vacuolar Iron by AtNRAMP3 and AtNRAMP4 Is Essential for Seed Germination on Low Iron. *EMBO J.* **2005**, *24*, 4041–4051. [CrossRef] [PubMed]
185. Bastow, E.L.; Garcia De La Torre, V.S.; Maclean, A.E.; Green, R.T.; Merlot, S.; Thomine, S.; Balk, J. Vacuolar Iron Stores Gated by NRAMP3 and NRAMP4 Are the Primary Source of Iron in Germinating Seeds. *Plant Physiol.* **2018**, *177*, 1267–1276. [CrossRef] [PubMed]
186. Li, Y.; Li, J.; Yu, Y.; Dai, X.; Gong, C.; Gu, D.; Xu, E.; Liu, Y.; Zou, Y.; Zhang, P.; et al. The Tonoplast-Localized Transporter OsNRAMP2 Is Involved in Iron Homeostasis and Affects Seed Germination in Rice. *J. Exp. Bot.* **2021**, *72*, 4839–4852. [CrossRef] [PubMed]
187. Conte, S.S.; Chu, H.-H.; Chan-Rodriguez, D.; Punshon, T.; Vasques, K.A.; Salt, D.E.; Walker, E.L. *Arabidopsis thaliana* Yellow Stripe1-Like4 and Yellow Stripe1-Like6 Localize to Internal Cellular Membranes and Are Involved in Metal Ion Homeostasis. *Front. Plant Sci.* **2013**, *4*, 283. [CrossRef] [PubMed]
188. Mary, V.; Schnell Ramos, M.; Gillet, C.; Socha, A.L.; Giraudat, J.; Agorio, A.; Merlot, S.; Clairet, C.; Kim, S.A.; Punshon, T.; et al. Bypassing Iron Storage in Endodermal Vacuoles Rescues the Iron Mobilization Defect in the *Natural Resistance Associated-Macrophage Protein3natural Resistance Associated-Macrophage Protein4* Double Mutant. *Plant Physiol.* **2015**, *169*, 748–759. [CrossRef] [PubMed]
189. Hoang, M.T.T.; Almeida, D.; Chay, S.; Alcon, C.; Corratge-Faillie, C.; Curie, C.; Mari, S. AtDTX25, a Member of the Multidrug and Toxic Compound Extrusion Family, Is a Vacuolar Ascorbate Transporter That Controls Intracellular Iron Cycling in *Arabidopsis*. *New Phytol.* **2021**, *231*, 1956–1967. [CrossRef] [PubMed]
190. Li, J.; Liu, Y.; Kong, L.; Xu, E.; Zou, Y.; Zhang, P.; Zhang, W.; Chen, X. An Intracellular Transporter OsNRAMP7 Is Required for Distribution and Accumulation of Iron into Rice Grains. *Plant Sci.* **2023**, *336*, 111831. [CrossRef] [PubMed]
191. Vert, G.; Barberon, M.; Zelazny, E.; Séguéla, M.; Briat, J.-F.; Curie, C. *Arabidopsis* IRT2 Cooperates with the High-Affinity Iron Uptake System to Maintain Iron Homeostasis in Root Epidermal Cells. *Planta* **2009**, *229*, 1171–1179. [CrossRef] [PubMed]
192. Hanikenne, M.; Esteves, S.M.; Fanara, S.; Rouached, H. Coordinated Homeostasis of Essential Mineral Nutrients: A Focus on Iron. *J. Exp. Bot.* **2021**, *72*, 2136–2153. [CrossRef] [PubMed]
193. Stanton, C.; Rodríguez-Celma, J.; Krämer, U.; Sanders, D.; Balk, J. BRUTUS-LIKE (BTSL) E3 Ligase-Mediated Fine-Tuning of Fe Regulation Negatively Affects Zn Tolerance of *Arabidopsis*. *J. Exp. Bot.* **2023**, *74*, 5767–5782. [CrossRef] [PubMed]
194. Remy, E.; Cabrito, T.R.; Batista, R.A.; Hussein, M.A.M.; Teixeira, M.C.; Athanasiadis, A.; Sá-Correia, I.; Duque, P. Intron Retention in the 5′UTR of the Novel ZIF2 Transporter Enhances Translation to Promote Zinc Tolerance in *Arabidopsis*. *PLoS Genet.* **2014**, *10*, e1004375. [CrossRef] [PubMed]
195. Lee, S.; Ricachenevsky, F.K.; Punshon, T. Functional Overlap of Two Major Facilitator Superfamily Transporter, ZIF1, and ZIFL1 in Zinc and Iron Homeostasis. *Biochem. Biophys. Res. Commun.* **2021**, *560*, 7–13. [CrossRef] [PubMed]
