



Published in final edited form as:

Future Virol. 2013 March ; 8(3): 301–311. doi:10.2217/fvl.13.6.

Role of cellular iron and oxygen in the regulation of HIV-1 infection

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Abstract

Despite efficient antiretroviral therapy, eradication of HIV-1 infection is challenging and requires novel biological insights and therapeutic strategies. Among other physiological and environmental factors, intracellular iron greatly affects HIV-1 replication. Higher iron stores were shown to be associated with faster progression of HIV-1 infection and to inversely correlate with the survival of HIV-1 infected patients. Iron is required for several steps in the HIV-1 life cycle, including reverse transcription, HIV-1 gene expression and capsid assembly. Here, the authors present a comprehensive review of the molecular mechanisms involved in iron- and oxygen-mediated regulation of HIV-1 replication. We also propose key intracellular pathways that may be involved in regulating HIV-1 replication, via protein kinase complexes, CDK9/cyclin T1 and CDK 2/cyclin E, protein phosphatase-1 and other host factors.

Keywords

CDK2; CDK9; HIV-1; hypoxia; iron chelators; protein phosphatase-1; Tat

Despite efficient antiretroviral therapy, eradication of HIV-1 infection continues to be a daunting challenge and requires new biological insights for the development of effective therapeutic strategies. Eradication of latent HIV-1 provirus still remains ineffective, as integrated HIV-1 is not affected by the existing antiretro-viral drugs until viral transcription is activated [1]. Both environmental and physiological factors can contribute to the progression of HIV-1 disease. For example, higher intracellular iron stores correlate with rapid progression of HIV-1 infection, thus associating with the lower rate of survival of HIV-1-infected patients [2]. Iron is required for several steps in the HIV-1 life cycle,

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Financial & competing interests disclosure

Work in S Nekhai's laboratory is supported by extramural NIH grants 1SC1GM082325, 1P30HL107253- 01, 5UH1 HL03679, AI043894, District of Columbia Developmental Center for AIDS Research (P30AI087714), 8G12MD0 07597, GW Project No. : 31440-16-CCLS90469F and intramural funding from Howard University. Work in S Dhawan's laboratory is supported by intramural funding from the US FDA. The authors have no other relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript apart from those disclosed.

No writing assistance was utilized in the production of this manuscript.

including reverse transcription, HIV-1 gene expression, and capsid assembly [3]. Lower levels of physiological oxygen concentrations also affect HIV-1 transcription and replication [4]. Here, the authors review the molecular mechanisms involved in the iron and hypoxia-mediated HIV-1 transcription regulation and discuss how these pathways could be potentially used to inhibit or activate HIV-1 for the development of future therapeutic interventions for the treatment of HIV-1 infections (Tables 1 & 2).

Iron overload & HIV-1 progression

The development of AIDS is accompanied by an increasing iron accumulation in macrophages, microglia, endothelial cells, myocytes, bone marrow, brain white matter, muscle and liver [5,6]. Increased iron stores correlate with rapid HIV-1 progression in AIDS patients, in iron-loaded thalassemia major patients, in HIV-positive patients administered with oral iron, and in those with the haptoglobin 2-2 polymorphism [2]. This association was supported by a retrospective study demonstrating the lower survival of HIV-1-infected individuals to be inversely correlated to higher iron stores [2]. Nonanemic HIV-1-positive women in Zimbabwe with high serum ferritin concentration are reported to exhibit increased viral load, which provides further evidence for the association of increased iron stores with more severe HIV-1 infection [7]. Elevated iron level has been suggested as a potential predictive marker for higher mortality in HIV-1-infected Gambian adults [8]. Different solute carrier family 11/natural resistance-associated macrophage protein 1 polymorphisms have been shown to be associated with either protection or greater mortality [9]. Therefore, iron metabolism is intrinsically connected to HIV-1 infection and disease progression.

