Transcriptional integration of the plant responses to iron availability
Fei Gao, Christian Dubos

To cite this version:
Fei Gao, Christian Dubos. Transcriptional integration of the plant responses to iron availability. Journal of Experimental Botany, Oxford University Press (OUP), 2020, 2056-2070 (6), pp.2056-2070. 10.1093/jxb/eraa556/6007775. hal-03031725

HAL Id: hal-03031725
https://hal.inrae.fr/hal-03031725
Submitted on 30 Nov 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives| 4.0 International License
Transcriptional integration of the plant responses to iron availability

Fei Gao\textsuperscript{1} & Christian Dubos\textsuperscript{1,*}

\textsuperscript{1} BPMP, Univ Montpellier, CNRS, INRAE, Institut Agro, Montpellier, France
* Corresponding author (Tel: 0033 (0)499 61 28 18)
E-mails: Fei Gao, fei.gao@supagro.fr; Christian Dubos, christian.dubos@inrae.fr

\textbf{Highlights:} Within this review, current knowledge on the control of iron homeostasis in plants is presented and future prospects to improve our understanding of this complex mechanism are provided.
Abstract

Iron is one of the most important micronutrients for plant growth and development. It functions as the enzyme cofactor or component of electron transport chains in various vital metabolic processes, including photosynthesis, respiration, and amino acid biosynthesis. For maintaining iron homeostasis, and therefore preventing any deficiency or excess that could be detrimental, plants have evolved complex transcriptional regulatory networks to tightly control iron uptake, translocation, assimilation, and storage. Such regulatory networks are composed of various transcription factors among them members from the basic helix-loop-helix (bHLH) family play an essential role. Here, we first review recent advances in understanding the roles of bHLH transcription factors involved in the regulatory cascade controlling iron homeostasis in the model plant Arabidopsis, extending it to rice and other plant species. The importance of other classes of transcription factors will also be discussed. Secondly, we elaborate on the posttranslational mechanisms involved in the regulation of these regulatory networks. Finally, we give some perspectives on future research that should be conducted in order to precisely depict how plants control the homeostasis of this micronutrient.

Key words: Arabidopsis thaliana, basic helix-loop-helix, bHLH, iron homeostasis, rice, transcription factor.
Introduction

Iron (Fe) is an essential micronutrient for almost all living organisms. In humans, iron deficiency anemia is a major global health issue affecting about one billion people worldwide (Camaschella, 2015). Therefore, increasing the iron content in plants, especially in crops (biofortification), would have enormous benefits for human health. To achieve this goal, a critical question is to uncover the mechanisms controlling iron homeostasis in plants. Like in humans, iron is an essential microelement for plant growth and development. It functions in various vital metabolic processes (e.g. photosynthesis, respiration, amino acid biosynthesis) by acting as cofactor for several metalloproteins or component of electron transport chains (Hänsch and Mendel, 2009; Touraine et al., 2019). However, the excess of iron is deleterious to plants because of its capacity to interact with oxygen, generating reactive oxygen species (ROS) via the Fenton Reaction. Thus, the levels of iron in plant cells must be tightly regulated to avoid iron deficiency or iron excess, both of which severely affecting crops yield and the quality of their derived products (Briat et al., 2015).

Although iron is the fourth most-abundant element on earth, much of it is not readily available for plant use due to the poor solubility of its main (hydro)oxides, especially in neutral-to-alkaline soils (Guerinot and Yi, 1994; Colombo et al., 2018). To adapt to low iron conditions and acquire iron from soil, higher plants have evolved two different strategies (Marschner and Römheld, 1994) (Figure 1). Dicots and non-graminaceous monocots (non-grass species) employ the reduction strategy (named Strategy I). The graminaceous utilize the chelation strategy (named Strategy II). In strategy I, non-grass plants are able to acidify the rhizosphere to promote iron solubility through protons release and mobilize Fe$^{3+}$ through coumarins (i.e. fraxetin and sideretin) or riboflavins secretion (Santi and Schmidt, 2009; Fourcroy et al., 2016; Robe et al., 2020). Following iron mobilization, Fe$^{3+}$ is reduced into Fe$^{2+}$ (a more soluble form of iron) that is subsequently transported into the root epidermal cells via high affinity iron transporters from the Zrt/Irt-like protein (ZIP) family.

In Arabidopsis thaliana, the release of protons into the rhizosphere is insured by the H$^+$-ATPASE 2 (AHA2; Santi and Schmidt, 2009) whereas the reduction of iron and its translocation into the roots are ensured by FERRIC REDUCTION OXIDASE 2 (FRO2) and IRON-REGULATED TRANSPORTER1 (IRT1), respectively (Brumbarova et al., 2015; Connorton et al., 2017). AHA2, FRO2 and IRT1 associate into a complex at the surface of the
root epidermal cells most likely allowing optimizing iron acquisition and therefore its uptake (Martín-Barranco et al., 2020). Coumarins secretion is ensure by the PLEIOTROPIC DRUG RESISTANCE 9/ATP-BINDING CASSETTE G37 (PDR9/ABCG37) transporter (Fourcroy et al., 2014; Fourcroy et al., 2016). In strategy II, plants biosynthesize and secrete phytosiderophores of the mugineic acid family (MAs) into the rhizosphere to chelate Fe$^{3+}$ (Kobayashi et al., 2014). Fe$^{3+}$-MAs complexes are then transported into root cells by transporters of the YELLOW STRIPE 1 (YS1) and YELLOW STRIPE 1–like (YSL) family (Inoue et al., 2009; Murata et al., 2006). Interestingly, it was recently shown that some plant species might use both strategies. For instance, when grown in waterlogged soil condition, rice (Oryza sativa), a graminaceous species, acquires Fe$^{2+}$ from the soil through the activity of two Fe$^{2+}$ transporters, OsIRT1 and OsIRT2 (Ishimaru et al., 2006). The secretion of caffeic and protocatechuic acids via the PHENOLICS EFFLUX ZERO 2 (PEZ2) transporter participates to Fe$^{3+}$ mobilization and reduction into Fe$^{2+}$ (Bashir et al., 2011). If iron acquisition is the first step that participates to the maintenance of iron homeostasis in plants, it should be noted that it is not the sole mechanism involved in this process. Iron translocation, compartmentalization, assimilation and storage are also important processes required for the maintenance of iron homeostasis at the cellular and subcellular levels, throughout the whole plant body (Kobayashi and Nishizawa, 2012; Kobayashi et al., 2019).

Gene regulation is a crucial step for coping with iron fluctuations. For instance, FRO2 and IRT1 expression is induced when iron availability is low whereas the expression of the genes encoding the iron storage ferritin proteins (i.e. FER1, 3 and 4) is induced in response to iron excess (Tissot et al., 2019). How plants control iron homeostasis, by regulating the expression of genes involved in the various facets of this complex mechanism, was a critical question for the past three decades. To address this question, several studies mostly based on forward and reverse genetic approaches were conducted, leading to the identification and characterization of several transcription factors (TFs). These studies, mostly conducted in Arabidopsis and rice, allowed establishing regulatory networks controlling iron homeostasis in which basic helix-loop-helix (bHLH) TFs play a preponderant role (Gao et al., 2019; Gao et al., 2020a; Li et al., 2019) (Figure 2 and Table 1). bHLH proteins form one of the largest families of TFs (Heim et al., 2003) known to modulate several facets of plant growth and development, including cell differentiation, secondary metabolite biosynthesis, hormone signaling or the responses to environmental factors (Carretero-Paulet et al., 2010). Indeed,
additional TFs and protein regulating TFs activity were also identified (Yan et al., 2016; Palmer et al., 2013; Rodríguez-Celma et al., 2019a).

