

Restriction factors of retroviral replication: the example of Tripartite Motif (TRIM) protein 5 α and 22

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Abstract Viral tropism, replication, and pathogenesis are determined by multiple interactions between the pathogen and the host. In the case of retroviruses, and in particular, the human immunodeficiency virus, the specific interaction of the envelope protein with the host receptors and co-receptors is essential to gain entry in the cells. After entry, the success of retroviruses to complete their life cycle depends on a complex interplay between the virus and host proteins. Indeed, the cell environment is endowed with a number of factors that actively block distinct stage(s) in the microbial life cycle. Among these restriction factors, Tripartite Motif-5 α (TRIM5 α) has been extensively studied; however, other TRIM family members have been demonstrated to be anti-retroviral effector proteins. This article reviews, in particular, the current knowledge on the anti-retroviral effects of TRIM5 α and TRIM22.

Keywords Retroviral infection · Host restriction factors · TRIM family proteins

Introduction

The concept of retroviral restriction dates back to 1957, when Charlotte Friend observed that different strains of

mice varied in their susceptibility to the Friend strain of murine leukemia virus (MLV), a member of the gamma-retroviral genus of the *Retroviridae* family of viruses (Friend 1957). Further genetic studies in mice revealed that virus susceptibility was determined by genetic traits termed “Friend virus susceptibility 1 (*Fv1*)” genes (Hartley et al. 1970; Lilly 1967; Pincus et al. 1971). Nearly 40 years after the first observation of a murine strain-specific block to MLV, *Fv1* was cloned (Best et al. 1996). From the analysis of mammalian species, however, no genes were found closely related to *Fv1* with the exception of mice (Besnier et al. 2003; Best et al. 1996). These findings were unexpected since a range of mammals, including humans, also demonstrated a specific resistance to MLV (Besnier et al. 2003; Towers et al. 2000). Thus, it has been suggested that human cells expressed the restriction factor 1 (Ref1) that inhibits MLV replication like the dominant *Fv1* gene product (Towers et al. 2000). Furthermore, primate lentiviruses, including the human immunodeficiency virus type-1 (HIV-1) and the simian immunodeficiency virus (SIV), encounter a similar dominant restriction activity in many non-human primate cells attributed to a gene named lentivirus susceptibility factor 1 (Lvl) (Besnier et al. 2002; Cowan et al. 2002; Munk et al. 2002). The gene responsible for Lvl activity was identified by introducing a cDNA expression library from HIV resistant Rhesus (Rh) macaque lung fibroblasts into HIV permissive human cells, and selecting for cells that expressed resistance to HIV-based vectors (Stremlau et al. 2004). The active Rh cDNA was found to encode the “alpha” spliced variant of Tripartite Motif 5 α (TRIM5 α), a member of a large family of proteins known as the TRIM proteins (Reymond et al. 2001). The expression of the Rh cDNA was sufficient to restrict incoming HIV-1, whereas its human ortholog was not. Afterwards, a number of groups demonstrated that the

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TRIM5 α protein of different primates has a comparable antiretroviral activity against a variety of retroviruses (Hatzioannou et al. 2004; Keckesova et al. 2004; Perron et al. 2004; Yap et al. 2004). These findings suggest that primate TRIM5 α proteins provide a general defense mechanism against retroviral infection.

TRIM protein structure

The members of the TRIM family were originally defined as proteins that contain Really New Interesting Protein (RING), either 1 or 2 B-boxes, and coiled-coil domains (RBCC) (Borden 1998; Reddy et al. 1992). The RBCC motif, located at the N-terminus, is well conserved among TRIM proteins, whereas the C-terminal domains vary. The C-terminal domains determine the classification of the 72 human TRIM proteins in 11 subfamilies while one group (including TRIM14 and TRIM20) remains unclassified due to the lack of a RING domain (Nisole et al. 2005; Ozato et al. 2008; Sardiello et al. 2008; Short and Cox 2006; Carthagen et al. 2009). Among others, the subfamily C-IV encompasses several members with anti-viral activity (Ozato et al. 2008). This subfamily is characterized by a SPRY domain in combination with a PRY domain to form a so-called B30.2 domain located at the C-terminus immediately following the RBCC motif (see Fig. 1). The B30.2 domain was originally identified as a protein domain encoded by a single exon (called B30.2) in the human major histocompatibility complex (MHC) class I region (Meyer et al. 2003), while the SPRY domain was identified as a conserved domain in the non-receptor tyrosine kinase spore lysis A of *Dictyostelium discoideum* and in mammalian ryanodine receptors (Ponting et al. 1997). The PRY domain was named for conserved sequences, located N-terminally to SPRY domains that appear to have arisen

relatively recently during evolution, distinguishing the B30.2 domain from the more ancient SPRY domain (Rhodes et al. 2005; Woo et al. 2006a, b).

