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## Iron homeostasis and organismal aging

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### Abstract

Iron is indispensable for normal body functions across species because of its critical roles in red blood cell function and many essential proteins and enzymes required for numerous physiological processes. Regulation of iron homeostasis is an intricate process involving multiple modulators at the systemic, cellular, and molecular levels. Interestingly, emerging evidence has demonstrated that many modulators of iron homeostasis contribute to organismal aging and longevity. On the other hand, the age-related dysregulation of iron homeostasis is often associated with multiple age-related pathologies including bone resorption and neurodegenerative diseases such as Alzheimer's disease. Thus, a thorough understanding on the interconnections between systemic and cellular iron balance and organismal aging may help decipher the etiologies of multiple age-related diseases, which could ultimately lead to developing therapeutic strategies to delay aging and treat various age-related diseases. Here we present the current understanding on the mechanisms of iron homeostasis. We also discuss the impacts of aging on iron homeostatic processes and how dysregulated iron metabolism may affect aging and organismal longevity.

### Keywords

Iron; Aging; Longevity; Homeostasis; Human diseases; C. elegans; Drosophila

### 1. Introduction

Iron is fundamentally important for cell survival, proliferation, and metabolism across multiple organisms. As a key element of many indispensable cellular players and co-factors (e.g., heme groups, iron sulfur clusters), iron is required for oxygen transport and involved in the biosynthesis of collagen, myelin, neurotransmitters, and many components of the mitochondrial electron transport chain (Gardi et al., 2002; T.H. Kim and Wessling-Resnick, 2014; J. Kim and Wessling-Resnick, 2014; Paul et al., 2017; Santiago González et al.,

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2019). In addition, iron is involved in multiple cellular catabolic and anabolic processes such as DNA synthesis, respiration, and energy metabolism (Abbaspour et al., 2014). Furthermore, iron plays a vital role in the innate immune response to infections, as the first-line host antimicrobial mechanisms often reduce iron availability to pathogens (Johnson and Wessling-Resnick, 2012).

Low concentrations of iron result in restricted erythropoiesis and consequently anemia. By contrast, high concentrations of labile iron are highly toxic to the cell by generating reactive oxygen species (ROS) that may inflict damages on cells and organs (Cabantchik et al., 2005). Thus, iron can act as a double-edged sword, which necessitates tight regulation of its cellular levels and exquisite equilibrium between iron storage and transport (Fig. 1) (Rivella and Crielaard, 2014). Iron uptake is a dynamic process that mainly depends on the absorption from digested food. However, unlike iron uptake, systemic iron excretion occurs at an almost steady basal rate regardless of the physiological concentration of iron (Coffey and Ganz, 2017; Mercadante et al., 2019). Therefore, excess iron can accumulate and result in iron overload. Iron overload could also result from hereditary disorders or pathologies like in the case of hemochromatosis (Piperno et al., 2020), a genetic disease that causes an increased intestinal iron absorption, eventually leading to the iron overload in body tissues and organs and causing tissue damages (Burke et al., 2002). In fact, many genetic variants of iron metabolism modulators have been linked to iron imbalance (Jallow et al., 2020).

Aging has a profound impact on iron homeostasis. In humans, age-related iron accumulation occurs in multiple organs including the liver, kidney, and brain (Cook and Yu, 1998), which has been linked to several age-related pathologies including liver diseases, renal disorders, and Alzheimer's disease (Anderson and Shah, 2013; Ashraf et al., 2018; Costa et al., 2014; Ward et al., 2014). Conversely, iron deficiency and various forms of anemia are also prominent among older adults as the intestinal dietary iron uptake becomes less efficient at advanced ages (Busti et al., 2014; Grubi Kezele and urko-Cofek, 2020). Notably, there are two major forms of iron deficiency, absolute and functional deficiency. While absolute iron deficiency is a decrease in the total body iron content and is usually due to a decrease in intestinal iron absorption, functional iron deficiency is in general due to iron flux to iron storage sites (McCranor et al., 2013), which leads to iron sequestration in macrophages and renders iron less bioavailable for erythropoeisis (Ganz and Nemeth, 2009). Functional anemia is also known as anemia of inflammation or anemia of chronic disease, and its occurrence mostly results from immune activation (Weiss et al., 2019). Importantly, iron deficiency in general is closely associated with impaired mental and immune functions as well as poor physical performance in the elderly (Beard, 2001; Jáuregui-Lobera, 2014; Penninx et al., 2003). Studies in rodents demonstrated that while restricted iron availability can jeopardize certain physiological processes in the body, ironenriched diets accelerate aging through increased oxidative stress and inflammation (Arruda et al., 2013). Collectively, a better understanding of the age-related dysregulation of iron homeostasis can help us develop strategies for fine-tuning the process, restoring the balance, and therefore mitigating the associated pathologies. In this review, we discuss our current understanding on the complex interactions between iron homeostasis and aging (Fig. 1).