Effect of cellular iron on HIV-1 replication

Iron serves as an important element during various steps in the life cycle of HIV-1 such as reverse-transcription, activation of NF- κ B, regulation of HIV-1 transcription, translation of viral mRNA, and viral assembly [3]. During viral entry, HIV-1 reverse transcription is dependent on the activity of host cell ribonucleotide reductase that contains nonheme iron, which is important for enzymatic activity [10]. Transcription of integrated HIV-1 proviral DNA is induced by HIV-1 Tat protein that relieves RNA polymerase II pausing by recruiting positive transcription elongation factor b (P-TEFb), which contains CDK9/cyclin T1 and other transcriptional regulatory factors, to the HIV-1 long terminal repeat [11].

Recent studies from the authors' laboratory have shown that HIV-1 transcription is inhibited by iron chelators that inhibit the enzymatic activity of CDK2 [12,13], and by the expression of the iron export protein, ferroportin [14]. The HIV-1 promoter contains several binding sites for host transcription factors, including two NF- κ B binding sites [15]. NF- κ B availability can be increased by iron efflux that activates I κ B kinase [16–18]. Cellular iron levels can also be increased by Nef, an HIV-1 accessory protein, that downregulates the expression of HFE, which controls iron uptake by macrophages and is mutated in hereditary hemochromatosis [5]. Deregulation of HFE by Nef increases iron levels, which coincides with increased HIV-1 gag expression, suggesting a beneficial effect of increased iron on the production of HIV-1 virions and viral replication [5].

Export of unspliced HIV-1 mRNA requires HIV-1 Rev protein and host eIF5 α . The eIF5 α protein contains *N*-epsilon-4-amino-2-hydroxybutyl-lysine (hypusine) that is produced by deoxyhypusine hydroxylase, an iron-containing enzyme [19]. The topical fungicide, ciclopirox, and the iron chelator, deferiprone, inhibit HIV-1 gene expression interfering with the hydroxylation step in the hypusine modification of eIF5 α [20]. Assembly of HIV capsid requires an ATP-binding cassette subfamily E member 1 protein, which contains iron-sulfur clusters [21] and binds to HIV-1 Gag protein [22].

Regulation of HIV-1 transcription

HIV-1 Tat protein recruits CDK9/cyclin T1, a component of P-TEFb, to transactivation response (TAR) element RNA, a hairpin-loop structure located at the 5'-end of all nascent HIV-1 transcripts (Figure 1) [23]. Inefficient transcription activation by Tat or the absence of essential transcription factors may contribute to the establishment of latency and protect HIV-1 provirus from anti-HIV-1 drugs, preventing HIV-1 eradication [1]. Formation of TAR RNA may disrupt the efficient recognition of HIV-1 TATA box by the cellular preinitiation complexes that require CTGC motifs for the accurate formation and also contribute to the establishment of latency [24]. HIV-1 transcription through the nucleosomal structure of integrated HIV-1 provirus requires chromatin-associated Spt6 and PAAF1 that protects Spt6 from proteasomal degradation [25]. Loss of Spt6 or PAAF1 leads to the synthesis of transcripts that are not efficiently translated [25].

Activation of HIV-1 transcription by Tat requires P-TEFb that exists in two molecular-weight forms. The lower-molecular-weight kinase active form of P-TEFb consists of CDK9 and cyclin T1 [26,27]. The high molecular weight inactive form of P-TEFb contains 7SK RNA, a dimer of CDK9/cyclin T1 and several additional proteins including HEXIM1 dimer, LARP7 protein [28–30] and MePCE [31,32]. HEXIM1 positions its inhibitory PY NT sequence to the active site of CDK9 inhibiting its enzymatic activity [33]. The high molecular weight P-TEFb complex serves as a source of CDK9/cyclin T1 for the recruitment by HIV-1 Tat [34].

HIV-1 Tat protein may also recruit CDK9/cyclin T1 to the HIV-1 promoter in inactive complex with 7SK RNA, and formation of TAR RNA can displace 7SK RNA [35]. Tat has recently been shown to facilitate the formation of a super-elongation complex containing active P-TEFb and additional elongation factors and co-activators [36,37]. P-TEFb triggers elongation of RNA polymerase II transcription by phosphorylating the negative elongation factor and the DRB-sensitivity inducing complex (DSIF/Spt4/Spt5), thus promoting the release of negative elongation factor [38]. P-TEFb can also phosphorylate Ser-5 residues of the C-terminal domain of the largest subunit of RNA polymerase II, especially when C-terminal domain is prephosphorylated on Ser-7 residues [39].

