



TYROSINE KINASES AS ESSENTIAL CELLULAR COFACTORS AND POTENTIAL THERAPEUTIC TARGETS FOR HUMAN IMMUNODEFICIENCY VIRUS INFECTION

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Abstract

The Human Immunodeficiency Virus (HIV) is the cause of the AIDS disease. To date, more than 30 million people worldwide are infected with HIV-1, which causes two millions deaths each year. The pandemic is still ongoing, with three million new infections every year. Even though the current arsenal of anti-HIV drugs is composed of more than twenty different molecules, it became clear that the chemotherapeutic approach will not be able to cure AIDS, at least in its current form. It is essential, in order to develop more effective ways of treating this disease, to better understand the interplay of HIV with its cellular host, in fact HIV-1 is an obligatory intracellular parasite that takes advantage of the host cell metabolism for its own replication. HIV-1 takes control of virtually every aspect of cell metabolism by changing the functional properties of key signaling cellular proteins, thus triggering virus-specific signal transduction pathways. In this review, we will summarize the current knowledge about the role(s) of cellular tyrosine kinases in HIV infection and their potential therapeutic exploitation.

Key words: HIV-1, tyrosine kinase, Vif, Nef.

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HIV and AIDS: an everlasting problem

The Acquired Immunodeficiency Syndrome (AIDS) emerged in the human population in 1981 as an outbreak of *Pneumocystis carinii* atypical pneumonia among homosexual men in the USA even if this syndrome was present in Africa for many decades earlier. To date, more than 30 million people worldwide are infected with HIV-1, which causes two millions deaths each year. The pandemic is still ongoing, with three million new infections every year. The Human Immunodeficiency Virus (HIV) is the cause of the AIDS disease. HIV is a retrovirus that is transmitted by sexual contact, injection of infected blood or blood-derived products (33). HIV exists in two serotypes, HIV-1 and HIV-2. The majority of the infections in the world are caused by HIV-1, whereas HIV-2 is mainly associated to smaller epidemics in West Africa and has a lower transmission efficacy.

AIDS is characterized by a progressive depletion of CD4+ helper T-cells, that allows opportunistic infections, including pulmonary tuberculosis (a frequent complication) and a variety of bacterial, viral, or parasitic infections, as well as cancer such as non-Hodgkin B cell lymphomas or Kaposi sarcoma (33). As all viruses, HIV-1 is an obligatory intracellular parasite that takes advantage of the host cell metabolism for its own replication. Due to the worldwide dimensions of the AIDS epidemic, HIV-1 has been the focus of intense research in the last 30 years, which allowed the uncovering of the extraordinary complexity of its interactions with the host cell. An early outcome of these studies was the development, about twenty years ago, of a chemotherapeutic approach, named highly active antiretroviral therapy HAART, based on the combination of three antiretroviral drugs, targeting different viral proteins. The HAART approach substantially decreased the number of AIDS-related deaths and current-

ly allows to keep the epidemic under control, at least in western countries, where this highly expensive therapy is available. However, HAART is not able to eradicate the infection; in addition, it is a lifelong therapy since its interruption is invariably followed by viral relapse in the patients. A consequence of this fact is the exacerbation of drug side effects, requiring continuous adjustments of the individual therapies and often causing a poor compliance of the treated individuals. On top of that, prolonged therapy favors the selection of viral drug resistant variants that cause the failure of first line therapies. Thus, even though the current arsenal of anti-HIV drugs is composed of more than twenty different molecules, it became clear that the chemotherapeutic approach will not be able to cure AIDS, at least in its current form. It is essential; in order to develop more effective ways of treating this disease, to better understand the interplay of HIV with its cellular host.

A short overview of the HIV-1 life cycle

CD4+T cells of the monocyte/macrophage lineage are the main target of HIV-1. HIV needs both the CD4 receptor and a chemokine receptor for entering the target cells. These chemokine receptors are CCR5 (a β -chemokine receptor) and CXCR4 (an α -chemokine receptor) (69). Attachment and entry of HIV-1 is mediated by the viral envelope glycoprotein Env (13). Env is a 160 kDa glycoprotein that is cleaved into a gp120 external subunit and a gp41 transmembrane subunit that together form trimeric spikes on the surface of the virion. The 9.5 kb molecule of single-stranded positive sense RNA encodes also for other two important structural virus proteins: Gag and Pol. Furthermore the RNA genome encodes the regulatory proteins Tat and Rev, and accessory proteins Nef, Vif, Vpr and Vpu (33).

Following entry into the cytosol the viral enzyme reverse transcriptase converts the RNA genome into double-

stranded DNA. A high-molecular weight structure, known as the pre-integration complex, translocates the newly synthesized viral DNA into the nucleus (10, 24, 34, 103, 113). A second viral enzyme, the integrase, is responsible for the integration of the viral DNA in the chromosome of the host cell. At this point the proviral DNA directs the transcription of viral RNAs, thanks to the action of the early genes Tat and Rev. These RNAs are transported in the cytoplasm where translation of viral proteins takes place. Env is processed in the endoplasmic reticulum and Golgi apparatus and is inserted in the cell cytoplasmic membrane. The Gag and Pol polyproteins and the two single stranded copies of full length viral RNA are then transported at the inner face of the plasma membrane to direct the assembly of new viral particles, which bud from the cell acquiring the viral envelope containing Env. Concomitantly with the release of new viral particle, the viral protease cleaves the Gag and Pol polyprotein precursors, triggering the formation of the mature virion.