### 2. Systemic, cellular, and molecular mechanisms involved in iron

### homeostasis

Maintaining safe iron levels is critical for sustaining steady iron stores, providing sufficient iron for erythropoiesis, and limiting iron availability to pathogens (Wang and Babitt, 2019). In adult humans, iron enters the body mainly from diet through intestinal dietary iron absorption in two major forms, heme and non-heme iron. Non-heme dietary iron is abundant in plant foods and iron-fortified foods (Monsen, 1988), and it can be in the ferric or more bioavailable ferrous states. Although the chemical nature of non-heme dietary iron is not very well understood, ferric citrate is thought to be the predominant species (Hider, 2002). Existing supplements mainly include ferrous sulfate, ferrous gluconate, ferric citrate, and ferric sulfate (Alleyne et al., 2008; Coates et al., 2010), and the low pH of the digestive system helps keep the non-heme iron in the soluble form. On the other hand, heme iron, which can be ingested from meat, seafood, and poultry, is bound to the porphyrin ring and less affected by diet and other factors, rendering its absorption more efficient (Monsen, 1988).

Iron homeostasis is achieved at both systemic and cellular levels. Cross-talks between the systemic and cellular iron metabolism are key to sensing iron levels, adjusting absorption and recycling accordingly. Below we discuss the underlying mechanisms of iron homeostasis at the systemic, cellular, and molecular levels.

#### 2.1. Systemic iron homeostasis

Systemic iron homeostasis, thoroughly reviewed by Ganz and Nemeth (Ganz and Nemeth, 2012), is maintained by balancing iron supply, utilization, and losses (Wang and Babitt, 2019). Iron is supplied by duodenal enterocytes that absorb dietary iron from the intestinal lumen and by reticuloendothelial macrophages that take iron from aged erythrocytes and supply it to the plasma (Gulec et al., 2014; Knutson and Wessling-Resnick, 2003; Knutson et al., 2005; Sharp and Srai, 2007). Duodenal enterocytes can uptake iron through their apical surface by different mechanisms depending on the type and redox status of iron (Gulec et al., 2014). After uptake, iron can be directly exported into the plasma through the cell's basolateral surface or stored for a few days (Mackenzie and Garrick, 2005). In humans, around 20 mg of iron are used each day to make 200 billion erythrocytes, which constitutes about 80% of the daily iron use (Girelli et al., 2018; Kautz and Nemeth, 2014). Unused iron can be stored in the liver in the forms of ferritin or hemosiderin (Bonkovsky, 1991). Under normal physiological conditions, iron losses are estimated to be about 1-2 mg per day (Bothwell et al., 1989), and these losses are mainly through shedding of intestinal and skin epithelial cells, menstruation, blood loss, as well as excretion through urine, sweat and stool (Anderson et al., 2009; Green et al., 1968; Hunt et al., 2009; Mercadante et al., 2019; Saito et al., 1964).

Notably, there are no known controlled iron excretion mechanisms in the human body, and thus efficient orchestration of iron absorption is critical for maintaining iron homeostasis. Systemically, this is mainly attained by the hormone hepcidin that is synthesized and secreted by liver hepatocytes (Fig. 2) (Rossi, 2005). Hepcidin is regulated by both the

amounts of cellular iron stores and circulating transferrin-bound iron levels (Nemeth and Ganz, 2009). An increase in plasma and tissue iron levels stimulates hepcidin production by activating the BMP-SMAD signaling cascade in hepatocytes (Yu et al., 2008). Hepcidin regulates iron homeostasis by modulating iron release into the circulation (Katsarou and Pantopoulos, 2020). At the cellular level, hepcidin decreases the levels of the iron exporter protein ferroportin (FPN) by directly binding to FPN (Fig. 2), which results in its internalization and subsequent degradation (Pagani et al., 2019). A decrease in intestinal FPN upon the elevated levels of hepcidin reduces iron release from the intestine to the bloodstream and leads to decreased iron absorption (De Domenico et al., 2007). In addition, reduction of FPN levels also occurs in reticuloendothelial macrophages which limits iron efflux from recycling macrophages. Conversely, a decrease in iron levels leads to downregulation of hepcidin production, which then causes upregulated intestinal iron absorption and increased iron release from macrophages (Ganz, 2011, 2005; Ganz and Nemeth, 2012). Interestingly, an increase in interleukin-6 (IL-6) from inflammation stimulates the production of hepcidin and leads to iron dyshomeostasis (Wang and Babitt, 2016). In such cases, iron serum levels decrease while ferritin levels increase (Pagani et al., 2019), a common phenomenon observed during inflammaging and associated anemia (McCranor et al., 2013).

### 2.2. Cellular iron homeostasis

Cellular iron uptake mechanisms vary depending on the cell type and the form of iron. As previously discussed, dietary iron exists in two forms: heme and non-heme. Non-heme iron can be either transferrin-bound (referred to as TBI) or non-transferrin-bound (known as NTBI). Under normal conditions, most of the iron in the circulation is transferrin-bound. However, in cases of iron overload, the potentially toxic NTBI can be found in the circulation at higher levels (Cabantchik et al., 2005; Jacobs et al., 2005). The cellular uptake and metabolism of iron are governed by complex pathways summarized in Fig. 3, and these processes seem to be fairly conserved across eukaryotic species, especially more complex ones (Dlouhy and Outten, 2013; Sherman et al., 2018).