196. Martinengo, S.; Santoro, V.; Schiavon, M.; Celi, L.; Martin, M.; Said-Pullicino, D. The Influence of Phosphorus Availability on Rice Root Traits Driving Iron Plaque Formation and Dissolution, and Implications for Phosphorus Uptake. *Plant Soil* **2024**, *494*, 603–616. [CrossRef]
197. Bournier, M.; Tissot, N.; Mari, S.; Boucherez, J.; Lacombe, E.; Briat, J.-F.; Gaymard, F. *Arabidopsis* Ferritin 1 (*AtFer1*) Gene Regulation by the Phosphate Starvation Response 1 (*AtPHR1*) Transcription Factor Reveals a Direct Molecular Link between Iron and Phosphate Homeostasis. *J. Biol. Chem.* **2013**, *288*, 22670–22680. [CrossRef] [PubMed]
198. Balzergue, C.; Dartevelle, T.; Godon, C.; Laugier, E.; Meisrimler, C.; Teulon, J.-M.; Creff, A.; Bissler, M.; Brouchoud, C.; Hagège, A.; et al. Low Phosphate Activates STOP1-ALMT1 to Rapidly Inhibit Root Cell Elongation. *Nat. Commun.* **2017**, *8*, 15300. [CrossRef] [PubMed]
199. Cai, Y.; Ping, H.; Zhao, J.; Li, C.; Li, Y.; Liang, G. IRON MAN Interacts with Cu-DEFICIENCY INDUCED TRANSCRIPTION FACTOR 1 to Maintain Copper Homeostasis. *New Phytol.* **2024**, *242*, 1206–1217. [CrossRef] [PubMed]
200. Castaings, L.; Caquot, A.; Loubet, S.; Curie, C. The High-Affinity Metal Transporters NRAMP1 and IRT1 Team up to Take up Iron under Sufficient Metal Provision. *Sci. Rep.* **2016**, *6*, 37222. [CrossRef] [PubMed]
201. Cailliatte, R.; Schikora, A.; Briat, J.-F.; Mari, S.; Curie, C. High-Affinity Manganese Uptake by the Metal Transporter NRAMP1 Is Essential for *Arabidopsis* Growth in Low Manganese Conditions. *Plant Cell* **2010**, *22*, 904–917. [CrossRef] [PubMed]
202. Connorton, J.M.; Jones, E.R.; Rodríguez-Ramiro, I.; Fairweather-Tait, S.; Uauy, C.; Balk, J. Wheat Vacuolar Iron Transporter TaVIT2 Transports Fe and Mn and Is Effective for Biofortification. *Plant Physiol.* **2017**, *174*, 2434–2444. [CrossRef] [PubMed]
203. Chu, H.-H.; Car, S.; Socha, A.L.; Hindt, M.N.; Punshon, T.; Guerinot, M.L. The *Arabidopsis* MTP8 Transporter Determines the Localization of Manganese and Iron in Seeds. *Sci. Rep.* **2017**, *7*, 11024. [CrossRef] [PubMed]
204. Roschzttardtz, H.; Conéjéro, G.; Curie, C.; Mari, S. Identification of the Endodermal Vacuole as the Iron Storage Compartment in the *Arabidopsis* Embryo. *Plant Physiol.* **2009**, *151*, 1329–1338. [CrossRef] [PubMed]

205. Paolacci, A.R.; Celletti, S.; Catarcione, G.; Hawkesford, M.J.; Astolfi, S.; Ciaffi, M. Iron Deprivation Results in a Rapid but Not Sustained Increase of the Expression of Genes Involved in Iron Metabolism and Sulfate Uptake in Tomato (*Solanum Lycopersicum* L.) Seedlings. *J. Integr. Plant Biol.* **2014**, *56*, 88–100. [CrossRef] [PubMed]
206. Astolfi, S.; Zuchi, S.; Hubberten, H.-M.; Pinton, R.; Hoefgen, R. Supply of Sulphur to S-Deficient Young Barley Seedlings Restores Their Capability to Cope with Iron Shortage. *J. Exp. Bot.* **2010**, *61*, 799–806. [CrossRef] [PubMed]
207. Astolfi, S.; Cesco, S.; Zuchi, S.; Neumann, G.; Roemheld, V. Sulfur Starvation Reduces Phytosiderophores Release by Iron-Deficient Barley Plants. *Soil Sci. Plant Nutr.* **2006**, *52*, 43–48. [CrossRef]
208. Vigani, G.; Briat, J.-F. Impairment of Respiratory Chain under Nutrient Deficiency in Plants: Does It Play a Role in the Regulation of Iron and Sulfur Responsive Genes? *Front Plant Sci.* **2016**, *6*, 1185. [CrossRef] [PubMed]