At this point the replication cycle of the virus is complete, and a new cycle of infection can be started from the mature virus particle (104).

Being an obligate intracellular pathogen, HIV-1 relies for its replication on several host factors. Over 1000 candidate host factors have been implicated in HIV-1 infection by a large scale siRNA and shRNA screens (5, 7, 12, 56, 57, 80, 87, 118, 123). This number is disproportionately higher than the number of proteins encoded by the viral genome (fifteen). However, these studies also revealed that the ability of HIV-1 to take control of virtually every aspect of cell metabolism through a limited number of its own proteins is made possible by the ability of the virus to directly modulate, through direct protein-protein interactions, key cellular proteins representing functional nodes at the intersection of diverse intracellular pathways. In such a way, by changing the functional properties of a limited number of proteins, HIV-1 triggers virus-specific signal transduction pathways which, in turn, profoundly affect the cellular metabolism.

Tyrosine kinases in HIV infection: novel antiretroviral targets?

Among the most important signal transduction components of the cellular metabolic pathways are the protein tyrosine kinases. The protein tyrosine kinases (TKs) are enzymes that catalyze the transfer of a phosphoryl group to tyrosine residues in protein substrates, using primarily ATP as the phosphate donor. In this large family there are, in the human genome, 58 receptor kinases (RTKs) and 32 non-receptor kinases (NRTKs). TKs regulate different aspects of the cellular metabolism: cell to cell communication, cellular growth, differentiation, motility, adhesion and death (91). TKs also play significant roles in many diseases like cancer and diabetes and they have also been linked to a variety of congenital syndromes (90).

RTKs and NRTKs are characterized by a different structural organization that reflects their different functions. RTKs are the main transducers of extracellular signals, due to their ability to be activated by the binding of specific protein ligands. The majority of RTKs in the absence of their ligand is monomeric and consists of a single polypeptide chain, with a central transmembrane domain, that separates the extracellular portion from the intracellular one. The catalytic activity is found in the cytoplasmic portion,

while the extracellular portion binds the specific polypeptide ligands that are responsible for TK activation. The extracellular region contains a diverse array of discrete globular domains (Ig-like domains, fibronectin type III-like domains, cysteine-rich domains and EGF-like domains), whereas the cytoplasmic domain is simpler and consists of a tyrosine kinase catalytic domain and a carboxyl-terminal region (48).

Most of NRTKs are localized in the cytoplasm (some of them are anchored to the inner face of the cell membrane through amino terminal modifications) and, as their name implies, they lack receptor-like features such a transmembrane-spanning region and an extracellular ligand-binding domain (79). In addition to their tyrosine kinase domain, they also have domains that mediate protein-protein, protein-lipid and protein-DNA interaction (48). Several studies indicated important roles of these enzymes for HIV-1 replication, however, the details of their action within the viral life cycle are, at best, still imperfectly understood (Figure 1).

Understanding the interplay among these enzymes and viral replication might offer new venues for HIV-1 chemotherapy. In fact, a strategy being pursued in order to overcome the problem of drug resistance is to target cellular factors of the host cell that interact with the virus during the infection. Since cellular proteins are much less prone to mutation, this could be a winning strategy for developing drugs to combat HIV (and other pathogens) avoiding, or at least substantially delaying, drug resistance. Tyrosine kinases are attractive targets, since they are already being studied as chemotherapeutic targets for the treatment of cancer and a significant amount of knowledge about their structure, functions and possible strategies to develop specific inhibitors is already available. Moreover, several tyrosine kinase inhibitors are already used in the clinics for the treatment of diverse malignancies and more are in advanced clinical trials. Thus, the discovery, among cellular tyrosine kinases, of a potential candidate for the treatment of HIV-1 infection, might very rapidly lead to the development of novel drugs.

In this review, we will summarize the current knowledge about the role(s) of cellular tyrosine kinases in HIV infection. The discussed tyrosine kinases, their biological functions and their proposed roles in HIV-1 replication are listed in Table 1.

Non-receptor tyrosine kinases

The Src family

The Src protein tyrosine kinase family (SFK) is composed of non-receptorial, cytoplasmic tyrosine kinases capable of communicating with a large number of different receptors (107). Eight members of non receptor tyrosine kinases are currently classified as SFK members: Src, Fyn, Yes, Lyn, Fgr, Hck, Lck, Blk. The first three are ubiquitously expressed, while there is a tissue-specific expression for the other five members (36). SFK family members have molecular weights between 52 and 56 kDa and are composed of six distinct functional regions: the Src homologous SH4 domain, the unique region (which is the N-terminal end), the SH3 domain, the SH2 domain, the catalytic domain (SH1), and a short negative regulatory tail (107).