**2.2.1. Non-transferrin-bound iron uptake**—Ferric iron (Fe<sup>3+</sup>) is reduced to ferrous iron (Fe<sup>2+</sup>) in order to enter the cell, and this can be achieved by ascorbate or membrane-bound reductases (Cain and Smith, 2021; Ganasen et al., 2018). Ascorbate, a known antioxidant, is a modulator of iron metabolism that can increase levels of cellular iron by increasing cellular ferritin (an iron storage protein) levels (Goralska et al., 1997). Ascorbate cycling across the plasma membrane is associated with ferric citrate iron uptake with this mechanism being more prominent in certain cell types like astrocytes (Lane and Richardson, 2014). As for iron absorption from food, non-heme iron is mainly absorbed by intestinal enterocytes expressing the ferric reductase duodenal cytochrome B (DCYTB), which reduces dietary iron from ferric Fe<sup>3+</sup> to ferrous Fe<sup>2+</sup> and facilitates its transport through the apical side of the enterocyte cell membrane by the divalent metal transporter DMT1 (Fig. 3) (Ems et al., 2021). In liver hepatocytes, ZIP14 (also known as SLC39A) mediates NTBI absorption by acting as a cellular iron importer (Liuzzi et al., 2006). ZIP8 (also called SLC39A8) is another iron importer that uptakes iron in placental cells (D. Wang et al., 2012; C.-Y. Wang et al., 2012). In addition, NTBI can enter the cell through bulk

Iron enters the circulation by being exported through FPN on the basolateral membrane of enterocytes (Fig. 3). FPN, the only known cellular iron export protein, is also responsible for releasing stored iron into the circulation from hepatocytes and macrophages (Donovan et al., 2005; Drakesmith et al., 2015; Zhang et al., 2012).

**2.2.2.** Transferrin-bound iron uptake—Iron in the circulation can be transported by transferrin that binds iron in the ferric state (Levine and Woods, 1990). After the ferrous iron is exported, multicopper ferroxidases, ceruloplasmin, hephaestin and hephaestin-like protein 1 (HephL1) then oxidize  $Fe^{2+}$  iron into the ferric state and allow it to bind to transferrin (Harris, 2019; Vashchenko and MacGillivray, 2013; Wierzbicka and Gromadzka, 2014). This is thought to facilitate iron release from intestinal enterocytes as well as absorption and release (Chen et al., 2004; Fuqua et al., 2014). Next, the formed TBI complex (ferric iron bound to transferrin) binds to the transferrin receptor TFR1, and TBI-TFR1 complex is then internalized into the cell through the clathrin-dependent receptor-mediated endocytosis (Harding et al., 1983; Muckenthaler et al., 2017). In short, endocytosis of TBI-TFR1 complex is initiated where the vesicle buds from the cell surface, forming a clathrin-coated pit that is separated from the cell membrane with the help of dynamin (Liu et al., 2010; Rosendale et al., 2019). Two populations of early endosomes will form depending on the maturation kinetics, and TBI-TFR1 randomly enters either one of these populations (Killisch et al., 1992; Stoorvogel et al., 1991). This TBI uptake pathway requires multiple trafficking molecules such as Sec1511 (exocyst complex component Sec15 A), Vps35 (vacuolar protein sorting-associated protein 35), Snx3 (sorting nexin-3) (Chen et al., 2013), as well as the vacuolar-type  $H^+$  – ATPase (V- ATPase) assembly factor coiled-coil domain containing 115 (CCDC115) (Sobh et al., 2020). After internalization, TBI-TFR1 eventually fuse with the lysosome, and the acidic pH (4.5–5.5) environment of the lysosome leads to the release of iron from transferrin (Karin and Mintz, 1981), as TFR1 has a higher affinity for the iron-free transferrin at the lower pH (Dautry-Varsat et al., 1983). Afterwards, while transferrin and its receptor are recycled back to the plasma membrane (Harding et al., 1983), six-transmembrane epithelial antigen of the prostate 3 (STEAP3) will reduce ferric Fe<sup>3+</sup> to ferrous Fe<sup>2+</sup>, and then Fe<sup>2+</sup> is released from the lysosome into the cytoplasmic LIP via DMT1 (Fig. 3) (Ohgami et al., 2005).

**2.2.3. Heme iron uptake**—In higher eukaryotes, heme iron is synthesized in the mitochondria or obtained from diet (Chung et al., 2012). Heme is thought to be internalized by receptor-mediated endocytosis (Fig. 3) (Sobh et al., 2020), where heme oxygenases (HO-1 in endoplasmic reticulum or HO-2 inside vesicles) degrade heme and release iron from its porphyrin ring (Yoshida and Migita, 2000). The released iron is then transported

into the cytoplasm through DMT1 and incorporated into the LIP (Fig. 3) (West and Oates, 2008). Additionally, in recycling macrophages, the heme importer HRG1 can transport heme from the phagolysosome to the cytoplasm (White et al., 2013). Besides the endocytosis route, heme might be taken by the proton-coupled folate transporter PCFT/HCP1 (encoded by *SLC46A1*) into the cytoplasm (Fig. 3) (West and Oates, 2008), although it has been argued that the main function of PCFT/HCP1 is to transport folate (Le Blanc et al., 2012). Notably, a genome-wide CRISPR screen in erythroleukemic K562 cells aiming to identify key-players in heme-trafficking revealed a clear role for endocytosis in heme import but did not uncover an explicit cellular heme importer (Sobh et al., 2020). As for the export of heme, feline leukemia virus subgroup C receptor-related protein 1b (FLVCR1b) has been shown to export the mitochondrial heme into the cytoplasm, while the cell membrane FLVCR1 is used to export heme outside of the cell (Fig. 3) (Khan and Quigley, 2013). Nonetheless, how species lacking FLVCR homologs export heme is still unknown.