209. Li, G.; Zhang, L.; Wu, J.; Wang, Z.; Wang, M.; Kronzucker, H.J.; Shi, W. Plant Iron Status Regulates Ammonium-Use Efficiency through Protein N-Glycosylation. *Plant Physiol.* **2024**, *195*, 1712–1727. [CrossRef] [PubMed]
210. Song, Y.; Wan, G.-Y.; Wang, J.-X.; Zhang, Z.-S.; Xia, J.-Q.; Sun, L.-Q.; Lu, J.; Ma, C.-X.; Yu, L.-H.; Xiang, C.-B.; et al. Balanced Nitrogen–Iron Sufficiency Boosts Grain Yield and Nitrogen Use Efficiency by Promoting Tillering. *Mol. Plant* **2023**, *16*, 1661–1677. [CrossRef] [PubMed]
211. Schuler, M.; Rellán-Álvarez, R.; Fink-Straube, C.; Abadía, J.; Bauer, P. Nicotianamine Functions in the Phloem-Based Transport of Iron to Sink Organs, in Pollen Development and Pollen Tube Growth in *Arabidopsis*. *Plant Cell* **2012**, *24*, 2380–2400. [CrossRef] [PubMed]
212. Deinlein, U.; Weber, M.; Schmidt, H.; Rensch, S.; Trampczynska, A.; Hansen, T.H.; Husted, S.; Schjoerring, J.K.; Talke, I.N.; Krämer, U.; et al. Elevated Nicotianamine Levels in *Arabidopsis halleri* Roots Play a Key Role in Zinc Hyperaccumulation. *Plant Cell* **2012**, *24*, 708–723. [CrossRef] [PubMed]
213. Cassin, G.; Mari, S.; Curie, C.; Briat, J.-F.; Czernic, P. Increased Sensitivity to Iron Deficiency in *Arabidopsis thaliana* Overaccumulating Nicotianamine. *J. Exp. Bot.* **2009**, *60*, 1249–1259. [CrossRef] [PubMed]
214. Chen, C.; Cui, Y.; Cui, M.; Zhou, W.; Wu, H.; Ling, H. A FIT-binding Protein Is Involved in Modulating Iron and Zinc Homeostasis in *Arabidopsis*. *Plant Cell Environ.* **2018**, *41*, 1698–1714. [CrossRef] [PubMed]
215. Pineau, C.; Loubet, S.; Lefoulon, C.; Chalies, C.; Fizames, C.; Lacombe, B.; Ferrand, M.; Loudet, O.; Berthomieu, P.; Richard, O. Natural Variation at the FRD3 MATE Transporter Locus Reveals Cross-Talk between Fe Homeostasis and Zn Tolerance in *Arabidopsis thaliana*. *PLoS Genet.* **2012**, *8*, e1003120. [CrossRef] [PubMed]
216. Charlier, J.-B.; Polese, C.; Nouet, C.; Carnol, M.; Bosman, B.; Krämer, U.; Motte, P.; Hanikenne, M. Zinc Triggers a Complex Transcriptional and Post-Transcriptional Regulation of the Metal Homeostasis Gene *FRD3* in *Arabidopsis* Relatives. *J. Exp. Bot.* **2015**, *66*, 3865–3878. [CrossRef] [PubMed]
217. Scheepers, M.; Spielmann, J.; Boulanger, M.; Carnol, M.; Bosman, B.; De Pauw, E.; Goormaghtigh, E.; Motte, P.; Hanikenne, M. Intertwined Metal Homeostasis, Oxidative and Biotic Stress Responses in the *Arabidopsis Frd3* Mutant. *Plant J.* **2020**, *102*, 34–52. [CrossRef] [PubMed]
218. Wu, H.; Chen, C.; Du, J.; Liu, H.; Cui, Y.; Zhang, Y.; He, Y.; Wang, Y.; Chu, C.; Feng, Z.; et al. Co-Overexpression *FIT* with *AtbHLH38* or *AtbHLH39* in *Arabidopsis*-Enhanced Cadmium Tolerance via Increased Cadmium Sequestration in Roots and Improved Iron Homeostasis of Shoots. *Plant Physiol.* **2012**, *158*, 790–800. [CrossRef] [PubMed]
219. Zhu, Y.; Dai, Y.; Jing, X.; Liu, X.; Jin, C. Inhibition of BRUTUS Enhances Plant Tolerance to Zn Toxicity by Upregulating Pathways Related to Iron Nutrition. *Life* **2022**, *12*, 216. [CrossRef] [PubMed]