We have shown that HIV-1 transcription is activated by Tat in the G1 phase, but not in the G2 phase [40,41], suggesting that Tat might function in concert with a host cell factor that is expressed in G1. Association of Tat with CDK2/cyclin E- and CDK2-activated HIV-1 transcription *in vitro* [42,43], and inhibition of HIV-1 transcription and replication in the CDK2 knock-down cells, further supports a close interaction of CDK2 with the HIV-1 promoter both *in vitro* and *in vivo* [44]. Inhibition of CDK2 with small-molecule inhibitor roscovitin [45] inhibits HIV-1 replication and prevents the association of CDK2 with the HIV-1 promoter [44]. Roscovitin and its analog CR8 also inhibit CDK9 activity [46], suggesting a cooperative interaction between CDK2 and CDK9 in regulating HIV-1 replication [47,48].

CDK9 contains several phosphorylation sites, including Thr-186, that are critical for its functional activity [49,50] and the association of CDK9/cyclin T1 with 7SK RNA snRNP [49,50]. Dephosphorylation of CDK9 at Thr-186 by protein phosphatase-1 (PP1) in stress-induced cells dissociates 7SK RNA and HEXIM1 and activates CDK9/cyclin T1 [51]. Additional phosphorylation sites on CDK9 include autophosphorylated Thr-29 [52] and the C-terminal residues Ser-329, Thr-330, Thr-333, Ser-334, Ser-347, Thr-350, Ser-353, and Thr-354 [49]. Dephosphorylation of CDK9's T-loop Ser-175 residue by PP1 induces CDK9 activity and activates HIV-1 transcription [53]. Accordingly, expression of the central domain of nuclear inhibitor of PP1 (cdNIPP1) in cultured cells, or as part of HIV-1 pNL4-3

in place of *nef*, efficiently inhibits HIV-1 transcription and replication [54]. Stable expression of cdNIPP1 disrupts the interaction of Tat with PP1, increases CDK9 phosphorylation of Thr-186, and induces association of CDK9 with 7SK RNA [54]. Expression of cdNIPP1 also increases CDK9's Ser-175 phosphorylation and inhibits the enzymatic activity of CDK9 [53].

The authors have recently developed small molecules that target a noncatalytic site of PP1 and identified inhibitors [55] as well as activators [Nekhai S & Kumari N, Unpublished Data] of HIV-1 transcription. The functional link between CDK2 and CDK9 is further supported by the inhibition of CDK2 by iron chelators (discussed in the next section) that also inhibit CDK9 activity and thus HIV-1 transcription [12,13]. It may be possible that CDK2 directly phosphorylates CDK9 (or Ser-90 of CDK9) and, therefore, may serve as a potentially key CDK2 phosphorylation site [56]. Phosphorylation of CDK9's Ser-90 may likely be a requirement for the functional CDK9 activity to activate HIV-1 transcription more efficiently because of the increased association with large P-TEFb complex [56]. Thus, recent studies may direct investigation to potentially novel and intriguing regulatory pathways linking CDK2 and CDK9 to cellular iron metabolism in the regulation of HIV-1 transcription.

Inhibition of HIV-1 transcription by iron chelators

In cultured T-cells, excess of iron is associated with an increased HIV-1 viral replication, whereas iron chelation with desferrioxamine correlates with lower viral replication [57]. Iron chelators deferoxamine and deferiprone inhibit HIV-1 replication in human primary peripheral blood lymphocytes and macrophages; however, the inhibition was largely attributed to decreased cellular proliferation [58]. Recently, the topical fungicide, ciclopirox, and the iron chelator, deferiprone, have been shown to inhibit HIV-1 gene expression at the level of transcription initiation by interfering with the hypusine modification of eIF5 α [20]. Iron chelators negatively affect the activity or expression of CDK2 [13,59,60] and thus mediate the deregulation of CDK2 and arrest cell cycle progress [61,62]. The iron chelator, desferrioxochelin, inhibits the binding of cyclin A and E to CDK2 in human mammary epithelial cells, whereas in human breast cancer cells the binding is increased [59]. On the other hand, iron chelator 311 inhibits the expression of cyclins D1, D2, D3, A and B1 and also CDK2, but not cyclin E [60]. HIV-1 transcription is inhibited in CEM T-cells by iron chelators 311 and ICL670 (deferasirox or Exjade[®], Novartis Oncology, NJ, USA) [13]. These iron chelators inhibit the cellular activity of CDK2 and inhibit both basal and Tat-induced HIV-1 transcription [13].