Within this review, current knowledge on the control of iron homeostasis by TFs, especially from the bHLH family, will be presented and discussed with a special emphasis on the latest findings. The transcriptional and posttranslational regulation of the iron homeostasis regulatory networks will also be documented. Last, some perspectives on future research to be conducted in order to improve our understanding of this complex mechanism will be provided.

The transcriptional regulation of iron homeostasis in strategy I plants, a preponderant role for bHLH TFs

The model plant Arabidopsis has allowed the identification of several factors involved in the regulation of iron homeostasis, notably by studying its response to iron deficiency. Such studies highlighted that the regulation of iron homeostasis was essentially occurring at the transcriptional level and was involving several TFs, in particular those of the bHLH family. This topic has also been covered in recent reviews by Gao et al., 2019; Kobayashi, 2019; Kobayashi et al., 2019; Wu and Ling, 2019; Schwarz and Bauer, 2020.

To date, at least six bHLH TF subfamilies (Heim et al., 2003), encoding 17 different proteins, are known to participate to the maintenance of iron homeostasis in Arabidopsis. These bHLH TFs form an intricate regulatory network composed of two interconnected regulatory modules (Figure 3).

The first module relies on the activity of FIT/bHLH29 (FER-LIKE IRON DEFICIENCY INDUCED TRANSCRIPTION FACTOR), a clade IIIa bHLH TF (Colangelo and Guerinot, 2004; Jakoby et al., 2004; Yuan et al., 2005). FIT/bHLH29 is a direct regulator of IRT1 and FRO2 expression, highlighting its central role for the regulation of the iron uptake machinery (Wang et al., 2013b). FIT/bHLH29 activity relies on its interaction with the four members of the Ib bHLH clade (i.e. bHLH38, bHLH39, bHLH100 and bHLH101), forming heterodimer complexes displaying partial redundant activities (Colangelo and Guerinot, 2004; Maurer et al., 2014; Yuan et al., 2008; Wang et al., 2013b) (Figure 3). Recently, the members of the IVa bHLH clade (i.e. bHLH18, bHLH19, bHLH20 and bHLH25) were identified as FIT/bHLH29 interacting proteins (Cui et al., 2018). These interactions were shown to
promote the degradation of FIT/bHLH29 via the 26S proteasome pathway, in a jasmonic acid-dependent manner (Cui et al., 2018). It is noteworthy that the Ib bHLH and the IVa bHLH TFs antagonize the activity of each other in regulating FIT/bHLH29 protein accumulation to tightly regulate the iron uptake machinery in response to different environmental stimuli (Cui et al., 2018) (Figure 3).

The second module acts upstream from FIT/bHLH29. It involves the four members of the IVc bHLH clade, namely ILR3/bHLH105 (IAA-LEUCINE RESISTANT 3), IDT1/bHLH34 (IRON DEFICIENCY TOLERANT 1), bHLH104 and bHLH115. These four TFs play additive roles in the iron deficiency responses and their activity is thought to rely, at least in part, on their ability to form homo- or heterodimers (Li et al., 2016; Zhang et al., 2015; Liang et al., 2017) (Figure 3). In response to iron deficiency, these TFs directly activate the expression of clade Ib bHLH and indirectly the one of FIT/bHLH29 (Li et al., 2016; Zhang et al., 2015; Liang et al., 2017).

Clade IVb bHLH TFs (i.e. PYE/bHLH47, bHLH11 and URI/bHLH121), also participate to the regulation of iron homeostasis in Arabidopsis. PYE/bHLH47 is a negative regulator (Long et al., 2010), which contains an EAR motif at its C-terminal region (i.e. DLNxxP; Kagale and Rozwadowski, 2011) that directly represses the expression of genes participating to the maintenance of iron homeostasis. Interaction studies highlighted that PYE/bHLH47 could heterodimerize with ILR3/bHLH105 and bHLH115 (Long et al., 2010; Zhang et al., 2015; Tissot et al., 2019). However, the role of these interactions was still a matter of debate until recently. In a recent study, ILR3/bHLH105 was found to play a central role in the regulation of iron homeostasis where it acts as both transcriptional activator and repressor of the plant responses to iron deficiency and excess, respectively (Kroh and Pilon, 2019; Tissot et al., 2019). In this study, the authors showed that the repressive activity of ILR3/bHLH105 was conferred by its dimerization with PYE/bHLH47 (Figure 3). The authors also highlighted that ILR3-PYE heterodimers might repress the expression of PYE/bHLH47 when iron availability is not limiting via a negative feedback regulatory loop (Figure 3). bHLH11 is another transcriptional repressor also containing an EAR motif (i.e. LxLxL) in its C-terminal domain (Tanabe et al., 2019). Overexpression studies suggest that bHLH11 inhibits the plant tolerance to iron deficiency and the expression of IRT1 and FRO2, most probably by indirectly repressing the expression of FIT/bHLH29 (Tanabe et al., 2019) (Figure 3). In contrast to PYE/bHLH47 and bHLH11, URI/ bHLH121 (UPSTREAM REGULATOR OF
IRT1) has been recently identified and characterized by three different groups as a positive regulator of the plant responses to iron deficiency (Lei et al., 2020; Lockhart, 2020; Gao et al., 2020a; Kim et al., 2019). URI/bHLH121 can form heterodimers with clade IVc bHLH TFs (Lei et al., 2020; Gao et al., 2020a; Kim et al., 2019) (Figure 3). These interactions participate to the relocation of URI/bHLH121 from the cytosol into the nucleus (Lei et al., 2020). It also suggests that the transcriptional activation of clade IVc bHLH target genes requires, at least in part, URI/bHLH121 (Lei et al., 2020; Gao et al., 2020a; Kim et al., 2019). In support of this assertion, it was demonstrated that several genes directly targeted by URI/bHLH121 are identical to that of clade IVc bHLH TFs (Figure 3). The expression of FIT/bHLH29 also relies on URI/bHLH121 activity, most probably via an indirect mechanism (Lei et al., 2020; Gao et al., 2020a; Kim et al., 2019). It is noteworthy that under iron deficiency condition, URI/bHLH121 accumulates in its phosphorylated form (Figure 3) that increases its binding capacity to the promoter region of its target genes such as the clade Ib bHLH TFs (Kim et al., 2019). Interestingly, both URI/bHLH121 transcript and protein accumulate constitutively regardless of iron status (Gao et al., 2020a; Kim et al., 2019). In contrast, URI/bHLH121 cellular localization in roots differs depending on iron availability (Gao et al., 2020a). When iron is not limiting, URI/bHLH121 mainly localizes in the stele and the endodermis, whereas under iron deficiency condition, URI/bHLH121 is primarily observed in the cortex and the epidermis cells, where it promotes iron uptake (Gao et al., 2020a). The thorough characterization of URI/bHLH121 indicates that it plays a key role in the control of plant iron homeostasis mainly because it directly or indirectly regulates the expression of most of the known genes involved in this regulatory network (Gao et al., 2020a; Kim et al., 2019) (Figure 3). Interestingly, it was recently reported that URI/bHLH121 directly activates FER1, FER3 and FER4 expression when iron availability is not in excess, indicating that URI/bHLH121 positively regulates the transient storage of iron in addition to the iron deficiency response (Gao et al., 2020b).