220. Shinkawa, H.; Kobayashi, T.; Murota, A.; Kamijima, A.; Nishizawa, N.K. Stability and Function of Rice OsHRZ Ubiquitin Ligases Are Regulated at Multiple Sites by the Iron–Zinc Balance. *Plant J.* **2025**, *122*, e70258. [CrossRef] [PubMed]
221. Zheng, L.; Huang, F.; Narsai, R.; Wu, J.; Giraud, E.; He, F.; Cheng, L.; Wang, F.; Wu, P.; Whelan, J.; et al. Physiological and Transcriptome Analysis of Iron and Phosphorus Interaction in Rice Seedlings. *Plant Physiol.* **2009**, *151*, 262–274. [CrossRef] [PubMed]
222. Liu, X.X.; Zhu, X.F.; Xue, D.W.; Zheng, S.J.; Jin, C.W. Beyond Iron-Storage Pool: Functions of Plant Apoplastic Iron during Stress. *Trends Plant Sci.* **2023**, *28*, 941–954. [CrossRef] [PubMed]
223. Ward, J.T.; Lahner, B.; Yakubova, E.; Salt, D.E.; Raghothama, K.G. The Effect of Iron on the Primary Root Elongation of *Arabidopsis* during Phosphate Deficiency. *Plant Physiol.* **2008**, *147*, 1181–1191. [CrossRef] [PubMed]
224. Chutia, R.; Scharfenberg, S.; Neumann, S.; Abel, S.; Ziegler, J. Modulation of Phosphate Deficiency-Induced Metabolic Changes by Iron Availability in *Arabidopsis thaliana*. *Int. J. Mol. Sci.* **2021**, *22*, 7609. [CrossRef] [PubMed]
225. Thibaud, M.-C.; Arrighi, J.-F.; Bayle, V.; Chiarenza, S.; Creff, A.; Bustos, R.; Paz-Ares, J.; Poirier, Y.; Nussaume, L. Dissection of Local and Systemic Transcriptional Responses to Phosphate Starvation in *Arabidopsis*: Local versus Systemic Responses to Phosphate Starvation. *Plant J.* **2010**, *64*, 775–789. [CrossRef] [PubMed]

226. Mora-Macías, J.; Ojeda-Rivera, J.O.; Gutiérrez-Alanís, D.; Yong-Villalobos, L.; Oropeza-Aburto, A.; Raya-González, J.; Jiménez-Domínguez, G.; Chávez-Calvillo, G.; Rellán-Álvarez, R.; Herrera-Estrella, L. Malate-Dependent Fe Accumulation Is a Critical Checkpoint in the Root Developmental Response to Low Phosphate. *Proc. Natl. Acad. Sci. USA* **2017**, *114*, E3563–E3572. [CrossRef] [PubMed]
227. Wang, X.; Wang, Z.; Zheng, Z.; Dong, J.; Song, L.; Sui, L.; Nussaume, L.; Desnos, T.; Liu, D. Genetic Dissection of Fe-Dependent Signaling in Root Developmental Responses to Phosphate Deficiency. *Plant Physiol.* **2019**, *179*, 300–316. [CrossRef] [PubMed]
228. Godon, C.; Mercier, C.; Wang, X.; David, P.; Richaud, P.; Nussaume, L.; Liu, D.; Desnos, T. Under Phosphate Starvation Conditions, Fe and Al Trigger Accumulation of the Transcription Factor STOP1 in the Nucleus of *Arabidopsis* Root Cells. *Plant J.* **2019**, *99*, 937–949. [CrossRef] [PubMed]
229. Mercier, C.; Roux, B.; Have, M.; Le Poder, L.; Duong, N.; David, P.; Leonhardt, N.; Blanchard, L.; Naumann, C.; Abel, S.; et al. Root Responses to Aluminium and Iron Stresses Require the SIZ1 SUMO Ligase to Modulate the STOP1 Transcription Factor. *Plant J.* **2021**, *108*, 1507–1521. [CrossRef] [PubMed]
230. Zheng, Z.; Liu, D. SIZ1 Regulates Phosphate Deficiency-Induced Inhibition of Primary Root Growth of *Arabidopsis* by Modulating Fe Accumulation and ROS Production in Its Roots. *Plant Signal. Behav.* **2021**, *16*, 1946921. [CrossRef] [PubMed]
231. Shen, N.; Hou, S.; Tu, G.; Lan, W.; Jing, Y. Transcription Factor WRKY33 Mediates the Phosphate Deficiency-Induced Remodeling of Root Architecture by Modulating Iron Homeostasis in *Arabidopsis* Roots. *Int. J. Mol. Sci.* **2021**, *22*, 9275. [CrossRef] [PubMed]