**2.2.4. LIP** iron utilization—To keep the low level of intracellular labile iron, the LIP iron can be exported outside of the cell through FPN or stored in the form of ferritin (Fig. 3) (Hynes, 1948). Poly r(C)-binding protein 1 and 2 (PCBP1 and PCBP2) are iron chaperones that are required for iron binding to ferritin (Leidgens et al., 2013). Moreover, the LIP iron can be imported into the mitochondrion through mitoferrin (MTFN1/2) (Paradkar et al., 2009), where it is used for heme biosynthesis, iron-sulfur clusters biosynthesis, tricarboxylic acid (TCA) cycle, or stored in the mitochondrial ferritin (MtFt) (Fig. 3) (Paul et al., 2017; Richardson et al., 2010; Ward and Cloonan, 2019). In addition to its use in the mitochondrion, iron is also widely used as a cofactor by various DNA metabolizing enzymes involved in DNA replication and repair (Puig et al., 2017).

Labile cellular iron is often regarded as a dynamic parameter since it depends on the cell type and the cell's fluctuating physiological conditions. On the one hand, LIP concentrations may vary within short durations in the same cell to meet the changing catalytic demands (Cabantchik, 2014). On the other hand, it can exist in both ferric and ferrous states with very low concentrations. This renders it difficult to reliably assess the real-time LIP status in living cells (Lv and Shang, 2018; Muir et al., 2019).

#### 2.3. Molecular mechanisms involved in iron homeostasis

Many transcriptional and post-transcriptional mechanisms play important roles in iron homeostasis. For example, hypoxia has been shown to increase the availability of iron in the body through the evolutionarily conserved transcription factors hypoxia inducible factors (HIFs) (Shah and Xie, 2014). HIFs control expression of multiple genes that maintain iron homeostasis, including transferrin, hepcidin, and ferroportin (Peyssonnaux et al., 2008). In the presence of oxygen, HIF-1 $\alpha$  is hydroxylated and degraded by the ubiquitin-proteasome degradation. However, when the oxygen level decreases, HIF-1 $\alpha$ accumulates and translocates to the nucleus, where it binds to the constitutively expressed HIF-1 $\beta$  subunits and forms a heterodimer to activate the expression of target genes through hypoxia response elements (HREs) (Dengler et al., 2014). Upon activation, the HIF pathway renders iron more available for erythrocyte production by downregulating hepcidin and upregulating transferrin, transferrin receptor, heme oxygenase 1, ferroportin,

and ceruloplasmin. Combined, these events enhance intestinal absorption, cellular import, and recycling of iron (Peyssonnaux et al., 2008, 2007; Renassia and Peyssonnaux, 2019). In addition to the transcriptional control, several post-transcriptional mechanisms also contribute to regulating the expression of iron homeostasis genes, including alternative splicing, iron regulatory proteins (IRPs), microRNAs (miRNAs), and proteolytic cleavage.

**2.3.1. Alternative splicing**—Depending on the splicing sites selection, expression of multi-exon genes can result in distinct proteins that have different sequences and activities (Greenberg and Soreq, 2013). Alternative splicing of several iron-related genes such as ferritin (Jiang et al., 2014), iron-sulfur cluster-containing aconitase 1 (ACO1) (Tejedor et al., 2015), and the most telomeric HLA class I gene HFE (Martins et al., 2011) all result in multiple transcript variants and protein isoforms that have different functions and efficiencies. For example, the HFE protein is expressed in several cell types to compete with transferrin-bound iron for transferrin receptor binding (Bennett et al., 2000), and a HFE splicing variant can regulate cellular transferrin uptake by hepcidin regulation of macrophage iron recycling and by controlling intestinal iron absorption (Laham et al., 2004; Martins et al., 2011). In addition, alternative splicing of *SLC11A2* results in two different proteins namely DMT1A and DMT1B. Unlike DMT1A that has an IRE motif at its three prime untranslated region (3' UTR), DMT1B does not and therefore is irresponsive to iron (Tabuchi et al., 2002). Furthermore, alternative splicing has been shown to contribute to the regulation of ferritin levels in the oriental fruit fly, *Bactrocera dorsalis* (Jiang et al., 2014).

**2.3.2. IRP-IRE pathway**—Iron regulatory proteins (IRPs) can bind to the IREcontaining RNA stem-loops in the untranslated regions (UTRs) of target mRNAs, which either negatively affects the expression of the mRNA by inhibiting translation (e.g., FPN1) (Liu et al., 2002) or positively by preventing degradation of the mRNA (e.g., DMT1 and TFR1) (Galy et al., 2008; Lymboussaki et al., 2003). Thus, the binding of iron to IRPs can alter the translation of target mRNAs by disrupting the interaction between IRPs and IRE (dos Santos et al., 2008). Importantly, IRE is present in many genes that are involved in iron uptake, export, transport (e.g., DMT1, TFR1, and ferritin), and utilization (e.g., ACO2 and 5-aminolevulinate synthase (ALAS)) (Muckenthaler et al., 2008; Steinbicker and Muckenthaler, 2013). Notably, IRP-IRE regulation of cellular iron uptake seems to be more prominent for TBI than NTBI (Brissot et al., 2012). Between the two IRPs (IRP1 and IRP2) encoded by the vertebrate genome, IRP2 only responds to iron-related signals and dominates regulation of iron homeostasis in mammals, whereas IRP1 can respond to both iron-dependent and -independent signals (Anderson et al., 2012; Meyron-Holtz et al., 2004; Wallander et al., 2006). Interestingly, IRP1 can also coordinate erythropoietin synthesis with oxygen and iron supply through translationally regulating HIF2a mRNA (Sanchez et al., 2007). Notably, alternative splicing is linked with the IRP-IRE pathway as certain alternatively spliced transcripts of ferroportin that lack the IRE domain can bypass iron deficiency-induced translational repression of its mRNA by IRPs in duodenal and erythroid precursor cells (Zhang et al., 2009). For more details on the post-transcriptional regulation of iron metabolism, readers are encouraged to check other related reviews (Rouault, 2002; Muckenthaler et al., 2008; Kühn, 2015).