Functional homologs of most of the above-described Arabidopsis bHLH TFs have been characterized in several dicots (Figure 2, Table 1) indicating that this regulatory mechanism is most likely conserved within strategy I plants.
bHLH TFs involved in the regulation of iron homeostasis in strategy II plants

As stated above, plants have developed two different strategies to take up iron from the soil, distinguishing the non-graminaceous (Strategy I, reduction strategy) and graminaceous (Strategy II, chelation strategy) species (Figure 1). However, the in-depth study of the responses to iron deficiency in rice has highlighted that the regulation of iron homeostasis in strategy II plants involves the activity of several bHLH TFs belonging to the same clades than those identified in strategy I plant species (Figures 2 and 4, Table 1; Kobayashi, 2019; Kobayashi et al., 2019).

OsFIT/OsbHLH156 was recently identified as a positive regulator of the iron deficiency responses (Liang et al., 2020; Wang et al., 2020). Loss-of-function of OsFIT/OsbHLH156 resulted in strong iron deficiency symptoms under upland condition, whereas no iron deficiency symptoms were observed when plants were grown in waterlogged soil (Wang et al., 2020). These results imply that the strategy II iron uptake system was impaired in the Osfit mutant, an hypothesis that is supported by the disruption of the expression of strategy II iron uptake related genes. It includes genes encoding enzyme involved in MA biosynthesis (e.g. NAS1 and NAS2, NICOTIANAMINE SYNTHASE 1 and 2) or Fe^{3+}-MA transport (e.g. OsYSL15, YELLOW STRIPE-LIKE 15) (Figure 1) (Liang et al., 2020; Wang et al., 2020). Interestingly, it was demonstrated that OsFIT/OsbHLH156 regulates the expression of OsIRT1 and therefore participates also to the regulation of strategy I iron uptake mechanism (Liang et al., 2020) (Figure 1). OsFIT/OsbHLH156 interacts with OsIRO2/OsbHLH56, a clade Ib bHLH, and promotes its nuclear accumulation (Figure 4) (Liang et al., 2020; Wang et al., 2020). OsIRO2/OsbHLH56 was the first characterized bHLH TF involved in the control of iron homeostasis in rice, where it acts as a positive regulator of the iron deficiency response (Ogo et al., 2006; Ogo et al., 2007). Expression analysis indicated that the regulation of OsIRT1 expression by OsFIT/OsbHLH156 might be different to that of Arabidopsis or that it might involve other Ib bHLH TFs than OsIRO2/OsbHLH56.

Three out of the four clade IVc bHLH TFs (i.e. OsPRI1/OsbHLH060, OsPRI2/OsbHLH058, OsPRI3/OsbHLH059; POSITIVE REGULATOR OF IRON HOMEOSTASIS 1, 2 and 3) have been identified in rice as playing a positive role in the iron deficiency responses (Zhang et al., 2017; Kobayashi et al., 2019; Zhang et al., 2020b). The characterization of loss-of-function mutants suggested that these three TFs directly regulate the expression of
OsIRO2/OsBHLH56, and indirectly the expression of OsNAS1, OsNAS2, and OsYSL15 via OsIRO2/OsBHLH56 (Figure 4) (Zhang et al., 2020b; Zhang et al., 2017). Among the potential direct targets of OsPRI1/OsBHLH060, OsPRI2/bHLH058 and OsPRI3/OsBHLH059, there is also OsIRO3/OsBHLH63 (Figure 4) (Zhang et al., 2020b; Zhang et al., 2017). OsIRO3/OsBHLH63 is a member of the IVb clade and the functional homolog of PYE/bHLH47 (Zheng et al., 2010). Like PYE/bHLH47, OsIRO3/OsBHLH63 functions as a negative regulator of the iron deficiency responses (Zheng et al., 2010). It is likely that OsIRO3/OsBHLH63 activity might antagonize OsIRO2/OsBHLH56 to tightly regulate iron uptake and avoid iron overload (Zhang et al., 2012; Zhang et al., 2020b; Zhang et al., 2017; Zheng et al., 2010). To date, there is no information on the role of OsbHLH057, the fourth member of the rice clade IVc bHLH. Indeed, based on the information gathered in Arabidopsis, it is likely that OsbHLH057 participates to the control of iron homeostasis in rice. Whether OsbHLH057 exerts a minor role in specific cell types or in specific environmental conditions remains to be determined.

OsbHLH133 functions as a negative regulator of iron translocation from roots to shoots (Wang et al., 2013a). It should be noted that OsbHLH133 is the only one member of the clade VIIIc reported to date as involved in the regulation of iron homeostasis in plants. The other members of this clade in Arabidopsis play a positive role in root hair development but have never been associated with the maintenance of iron homeostasis (Bruex et al., 2012). Whether these bHLHs have a similar and conserved role, as that of OsbHLH133 in the regulation of iron homeostasis in strategy II plants, is to be investigated.

The transcriptional regulation of iron homeostasis is not restricted to the activity of bHLH TFs.

TFs from other families are involved in regulatory networks acting for iron homeostasis in both strategy I and strategy II plants (Figures 3 and 4, Table 2).

Several R2R3-MYB TFs from different plant species have been shown to be involved in the regulation of iron deficiency responses. In Arabidopsis, MYB10 and MYB72 are two iron deficiency inducible TFs required for proper iron uptake and whose expression is partially dependent on FIT/bHLH29 and URI/bHLH121 activities (Figure 3) (Gao et al., 2020a; Palmer et al., 2013; Zamioudis et al., 2014). Furthermore, MYB72 has been identified as a
transcriptional activator of genes associated with the biosynthesis and secretion of iron-mobilizing coumarins, highlighting its role in strategy I iron uptake system (Stringlis et al., 2018; Zamioudis et al., 2014) (Figure 1). Recently, it was shown that the Arabidopsis MYB28 and MYB29 are at the interface of the plant sensitivity to ammonium stress and the modulation of iron homeostasis (Coleto et al., 2020). Notably, the ammonium-dependent decrease of MYB28 and MYB29 expression (or the loss-of-function of both genes) leads to defects in iron translocation from roots to shoots and to the induction of the expression of FIT/bHLH29, clade Ib bHLHs, MYB72 as well as IMA1/FEP3 and IMA3/FEP1 in roots. MdMYB58, a close homolog of MYB72, was recently characterized as a positive regulator of iron uptake and translocation in apple (Wang et al., 2018). Further investigation showed that MdMYB58 transcriptional activity is inhibited by its heterodimerization with MdSAT1/MdbHLH18, a IVa clade bHLH TF (Wang et al., 2018). In contrast to the above-mentioned MYB TFs, MxMYB1 may function as a negative regulator of iron uptake and storage (Shen et al., 2008).

In Arabidopsis, WRKY46 plays a role in iron translocation between root and shoot by directly regulating the expression of VITL1 (VACUOLAR IRON TRANSPORTER-LIKE 1), a potential iron transporter involved in iron sequestration into the vacuoles (Yan et al., 2016; Gollhofer et al., 2014). HAP5A/NF-YC1 is also involved in iron translocation between root and shoot by regulating the expression of NAS1 (Zhu et al., 2020). ERF4 and ERF72 are two Arabidopsis TFs belonging to AP2/ERF family that have been reported as potential negative regulators of iron deficiency responses by repressing the expression of genes involved in iron uptake such as IRT1 (Liu et al., 2017a; Liu et al., 2017b). Similarly, MbERF4 and MbERF72 from Malus baccata as well as MxERF4 from Malus xiaojinensis act as negative regulators of the iron deficiency responses in these two apple species (Liu et al., 2018; Zhang et al., 2020a). In contrast, ERF95 was recently proposed to promote iron storage in Arabidopsis seeds (Sun et al., 2020). However, how iron distribution is controlled in seeds is not clearly established even if it was recently proposed that B3 TFs, which are involved in the regulation of embryo development and seed maturation, might be good candidates (Roschztarttz et al., 2020).