The SH4 domain has a sequence of 15 amino-acids that contains signals for lipid modification of SFKs (107), while

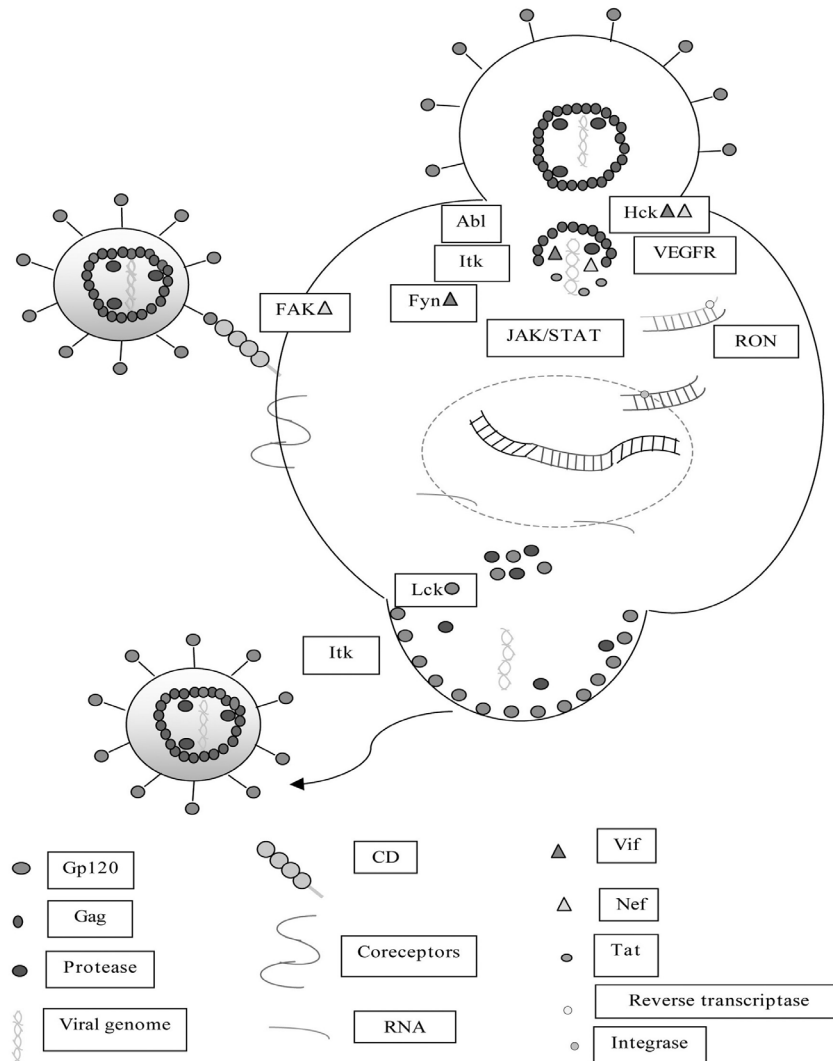


Figure 1. Tyrosine kinases are involved in different stages of the HIV-1 life cycle. Schematic representation of the HIV-1 life cycle from entry to budding. The various tyrosine kinases involved in HIV-1 infection are indicated at each stage of the viral life cycle along with the respective viral interactors.

the unique domain is responsible for the association of SFKs to the inner face of the plasma membranes. The SH3 domain is a protein-protein interaction motif, responsible for recognizing the proline-rich consensus sequence PxxP. The SH2 domain recognizes proteins with phosphorylated tyrosines within the consensus sequence pYEEI. The catalytic site resides in the SH1 domain, where is also present a kinase-activation loop containing a specific tyrosine (activating tyrosine, YA) that can be autophosphorylated leading to fully active kinase (36).

The SFKs are found in the cell in two different functional states, active or inactive, corresponding to particular protein conformations. The inactive conformation is maintained by specific intramolecular inhibitory interactions: the SH3 domain binds to a polyproline type II helical motif located in the linker between the SH2 and SH1 domains, this binding is stabilized by the interaction of a phosphorylated tyrosine located in the C-terminal tail (tail tyrosine, YT) with the SH2 domain. The active conformation is assumed by protein following dephosphorylation of YT, which in turn, promotes the release of the linker domain from SH3, exposing the active site and enabling autophosphorylation of the YA residue. The balance between the active and inactive forms of SFKs in the cell is regulated through phosphorylation of YT and dephosphorylation of YA that are mediated by the C-terminal Src kinase (Csk)

and C-terminal Src homologous kinase (CHK), and various protein phosphatases, respectively (78, 102, 109).

SFKs and HIV

Many members of the SFK are involved in the HIV-1 infection.

Hematopoietic cell kinase, Hck

The expression of Hck is mainly present in promonocytic cells, including monocyte-derived macrophages, where it mediates relevant functions such as induction of cytokine production triggered by bacterial lipopolysaccharide, FcγRI receptor signaling, phagocytosis, and cell spreading (22, 66, 72). Hck is the first cellular protein that has been identified as interacting with the auxiliary HIV-1 protein Vif (44). In the C-terminal domain of Vif is localized a proline-rich motif (PPLP) that can interact with the SH3 domain of the tyrosine kinases and adaptor proteins. Hassaine *et al.* (44) demonstrated that Vif binds preferentially to the SH3 domain of the tyrosine kinase Hck and not significantly to other SH3 domains of the members of SFK and of adaptor proteins.

It has been demonstrated that in absence of Vif, T cells were less permissive for HIV-1 replication. Moreover, when Vif was lacking and Hck was expressed, release of HIV-1 viral particles was strongly inhibited and virion in-

Table 1. Human Tyrosine kinases involved in HIV-1 infection.