**2.3.3. microRNAs**—miRNAs are single-stranded, noncoding RNA molecules that can interact most commonly with the 3' UTR region of an mRNA and usually silences the target gene and negatively regulates its expression (O'Brien et al., 2018). Multiple types of miRNAs have been shown to regulate expression of genes involved in iron import, export, storage, and utilization (Davis and Clarke, 2013). For example, miR-122 regulates the expression of hepcidin (Castoldi et al., 2011), while miR-210 (Yoshioka et al., 2012) and miR-148a regulate the expression of transferrin receptor 1 (Babu and Muckenthaler, 2019). Interestingly, miRNAs have also been depicted in the modulation of aging such that upregulation of miR-29 can delay aging by limiting iron delivery to neurons and therefore counteracting the age-associated effects of iron accumulation in these cells (Ripa et al., 2017).

**2.3.4. Proteases**—In addition to the regulatory mechanisms mentioned above, a role for proteases in the regulation of iron homeostasis was recently revealed. Martipase-2, a serine protease encoded by *TMPRSS6*, has been shown to be sensitive to the cellular iron levels and negatively regulate the expression of hepcidin (Meynard et al., 2011). In addition, martipase-2 regulates the expression of hemojuvelin, a protein responsible for the increased iron levels in juvenile hemochromatosis (Du et al., 2008; Folgueras et al., 2008; Malyszko, 2009; Ramsay et al., 2009). In fact, different allelic variants of martipase-2 cause altered serum iron and transferrin saturation levels (An et al., 2012; Benyamin et al., 2009; Chambers et al., 2009; Nai et al., 2011; Tanaka et al., 2010), indicating that martipase-2 may act as a global modulator of serum iron concentration and transferrin saturation levels (Wang et al., 2014). Regulation of iron homeostasis by protein degradation has been thoroughly reviewed elsewhere (Thompson and Bruick, 2012; Wang et al., 2014).

### 3. The impacts of aging on iron homeostasis

As discussed above, we have gained plenty of knowledge about the biological mechanisms underlying iron homeostasis in the past several decades. More recently, emerging evidence suggested that iron homeostasis is interconnected with aging. Older people not only suffer from cellular iron accumulation that can result in multiple pathologies and tissue degeneration, but also are negatively impacted by anemia due to deterrent iron absorption. In fact, anemia in the elderly is considered a significant risk factor for several adverse outcomes including death (den Elzen et al., 2013). Multiple studies have identified unexplained anemia of the elderly (UAE) as one of the most common types of anemia among people 65 years and older (Artz and Thirman, 2011). A dissection of the onset and key players of age-induced dysregulation of iron homeostasis might provide an insight into the etiology of many age-related diseases, thus helping mitigate the effects of iron dyshomeostasis in elderly.

#### 3.1. Age-related decline in systemic iron homeostasis

The most common causes underlying iron-deficiency anemia are gastrointestinal (GI) diseases including ulcers, GI tract malignancies, inflammatory bowel disease, and other pathophysiological conditions that cause bleeding in the GI tract, as these conditions cause iron malabsorption and iron loss (blood loss) (Busti et al., 2014). While the levels of

many key modulators of iron homeostasis do not seem to vary steadily with age under normal conditions, certain age-related pathological conditions may alter their levels (Fig. 4). Hepcidin, for instance, does not seem to change with age under normal conditions (Goodnough and Schrier, 2014). However, patients with anemia of inflammation and those at risk for developing Alzheimer's disease have higher levels of hepcidin, whereas those suffering from iron deficiency anemias have lower plasma hepcidin levels (Chatterjee et al., 2020; den Elzen et al., 2013; Picca et al., 2019). This increase in hepcidin and subsequent sequestration of iron in cells are then associated with the functional iron deficiency and decreased hematopoiesis noted in older adults (Nemeth et al., 2004). In fact, chronic inflammation is known to increase circulating hepcidin levels that lead to a decrease in systemic iron levels and decreased hematopoiesis, which can eventually cause anemia commonly seen in older adults (Cunietti et al., 2004).