IDEF1 and IDEF2 (IRON DEFICIENCY-RESPONSIVE ELEMENT FACTOR 1 and 2) are two rice TFs belonging to two different families, the ABI3/VP1 and NAC, respectively (Figure 4) (Kobayashi et al., 2007; Ogo et al., 2008). These two TFs participate to the regulation of iron homeostasis in rice. IDEF1 is required for the coordinated activation of
genes related to iron uptake and translocation, including OsIRT1, OsNAS1, OsNAS2 and OsYSL15 (Kobayashi et al., 2009; Kobayashi et al., 2007). In addition, IDEF1 positively regulates the expression of OsIRO2, indicating that IDEF1 functions upstream of OsIRO2 in the iron deficiency regulatory network (Figure 4) (Kobayashi et al., 2009; Kobayashi et al., 2007). Interestingly, it was shown that IDEF1 could bind to iron and zinc atoms and that this capacity was necessary for its activity (Kobayashi et al., 2012). It was therefore proposed that IDEF1 could sense the cellular metal ion balance caused by changes in iron availability, suggesting that IDEF1 could be a cellular iron sensor allowing the tight regulation of the iron deficiency responses (Kobayashi et al., 2012). Similarly to IDEF1, IDEF2 plays a positive role in the plant response to iron deficiency (Ogo et al., 2008).

A family of peptides named IMA/FEP (IRONMAN/FE-UPTAKE-INDUCING PEPTIDE) has been reported to play a positive role in iron deficiency responses in Arabidopsis, by regulating a set of deficiency-inducible genes including Ib bHLH TFs, a function that seems to be conserved across plant species (Grillet et al., 2018; Hirayama et al., 2018). Two recent studies showed that URI/bHLH121 is a direct positive regulator of IMA1/FEP3 and IMA2/FEP2 expression (Gao et al., 2020a; Kim et al., 2019). These results indicate that IMAs/FEPs are implicated in the bHLH-dependent regulatory network regulating iron homeostasis. However, the precise regulatory mechanisms by which IMAs/FEPs act are still unknown.

**Post-translational regulation of the iron homeostasis regulatory networks**

Protein-protein interactions as well as post-translational modifications (i.e. ubiquitination, sumoylation, phosphorylation) can significantly affect the regulatory activities of TFs. Such mechanisms were shown to play an important role in the maintenance of iron homeostasis in plants. This topic has also been covered in recent reviews by Kobayashi, 2019; Rodríguez-Celma et al., 2019a; Schwarz and Bauer, 2020; Spielmann and Vert, 2020; Wu and Ling, 2019.

As described earlier, the transcriptional activity of bHLH TFs involved in the control of iron homeostasis is extensively dependent on *in vivo* protein-protein interactions, in the form of homo- or heterodimers (Figures 3 and 4, Tables 1 and 2). For instance, FIT/bHLH29 heterodimerization with clade Ib bHLH TFs is required for its transcriptional activity and
stability, whereas its interaction with clade IVa members promotes its degradation via the 26S proteasome pathway (Cui et al., 2018). bHLH39 nuclear localization also depends on its interaction with FIT/bHLH29 since in the cells lacking FIT/bHLH29, bHLH39 localizes predominantly in the cytoplasm (Trofimov et al., 2019). Similarly, OsFIT/OsbHLH156 facilitates the nuclear localization of OsIRO2/OsbHLH156, the functional homolog of bHLH39 in rice, suggesting that this post-translational regulatory mechanism is conserved within the plant kingdom (Liang et al., 2020; Wang et al., 2020). FIT/bHLH29 activity and/or stability are also modulated by its interaction with several additional protein partners that do not belong to the bHLH family of TFs (Figures 3, Tables 1) (reviewed in Kobayashi, 2019; Schwarz and Bauer, 2020; Spielmann and Vert, 2020; Wu and Ling, 2019).

Several ubiquitin E3 ligases have been identified and characterized as negative regulators of iron uptake to avoid potential iron overload by targeting bHLH TFs for their degradation (for details, see Spielmann and Vert, 2020; Rodríguez-Celma et al., 2019a) (Figures 3 and 4). BTS (BRUTUS), whose expression is induced by iron deficiency in roots, is proposed to be a critical iron sensing E3 ubiquitin ligase in Arabidopsis (Long et al., 2010). BTS interacts with ILR3/bHLH105 and bHLH115 to facilitate their degradation via the 26S proteasome pathway, allowing the fine tuning of the expression of downstream iron deficiency response genes (Figure 3) (Selote et al., 2015; Long et al., 2010). Similarly, OsHRZ1 and OsHRZ2 (HAEMERYTHRIN MOTIF-CONTAINING REALLY INTERESTING NEW GENE (RING) AND ZINC-FINGER PROTEIN 1 and 2), two rice ubiquitin E3 ligases displaying strong sequence similarities with BTS, have been reported as potential iron sensors playing a negative role in iron acquisition under iron sufficient conditions (Kobayashi et al., 2013). It was shown that OsHRZ1 could interact with OsPRI1/OsbHLH60, OsPRI2/OsbHLH58 and OsPRI3/OsbHLH59 and mediate their degradation via the 26S proteasome (Figure 4) (Zhang et al., 2020b; Zhang et al., 2017). However, different results were reported in another study only validating the sole interactions between OsHRZ1 and OsHRZ2 with OsPRI1/OsbHLH60 and OsPRI2/OsbHLH58 (Kobayashi et al., 2019). Another in vitro ubiquitination study showed that neither OsPRI1/OsbHLH60, nor OsPRI2/OsbHLH58 or OsPRI3/OsbHLH59 were ubiquitinated by OsHRZ1 or by OsHRZ2 (Kobayashi et al., 2019). These discrepancies may be due to the different methodologies and materials used in these studies. Whether these interactions participate to the ubiquitination and degradation of OsPRI1/OsbHLH60, OsPRI2/OsbHLH58 and OsPRI3/OsbHLH59 remains to be further demonstrated and confirmed. IDEF1, whose activity is necessary for HRZs expression, is also
degraded via the 26S proteasome pathway through a yet uncharacterized mechanism (Zhang et al., 2014). However, IDEF1 degradation is inhibited by its interaction with the IBP1.1 (IDEF1-BINDING PROTEINS 1.1) Bowman–Birk trypsin inhibitor protein (Figure 4) (Zhang et al., 2014). BTSL1 and BTSL2, two Arabidopsis homologs of BTS, function redundantly as negative regulators of the iron deficiency response (Hindt et al., 2017). In addition, BTSL1 and BTSL2 could directly target FIT/bHLH29 and promote its ubiquitination and subsequent degradation via the 26S proteasome pathway, thus negatively regulating the expression of iron uptake related genes (Figure 3) (Rodríguez-Celma et al., 2019b; Rodríguez-Celma et al., 2019a). In apples, MdBT1 and MdBT2, two BTB-TAZ proteins, interact with MdbHLH104. MdBT proteins interact as well with MdCUL3 (CULLIN-RING UBIQUITIN LIGASE 3) to form MdBT-MdCUL3 complexes required for MdbHLH104 ubiquitination and degradation via the 26S proteasome pathway (Zhao et al., 2016a). In contrast, MdSIZ1, a SIZ/PIAS-type SUMO E3 ligase, directly sumoylates MdbHLH104, especially under iron deficiency conditions, to enhance its stability (Zhou et al., 2019). Recently, it was shown that the mutation of an alanine into valine within IDT1/bHLH34 enhances both its stability and nuclear localization (Sharma and Yeh, 2020). Since this amino acid is conserved among clade IVc bHLH TFs in both monocots and dicots (Sharma and Yeh, 2020), one might speculate that this amino acid plays an important role in regulating the stability of clade IVc bHLH and thus their degradation via the 26S proteasome.