232. Xu, Z.-R.; Cai, M.-L.; Yang, Y.; You, T.-T.; Ma, J.F.; Wang, P.; Zhao, F.-J. The Ferroxidases LPR1 and LPR2 Control Iron Translocation in the Xylem of *Arabidopsis* Plants. *Mol. Plant* **2022**, *15*, 1962–1975. [CrossRef] [PubMed]
233. Ticconi, C.A.; Lucero, R.D.; Sakhonwasee, S.; Adamson, A.W.; Creff, A.; Nussaume, L.; Desnos, T.; Abel, S. ER-Resident Proteins PDR2 and LPR1 Mediate the Developmental Response of Root Meristems to Phosphate Availability. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 14174–14179. [CrossRef] [PubMed]
234. Müller, J.; Toev, T.; Heisters, M.; Teller, J.; Moore, K.L.; Hause, G.; Dinesh, D.C.; Bürstenbinder, K.; Abel, S. Iron-Dependent Callose Deposition Adjusts Root Meristem Maintenance to Phosphate Availability. *Dev. Cell* **2015**, *33*, 216–230. [CrossRef] [PubMed]
235. Gao, Y.-Q.; Bu, L.-H.; Han, M.-L.; Wang, Y.-L.; Li, Z.-Y.; Liu, H.-T.; Chao, D.-Y. Long-Distance Blue Light Signalling Regulates Phosphate Deficiency-Induced Primary Root Growth Inhibition. *Mol. Plant* **2021**, *14*, 1539–1553. [CrossRef] [PubMed]
236. Li, T.; Zhang, R.; Satheesh, V.; Wang, P.; Ma, G.; Guo, J.; An, G.; Lei, M. The Chromatin Remodeler BRAHMA Recruits HISTONE DEACETYLASE6 to Regulate Root Growth Inhibition in Response to Phosphate Starvation in *Arabidopsis*. *J. Integr. Plant Biol.* **2022**, *64*, 2314–2326. [CrossRef] [PubMed]
237. Joon, R.; Singh, G.; Tyagi, D.; Meena, V.; Shukla, V.; Agrwal, K.; Saini, S.; Mankiran; Banoo, H.; Satbhai, S.B.; et al. Integrative Spatial Transcriptomic Analysis Pinpoints the Role of the Ferroxidase, TaMCO3, in Wheat Root Tip Iron Mobilization. *Plant J.* **2025**, *122*, e70188. [CrossRef] [PubMed]
238. Clúa, J.; Montpetit, J.; Jimenez-Sandoval, P.; Naumann, C.; Santiago, J.; Poirier, Y. A CYBDOM Protein Impacts Iron Homeostasis and Primary Root Growth under Phosphate Deficiency in *Arabidopsis*. *Nat. Commun.* **2024**, *15*, 423. [CrossRef] [PubMed]
239. Maniero, R.A.; Picco, C.; Hartmann, A.; Engelberger, F.; Gradogna, A.; Scholz-Starke, J.; Melzer, M.; Künze, G.; Carpaneto, A.; von Wirén, N.; et al. Ferric Reduction by a CYBDOM Protein Counteracts Increased Iron Availability in Root Meristems Induced by Phosphorus Deficiency. *Nat. Commun.* **2024**, *15*, 422. [CrossRef] [PubMed]
240. Wang, L.; Qian, J.; Li, M.; Zheng, H.; Yang, X.; Zheng, M.; Hsu, Y.-F. *Arabidopsis* PDE1 Confers Phosphate-Deficiency Tolerance in Primary Root Growth. *Plant Cell Rep.* **2023**, *43*, 8. [CrossRef] [PubMed]
241. Yang, X.; Ding, Y.; Wang, Y.; Wu, T.; Liu, H.; Yuan, P.; Hammond, J.P.; Kant, S.; Wang, S.; Cai, H.; et al. The PHR1–RSL2 Module Regulates Root Hair Elongation Induced by Phosphate Deficiency. *Plant J.* **2026**, *127*, e71068. [CrossRef] [PubMed]
242. Zhang, G.; Wang, H.; Ren, X.; Xiao, Y.; Liu, D.; Meng, W.; Qiu, Y.; Hu, B.; Xie, Q.; Chu, C.; et al. Brassinosteroid-Dependent Phosphorylation of PHOSPHATE STARVATION RESPONSE2 Reduces Its DNA-Binding Ability in Rice. *Plant Cell* **2024**, *36*, 2253–2271. [CrossRef] [PubMed]
243. Guo, M.; Ruan, W.; Zhang, Y.; Zhang, Y.; Wang, X.; Guo, Z.; Wang, L.; Zhou, T.; Paz-Ares, J.; Yi, K. A Reciprocal Inhibitory Module for Pi and Iron Signaling. *Mol. Plant* **2022**, *15*, 138–150. [CrossRef] [PubMed]