Unlike hepcidin whose levels do not usually fluctuate with age under normal conditions, the levels of iron storage protein ferritin increase with age (Fig. 4) (Pusch et al., 1981), and this age-related increase of ferritin is typically induced by aging-driven systemic inflammation, or inflammaging. Although in normal situations iron deficiency leads to decreased ferritin levels, geriatric patients tend to have high ferritin levels even with iron deficiency because of inflammaging, which makes ferritin a potential biomarker for the age-associated inflammation (den Elzen et al., 2013). A 2010 study with 252 geriatric patients showed that 25.4% of the population had anemia while 41% had inflammation (Fairweather-Tait et al., 2014; Lopez-Contreras et al., 2010). Importantly, this study confirmed the link between inflammation markers and ferritin. In addition to anemia, inflammaging is closely associated with many other age-related conditions such as osteoporosis, malignancies, cognitive impairments, atherosclerosis, sarcopenia, and cardiovascular diseases (Ferrucci and Fabbri, 2018; Krabbe et al., 2004; Lencel and Magne, 2011). Thus, a better comprehension of the effect of inflammation on iron homeostasis and vice versa may provide important insights into a better understanding of age-associated diseases.

### 3.2. Age-related changes in cellular and molecular iron homeostasis

Although heme levels have been clearly shown to decrease with age (Bitar and Weiner, 1983), the change of total iron content with age seems to be less clear. In general, serum iron and soluble transferrin receptor levels decrease with age (Gayar and Deghady, 2015), while ferritin levels increase with age (Cankurtaran et al., 2012) although there are conflicting results from different studies (Fairweather-Tait et al., 2014). In older individuals, iron seems to accumulate in an age-related and tissue/organ-specific manner. For example, the age-associated increase in iron deposition varies between different brain regions and cell types in humans (C.-Y. Wang et al., 2012; D. Wang et al., 2012). In rodent liver and spleen, ferritin levels and ferritin iron saturation increase with age (Bulvik et al., 2012), while old rats have higher iron levels and lower levels of TfR1 and FPN in skeletal muscles (Xu et al., 2012a). Nonetheless, other iron-related factors such as DcytB, DMT1 and FPN1 exhibit the highest levels during the first few weeks in life and then keep decreasing with age, with the lowest levels reported in the oldest rats (Kong et al., 2015). Collectively, aging seems to have complex impacts on the expression levels of distinct systemic, cellular, and molecular factors involved in iron homeostasis.

### 4. Iron metabolism dysregulation contributes to cellular and organismal

### aging

The intricate balance of physiological iron levels and proper maintenance of iron homeostasis are key to healthy aging. Iron-induced oxidative stress is linked to age-related pathologies (Smith et al., 1997) and considered as a major contributing factor of aging in humans (Kregel and Zhang, 2007). Intriguingly, suppressing the age-related iron accumulation by limiting iron intake (Polla, 1999) with iron chelators (Bogdan et al., 2016; Kell, 2009; Pouillot et al., 2013) or dietary restriction has been suggested to reduce oxidative stress (Cook and Yu, 1998). Moreover, the rate of iron accumulation is proportional to the rate of aging in *Drosophila melanogaster* (Massie et al., 1985). Therefore, manipulating iron homeostasis might have direct impacts on aging and longevity.

### 4.1. Age-associated iron deposition in cellular senescence

Age-related cellular iron deposition can exist in several forms, including labile iron, lipofuscin, and ferritin. As ferritin levels tend to increase with age (Casale et al., 1981; Jung et al., 2008), this could potentially explain the phenomenon of age-related cellular iron sequestration. Very interestingly, senescent cells can have a 10-fold higher concentration of iron compared to younger cells (Killilea et al., 2003), and increased cellular ferritin levels is considered a strong biomarker of cellular aging and senescence (Liu et al., 2019). Furthermore, the increased accumulation of iron is associated with impaired ferritin degradation, altered ferroptosis sensitivity, as well as increased expression of p16, p21 and IL-6 in senescent fibroblasts (Masaldan et al., 2018), all of which are considered as biomarkers of aging (Bernardes de Jesus and Blasco, 2012; González-Gualda et al., 2021).

The iron-dependent ferroptosis process is typically accompanied by iron accumulation and lipid peroxidation (Conrad and Pratt, 2019; Hadian and Stockwell, 2020). Senescent cells often exhibit severely impaired ferritinophagy, a lysosomal degradation process that degrades ferritin and promotes ferroptosis. Thus, the large amount of iron accumulated in senescent cells is primarily trapped in ferritin due to defective ferritinophagy, and cells actually perceive it as iron deficiency (Masaldan et al., 2018). As a result, senescent cells are often resistant to ferroptosis (Masaldan et al., 2018). On the other hand, multiple studies have indicated that cellular free iron is a major driver of both senescence and ferroptosis, and increased ferroptosis might contribute to age-associated neurodegeneration (Cozzi et al., 2019; Do Van et al., 2016; Guiney et al., 2017; Kenny et al., 2019; Morris et al., 2018). It is possible that the amount of LIP iron, but not sequestered iron, might determine the final outcome of ferroptosis in different cell types. Therefore, it is important to decipher whether the mechanisms and initiators of ferroptosis vary among distinct types of cells. A better understanding of the etiology of ferroptosis in aging cells could assist in targeting ferroptosis for various age-related diseases.

Ferritin can accumulate in the cytosol, mitochondria, or form aggregates as dimers, trimers, tetramers and even oligomers (Ashraf et al., 2018). Cytosolic ferritin is degraded by autophagy to release redox-active iron and increase the concentration of LIP (Yu et al., 2003). Notably, ferritin holds large amounts of free iron (theoretically up to 4500 Fe<sup>3+</sup>

but biologically around 2000  $\text{Fe}^{3+}$  per ferritin molecule), and therefore its degradation can release a large amount of iron (Arosio et al., 2009; Watanabe et al., 2001; Worwood et al., 1976). Excess free irons increase cellular oxidative stress and lead to deteriorating effects on health and longevity (Murillo-Ortiz et al., 2016).