Previously described di-2-pyridylketone thiosemicarbazone- and 2-benzoylpyridine thiosemicarbazone-based tridentate iron chelators markedly inhibit HIV-1 transcription and virus replication at much lower concentrations than 311 or ILC670 [12]. Whilst the Bp4aT and Bp4eT iron chelators inhibit CDK2 activity, as expected, they also inhibit CDK9 activity [12]. CDK2 is positively regulated by the binding of cyclin E (G1/S transition) or cyclin A (S phase transition) and by CDK7-mediated phosphorylation of Thr-160 [63].

Negative regulation of CDK2 includes its association with the p21 (CIP1/WAF1) and p27 (Kip1) inhibitory proteins and Tyr15 phosphorylation by Wee1 kinase [64]. The mechanism of CDK2 inhibition by iron chelators may be related to the expression of the cyclin-dependent kinase inhibitors p21 or p27 [65,66]. Iron depletion removes iron from prolyl hydroxylase and increases HIF-1 α and HIF-2 α protein levels, mimicking the effect of hypoxia [67]. Induction of p21 expression by 9-aminoacridine inhibits HIV-1 transcription [68,69]. In a recent study, overexpression of p21 was found in a group of elite HIV-1 controllers [70]. Blockade of p21 in CD4⁺ T cells from elite controllers markedly increased

viral reverse transcripts and mRNA production, leading to higher enzymatic activities of CDK9, indicating p21 as a barrier against HIV-1 infection in CD4⁺ T cells [70]. Thus, based on the earlier observation that CDK2 and CDK9 associate in a complex with HIV-1 Tat [71], and the fact that CDK9 is directly phosphorylated by CDK2 [56], it is likely that p21 inhibits CDK9 indirectly by interacting with CDK2 and inhibiting its activity.

HIV-1 infection & iron metabolism regulation in macrophages

HIV-1 infection of macrophages has been recognized as an important component of viral pathogenesis [72]. An important function of human macrophages is a recycling of iron to the bone marrow from aged red blood cells, which involves iron export by ferroportin [73]. Macrophages recycle approximately 20–25 mg of iron per day, meeting the bioavailability of iron requirement for erythropoiesis [74]. After degradation of red blood cells in phagolysosomes, heme reaches the cytoplasm, where it activates the transcription of several cellular genes, including HO-1 and ferroportin [74]. HO-1 degrades heme to release CO, biliverdin and iron, which is stored in ferritin barrels or exported back to the plasma by ferroportin [74].

Activation of HO-1 and production of CO by HO-1 has recently been shown to protect against cerebral malaria in A/S sickle cell trait individuals [70], and may explain the survival advantage of sickle cell trait against malaria [75,76]. Hemin-induced HO-1 induction also efficiently inhibits HIV-1 infection *in vitro* and *in vivo* [77,78]. Hemoglobin-stimulated macrophages undergo a selective differentiation program and demonstrate increased ferroportin expression and reduced iron levels [79].

Ferroportin is the only iron exporter found in mammals [80] and is present in cells and tissues where major iron flows are regulated, such as red blood cells, placenta, hepatocytes and macrophages [81–83]. Ferroportin is also expressed on the basolateral side of duodenal enterocytes and helps to release iron into plasma, thus controlling both systemic iron absorption and iron recycling [84]. Mutations in the ferroportin gene, A77D, V162del and G490D, result in reduced iron export leading to iron accumulation in macrophages [85,86]. Mutations affecting the interaction with hepcidin prevent its proper functioning and cause hereditary iron overloads [84]. Because reduction of cellular iron inhibits HIV-1 transcription, depletion of cellular iron through the expression of ferroportin is thought to inhibit HIV-1 gene expression [14]. Expression of ferroportin is negatively regulated by hepcidin, a hepatocyte peptide hormone, resulting in the hepatic iron overload condition similar to hemochromatosis [87]. Hepcidin is secreted by hepatocytes and macrophages, and interacts with ferroportin, leading to its internalization and degradation by lysosomes [84].