Tyrosine Kinase	Physiological functions	HIV-1 related functions
Hck	Mediates induction of cytokine production, neutrophils migration and degranulation	- Inhibited by Vif - Activated by Nef
Fyn	Control of cell growth	- Interacts with Vif - Phosphorylates APOBEC3G
Lck	Selection and maturation of developing T-cells in the thymus and in mature T-cells function	- Binds Gag during virus assembly - Has a role during viral packaging - Involved in Nef signaling
Abl	Role in morphogenesis and F-actin dynamics, survival and cell growth	- Phosphorylates Wave 2 complex
Itk	Role in T-cell proliferation and differentiation	- Is required for actin polarization and activation of Rac and gp120 induced actin rearrangement. - Stimulates virion assembly and release - Increases intracellular Ca ²⁺
Fak	Influence proliferation, migration attachment and survival of cells	- Phosphorylated when is recruited on the plasma membrane by gp120, induces apoptosis - Competes with Nef
RON	Regulates macrophage function and inflammation	- Inhibits virus transcription
VEGFR	Vasculogenesis and angiogenesis	- Mediates Tat signaling
JAK/STAT	Involved in signaling pathways mainly activated by cytokines	- Inhibits HIV replication in monocytes

fectivity was reduced. This Hck-dependent inhibition was overcome by the presence of Vif. Douaisi *et al.* (21) demonstrated that the autophosphorylation of Hck was dramatically reduced by Vif, causing a decrease of the active form of Hck concurrently with an increased expression of Vif.

Nef is an accessory gene unique to the primary lentiviruses HIV-1, HIV-2 and SIV. Nef manipulates HIV-infected cells by altering a variety of protein sorting and signal transduction pathways like T cell receptor (TCR) signal transduction pathway (38) and Hck regulation. Nef binds Hck, increasing its catalytic activity and promoting viral growth (52). Nef interacts with the Hck SH3 domain via

its polyproline motif and this interaction was proposed to upregulate the Hck kinase activity by displacing the intramolecular SH3/linker domain interaction characteristic of the inactive form of Hck. The HIV-1 protein Vif is also important to counteract the cellular antiviral cytidine deaminase APOBEC3G (93). During the viral assembly of HIV-1, in the absence of the Vif protein APOBEC3G is packaged in the virions (71) and, upon infection of cell by the virus, catalyzes the cytosine deamination of the single-stranded DNA intermediates which are formed during the reverse transcription step, blocking viral replication (43, 60, 70, 122).

The antiviral factor Vif limits the APOBEC3G packaging into virions by targeting the deaminase to ubiquitin-dependent degradation by the proteasome (71). APOBEC3G can be phosphorylated on tyrosine in the presence of Hck, and this tyrosine kinase can inhibit the packaging of APOBEC3G into HIV-1 particles, independently of Vif. Thus, the functional interaction between APOBEC3G and the HIV-1 assembly complex is modified by the activation of Src kinases, resulting in an enrichment of the phosphorylated form of APOBEC3G at the viral budding site (21). These diverse effects of Hck on viral replication suggest that the activity of this kinase must be finely tuned within the HIV-1 life cycle, an observation that justifies the presence of two viral proteins acting on this kinase with opposite effects (inhibition by Vif / activation by Nef). However, the molecular details of this mechanism are currently unknown.

Fgr- and Yes-related protein kinase, Fyn

The Vif protein also interacts with another SFK member: Fyn. This interaction is mediated by Fyn SH3 domain and reduces the catalytic activity of the kinase (21). Auto-phosphorylation of Fyn is reduced by Vif and the increased expression of Vif causes the decrease of active Fyn. Vif is not itself a substrate of either Fyn or Hck, however Fyn has been shown to phosphorylate APOBEC3G reducing its packaging into HIV-1 particles.

Lymphoid T-cell protein kinase, Lck

Various studies have suggested that Lck is involved in HIV-1 transcription, replication and pathogenesis (101). Strasner *et al.* (101) have demonstrated that Lck promotes efficient HIV-1 replication in T-cells. They showed that Lck regulates Gag trafficking from the intracellular compartments to the plasma membrane during HIV-1 assembly in T-cells. Moreover, the unique domain (UD) of Lck binds HIV-1 Gag during virus assembly facilitating efficient virus release. So Lck has a role during viral packaging (101). The palmitoylation and plasma membrane localization of Lck UD are critical for the ability of Lck to favor HIV-1 assembly (101). The palmitoylation of Lck is catalyzed in the early exocytic pathway and it allows for subsequent transport of the protein to the plasma membrane. Thus, this HIV-1 Gag can take advantage of this property of Lck for its targeting to the plasma membrane (101).

The physiologically exogenous TCR activation occurs through formation of the immunological synapse (IS) between an antigen presenting cell (APC) and a T-cell. The transduction of the signals occurs through Lck (63). Several reports indicate that, during exogenous TCR activation, Nef expression can reduce signal transmission, preventing cell activation and prolonging the lifespan of infected cells (37, 92, 108). It has been suggested that Nef interferes with the intracellular sorting of Lck, the IS proximal kinase, in HIV-1 infected primary human T lymphocytes (108) determining a significant change in the normal subcellular localization of this kinase in T lymphocytes. In addition, Thoulouze *et al.* also reported that Nef impairs the recruitment of Lck to the IS following TCR engagement (108).