244. Sheng, H.; Jiang, Y.; Rahmati, M.; Chia, J.-C.; Dokuchayeva, T.; Kavulych, Y.; Zavodna, T.-O.; Mendoza, P.N.; Huang, R.; Smieshka, L.M.; et al. YSL3-Mediated Copper Distribution Is Required for Fertility, Seed Size and Protein Accumulation in *Brachypodium*. *Plant Physiol.* **2021**, *186*, 655–676. [CrossRef] [PubMed]
245. Waters, B.M.; McInturf, S.A.; Stein, R.J. Rosette Iron Deficiency Transcript and microRNA Profiling Reveals Links between Copper and Iron Homeostasis in *Arabidopsis thaliana*. *J. Exp. Bot.* **2012**, *63*, 5903–5918. [CrossRef] [PubMed]
246. Yan, J.; Chia, J.-C.; Sheng, H.; Jung, H.-I.; Zavodna, T.-O.; Zhang, L.; Huang, R.; Jiao, C.; Craft, E.J.; Fei, Z.; et al. *Arabidopsis* Pollen Fertility Requires the Transcription Factors CITF1 and SPL7 That Regulate Copper Delivery to Anthers and Jasmonic Acid Synthesis. *Plant Cell* **2017**, *29*, 3012–3029. [CrossRef] [PubMed]
247. Waters, B.M.; Armbrust, L.C. Optimal Copper Supply Is Required for Normal Plant Iron Deficiency Responses. *Plant Signal. Behav.* **2013**, *8*, e26611. [CrossRef] [PubMed]

248. Chia, J.; Vatamaniuk, O.K. Shall We Talk? New Details in Crosstalk between Copper and Iron Homeostasis Uncovered in *Arabidopsis thaliana*. *New Phytol.* **2024**, *242*, 832–835. [CrossRef] [PubMed]
249. Cai, Y.; Liang, G. CITF1 Functions Downstream of SPL7 to Specifically Regulate Cu Uptake in *Arabidopsis*. *Int. J. Mol. Sci.* **2022**, *23*, 7239. [CrossRef] [PubMed]
250. Zhu, J.; Li, J.; Hu, X.; Wang, J.; Fang, J.; Wang, S.; Shou, H. Role of Transcription Factor Complex OsbHLH156-OsIRO2 in Regulating Manganese, Copper, and Zinc Transporters in Rice. *J. Exp. Bot.* **2024**, *75*, 1112–1127. [CrossRef] [PubMed]
251. Xu, C.; Yang, H.; Huang, C.; Lan, M.; Zou, Z.; Zhang, F.; Zhang, L. Interaction Mechanism of Fe, Mg and Mn in Karst Soil-Mango System. *Land* **2023**, *12*, 256. [CrossRef]
252. Vert, G.; Grotz, N.; Dédaldéchamp, F.; Gaymard, F.; Guerinot, M.L.; Briat, J.-F.; Curie, C. IRT1, an *Arabidopsis* Transporter Essential for Iron Uptake from the Soil and for Plant Growth. *Plant Cell* **2002**, *14*, 1223–1233. [CrossRef] [PubMed]
253. Castaings, L.; Alcon, C.; Kosuth, T.; Correia, D.; Curie, C. Manganese Triggers Phosphorylation-mediated Endocytosis of the *Arabidopsis* Metal Transporter NRAMP1. *Plant J.* **2021**, *106*, 1328–1337. [CrossRef] [PubMed]
254. Lanquar, V.; Ramos, M.S.; Lelièvre, F.; Barbier-Brygoo, H.; Krieger-Liszkay, A.; Krämer, U.; Thomine, S. Export of Vacuolar Manganese by AtNRAMP3 and AtNRAMP4 Is Required for Optimal Photosynthesis and Growth under Manganese Deficiency. *Plant Physiol.* **2010**, *152*, 1986–1999. [CrossRef] [PubMed]
255. Eroglu, S.; Giehl, R.F.H.; Meier, B.; Takahashi, M.; Terada, Y.; Ignatyev, K.; Andresen, E.; Küpper, H.; Peiter, E.; von Wirén, N. Metal Tolerance Protein 8 Mediates Manganese Homeostasis and Iron Reallocation during Seed Development and Germination. *Plant Physiol.* **2017**, *174*, 1633–1647. [CrossRef] [PubMed]
256. Eroglu, S.; Meier, B.; von Wirén, N.; Peiter, E. The Vacuolar Manganese Transporter MTP8 Determines Tolerance to Iron Deficiency-Induced Chlorosis in *Arabidopsis*. *Plant Physiol.* **2016**, *170*, 1030–1045. [CrossRef] [PubMed]