The ferroportin mutants Y64N, N144D, N144H, and C326Y, which have a reduced sensitivity to hepcidin, lead to a higher dietary iron uptake, more iron recycling by macrophages and higher serum transferrin saturation [85]. Hepcidin has recently been shown to induce HIV-1 transcription in 293 T cells expressing WT ferroportin, but not the C326Y mutant [14]. In addition, hepcidin treatment of HIV-1-infected primary macrophages and T cells cultured in the presence of iron significantly induced HIV-1 replication [14]. These findings suggest that the interplay between ferroportin expression and its degradation by hepcidin may play a regulatory role in HIV-1 transcription and that HIV-1 transcription can be transiently activated by hepcidin. However, the role of ferroportin or hepcidin in the progression of HIV-1 disease has remained undefined. Hepcidin expression is facilitated by IL-6 and other proinflammatory cytokines that are elevated during inflammation [88] and constitute a risk factor for the progression of HIV-1 disease and pathogenesis [89].

Effect of hypoxia on HIV-1

The role of physiological factors in the regulation of HIV-1 transcription is not well defined. Our knowledge about the activation of HIV-1 transcription is primarily based on observations from cell culture experiments, which are typically conducted at atmospheric oxygen level (21% O₂). However, the physiologic level of O₂ is significantly less than that present in these *in vitro* experimental conditions. For example, in lungs, liver, kidneys and heart, O₂ varies between 4 and 14%; in the brain, from 0.5 to 7%; in the eye, from 1 to 5%; and in the bone marrow, from 0 to 4% [90]. Thus, the function of cellular and viral proteins may differ under the lower-than-atmospheric oxygen tension. This is exemplified by the iron-responsive proteins, IRP-1 and IRP-2, where IRP-1 is the major sensor of intracellular labile iron in tissue culture experiments at 21% O₂ but IRP-2 is the main iron sensor *in vivo* and in cells cultured at 3% O₂ [91].

Hypoxia can induce some viruses and inhibit the others. Hypoxia (1% O₂) induces lytic replication of EBV [92] and Kaposi sarcoma-associated herpesvirus [93], but suppresses replication of oncolytic parvovirus Minute virus of mice [94], adenovirus [95] or Moloney murine leukemia virus [96]. Primary T cells cultured at 3–6% O₂ maintain an intracellular redox environment similar to the *in vivo* situation, as opposed to T cells cultured at atmospheric 21% O₂, in which the intracellular redox state is significantly altered [97]. Peripheral blood mononuclear cells (PBMCs) cultured at 5% O₂ are efficiently activated by extracellular HIV-1 Tat protein, which mimicks the activation by IL-2 and PMA, and the activated cells support HIV 1 replication [98].

Iron chelators deplete iron from cellular enzymes including prolyl hydroxylase, which decreases prolyl hydroxylase activity and increases the protein level of HIF-1 α , thus mimicking the effect of hypoxia [99]. Therefore, it may be argued that HIV-1 transcription and replication could also be reduced in cells cultured in lower levels of oxygen as compared with the atmospheric oxygen concentration [4]. Interestingly, HIF-1 α expression is seen only at low 1% O₂, but not at physiological 3% O₂, and CDK2 activity remains unchanged at 3% O₂ [4]. In contrast, CDK9/cyclin T1 activity is significantly reduced in T cells cultured at 3% oxygen [4]. This is due to reduced association of CDK9 with cyclin T1, and not because of the reduced expression of CDK9 or cyclin T1 [4]. Accordingly, the CDK9 inhibitor ARC, which efficiently inhibits HIV-1 transcription [100], has significantly less effect on HIV-1 transcription in cells cultured at 3% O₂ [4], suggesting that CDK9 activity may be decreased and less critical for the regulation of HIV-1 transcription in the cells cultured at 3% O₂.