Labile cellular iron can also catalyze the formation of lipofuscin whose accumulation is a hallmark of aging and senescence. As intralysosomal aggregates mainly composed of lipids and oxidized proteins, lipofuscin is resistant to ubiquitin-proteasome degradation (Katz and Robison, 2002). Lipofuscin usually accumulates with age and has cytotoxic effects by the chronic production of oxidants (Höhn et al., 2010). The iron in lipofuscin jeopardizes the stability of the lysosome and triggers apoptosis after lysosome disruption and contents release (Brunk and Terman, 2002). Interestingly, iron chelation has been suggested to alleviate the deteriorating effects lipofuscin on age-related macular degeneration (Ueda et al., 2018).

### 4.2. Iron metabolism-related genes in animal lifespan regulation

Unlike humans with long lifespan, invertebrate model organisms such as *C. elegans* and *Drosophila* feature short lifespan and powerful genetics. As a result, it is more convenient to use these genetic model organisms to investigate the potential impact of iron metabolism-related genes on longevity. In *C. elegans*, increased dietary iron intake significantly accelerates age-related protein aggregation and negatively affects organismal longevity (Klang et al., 2014). Conversely, reducing overall iron levels using intracellular iron scavengers is sufficient to extend lifespan (Fig. 5A) (Jenkins et al., 2020). Moreover, blocking the iron-dependent ferroptosis can also slow down the aging process and extend lifespan (Jenkins et al., 2020). Furthermore, several core components of the iron-sulfur cluster (ISC) assembly machinery (e.g., ISCU-1, NFS-1) have been recently shown to modulate longevity (Sheng et al., 2021). Interestingly, while ISCU-1 is required for the normal development of larval worms to adults (Fig. 5B), it suppresses longevity during adulthood (Fig. 5C). Thus, the ISC assembly machinery might exhibit antagonistic pleiotropy by being beneficial early in life at the cost of aging.

In line with the results of *C. elegans*, studies in *Drosophila* have revealed the age-dependent accumulation of iron and holoferritin in addition to altered mitochondrial iron homeostasis and autophagy (Jacomin et al., 2019). In fact, increased dietary iron intake was even considered as an "initiator of senescence" in flies (Massie et al., 1985). On a similar note, green tea can prolong the lifespan of *Drosophila* through regulating mitoferrin and reducing mitochondrial iron levels (Lopez et al., 2016; Massie et al., 1993). However, improper iron chelation that results in poor liganding of iron species can increase inflammation, demote the fly's overall health, and decrease its lifespan (Kell, 2009).

Besides *C. elegans* and *Drosophila*, studies with several other species have shown that increased cellular iron concentration has negative health impacts that can be potentially ameliorated by iron chelation, including water flea (Dave, 1984), zebrafish (Hamilton et al., 2014; Nakamura et al., 2020), killifish (Kelmer Sacramento et al., 2020; Poeschla and Valenzano, 2020), mouse (Garringer et al., 2016; Song et al., 2014), rat (Bloomer et al., 2008), dog (Bergeron et al., 2004), pig (Gu et al., 2011), and pin monkey (Bergeron et al.,

2004, 1999). For example, iron chelation by deferiprone in mouse embryonic fibroblasts with high ferritin levels has been shown to significantly decrease cellular iron content and increase cell viability (Garringer et al., 2016). In addition, iron chelation also decreases oxidative stress during retinal degeneration in mice suffering from iron overload (Song et al., 2014). Although the underlying mechanisms are not thoroughly understood, ferritin, transferrin, and mitochondrial signaling seem to be the key players (Shen, 2020; Shin and Baik, 2017; Whittemore et al., 2019).

### 4.3. Dysregulated iron homeostasis is a hallmark of human aging

Age-related dysregulation of iron homeostasis contributes to a plethora of human disorders (Fig. 6), including impaired bone homeostasis (Balogh et al., 2018) and osteopenia (Liu et al., 2006), muscle aging (Picca et al., 2019), sarcopenia and skeletal muscle atrophy (DeRuisseau et al., 2013), renal dysfunction (Bloomer et al., 2020), liver disease (Milic et al., 2016), cardiomyopathies (Johnson et al., 1994; Nordestgaard et al., 2010), neurodegenerative diseases such as Alzheimer's disease (Liu et al., 2018) and Parkinson's disease (Ayton and Lei, 2014; Rhodes and Ritz, 2008), vision loss (Błasiak et al., 2009), impaired immune system (Dao and Meydani, 2013), and lung damage (Philippot et al., 2014). Alterations in iron homeostasis have been also linked to endocrine system disruptions (Abdulzahra et al., 2011) and gut microbiota imbalance (Yilmaz and Li, 2018). Intriguingly, reduced iron deposition leads to improved motor performance in aging individuals (Kastman et al., 2012), whereas iron supplements negatively affect gut microflora by favoring the pathogenic bacteria and thus potentially leading to gut inflammation (Jaeggi et al., 2015; Zimmermann et al., 2010). Moreover, the serum ferritin level is significantly higher in both women and men with sarcopenia compared to those without sarcopenia (J. Kim et al., 2014; T.H. Kim et al., 2014). Collectively, dysregulated iron homeostasis appears to be intuitively linked to human aging.