About their structure, TRIM proteins form high-molecular-mass complexes that localize to specific subcellular compartments present either in the cytoplasm or in the nucleus (Reymond et al. 2001). For example, TRIM19, also known as Promyelocytic Leukemia (PML) protein, exists in subnuclear structures known as “nuclear bodies”, whereas TRIM5 is normally located in distinct cytoplasmic aggregates designated as “cytoplasmic bodies”. These bodies are mobile, highly dynamic structures that turn over rapidly due to exchange of protein between the nucleus and the cytoplasm (Campbell et al. 2007). The formation of cytoplasmic bodies, however, is not a requirement for retroviral restriction (Perez-Caballero et al. 2005a; Song et al. 2005).

TRIM protein function

TRIM family proteins have been involved in a variety of cellular processes, such as signal transduction, transcriptional regulation, cell proliferation, oncogenesis, and apoptosis (Meroni and Diez-Roux 2005; Ozato et al. 2008). Furthermore, a number of TRIM proteins have been found to interfere with the replication cycle of different viruses (see Table 1). TRIM19, for example, has been implicated in the regulation of infection by a variety of RNA and DNA viruses, including adenoviruses, herpes simplex viruses (HSV) and human cytomegalovirus (CMV) (Everett and Chelbi-Alix 2007). These findings, together with the observation that the expression of many TRIM proteins is induced by interferons (IFNs) (Carthagen et al. 2009), suggest that they likely represent important mediators of innate immunity. In this regard, it has been recently shown that TRIM21 plays a negative role in the regulation of the NF- κ B dependent pro-inflammatory cytokine response in mice (Yoshimi et al. 2009). Another member, i.e. TRIM30, inhibits the Toll-like receptor (TLR) signaling by degrading TAK1-binding protein (TAB) 2 and 3 and it contributes to the inhibition of TLR-mediated NF- κ B activation (Shi et al. 2008).

In regard to retroviruses, multiple TRIM proteins beside TRIM5 display antiviral activities against a panel of distantly related retroviruses when exogenously expressed (see Table 1) (Li et al. 2007; Uchil et al. 2008; Zhang et al. 2006). For example, mouse TRIM28 was shown to restrict MLV replication by promoting gene silencing (Wolf and Goff 2007). In particular, TRIM28 functions as a transcriptional co-repressor recruiting several other factors involved in transcriptional silencing and heterochromatin formation (Le Douarin et al. 1996; Schultz et al. 2002).

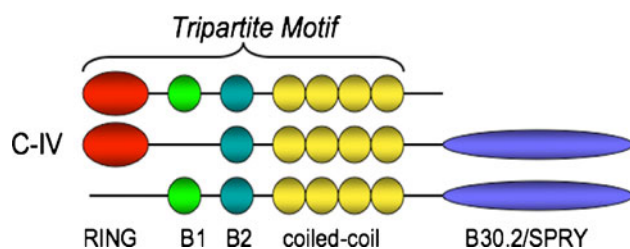


Fig. 1 Schematic structure of the domains present in the C-IV class of TRIM/RBCC family. The TRIM/RBCC proteins share RING, B1, B2 and coiled-coil domains whereas the C-terminals are variable. The C-terminal domains determine the classification of the 72 human TRIM proteins in 11 subfamilies while one group (including TRIM14 and TRIM20) remains unclassified due to the lack of a RING domain (Carthagen et al. 2009). The C-IV subfamily that includes the TRIM5 and TRIM22 members is characterized by the presence of the only B-box 2