CDK9 activity is regulated in part by PP1 [53,54,101]. Previously, PP1 has been shown to be negatively affected by hypoxia either through a decrease of mRNA expression [102] or increased association with its regulatory subunit, nuclear inhibitor of PP1 [103]. Thus, PP1 inhibition may lead to changes in CDK9 phosphorylation and modulation of its activity. Hypoxia also modulates the activity of CDK9 through the expression of p27 protein [104], which may also have a downstream effect on CDK9.

Low prevalence of HIV-1 infection in sickle cell disease

In sickle cell disease (SCD), a hereditary disorder that affects approximately 100,000 people in the USA, primarily of African descent [105], a single V6G mutation in the β -globin gene can lead to the production of hemoglobin S, development of chronic hemolytic anemia, adhesion of sickle erythrocytes to endothelium, immune activation and abnormal cytokine production [106]. Despite frequent blood transfusion, SCD patients have lower risk for HIV-1 infection in comparison with Human T-lymphotropic virus type I (HTLV-1) infection (0% HIV-1⁺ vs 7.9% HTLV-1⁺) [107] and higher frequency of HIV-1 long-term

nonprogressors compared with the general HIV⁺ population (44% in SCD patients vs. 13.9% in controls) [108]. Out of 116 SCD patients, 88 patients received an average 18 transfusions between 1978 and 1985, and negative for the HIV antibody. Among the same patient population, nine (7.8%) were tested positive for HTLV-I antibodies. A recent study conducted among five University Centers, including Howard University, revealed a higher frequency of HIV-1 long-term nonprogressors among HIV-1-infected SCD patients (44%) as compared with HIV-1-infected controls (13.9%) [108]. Another recently published report from Republic of Congo indicated that frequency of HIV among 127 SCD patients was lower than among 3390 blood donors [109,110]. Our recent analysis of national hospital discharge surveys (1997–2009) showed that SCD is associated with lower frequency of HIV-1 diagnosis (odds ratio 0.33) as compared with other diagnosis [111].

The level of hepcidin that regulates internalization and degradation of the iron export protein ferroportin is reduced in some SCD patients [112]. Gene expression analysis showed increased expression of HO-1, biliverdin reductase and p21 in PBMCs from SCD patients in steady-state SCD [113]. Our unpublished observations show that HIV-1 replication is reduced in PBMCs obtained from SCD patients, suggesting that chronic hemolysis and local ischemia may contribute to protection against HIV-1 infection in SCD.

Conclusion

In this review, the authors have discussed cellular factors involved in the iron and oxygen homeostasis that affect HIV-1. Understanding the role of these cellular factors in HIV-1 replication may provide new targets for HIV-1 therapy. Also, information on the emerging roles of iron and oxygen-regulatory pathways in antiviral immune response may provide a supplemental strategy for controlling HIV-1 infection in addition to the existing antiretroviral therapy or vaccination trials.

Future perspective

As outlined in this review, iron- and oxygen-related metabolic pathways emerge as important regulatory players in HIV-1 infection. With the failure of anti-HIV-1 vaccines targeted to gp120 and HIV-1 Gag, Pol and Nef proteins, and the low (31%) efficacy of a combined vaccine recently tested among community-risk Thai participants [114], additional strategies are needed to curb HIV-1 epidemics. As proteins regulating cellular iron metabolism, such as ferroportin and hepcidin, emerge as major regulators of innate immune response [115], therapeutic strategies that provide iron chelation or control iron absorption could be developed as supplemental approaches that may be combined with and augment vaccination. Iron supplementation strategy has to be taken with caution in this situation, especially because of the high rates of HIV-1 coinfection with tuberculosis [116], HBV and HCV [117], and thus the possibility of increased adverse effects due to the augmentation of coinfections [118,119].

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Executive summary

Increased iron levels associate with severe HIV-1 disease progression

- A number of studies showed association between increased iron stores and severity of HIV-1 infection.

Cellular iron affects HIV-1 replication

- Cellular iron affects HIV-1 transcription through the control of CDK 2 activity; splicing through Rev and eIF5 α ; and viral assembly through Nef, HFE, and ABCE1.