Abelson leukemia kinase, Abl

c-Abl is a non-receptor tyrosine kinase which is localized both in the nucleus and the cytoplasm, and is implicated in the morphogenesis, survival of the cell and in cell growth

(95). The organization of Abl proteins is similar to the one of Src, comprising a unique N-terminus followed by a SH3 domain, a SH2 domain and the catalytic core. The difference with Src is in the C-terminus tail, where there is a large and unique sequence, encoded by the last exon, comprising F-(filamentous) and G-(globular) actin-binding domains, NESs (nuclear export sequences) and proline-rich sequences. There is also NLSs (nuclear localization signal) and a DNA-binding sequence that are important for nuclear functions (82). c-Abl alternates between nuclear and cytoplasmic compartments. The function of nuclear c-Abl has been well documented (111); it is implicated in promotion of apoptosis, cell growth inhibition and modulation of the cellular response induced by DNA damage. The cytoplasmic form of c-Abl has a central role in morphogenesis and F-actin dynamics, as revealed by genetic and biochemical analysis (115) and c-Abl has some role even in receptor endocytosis (95). Several reports underline that c-Abl is involved in different cytoplasmic signaling cascades induced by various extracellular stimuli (18, 81, 89, 110, 115, 124). Similar to SFKs, c-Abl alternates between two forms: active and inactive. The inactive form is characterized by a closed conformation of the kinase domain due to intramolecular interactions involving the SH3 domain and the proline-rich sequence in SH2-kinase linker domain (3). The catalytic activation is induced by the opening of the closed conformation. When a mutation induces the disruption of these interactions the activity is transformed, as observed in oncogenic Abl alleles such as the fusion BCR-Abl kinase (40). Activity of c-Abl is regulated by its phosphorylation status. The phosphorylation on Tyr 245 and Tyr 412 (functionally analogous to YA and YT of SFKs) is required for c-Abl activation; moreover c-Abl is phosphorylated also on serine and threonine residues which are involved in the catalytic regulation (39).

Abl and HIV

HIV infects the cells by fusion at the plasma membrane, in a pH-independent manner (27, 35, 75). The entry of HIV-1 involves critical conformational changes in the HIV-1 glycoprotein, as well as rearrangements of the actin cytoskeleton at the entry site (20, 29, 41, 49, 50, 84, 85). These events are triggered when the Env subunit gp120 binds the primary receptor CD4 and the CCR5 or CXCR4 chemokine coreceptors (35, 85). This interaction determines the activation of many signaling events in the cell, such as Ca²⁺ mobilization, activation of RhoGTPases and phosphorylation of several tyrosine kinases, such as Pyk2, Zap70 and Lck (41, 85, 99). In particular, the signaling from the membrane receptors to the actin cytoskeleton is mediated by the Rho family GTPases, which include the Cdc42, Rac and Rho subfamilies (42).

It has been shown that when HIV-1 Env binds target cells, it induces activation of Rac. Conversely, overexpression of a dominant negative mutant of Rac, inhibits HIV fusion (84, 85). Among the fusion specific effectors of Rac, essential for the actin cytoskeleton rearrangements that mediate membrane fusion, there is the Arp2/3 complex that induces actin polymerization (42). Arp2/3 is activated by the Wave2 complex through the IRSp53 adaptor protein that binds Rac and Wave2 (11). The Wave2 complex, in turn, is associated with Abl, and phosphorylation mediated by Abl promotes Wave2 activation (29, 97). This modification is essential for the subsequent activation of Arp2/3-mediated

actin rearrangements which facilitate pore formation, pore enlargement, and entry of HIV-1. Recent studies demonstrated that the Env-mediated membrane fusion process is arrested by Abl kinase inhibitors (like imatinib, nilotinib and dasatinib) (42). Abl actin remodeling can act both upstream and downstream of Rac (120, 121). Harmon *et al.* (42) used siRNA and specific inhibitors to show that the activity of Abl kinase is required both upstream and downstream of Rac for the Env-induced membrane fusion.

Tyrosine kinase expressed in hepatocellular carcinoma, Tec and its family

The Tec family of tyrosine kinases (TEK) are important mediators of antigen receptor signaling in lymphocytes. TEKs are a group of five non-receptor tyrosine kinases: Tec, Btk, Itk, Rlk and Bmx, and they are primarily expressed in hematopoietic cells. These kinases are involved in different roles: TCR-mediated activation of phospholipase C- γ , regulation of actin cytoskeletal reorganization and cellular adhesion. Moreover they play parallel roles in the regulation of Rho GTPases, cell polarization, adhesion, and migration after their activation of phospholipase C- γ mediated by TCR (4).

The five members of Tec family kinases share a similar domain organization that recalls the organization of the Src family tyrosine kinases (96). In the C-terminus there is the kinase domain which is followed by a single SH2 and a single SH3 domain. However, there are also significant differences with the Src family kinases. Particularly, in the N-terminal side of the SH3 domain, all Tec kinases apart Bmx, have a proline-rich region (PRR). In Btk and Tec there is a second tandem PRR, near to a Zn²⁺-binding region, called Btk homology (BH) motif. This BH motif is also found in Itk, adjacent to its single PRR.