Phosphorylation plays also an important role in determining TF activity in the iron homeostasis networks (Figure 3). In Arabidopsis, FIT/bHLH29 phosphorylation by the calcium-dependent protein kinase CIPK11 (CBL-INTERACTING PROTEIN KINASE 11) positively regulates its activity by favoring its nuclear accumulation and dimerization with bHLH39 (Gratz et al., 2019). CIPK11 is induced and activated via a CBL1/9-mediated Ca²⁺ sensing pathway under iron deficiency conditions. CIPK21 could also interact with FIT/bHLH29, indicating that this protein kinase might have a potential role in the regulation of the FIT/bHLH29-dependent iron deficiency responses (Gratz et al., 2019). Recently, the phosphorylation of URI/bHLH121 was also reported as a key mechanism that regulates its activity (Kim et al., 2019). It was shown that the phosphorylated form of URI/bHLH121 only accumulates in response to iron deficiency, whereas the turnover of phosphorylated URI/bHLH121 is dependent on BTS activity (Kim et al., 2019). Under iron deficiency, URI/bHLH121 showed enhanced heterodimerization capability with IVc bHLH TFs and increased binding ability to the promoter of its target genes, indicating that the
phosphorylation of URI/bHLH121 plays a positive role in the iron deficiency responses (Kim et al., 2019). Nevertheless, since URI/bHLH121 can activate the expression of FER1, FER3 and FER4 in the stele when iron availability is not limiting (Gao et al., 2020b), a growth condition where the phosphorylated form of bHLH121 is degraded (Kim et al., 2019), it is likely that URI/bHLH121 is transcriptionally active independently of its phosphorylation state. Interestingly, as stated earlier, the pattern of accumulation of URI/bHLH121 within the root cells is controlled by an iron-dependent mechanism. URI/bHLH121 is preferentially accumulated in the epidermis and the cortex when plants are grown under iron deficiency and in the stele when grown under iron sufficiency. From these observations, one might hypothesize that URI/bHLH121 cellular distribution, rather than its transcriptional activity, is regulated by its phosphorylation state. However, the precise regulatory mechanism leading to the phosphorylation of URI/bHLH121 remains to be characterized.

Conclusions and future prospects

In the past two decades, remarkable progresses have been made in decrypting the molecular mechanisms that regulate iron homeostasis in both strategy I and strategy II plants (Figure 1). They highlighted that iron homeostasis in plants is regulated at the transcriptional level and involves several bHLH TFs that function in intricate regulatory networks (Figures 2 to 4).

The function of most of these bHLH TFs (i.e. clades Ib, IIIa, IVb and IVc) is conserved among grass and non-grass species (Figure 2), in contrast to the downstream target genes of iron acquisition machinery, which are distinctive in strategy I and strategy II plants (Figure 1). How these bHLH functional homologs have evolved to target different genes is an intriguing question. bHLH from clade IVa are involved in the regulation of iron homeostasis in Arabidopsis but whether or not this clade of bHLH TFs has a similar role in other plant species needs to be investigated. Additional investigations will also be necessary to determine if the non-grass homologs of OsbHLH133 (clade VIIIc) play a role in the control of iron homeostasis. Other regulatory proteins are also conserved between plants from both strategies. It is for instance the case for MYB and ERF TFs (Table 2) or for haemerythrin E3-ubiquitin ligases. Interestingly, BTB-TAZ-CUL3 ubiquitin ligase complexes participate to the degradation of clade IVc bHLH in apples. To date, such mechanism has only been observed in apple, raising the question of the conservation of this regulatory mechanism in other plants species, from non-grass to grass and from perennials to annuals. Ubiquitination,
as well as phosphorylation and sumoylation, are crucial posttranslational modifications for the regulation of key bHLH TFs activities involved in the iron homeostasis networks, notably clade IVc bHLH FIT/bHLH29 and URI/bHLH121. Whether such modifications participate to the regulation of other TF activities within this network is still to be assessed. Determining the degree of conservation of this regulatory network between plants from strategy I and strategy II, and between annual and perennial species, is still on its own a question that deserves to be addressed.

How plants sense iron status and switch on or repress the downstream regulatory network to regulate iron uptake, translocation, storage or assimilation has remained elusive. To date, haemerythrin E3-ubiquitin ligases are the main candidates (Rodríguez-Celma et al., 2019a). These E3-ubiquitin ligases are induced in response to iron deficiency, participate to the degradation of key bHLH TFs (i.e. clade IVc and FIT/bHLH29) and are destabilized upon iron binding at their haemerythrin motifs. IDEF1, the rice iron binding TF mentioned earlier, was also proposed as a potential iron sensor (Kobayashi et al., 2012; Kobayashi et al., 2009; Kobayashi et al., 2007). The characterization of IDEF1 functional homologs in non-grass species would be an additional element in support of this later hypothesis. Another important question concerns the regulation of the most upstream bHLH TFs. For instance, the main challenges would be to determine how the expression of clade IVc bHLH is controlled and to identify which protein kinase modulates URI/bHLH121 activity.

Recently, epigenetic regulation has emerged as playing important role in the control of iron homeostasis, by regulating DNA accessibility to promoters, and thus the expression of both TFs and iron uptake genes. This is for instance the case in Arabidopsis with the iron-dependent deposition of repressive marks on H3 histone (i.e. H3K27m3) at the promoter loci of FIT/bHLH29, IRT1 and FRO2 (Park et al., 2019). This additional layer of regulation in the transcriptional networks controlling iron homeostasis raises questions on the importance and the significance of such regulatory mechanism in this process.

Within this review, it is possible to grasp the extent of the complexity of the regulatory networks that regulate iron homeostasis in plants. Nevertheless, another level of complexity still to be investigated concerns the apparent redundancies existing between several TFs, the localization of their target genes, and thus the physiological functions that are controlled. This will be achieved by the in depth study of the tissue and cellular localization of the
different TFs as well as the proteins involved in their regulation. Such knowledge is necessary to fully decrypt and understand the dynamics of this regulatory process. Unfortunately, such data are only available for a few of these proteins (Long et al., 2010; Gao et al., 2020a; Samira et al., 2018).

In conclusion, much work still lies ahead to fully comprehend the transcriptional regulatory network that regulate iron homeostasis in plants, which might offer novel opportunities for improving plant growth and health and for generating iron-fortified crops.
Acknowledgements
This work was supported by grants from the “Agence Nationale de la Recherche (ANR)” to C.D. Support was provided by the China Scholarship Council to F.G. We thank Florence Vignols for help in preparing this article.

Author Contribution
FG and CD wrote the manuscript
References


transporter1-like proteins mediate iron homeostasis in Arabidopsis. PLoS One 9, 
e110468.