Regulation of HIV-1 transcription

- HIV-1 Tat engages CDK2/cyclin E and protein phosphatase-1 that phosphorylates and dephosphorylates CDK9 on Ser-90 and Ser-175 respectively and which are subject to a regulation by cellular iron and hypoxia.

HIV-1 infection and iron metabolism regulation in macrophages

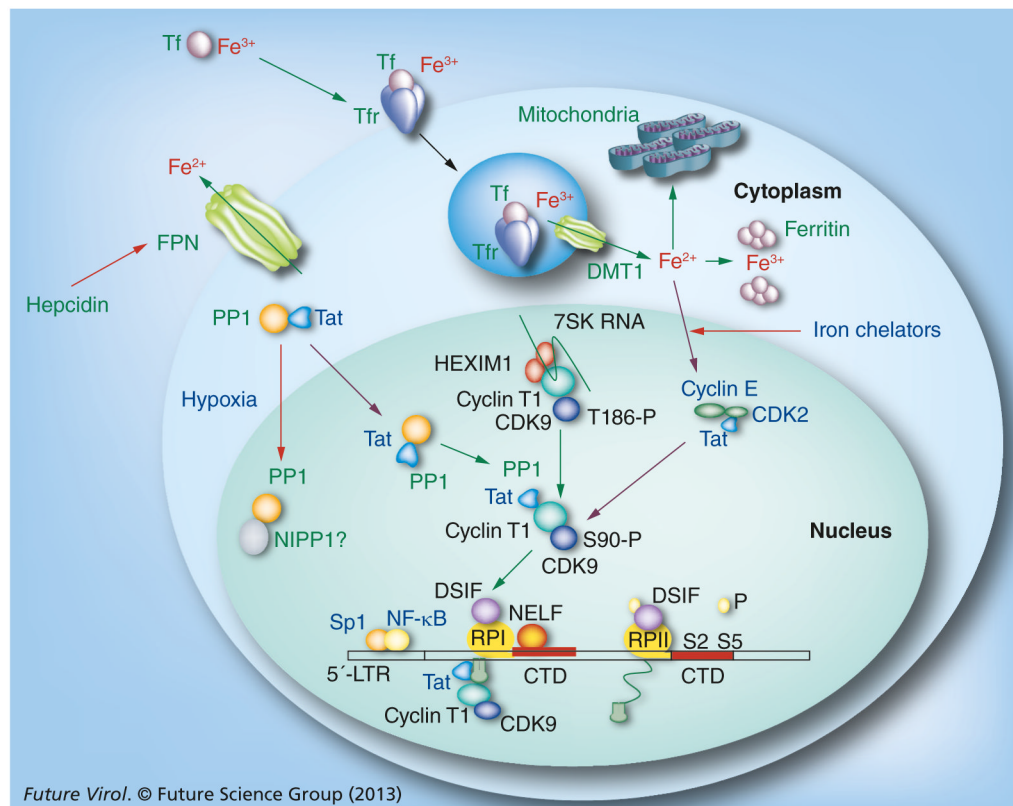
- Heme processing by macrophages leads to induction of HO-1 and ferroportin, inhibiting HIV-1. The negative regulator of ferroportin expression, hepcidin, induces HIV-1 transcription and replication.

Effect of hypoxia on HIV-1

- Hypoxia inhibits HIV-1 by decreasing CDK9/cyclin T1 activity. The effect of hypoxia could be due to deregulation of protein phosphatase-1 and/or increased expression of p27.

Low prevalence of HIV-1 in sickle cell disease

- Sickle cell disease associates with lower rates or slower progression of HIV-1 infection. Decreased hepcidin levels and increased levels of HO-1 and p21 may reduce HIV-1 replication.