257. Zhang, Z.; Fu, D.; Sun, Z.; Ju, C.; Miao, C.; Wang, Z.; Xie, D.; Ma, L.; Gong, Z.; Wang, C. Tonoplast-Associated Calcium Signaling Regulates Manganese Homeostasis in *Arabidopsis*. *Mol. Plant* **2021**, *14*, 805–819. [CrossRef] [PubMed]
258. Ishimaru, Y.; Masuda, H.; Bashir, K.; Inoue, H.; Tsukamoto, T.; Takahashi, M.; Nakanishi, H.; Aoki, N.; Hirose, T.; Ohsugi, R.; et al. Rice Metal-Nicotianamine Transporter, OsYSL2, Is Required for the Long-Distance Transport of Iron and Manganese. *Plant J.* **2010**, *62*, 379–390. [CrossRef] [PubMed]
259. Koike, S.; Inoue, H.; Mizuno, D.; Takahashi, M.; Nakanishi, H.; Mori, S.; Nishizawa, N.K. OsYSL2 Is a Rice Metal-Nicotianamine Transporter That Is Regulated by Iron and Expressed in the Phloem. *Plant J.* **2004**, *39*, 415–424. [CrossRef] [PubMed]
260. Schaaf, G.; Ludewig, U.; Erenoglu, B.E.; Mori, S.; Kitahara, T.; von Wirén, N. ZmYS1 Functions as a Proton-Coupled Symporter for Phytosiderophore- and Nicotianamine-Chelated Metals. *J. Biol. Chem.* **2004**, *279*, 9091–9096. [CrossRef] [PubMed]
261. Przybyla-Toscano, J.; Roland, M.; Gaymard, F.; Couturier, J.; Rouhier, N. Roles and Maturation of Iron–Sulfur Proteins in Plastids. *J. Biol. Inorg. Chem.* **2018**, *23*, 545–566. [CrossRef] [PubMed]
262. Astolfi, S.; Zuchi, S.; Neumann, G.; Cesco, S.; Sanità di Toppi, L.; Pinton, R. Response of Barley Plants to Fe Deficiency and Cd Contamination as Affected by S Starvation. *J. Exp. Bot.* **2012**, *63*, 1241–1250. [CrossRef] [PubMed]
263. Zuchi, S.; Watanabe, M.; Hubberten, H.-M.; Bromke, M.; Osorio, S.; Fernie, A.R.; Celletti, S.; Paolacci, A.R.; Catarcione, G.; Ciaffi, M.; et al. The Interplay between Sulfur and Iron Nutrition in Tomato. *Plant Physiol.* **2015**, *169*, 2624–2639. [CrossRef] [PubMed]
264. Zuchi, S.; Cesco, S.; Varanini, Z.; Pinton, R.; Astolfi, S. Sulphur Deprivation Limits Fe-Deficiency Responses in Tomato Plants. *Planta* **2009**, *230*, 85–94. [CrossRef] [PubMed]
265. Forieri, I.; Sticht, C.; Reichelt, M.; Gretz, N.; Hawkesford, M.J.; Malagoli, M.; Wirtz, M.; Hell, R. System Analysis of Metabolism and the Transcriptome in *Arabidopsis thaliana* Roots Reveals Differential Co-regulation upon Iron, Sulfur and Potassium Deficiency. *Plant Cell Environ.* **2017**, *40*, 95–107. [CrossRef] [PubMed]
266. Bouranis, D.L.; Chorianopoulou, S.N.; Protonotarios, V.E.; Siyiannis, V.F.; Hopkins, L.; Hawkesford, M.J. Leaf Responses of Young Iron-Inefficient Maize Plants to Sulfur Deprivation. *J. Plant Nutr.* **2003**, *26*, 1189–1202. [CrossRef]
267. Wu, Z.; Zhang, C.; Dai, C.; Ge, Y. Sufficient Sulfur Supply Promotes Seedling Growth, Alleviates Oxidation Stress, and Regulates Iron Uptake and Translocation in Rice. *Biol. Plant.* **2015**, *59*, 788–792. [CrossRef]
268. Ciaffi, M.; Paolacci, A.R.; Celletti, S.; Catarcione, G.; Kopriva, S.; Astolfi, S. Transcriptional and Physiological Changes in the S Assimilation Pathway Due to Single or Combined S and Fe Deprivation in Durum Wheat (*Triticum durum* L.) Seedlings. *J. Exp. Bot.* **2013**, *64*, 1663–1675. [CrossRef] [PubMed]
269. Astolfi, S.; Zuchi, S.; Passera, C.; Cesco, S. Does the Sulfur Assimilation Pathway Play a Role in the Response to Fe Deficiency in Maize (*Zea mays* L.) Plants? *J. Plant Nutr.* **2003**, *26*, 2111–2121. [CrossRef]