The four members Itk, Btk, Tec and Bmx at the very N-terminus of the protein share a PH (pleckstrin homology) domain, whereas Rlk contains a cysteine-string motif. This PH domain binds to the products of phosphoinositide 3-kinase (PI3K), a property unique to TEKs. All the domains mentioned above (SH2, SH3, PRR, BH) mediate protein-protein interactions which regulate the binding partners of the TEKs determining their proximity to signaling complexes and potential substrates. Itk, Rlk and Tec are the three major TEKs that are expressed in T lymphocytes and they phosphorylate on specific tyrosines upon T cell receptor (TCR) stimulation (19, 32, 46, 117). These three TEKs have distinct patterns and levels of expression in response to their functions in different T cell subsets and stages of development. The predominant Tec kinase in T cell is Itk, which is expressed in thymocytes and mature T cells, mast cells, natural killer cells (31, 45, 94, 106, 116). Rlk is expressed like Itk in thymocytes, mature resting T cells, and mast cells (47, 98). The pattern of expression of Tec is broader and this kinase is present both in hematopoietic and other cell types (4).

Itk and HIV

Itk plays a critical role in HIV replication. As mentioned above the expression of Itk is important for TCR-mediated activation of T-cells, where it has a role in the regulation of PLC γ -1, Ca²⁺ mobilization and downstream activation of transcription factors (4). Thanks to its ability to coordinate cytoskeleton reorganization, signaling downstream the TCR and chemokine receptors, Itk could be viewed as

a critical factor in regulating HIV infection and replication in T cells (88). For example, in response to stimulation of CXCR4 by SDF1 α , ITK is activated and its tyrosine kinase activity is required for actin polarization and activation of Rac in response to SDF1 α (26, 105). Readinger *et al.* (88) demonstrated that Itk is required for gp120-induced actin rearrangement, a process that is fundamental for efficient HIV entry into host cells, while viral reverse transcription or proviral DNA integration are not altered by the expression and/or function of Itk. Moreover, Itk stimulates virion assembly and release and it has been found that the suppression of HIV replication can be reached with inhibition of Itk either before or post-infection (88). Other cellular processes that modulate HIV infection in T cells may be influenced by Itk, like the interaction of Gag with the cyclophilin (28), a protein that also interacts with Itk (8), or increased intracellular Ca²⁺, a process that has been linked to the production of viral particles and it is influenced by Itk in T cells (83).

Focal adhesion kinase, FAK

The focal adhesion kinase (FAK) is important for the assembly, signaling and disassembly of focal adhesions (FAs) and its activity influences key cellular processes, including proliferation, migration, attachment and survival (30). The kinase activity of FAK is activated upon phosphorylation by the non-receptor tyrosine kinase Src, which binds to an autophosphorylated tyrosine of FAK through its SH2 domain. Upon activation, FAK interacts with a number of downstream signaling proteins (paxillin, Grb2 and p85 subunit of phosphatidylinositol 3 kinase). FAK is a protein of 125kDa composed of a N-terminal 4.1-ezrin-radixin-moesin domain (also called FERM domain, that allow the ezrin, radixin and moesin proteins to interact with proteins of the plasma membrane) and a C-terminal FA targeting (FAT) domain, which is linked via a 220-amino-acid proline-enriched region to a central tyrosine kinase domain near to the N-terminal domain. FAK is recruited, through an interaction between its FAT domain and LD motifs of paxillin (the amino-terminal domain of paxillin that contains five leucine-rich sequences, called LD motifs), to integrin clusters at the site of cellular attachment. FAK is also implicated in T-cell signaling events, together with its close homolog (45% identical) proline-rich tyrosine kinase 2 (PYK2).

FAK and HIV

Both FAK and PYK2 are linked to immune system dysfunctions caused by HIV infection. When the HIV-1 envelope glycoprotein gp120 interacts with the extracellular domains of CD4 and CCR5, FAK colocalizes with these receptors on the inner face of the plasma membrane (15). After its recruitment, FAK becomes phosphorylated and then it is cleaved by the cellular proteases caspase-3 and caspase-6, this causes the inactivation of FAK and promotes apoptosis (15-16).

FAK has also been linked to T-cell receptor (TCR) signaling. When the TCR complex is stimulated, FAK becomes phosphorylated and associates with the SH2 domain of Lck (a tyrosine kinase of Src family that is most commonly found in T cells) causing CD4 dissociation from Lck and FAK association with CD4. This interaction occurs through the FAT domain of FAK and is specific and almost identical to the FAT-LD interaction (30). Further-

more, the interaction surface of FAT-CD4 shows striking similarities with the binding surface of CD4-Nef (a HIV infection protein), in fact FAK and Nef bind the same region of CD4 with the same affinity (86). This interaction causes, however, different results. The FAK-CD4 gp120 mediated interaction determines the facilitation of viral post-entry stages and triggers apoptosis in uninfected T cell, through FAK inactivation by caspases, whereas Nef action on CD4 causes the block of the super infection and the proapoptotic signaling (67, 114).

All together these observations imply that gp120 signaling might be counteracted by Nef through displacing of FAK from CD4 and Lck (because they compete for binding); so, the ability of Nef to compete, in infected cell, with FAK avoiding apoptosis and super infection would be really important for virus replication (30).