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Figure 1. Schematic representation of the effect of iron and hypoxia on Tat-mediated HIV-1 transcription

Tf-bound iron is uptaken through the Tfr and then exported to cytoplasm by DMT1. Ferritin stores cellular iron. Excess iron is exported by ferroportin, which is negatively regulated by extracellular hepcidin that binds to ferroportin and leads to its internalization and degradation. HIV-1 transcription is activated by Tat protein, which recruits CDK9/cyclin T1 to the HIV-1 5' LTR promoting the phosphorylation of NELF, DSIF and the CTD of RPII. CDK2/cyclin E activates CDK9 by phosphorylation on Ser-90. Iron chelation inhibits CDK2 and CDK9 activities. Tat also shuttles PP1 to the nucleus, where PP1 dephosphorylates CDK9 and facilitates the dissociation of CDK9/cyclin T1 from the inactive complex containing 7SK RNA and HEXIM1. Hypoxia affects PP1, facilitating its binding to NIPP1. Expression of ferroportin inhibits HIV-1, and inhibition of ferroportin by hepcidin induces HIV-1.

CTD: C-terminal domain; DMT1: Divalent metal transporter 1; DSIF: DRB-sensitivity inducing complex; HEXIM1: Hexamethylene bis-acetamide-inducible protein 1; LTR: Long terminal repeat; NELF: Negative elongation factor; NIPP1: Nuclear inhibitor of PP1; PP1: Protein phosphatase-1; RPII: RNA polymerase; Sp1: Transcription factor; Tat: HIV-1 transcription factor; Tfr: Transferrin receptor.

Table 1

Iron and oxygen regulatory pathways and their effect on HIV-1.

| Modulation | Mechanism | Mediating pathways | HIV-related consequence | Ref. |
|------------|------------------------------|--|--|---------|
| ↑ Iron | Iron suppl. | Unknown | ↑ HIV-1 replication | [57] |
| ↑ Iron | Hepcidin. | Ferroportin degradation | ↑ HIV-1 replication | [14] |
| ↓ Iron | Iron chelation | ↓ CDK2 activity, ↓ CDK9 activity | ↓ HIV-1 transcription | [12,13] |
| ↓ CDK2 | siRNA | ↓ CDK9 Ser-90 phosphorylation | ↓ HIV-1 transcription, ↓ HIV-1 replication | [56] |
| ↓ CDK9 | Inhibition by ARC | ↓ CDK9 activity | ↓ HIV-1 transcription, ↓ HIV-1 replication | [100] |
| ↓ Iron | Ferroportin | Unknown | ↓ HIV-1 replication | [14] |
| ↑ HO-1 | Heme suppl. | Unknown | ↓ HIV-1 replication | [77,78] |
| ↓ Oxygen | 3% O ₂ culture | ↓ CDK9 activity | ↓ HIV-1 transcription, ↓ HIV-1 replication | [4] |
| ↓ Oxygen | 1% O ₂ culture | ↓ PP1 activity due to association with NIPP1 | Unknown | [103] |
| ↓ Oxygen | 1% O ₂ culture | p27 expression | Unknown | [104] |
| ↓ PP1 | Expression of PP1 inhibitors | CDK9 Ser-175 and Thr-186 phosphorylation | ↓ HIV-1 transcription | [53-55] |

Table 2

Epidemiological evidence for iron and oxygen pathways effect on HIV-1.

| Epidemiological evidence | Hypothesized mechanism | HIV-1 related consequence | Ref. |
|---|------------------------|--|---------------|
| Thalassemia major, oral iron administration, haptoglobin 2-2 polymorphism | ↑ Iron, ↑ ferritin | ↑ Mortality | [2] |
| Zimbabwe HIV cohort | ↑ Ferritin | ↑ HIV-1 infection | [7] |
| Gambian HIV cohort | ↑ Iron, ↑ ferritin | ↑ Mortality | [8] |
| <i>SLC11A1</i> (NRAMP1) polymorphisms | ↑ ↓ Ferritin | ↑ ↓ Mortality | [9] |
| Sickle cell disease | ↑ Hemolysis | ↓ HIV-1 infection; ↓ HIV-1 progression | [107,108,111] |
| Sickle cell disease | ↑ HO-1, ↑ p21 | Unknown | [113] |
| Gambian HIV cohort | ↑ Iron, ↑ ferritin | ↑ Mortality | [8] |
| HIV-1 elite controllers | ↑ p21, ↓ CDK9 activity | ↓ HIV-1 progression | [74] |