Meiser J, Mai H-J, Drerup M. 2019. CIPK11-dependent phosphorylation modulates 
FIT activity to promote Arabidopsis iron acquisition in response to calcium signaling. 
Developmental cell 48, 726-740. e710.

Grillet L, Lan P, Li W, Mokkapati G, Schmidt W. 2018. IRON MAN is a ubiquitous 
family of peptides that control iron transport in plants. Nature plants 4, 953-963.

Physiology 104, 815-820.

Hänsch R, Mendel RR. 2009. Physiological functions of mineral micronutrients (cu, zn, 
Mn, Fe, Ni, Mo, B, cl). Current Opinion in Plant Biology 12, 259-266.

basic helix–loop–helix transcription factor family in plants: a genome-wide study of 
protein structure and functional diversity. Molecular biology and evolution 20, 735- 
747.

Hindt MN, Akmakjian GZ, Pivarski KL, Punshon T, Baxter I, Salt DE, Guerinot 
ML. 2017. BRUTUS and its paralogs, BTS LIKE1 and BTS LIKE2, encode important 
negative regulators of the iron deficiency response in Arabidopsis thaliana. 
Metallomics 9, 876-890.

Hirayama T, Lei GJ, Yamaji N, Nakagawa N, Ma JF. 2018. The putative peptide gene 
FEP1 regulates iron deficiency response in Arabidopsis. Plant and Cell Physiology 59, 
1739-1752.

Huang D, Dai W. 2015. Molecular characterization of the basic helix-loop-helix (bHLH) 
genes that are differentially expressed and induced by iron deficiency in Populus. 
Plant cell reports 34, 1211-1224.

Inoue H, Kobayashi T, Nozoye T, Takahashi M, Kakei Y, Suzuki K, Nakazono M, 
Nakanishi H, Mori S, Nishizawa NK. 2009. Rice OsYSL15 is an iron-regulated iron 
(III)-deoxymugineic acid transporter expressed in the roots and is essential for iron


Zhang H, Li Y, Pu M, Xu P, Liang G, Yu D. 2020b. Oryza sativa POSITIVE REGULATOR OF IRON DEFICIENCY RESPONSE 2 (OsPRI2) and OsPRI3 are involved in the maintenance of Fe homeostasis. Plant, cell & environment 43, 261-274.


Table 1. bHLH TFs involved in the regulation of iron homeostasis in plants.

<table>
<thead>
<tr>
<th>Name</th>
<th>Clade</th>
<th>Species</th>
<th>Interacting proteins</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>AtbHLH38*</td>
<td>Ib</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29, DELLAs</td>
<td>Yuan et al., 2008; Wang et al., 2013</td>
</tr>
<tr>
<td>AtbHLH39*</td>
<td>Ib</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29, DELLAs</td>
<td>Yuan et al., 2008; Wang et al., 2013</td>
</tr>
<tr>
<td>AtbHLH100*</td>
<td>Ib</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Wang et al., 2013</td>
</tr>
<tr>
<td>AtbHLH101*</td>
<td>Ib</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Wang et al., 2013</td>
</tr>
<tr>
<td>FIT/AtbHLH29 *</td>
<td>IIIa</td>
<td>A. thaliana</td>
<td>AtbHLH38, AtbHLH39, AtbHLH100, AtbHLH101, AtbHLH18, AtbHLH19, AtbHLH20, AtbHLH25, BTSL1, BTSL2, CIPK11, DELLAs, EIL1, EIN3, MED16, ZAT12</td>
<td>Colangelo and Guerinot, 2004; Jakoby et al., 2004; Yuan et al., 2005</td>
</tr>
<tr>
<td>MYC2/AtbHLH6</td>
<td>IIIe</td>
<td>A. thaliana</td>
<td></td>
<td>Cui et al., 2018</td>
</tr>
<tr>
<td>AtbHLH18*</td>
<td>IVa</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Cui et al., 2018</td>
</tr>
<tr>
<td>AtbHLH19*</td>
<td>IVa</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Cui et al., 2018</td>
</tr>
<tr>
<td>AtbHLH20*</td>
<td>IVa</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Cui et al., 2018</td>
</tr>
<tr>
<td>AtbHLH25*</td>
<td>IVa</td>
<td>A. thaliana</td>
<td>FIT/AtbHLH29</td>
<td>Cui et al., 2018</td>
</tr>
<tr>
<td>AtbHLH11</td>
<td>IVb</td>
<td>A. thaliana</td>
<td>IDT1/AtbHLH34, AtbHLH104, ILR3/AtbHLH105, AtbHLH115</td>
<td>Tanabe et al., 2019</td>
</tr>
<tr>
<td>PYE/AtbHLH47</td>
<td>IVb</td>
<td>A. thaliana</td>
<td>ILR3/AtbHLH105, AtbHLH115</td>
<td>Long et al., 2010</td>
</tr>
<tr>
<td>URI/AtbHLH121</td>
<td>IVb</td>
<td>A. thaliana</td>
<td>IDT1/AtbHLH34, AtbHLH104, ILR3/AtbHLH105, AtbHLH115</td>
<td>Gao et al., 2020b; Kim et al., 2019; Lei et al., 2020</td>
</tr>
<tr>
<td>IDT1/AtbHLH34</td>
<td>IVc</td>
<td>A. thaliana</td>
<td>IDT1/AtbHLH34, AtbHLH104</td>
<td>Li et al., 2016</td>
</tr>
<tr>
<td>GenBank Accession</td>
<td>Gene Symbol</td>
<td>Organism</td>
<td>Species</td>
<td>Description</td>
</tr>
<tr>
<td>-------------------</td>
<td>-------------</td>
<td>----------</td>
<td>---------</td>
<td>-------------</td>
</tr>
<tr>
<td>OsIRO2/OsbHLH56</td>
<td>Os. sativa</td>
<td>Ib</td>
<td>O. sativa</td>
<td>OsFIT/OsbHLH156</td>
</tr>
<tr>
<td>OsIRO3/OsbHLH63</td>
<td>Os. sativa</td>
<td>IVb</td>
<td>O. sativa</td>
<td></td>
</tr>
<tr>
<td>OsFIT/OsbHLH156</td>
<td>Os. sativa</td>
<td>IIIa</td>
<td>Os. sativa</td>
<td>OsIRO2/OsbHLH56</td>
</tr>
<tr>
<td>OsPRI1/OsbHLH60</td>
<td>Os. sativa</td>
<td>IVc</td>
<td>O. sativa</td>
<td>OsHRZ1</td>
</tr>
<tr>
<td>OsPRI2/OsbHLH58</td>
<td>Os. sativa</td>
<td>IVc</td>
<td>O. sativa</td>
<td>OsHRZ1</td>
</tr>
<tr>
<td>OsPRI3/OsbHLH59</td>
<td>Os. sativa</td>
<td>IVc</td>
<td>O. sativa</td>
<td>OsHRZ1</td>
</tr>
<tr>
<td>OsbHLH133</td>
<td>Os. sativa</td>
<td>VIIlc</td>
<td>O. sativa</td>
<td></td>
</tr>
<tr>
<td>GmbHLH57</td>
<td>G. max</td>
<td>IIIa</td>
<td>G. max</td>
<td>GmbHLH300</td>
</tr>
<tr>
<td>GmbHLH300</td>
<td>G. max</td>
<td>Ib</td>
<td>G. max</td>
<td>GmbHLH57</td>
</tr>
<tr>
<td>FER</td>
<td>S. lycopersicum</td>
<td>IIIa</td>
<td>S. lycopersicum</td>
<td>SlbHLH68</td>
</tr>
<tr>
<td>SlbHLH68</td>
<td>S. lycopersicum</td>
<td>Ib</td>
<td>S. lycopersicum</td>
<td>FER</td>
</tr>
<tr>
<td>MxIRO2</td>
<td>M. xiaojinensis</td>
<td>Ib</td>
<td>M. xiaojinensis</td>
<td></td>
</tr>
<tr>
<td>MxFIT</td>
<td>M. xiaojinensis</td>
<td>IIIa</td>
<td>M. xiaojinensis</td>
<td>MxERF4</td>
</tr>
<tr>
<td>PtFIT</td>
<td>P. tremula</td>
<td>IIIa</td>
<td>P. tremula</td>
<td></td>
</tr>
<tr>
<td>PtIRO</td>
<td>P. tremula</td>
<td>Ib</td>
<td>P. tremula</td>
<td></td>
</tr>
<tr>
<td>SAT1/MdbHLH18</td>
<td>M. domestica</td>
<td>IVa</td>
<td>M. domestica</td>
<td>MdMYB58</td>
</tr>
<tr>
<td>Gene</td>
<td>IV</td>
<td>Species</td>
<td>Proteins</td>
<td>Reference</td>
</tr>
<tr>
<td>--------------</td>
<td>------</td>
<td>--------------</td>
<td>------------------------------------</td>
<td>------------------------------------</td>
</tr>
<tr>
<td>MdbHLH104</td>
<td>IVc</td>
<td><em>M. domestica</em></td>
<td>MdB1, MdB2, MdBHLH104, MdBHLH105, MdBHLH115, MdBHLH11, MdBHLH121, MdPYE</td>
<td>Zhao <em>et al.</em>, 2016b</td>
</tr>
<tr>
<td>NtbHLH1</td>
<td>IVb</td>
<td><em>N. tabacum</em></td>
<td></td>
<td>Li <em>et al.</em>, 2020</td>
</tr>
<tr>
<td>CmbHLH1</td>
<td>IVc</td>
<td><em>C. morifolium</em></td>
<td></td>
<td>Zhao <em>et al.</em>, 2014</td>
</tr>
<tr>
<td>FEFE/CmbHLH38</td>
<td>Ib</td>
<td><em>C. melo</em></td>
<td>CmFIT</td>
<td>Ramamurthy and Waters, 2017</td>
</tr>
<tr>
<td>GmORG3</td>
<td>Ib</td>
<td><em>G. max</em></td>
<td></td>
<td>Xu <em>et al.</em>, 2017</td>
</tr>
</tbody>
</table>