Table 1 Role of TRIM family members in viral infections

Member	Virus(es)	Viral target(s)	Note(s)	Key references
TRIM1	MLV	CA	Restriction activity	Yap et al. (2004), Zhang et al. (2006)
TRIM5	HIV, MLV, SIV, FIV, EIAV	CA	Restriction activity	Stremlau et al. (2004), Keckesova et al. (2004), Yap et al. (2004)
TRIM6	HIV	CA	No restriction activity	Li et al. (2007)
TRIM8	HIV, MLV	Unknown	Inhibition of entry, inhibition of MLV particle release	Uchil et al. (2008)
TRIM9	Unknown	Unknown	Up-regulated in FcγR-activated macrophages	Carthagen et al. (2009)
TRIM10	HIV	Unknown	Inhibition of entry	Uchil et al. (2008)
TRIM11	HIV, MLV	Unknown	Inhibition of HIV entry, particle production and release. Enhancement of MLV entry	Uchil et al. (2008)
TRIM13	MLV	Unknown	Inhibition of particle production and release	Uchil et al. (2008)
TRIM14	HIV, MLV	Unknown	Inhibition of particle production and release	Uchil et al. (2008)
TRIM15	HIV, MLV	Unknown	Inhibition of particle release	Uchil et al. (2008)
TRIM19	MLV, VSV, Influenza A, CMV, HSV-1, Ebola and Lassa viruses, LCMV, human foamy virus, adenovirus, HIV	LCMV Z protein, HCV core protein	Inhibition of p53, inhibition of particle release	Everett and Chelbi-Alix (2007), Turelli et al. (2001), Uchil et al. (2008)
TRIM21	HIV	Unknown	Enhancement of entry	Uchil et al. (2008)
TRIM22	HIV	LTR and Gag	Inhibition of transcription, assembly and release	Tissot and Mechti (1995), Barr et al. (2008)
TRIM25	MLV, Sendai virus, New Castle disease virus, VSV	Unknown	Ubiquitination of retinoic acid-inducible gene I product (RIG-I)	Gack et al. (2007), Uchil et al. (2008)
TRIM26	HIV, MLV	Unknown	Inhibition of entry and particle release	Uchil et al. (2008)
TRIM28	MLV, HTLV-1	PBS	Inhibition of transcription and particle release	Wolf and Goff (2007), Uchil et al. (2008)
TRIM30	MLV	Unknown	Enhancement of entry	Uchil et al. (2008)
TRIM31	HIV	Unknown	Inhibition of entry	Uchil et al. (2008)
TRIM32	HIV-1, HIV-2 and EIAV	Tat	Transcription regulation	Fridell et al. (1995)
TRIM34	SIV	CA	Weak restriction activity	Li et al. (2007), Zhang et al. (2006)
TRIM35	MLV	Unknown	Inhibition of particle release	Uchil et al. (2008)
TRIM38	HIV	Unknown	Enhancement of entry	Uchil et al. (2008)
TRIM54	Unknown	Unknown	Up-regulated in FcγR-activated macrophages	Carthagen et al. (2009)
TRIM56	HIV	Unknown	Inhibition of entry	Uchil et al. (2008)
TRIM62	MLV	Unknown	Inhibition of entry	Uchil et al. (2008)

EIAV Equine infectious anemia virus, *VSV* vesicular stomatitis virus, *LCMV* lymphocytic choriomeningitis virus, *R* receptor, *CA* capsid, *LTR* long terminal repeat, *PBS* primer binding site

TRIM28-mediated MLV restriction is effective in embryonic stem cells since this TRIM protein is part of a nuclear repressor complex that binds to the retroviral “Primer Binding Site (PBS)”. In the case of MLV, PBS is a sequence complementary to the cellular tRNA for proline (tRNA^{Pro}) that is used to prime minus-strand DNA

synthesis during reverse transcription (Harada et al. 1979). However, the PBS overlaps with a so-called “Repressor-Binding Site (RBS)” (Wolf and Goff 2007). Since TRIM28, in spite of being recruited to different PBS including the tRNA of Lysine 1 and 2 (Wolf et al. 2008), does not bind to DNA, other factors must recruit TRIM28

to mediate the specific silencing induced by different DNA-binding proteins. In this regard, Wolf and Goff (2009) have recently identified a novel zinc finger protein, ZFP208, that functions as a recognition molecule bridging the integrated proviral DNA with TRIM28. Expression of ZFP208 is sufficient to render even differentiated cells resistant to MLV infection. In addition, ZFP208 potently inhibits transcription from DNA constructs of the human T cell lymphotropic virus-1 (HTLV-1) that utilizes the same primer tRNA (Wolf and Goff 2009). Thus, this novel zinc finger protein is a new DNA binding factor that specifically recognizes a large subset of mammalian retroviruses and retroelements and targets them for transcriptional silencing. This breakthrough observation suggests that ZFP809 has evolved as a stem cell-specific retroviral restriction factor constituting a novel component of the intrinsic defense of stem cells.

TRIM5 α

In spite of the presence of 72 family members, only a few proteins have been extensively studied and, among others, TRIM5 α . Indeed, TRIM5 possesses multiple spliced isoforms, each characterized by an alternative C-terminus (see Fig. 2). The longest isoform, TRIM5 α , is the only one that encodes a C-terminal B30.2 domain and exhibits antiviral activity (Stremlau et al. 2004). The shorter isoforms, TRIM5 γ and TRIM5 δ , lack the C-terminus and, when overexpressed, act in a dominant negative fashion on