Receptorial tyrosine kinases

Recepteur d'origine nantais" tyrosine kinase, RON

RON is a receptor tyrosine kinase that has been shown to be a regulator of macrophage function and inflammation (17). This protein is a member of the MET family of receptor tyrosine kinases, and regulates a variety of cellular responses, including proliferation, differentiation, apoptosis and cell movement (17). RON binds the macrophage-stimulating protein (MSP), a serum protein that shares high homology with the MET ligand, the hepatocyte growth factor (61). The production of proinflammatory mediators such as IL-2, TNF- α , and NO is inhibited by activation of RON by MPS, which also induces the expression of genes associated with inhibition of inflammation, including scavenger receptor A, IL-1Ra, and arginase (14, 65, 76, 77). Phagocytosis and adhesion of macrophages are also promoted by RON activation (68).

On chromosome 3p21 is located the RON gene that contains 20 exons and 19 introns, and this region has been observed to be frequently altered in cancer. RON is first synthesized as a single chain called pro-RON. The mature RON is generated as a result of a proteolytic conversion in a specific site and results in a 180kDa heterodimer protein composed of a 40kDa α -chain (284 amino acids) that is completely extracellular and a 150kDa transmembrane β -chain (which comprises an extracellular domain, a short transmembrane segment and a large cytoplasmic portion) linked by a disulfide bond. In the cytoplasmic portion of the β -chain is located the tyrosine kinase activity. When MSP binds to RON, it causes the phosphorylation of two tyrosine residues (Y1238 and Y1239) that reside in the catalytic domain and lead to an increase of kinase activity (112).

RON and HIV

RON has been shown to negatively regulate inflammation and macrophage function (17). In addition, Lee *et al.* (61) demonstrated that RON inhibits HIV-1 infection through the inhibition of virus transcription. In fact, RON activation inhibits NF- κ B activity (65) which, besides being involved in the pro-inflammatory response, is a critical factor for efficient HIV-1 transcription in monocyte/macrophages, since it binds the LTR enhancer element of the HIV-1 proviral promoter. Thus, inhibition of NF- κ B can compromise HIV-1 LTR activity and proviral transcription.

Klatt *et al.* (54) demonstrated that RON doesn't interfere with the formation of the pre-initiation complex, but it represses HIV-1 transcription by inhibiting elongation through the suppression of RNA pol II processivity. The HIV transcription in unstimulated cells is inhibited by RON signalling by promoting the association to RNA pol II with negative elongation factors NELF, DRB sensitivity-inducing factor (DSIF), and Pcf11 a transcription termination factor.

Another function of RON is its ability of altering the nucleosome organization. In fact, RON negatively regulates histone acetylation, inducing a transcriptionally repressed chromatin organization that correlates with pausing of RNA pol II and reduced HIV-1 provirus transcription in monocytic cells (54). Recently, it has been shown that Tat specifically induces downregulation of RON by targeting this receptor tyrosine kinase for ubiquitin-mediated proteosome degradation (53). Since RON has an important role in regulating tissue resident macrophage activity and the inflammation response, these findings can explain an additional mechanism by which HIV creates a microenvironment that favors virus replication (53).

VEGFR

The family of vascular endothelial growth factor (VEGF) is composed of five members: VEGFA, VEGFB, VEGFC, VEGFD and PIGF (placental growth factor), which are homodimeric polypeptides (although natural occurring heterodimers of VEGFA and PIGF have been described). Alternative splicing of VEGFA, VEGFB and PIGF and processing of VEGFC and VEGFD, make this family even more complex (25). This splicing and processing regulates the ability of the ligand to bind to VEGF receptors (VEGFR).

In humans, three structurally related VEGF receptor tyrosine kinases (VEGFR) have been identified: VEGFR1, VEGFR2, VEGFR3. These receptors show a similar organization; they have a C-terminal tail, a split tyrosine kinase domain, a juxtamembrane domain, a transmembrane domain and an extracellular, ligand-binding, domain composed of immunoglobulin-like loops. VEGFR1 is expressed in monocytes and macrophages, VEGFR2 in vascular endothelial cells and VEGFR3 in lymphatic endothelial cells.

The binding of VEGF to its receptor can occur in *cis* or in *trans*, on the N-terminal extracellular domain. This binding causes both the receptor dimerization and changes in the intracellular domain conformation. These changes lead to the exposure, in the intracellular kinase domain, of the ATP-binding site followed by binding of ATP and auto- or trans- phosphorylation of tyrosine residues on the receptor (55).

VEGFR and HIV

The HIV-1 infected cells can release soluble Tat protein in the extracellular medium that can activate mesenchymal cells. For example, it has been shown that in response to Tat release, monocytes migrate into tissues and release inflammatory mediators. Tat signaling inside the cells is mediated by the receptor for vascular endothelial growth factor, a tyrosine kinase (VEGFR-1/Flt-1) (74). Previously it was also shown that Tat binding to another related receptor, VEGFR-2/KDR, expressed on endothelial cells, activated its tyrosine kinase activity(2). Thus, the activation

of monocyte VEGFR-1/Flt-1 by Tat present in serum or tissue (74) could play an active role in the movement of monocyte out of the circulatory system and subsequent tissue damage in AIDS patients.

The Janus Kinase/Signal Transducer and Activator of Transcription, JAK/STAT pathway

In mammals there are four JAK kinases and seven STAT proteins. The pathway is initiated when a peptide ligand binds the transmembrane receptors. The receptor dimerizes and this causes the cross-activation of receptor-associated JAK kinases, which in turn phosphorylate tyrosine residues in the cytoplasmic tail of the receptor. JAK, then phosphorylates STAT proteins on a crucial C-terminus residue. This phosphorylation of STAT is possible because they are recruited from the cytoplasm after the phosphorylation of tyrosine residue of receptor that functions as docking site for STAT (64).