Studies on centenarians have associated healthy aging and increased longevity with increased immune system and systemic anti-inflammatory performance (Balistreri et al., 2012), both of which are modulated by proper iron homeostasis. Intriguingly, a recent GWAS study has linked heme metabolism pathways with human aging (Timmers et al., 2020). It would be very interesting to examine whether the iron homeostasis dysregulation and consequently aging acceleration can be mitigated by reducing iron intake.

### 5. Conclusions and perspectives

Although the mechanisms and etiologies remain unknown, the negative impacts of agerelated iron dyshomeostasis on human health have been well documented (Xu et al., 2012b, 2008). Our knowledge and understanding of iron biology have advanced remarkably during the last couple of decades. However, many key players involved in iron metabolism and homeostasis remain unidentified. For instance, the precise mechanism in cellular heme uptake remains to be identified. In addition, how iron accumulates with age and triggers the associated pathologies are still poorly understood. A better understanding of these questions could help develop diagnostics and therapies for various geriatric pathologies.

Since the age-related increase of ferritin levels appears to underlie the cellular iron accumulation even under conditions of decreased serum iron levels and anemia, mobilizing ferritin iron could potentially mitigate the occurrence of age-associated cellular iron accumulation and its related pathologies. Notably, a recent study has demonstrated that chelating or reducing agents do not mobilize ferritin iron (La et al., 2018). Other studies have investigated the potential overexpression of mitochondrial ferritin to limit the availability of cytosolic active iron by shunting iron to the mitochondria (Nie et al., 2005). The development of real-time iron probes might facilitate studies on ferritin iron mobilization and other aspects of iron homeostasis. Recent advancements in selective fluorescent and genetic iron probes may offer a better monitoring of biological iron in living cells and tissues, which could lead to a better understanding of its involvement in age-related pathologies (Aron et al., 2018; Sahoo and Crisponi, 2019; Weissman et al., 2021).

Taken together, in this review we summarized key players involved in animal iron homeostasis. We also highlighted the link between progressive iron accumulation and agerelated pathologies and organ dysfunction. As genetic studies in model organisms suggest that iron accumulation might have a negative impact on aging and longevity, cellular iron homeostasis machineries may present an attractive target to combat aging and age-related diseases.

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#### Fig. 1. Iron homeostasis is maintained by balancing iron uptake with turnover.

Aging and inflammation can disrupt iron homeostasis by enhancing iron accumulation in different tissues, which may lead to oxidative stress, neurodegeneration, organ damage, as well as cancer. Meanwhile, iron deficiencies are common with old age since dietary iron uptake via intestinal absorption becomes less efficient in the elderly.



### **Systemic Iron Homeostasis**

#### Fig. 2. The regulation of systemic iron homeostasis.

An increase in plasma (circulating) and tissue (stored) iron levels leads to production and secretion of the hormone hepcidin. Hepcidin decreases the levels of ferroportin (FPN) by direct binding, which leads to its internalization and degradation. The reduction of FPN causes a decrease in iron absorption at the intestinal level as well as a decrease in iron efflux by reticuloendothelial macrophages.



#### Fig. 3. Important regulators involved in cellular iron homeostasis.

Non-heme iron can enter the cell in two forms: transferrin bound (TFB) and non-transferrin bound (aka NTBI). Ferrous iron or NTBI enters the cell through DMT1. Ferric iron is reduced to ferrous iron by DcytB, whereas ferrous iron is oxidized into ferric iron by the multicopper ferroxidases ceruloplasmin, hephaestin and HephL1. Ferric iron binds to transferrin that in turn binds to the transferrin receptor and gets internalized into the cell via endocytosis. Inside the internalized vesicles, iron is released and transformed into ferrous iron by STEAP3. Ferrous iron will then be exported out of the vesicle and into the cytoplasm by DMT1. Ferrous iron in the cytoplasm constitutes the labile iron pool (LIP), and it can be exported out of the cell by ferroportin, stored in the cell by ferritin, or utilized in different cellular processes. As for heme, it is synthesized in the mitochondria and can be exported to the outside of the cell by FLVCR1. Once in the cytoplasm, heme is cleaved by heme oxygenase (HO1) to release ferrous iron.



#### Fig. 4. Age-related changes in iron homeostasis.

Transferrin receptor levels seem to decrease with age, while ferritin levels increase. Various studies with different animal models also suggest that depending on the organ studied, the levels of certain iron-regulating proteins can vary with age.



### Fig. 5. Iron metabolism and lifespan regulation in C. elegans.

**A**, excessive iron accumulation suppresses longevity in *C. elegans*, where ROS accumulation, ferroptosis, and cellular senescence may act as contributing factors. **B**, ISCU-1/ISCU, a central mitochondrial protein required for *de novo* biosynthesis of iron sulfur clusters, is essential for normal development during larval stages but accelerates aging during adulthood. **C**, suppressing the functions of ISCU-1 by *iscu-1* RNAi extends lifespan and promotes stress resistance.

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**Fig. 6. Organ-specific effects of age-related iron accumulation in humans.** Depending on the tissue and organ affected, age-related iron accumulation can lead to various pathologies in humans.