*: for details on posttranslational regulation of FIT activity, see Wu and Ling, 2020 and Schwarz and Bauer, 2020.
Table 2. TFs other than bHLHs involved in the regulation of iron homeostasis in plants.

<table>
<thead>
<tr>
<th>TF family</th>
<th>Gene name</th>
<th>Species</th>
<th>Interacting proteins</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABI3/VP1</td>
<td>IDEF1</td>
<td><em>O. sativa</em></td>
<td>IBP1</td>
<td>Kobayashi et al., 2007</td>
</tr>
<tr>
<td>ARF</td>
<td>OsARF12</td>
<td><em>O. sativa</em></td>
<td></td>
<td>Qi et al., 2012</td>
</tr>
<tr>
<td>ARF</td>
<td>OsARF16</td>
<td><em>O. sativa</em></td>
<td></td>
<td>Shen et al., 2016</td>
</tr>
<tr>
<td>C2H2</td>
<td>ZAT12*</td>
<td><em>A. thaliana</em></td>
<td>FIT/bHLH29</td>
<td>Le et al., 2016</td>
</tr>
<tr>
<td>EIL</td>
<td>EIN3*</td>
<td><em>A. thaliana</em></td>
<td>FIT/bHLH29</td>
<td>Lingam et al., 2011</td>
</tr>
<tr>
<td>EIL</td>
<td>EIL1*</td>
<td><em>A. thaliana</em></td>
<td>FIT/bHLH29</td>
<td>Lingam et al., 2011</td>
</tr>
<tr>
<td>ERF</td>
<td>ERF4</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Liu et al., 2017a</td>
</tr>
<tr>
<td>ERF</td>
<td>ERF72</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Liu et al., 2017b</td>
</tr>
<tr>
<td>ERF</td>
<td>ERF95</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Sun et al., 2020</td>
</tr>
<tr>
<td>ERF</td>
<td>MxERF4</td>
<td><em>M. xiaojinensis</em></td>
<td>MxFIT</td>
<td>Liu et al., 2018</td>
</tr>
<tr>
<td>ERF</td>
<td>MbERF4</td>
<td><em>M. baccata</em></td>
<td>MbERF72</td>
<td>Zhang et al., 2020a</td>
</tr>
<tr>
<td>ERF</td>
<td>MxERF72</td>
<td><em>M. baccata</em></td>
<td>MbERF4</td>
<td>Zhang et al., 2020a</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MYB10</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Palmer et al., 2013</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MYB28</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Coletto et al., 2020</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MYB29</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Coletto et al., 2020</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MYB72</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Palmer et al., 2013</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MdMYB58</td>
<td><em>M. domestica</em></td>
<td>MdSAT1/MdbHLH18</td>
<td>Wang et al., 2018</td>
</tr>
<tr>
<td>MYB (R2R3)</td>
<td>MxMYB1</td>
<td><em>M. xiaojinensis</em></td>
<td></td>
<td>Shen et al., 2008</td>
</tr>
<tr>
<td>NAC</td>
<td>IDEF2</td>
<td><em>O. sativa</em></td>
<td></td>
<td>Ogo et al., 2008</td>
</tr>
<tr>
<td>NF-YC</td>
<td>HAP5A/NF-YC1</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Zhu et al., 2020</td>
</tr>
<tr>
<td>WRKY</td>
<td>WRKY46</td>
<td><em>A. thaliana</em></td>
<td></td>
<td>Yan et al., 2016</td>
</tr>
</tbody>
</table>

*: for details on posttranslational regulation of FIT activity, see Wu and Ling, 2020 and Schwarz and Bauer, 2020.
Figure legends

Figure 1. Schematic diagram of iron uptake strategies in Arabidopsis and rice. In Arabidopsis, AHA2 secretes protons into the rhizosphere to increase Fe$^{3+}$ solubility; PDR9 secretes Fe-mobilizing coumarins (i.e. fraxetin and sideretin) to mobilize and chelate Fe$^{3+}$. Fe$^{3+}$ is reduced into Fe$^{2+}$ and is subsequently transported into the root epidermal cells by FRO2 and IRT1, respectively. AHA2, FRO2 and IRT1 form a protein complex optimizing Fe acquisition by creating a local environment with low pH and high Fe$^{2+}$ concentration. Rice biosynthesizes and secretes DMA (2-deoxy-mugineic acid) to chelate Fe$^{3+}$. Fe$^{3+}$-DMA complexes are transported into root cells via YSL15 and YSL16. In addition, rice also uptakes Fe$^{2+}$ from the soil through the activity of two Fe$^{2+}$ transporters, OsIRT1 and OsIRT2 under waterlogged soil condition. The secretion of CA and PCA via the PEZ2 phenolics efflux transporter participates to Fe$^{3+}$ mobilization and reduction into Fe$^{2+}$. AHA2: H$^+$-ATPase 2; PDR9: PLEIOTROPIC DRUG RESISTANCE 9/ATP-BINDING CASSETTE G37; FRO2: FERRIC REDUCTION OXIDASE 2; IRT1: IRON-REGULATED TRANSPORTER 1, F6'H1: FERULOYL CoA 6’ HYDROXYLASE 1; S8H: SCOPOLETIN 8-HYDROXYLASE; CYP82C4: FRAXETIN 5-HYDROXYLASE; TOM1: TRANSPORTER OF MUGINEIC ACID 1; YSL15/16: YELLOW STRIPE-LIKE 15/16; OsIRT1/2: Rice IRON-REGULATED TRANSPORTER 1/2; PEZ2: PHENOLICS EFFLUX ZERO 2; OsNAS: NICOTIANAMINE SYNTHASE; OsNAAT: NICOTIANAMINE AMINOTRANSFERASE; OsDMAS: DEOXYMUGINEIC ACID SYNTHASE; SAM: S-adenosyl methionine; NA: nicotianamine; CA: caffeic acid; PCA: protocatechuic acid.