Now, via Src-homology 2-domain-phospho-tyrosine interaction, the phosphorylated STAT proteins dimerize and translocate to the nucleus where induce the expression of target genes, working as transcriptional activators (1, 62). The JAK/STAT pathway regulates many cellular events and accumulating evidence indicates that its dysregulation causes human diseases and cancer (9, 119).

JAK/STAT and HIV

Infection by HIV-1 can up- or down-regulate the expression of several interferons and cytokines, whose signals are transduced by the JAK/STAT pathway (6). Several cytokines may have a direct or indirect effect on HIV-infected cells by inducing different response on virus replication. Bovolenta *et al.* (6) had found evidence indicating a clear role of the IFN γ and IFN α mediated JAK/STAT pathways in inhibiting HIV replication in human monocytes. In fact, it has been shown that stimulation of glial cells by HIV gp120 envelope glycoprotein induces STAT1 and JAK2 activation. Furthermore, it has been reported that inhibition of interleukin-2 receptor (IL-2R) expression in T lymphocytes is due to the binding of gp120 Env with CD4, and this effect has been correlated with the inhibition of both expression and activation of JAK3. Bovolenta *et al.* (6) demonstrated that a constitutive activation of STAT proteins occurs in the majority of HIV-infected individuals. JAK-dependent phosphorylation of one or more tyrosine residues is required for STAT binding to DNA, thus deregulated expression of specific cytokines or other factors, resulting in a constitutive JAK activation, could be the key event underlying STAT activation in HIV-infected individuals (6). During HIV infection the levels of phosphorylated STAT proteins is increased. According to Miller *et al.* (73) this is due to the inability of the SOCS-1 and SOCS-3 proteins to control the JAK/STAT pathway in infected cells. SOCS proteins are key feedback inhibitors of the JAK/STAT pathway. SOCS-1 deficient-mice show a constitutive and sustained activation of the JAK/STAT pathway, and these mice have a clinical phenotype reminiscent of advanced HIV disease. Accordingly, it was shown that T cells from patients had increased phospho-STAT-1,-3 and -5 levels and reduced SOCS-1 and SOCS-3 protein levels.

It is known that the activation of the JAK/STAT signaling pathway plays a critical role in IL-2 induced T-lymphocyte proliferation and that activation of STAT5 is

important in cell cycle progression and protection from apoptosis. Lack of IL-2 dependent STAT activation, could have a negative impact on the maintenance of a CD8 T cell population responsive to HIV infection. It has been observed that CD8 T cells from HIV infected patients are inactive and more prone to spontaneous apoptosis than those isolated from healthy individuals. This effect correlates with an impaired activation, in CD8T lymphocytes of HIV-infected individuals, of the upstream kinase JAK-3, which blocks the pathway of STAT5. Highly active anti-retroviral therapy (HAART) has been observed to restore JAK/STAT and IL-2 responses (58).

Another important interleukin involved in maturation of lymphocytes is IL-7 that plays a central role in controlling CD4 T-cell homeostasis and T-cell proliferation. In HIV infection, the IL-7/CD4 regulatory loop is activated by increased plasma IL-7 levels that correlate with the decline CD4+ T-cell counts of patients. Juffroy *et al.* (51) provided evidence that HIV infection perturbs IL-7 response by decreasing the IL-7 binding capacity of memory CD4T cells and by inducing abnormal activation of the JAK/STAT5 signaling pathway (51).

Tyrosine kinases inhibitors

The efficacy of tyrosine kinase inhibitors in treating HIV-1 infection has been demonstrated in some works. Stantchev *et al.* (100) analyzed the role of the broad spectrum tyrosine kinase inhibitor Genestein in HIV infection, demonstrating that Genestein was able to affect both entry and early post-entry steps of the virus life cycle. Unfortunately the use of a broad spectrum inhibitor does not allow to identify the specific tyrosine kinases required for HIV-1 entry/infection. Nowadays there are few studies that focus on the efficacy of tyrosine kinase inhibitors on HIV-1 infection. However, compounds that interact with Nef specifically impeding Hck activation, showed to be strong inhibitors of HIV-1 replication (23), posing Hck as an attractive pharmacological target. Moreover, the efficacy of specific tyrosine kinase inhibitors was proved in other viral diseases. In fact a recent work (59) demonstrated that selective inhibitors of the platelet-derived growth factor receptor (PDGFR), as well as inhibitors of nerve growth factor receptor (TrkA) and heregulin receptor erbB-2 (HER-2), are effective against a variety of RNA and DNA viruses, including Influenza A virus, Sendai virus, herpes simplex virus, mouse hepatitis virus and rhesus rotavirus.

Taken together these data underline the emerging knowledge on the role of tyrosine kinases in HIV-1 life cycle and the growing interest on these enzymes as potential targets for innovative anti-HIV-1 treatments. The availability of inhibitors of several tyrosine kinases already approved for cancer therapy could represent an opportunity for the rapid discovery of new effective pharmacological HIV-1 therapies.

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Other articles in this theme issue include references (125-152).

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