270. Astolfi, S.; Zuchi, S.; Cesco, S.; Sanità Di Toppi, L.; Pirazzi, D.; Badiani, M.; Varanini, Z.; Pinton, R. Iron Deficiency Induces Sulfate Uptake and Modulates Redistribution of Reduced Sulfur Pool in Barley Plants. *Funct. Plant Biol.* **2006**, *33*, 1055–1061. [CrossRef] [PubMed]
271. Aciksoz, S.B.; Yazici, A.; Ozturk, L.; Cakmak, I. Biofortification of Wheat with Iron through Soil and Foliar Application of Nitrogen and Iron Fertilizers. *Plant Soil* **2011**, *349*, 215–225. [CrossRef]

272. Chen, H.; Zhang, Q.; Cai, H.; Zhou, W.; Xu, F. H2O2 Mediates Nitrate-Induced Iron Chlorosis by Regulating Iron Homeostasis in Rice. *Plant Cell Environ.* **2018**, *41*, 767–781. [CrossRef] [PubMed]
273. Sun, W.-J.; Zhang, J.-C.; Ji, X.-L.; Feng, Z.-Q.; Wang, X.; Huang, W.-J.; You, C.-X.; Wang, X.-F.; Hao, Y.-J. Low Nitrate Alleviates Iron Deficiency by Regulating Iron Homeostasis in Apple. *Plant Cell Environ.* **2021**, *44*, 1869–1884. [CrossRef] [PubMed]
274. De La Peña, M.; Marín-Peña, A.J.; Urmeneta, L.; Coleto, I.; Castillo-González, J.; Van Liempd, S.M.; Falcón-Pérez, J.M.; Álvarez-Fernández, A.; González-Moro, M.B.; Marino, D. Ammonium Nutrition Interacts with Iron Homeostasis in *Brachypodium distachyon*. *J. Exp. Bot.* **2022**, *73*, 263–274. [CrossRef] [PubMed]
275. Zhang, X.; Liu, H.; Zhang, S.; Wang, J.; Wei, C. NH^{4+}-N Alleviates Iron Deficiency in Rice Seedlings under Calcareous Conditions. *Sci. Rep.* **2019**, *9*, 12712. [CrossRef] [PubMed]
276. Zhu, X.F.; Dong, X.Y.; Wu, Q.; Shen, R.F. Ammonium Regulates Fe Deficiency Responses by Enhancing Nitric Oxide Signaling in *Arabidopsis thaliana*. *Planta* **2019**, *250*, 1089–1102. [CrossRef] [PubMed]
277. Wu, J.; Zhang, Z.-S.; Xia, J.-Q.; Alfatih, A.; Song, Y.; Huang, Y.-J.; Wan, G.-Y.; Sun, L.-Q.; Tang, H.; Liu, Y.; et al. Rice NIN-LIKE PROTEIN 4 Plays a Pivotal Role in Nitrogen Use Efficiency. *Plant Biotechnol. J.* **2021**, *19*, 448–461. [CrossRef] [PubMed]
278. Coleto, I.; Bejarano, I.; Marín-Peña, A.J.; Medina, J.; Rioja, C.; Burow, M.; Marino, D. *Arabidopsis thaliana* Transcription Factors MYB28 and MYB29 Shape Ammonium Stress Responses by Regulating Fe Homeostasis. *New Phytol.* **2021**, *229*, 1021–1035. [CrossRef] [PubMed]
279. Liu, X.X.; Zhang, H.H.; Zhu, Q.Y.; Ye, J.Y.; Zhu, Y.X.; Jing, X.T.; Du, W.X.; Zhou, M.; Lin, X.Y.; Zheng, S.J.; et al. Phloem Iron Remodels Root Development in Response to Ammonium as the Major Nitrogen Source. *Nat. Commun.* **2022**, *13*, 561. [CrossRef] [PubMed]
280. Pandey, A.; Devi, L.L.; Gupta, S.; Prasad, P.; Agrwal, K.; Asif, M.H.; Pandey, A.K.; Bandyopadhyay, K.; Singh, A.P. Jasmonate Signaling Modulates Root Growth by Suppressing Iron Accumulation during Ammonium Stress. *Plant Physiol.* **2024**, *196*, 2213–2231. [CrossRef] [PubMed]
281. Maurer, F.; Müller, S.; Bauer, P. Suppression of Fe Deficiency Gene Expression by Jasmonate. *Plant Physiol. Biochem.* **2011**, *49*, 530–536. [CrossRef] [PubMed]
282. Jian, S.; Liao, Q.; Song, H.; Liu, Q.; Lepo, J.E.; Guan, C.; Zhang, J.; Ismail, A.M.; Zhang, Z. NRT1.1-Related NH_4^+ Toxicity Is Associated with a Disturbed Balance between NH_4^+ Uptake and Assimilation. *Plant Physiol.* **2018**, *178*, 1473–1488. [CrossRef] [PubMed]

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