Figure 2. Phylogenetic tree of bHLH TFs involved in the regulation of iron homeostasis in plants. The tree was constructed by using the neighbor-joining method with the MEGA software (v10.0.5) using full-length bHLH amino acid sequences. The bootstrap analysis was carried out with 1000 replicates. Sequences were aligned prior to the construction of the phylogenetic tree using the ClustalX software (v2.0.11). The different bHLH clades are designated as previously reported (Heim et al., 2003). Species abbreviations: At, Arabidopsis thaliana; Md, Malus domestica; Nt, Nicotiana tabacum;
Os, *Oryza sativa*; Sl, *Solanum lycopersicum*; Gm, *Glycine max*; Mx, *Malus xiaojinensis*; Cm, (*CmbHLH1*), Chrysanthemum *morifolium*; Cm (*CmbHLH38*), Cucumis *melo*; Pt, *Populus tremula*.

**Figure 3.** *bHLH TFs network that regulates iron homeostasis in Arabidopsis.* Question marks indicate protein complexes for which transcriptional activities have not yet been clearly demonstrated. The colour code for the *bHLH* TFs refers to the clades described Figure 2. Non *bHLH* proteins are in grey. EIN3 and EIL1 favor FIT stability whereas MED16 and MED25 mediate the FIT/bHLH29-dependent iron deficiency responses (for additional details on posttranslational regulation of FIT, see Kobayashi, 2019; Schwarz and Bauer, 2020; Spielmann and Vert, 2020; Wu and Ling, 2019). EIN3: ETHYLENE INSENSITIVE 3; EIL1: ETHYLENE INSENSITIVE 3-LIKE1; FBP: FIT-BINDING PROTEIN; MED16 AND 25: MEDIATOR SUBUNIT 16 and 25; ZAT12: ZINC FINGER OF ARABIDOPSIS THALIANA 12.

**Figure 4.** *bHLH TFs network that regulates iron homeostasis in rice.* Question mark indicates the putative degradation mechanism for OsPRI1 and OsPRI2 via OsHRZ2. The colour code for the *bHLH* TFs refers to the clades described Figure 2. Non *bHLH* proteins are in grey. IBP1.1: IDEF1-BINDING PROTEINS 1.1.
Figure 1. Schematic diagram of iron uptake strategies in Arabidopsis an rice. In Arabidopsis, AHA2 secretes protons into the rhizosphere to increase Fe³⁺ solubility; PDR9 secretes Fe-mobilizing coumarins (i.e. fraxetin and sideretin) to mobilize and chelate Fe³⁺. Fe³⁺ is reduced into Fe²⁺ and is subsequently transported into the root epidermal cells by FRO2 and IRT1, respectively. AHA2, FRO2 and IRT1 form a protein complex optimizing Fe acquisition by creating a local environment with low pH and high Fe²⁺ concentration. Rice biosynthesizes and secretes DMA to chelate Fe²⁺. Fe³⁺-DMA complexes are transported into root cells via YSL15 and YSL16. In addition, rice also uptake Fe²⁺ from the soil through the activity of two Fe²⁺ transporters, OsIRT1 and OsIRT2 under waterlogged soil condition. The secretion of CA and PCA via the PEZ2 phenolics efflux transporter participates to Fe²⁺ mobilization and reduction into Fe²⁺. AHA2: H⁺-ATPase 2, PDR9: PLEIOTROPIC DRUG RESISTANCE 9/ATP-BINDING CASSETTE G37, FRO2: FERRIC REDUCTION OXIDASE 2; IRT1: IRON-REGULATED TRANSPORTER 1, F6H1: FERULOYL CoA 6 HYDROXYLASE 1; S9H1: SCOPOLETIN 8-HYDROXYLASE; CYP82C4: FRAXETIN 5-HYDROXYLASE; TOM1: TRANSPORTER OF MUGINEIC ACID 1; YSL15/16: YELLOW STRIPE-LIKE 15/16; OsIRT1/2: RICE IRON-REGULATED TRANSPORTER 1/2; PEZ2: PHENOLICS EFFLUX ZERO 2; OsNAS: NICOTIANAMINE SYNTHASE; OsNAAT: NICOTIANAMINE AMINOTRANSFERASE; OsDMAS: DEOXYMUGINEIC ACID SYNTHASE; SAM: S-adenosyl methionine; NA: nicotianamine; CA: caffeic acid; PCA: protocatechuc acid.
Figure 2. Phylogenetic tree of bHLH TFs involved in the regulation of iron homeostasis in plants. The tree was constructed by using the neighbor-joining method with the MEGA software (v10.0.5) using full-length bHLH amino acid sequences. The bootstrap analysis was carried out with 1000 replicates. Sequences were aligned, prior to the construction of the phylogenetic tree, using the ClustalX software (v2.0.11). The different bHLH clades are designated as previously reported (Heilm et al., 2003). Species abbreviations: At, Arabidopsis thaliana; Md, Malus domestica; Nt, Nicotiana tabacum; Os, Oryza sativa; Sl, Solanum lycopersicum; Gm, Glycine max; Mx, Malus xiaojinensis; Cm, (CmbHLH1), Chrysanthemum morifolium; Cm (CmbHLH38), Cucumis melo; Pt, Populus tremula.
Figure 3. BHLH TFs network that regulates iron homeostasis in Arabidopsis. Question marks indicate protein complexes for which transcriptional activities have not yet been clearly demonstrated. The color code for the bHLH TFs refers to the clades described Figure 2. EIN3 and EIL1 favor FIT stability whereas MED16 and MED25 mediate the FIT/bHLH25-dependent iron deficiency responses (for additional details on posttranslational regulation of FIT see Kobayashi, 2019; Schwarz and Bauer, 2020; Spielmann and Vert, 2020; Wu and Ling, 2019). Non bHLH proteins are in grey. EIN3: ETHYLENE INSENSITIVE 3; EIL1: ETHYLENE INSENSITIVE 3-LIKE1; MED16 and 25: FBP: FIT-BINDING PROTEIN; MED16 AND 25: MEDIATOR SUBUNIT 16 and 25; ZAT12: ZINC FINGER OF ARABIDOPSIS THALIANA 12.
Figure 4. bHLH TFs network that regulates iron homeostasis in rice. Question mark indicates the putative degradation mechanism for OsPRI1 and OsPRI2 via OsHRZ2. The color code for the bHLH TFs refers to the clades described Figure 2. Non bHLH proteins are in grey. IBP1.1: IDE1 BINDING PROTEINS 1.1.