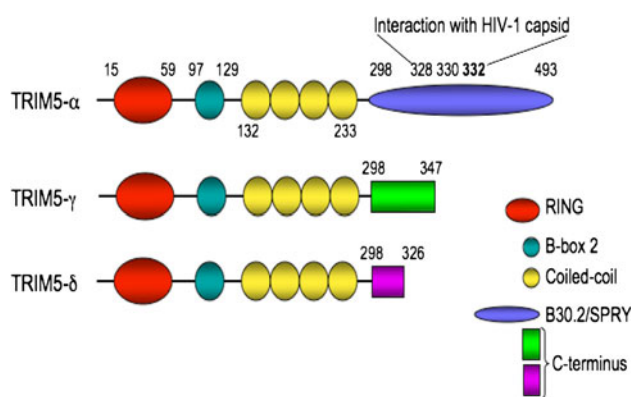


Fig. 2 Schematic representation of the main splice variants of TRIM5. The TRIM5 gene is endowed with multiple isoforms that are characterized by alternative C-terminus. The TRIM5 α possesses the B30.2/SPRY domain whereas the TRIM5 γ and TRIM5 δ undergo alternative splicing within the coding region resulting in a frameshift and use of upstream termination codons. The B30.2/SPRY domain of TRIM5 α contains the amino acids critical for the interaction with the HIV-1 capsid. In particular, the amino acid at position 332 accounts for full HIV-1 restriction in human TRIM5 α (arginine) when it is replaced with that of the rhesus TRIM5 α protein (proline) (Stremlau et al. 2005; Yap et al. 2005)

TRIM5 α targets therefore promoting the rescue of restricted infection (Passerini et al. 2006; Stremlau et al. 2004). TRIM5 α is a protein responsible for the species-specific restriction of HIV entry via binding to incoming retroviral capsid (CA) protein mediated by its C-terminal B30.2 domain causing premature disassembly of the CA (Sawyer et al. 2005; Stremlau et al. 2005; Yap et al. 2005). In addition, TRIM5 α has been postulated to interfere with late events in the viral life cycle affecting particle release by promoting the degradation of nascent Gag (Sakuma et al. 2007). This interpretation, however, has been debated since it requires high levels of TRIM5 α expression (Zhang et al. 2008). Indeed, the precise mechanism of restriction mediated by TRIM5 α remains still unknown, although the role of the B30.2 domain of TRIM5 α in restricting retroviruses became apparent in early experiments in which Rh and hu TRIM5 α were shown to directly interact with the CA protein of HIV-1 and MLV, respectively (Sebastian and Luban 2005; Stremlau et al. 2006). The B30.2 domain is required for binding CA and restriction, as demonstrated by the observation that both deletion mutants and naturally occurring isoforms of Rh TRIM5 α , lacking the B30.2 domain fail to restrict HIV-1 (Stremlau et al. 2004, 2006). Furthermore, the replacement of segments in the B30.2 variable region of hu TRIM5, which fails to restrict HIV-1, with analogous sections from Rh TRIM5 α , has demonstrated restriction activity against HIV-1 (Stremlau et al. 2005). Additional mutagenesis experiments have shown that a single amino acid change in hu TRIM5 α (R332P), matching the analogous residue in the B30.2 variable region of Rh TRIM5 α , confers antiviral activity against HIV-1 (Fig. 2) (Perron et al. 2006; Stremlau et al. 2005; Yap et al. 2005). In this regard, it has recently been shown by experiments of site-directed mutagenesis of 9 clusters of 3 charged amino acids in the conserved regions of the B30.2 domain that retroviral restriction is dependent on the interaction of TRIM5 α with CA (Sebastian et al. 2009). Furthermore, a highly conserved surface patch on the TRIM5 α B30.2 domain has been described as crucial for the restriction of the incoming virions independently of CA binding (Sebastian et al. 2009).

By analyzing TRIM5 α orthologous sequences, it has been proposed that the TRIM5 gene is under positive purifying selection in that the ratio between non-synonymous coding mutations (dN) and synonymous non-coding mutations (dS) is >1.0 (Sawyer et al. 2005). In particular, a variable region of the B30.2 domain was predicted to be under positive selection (Sawyer et al. 2005). Intriguingly, this variable region lies within the PRY domain (amino acids 298–355) of the B30.2 domain, a relatively recent addition to the older SPRY domain since B30.2 domains are only found in vertebrates (Sawyer et al. 2005). These observations support the notion that a positive selective

pressure during evolution led to a species-specific block of retroviral infections and that the B30.2 domain of TRIM5 α is a determinant of a species-specific retroviral tropism.

The importance of TRIM5 α in retroviral infection is highlighted by a retrotransposition event that occurred in Owl monkeys (*Aotus trivirgatus*) leading to the generation of an ortholog of TRIM5 α that blocks HIV-1 infection in this species. The retrotransposition event deleted the B30.2 domain of TRIM5 α and replaced it by the coding sequence of Cyclophilin A (CypA), a well known target of immunosuppressive drugs, such as Cyclosporine A (CsA), leading to a fusion protein termed TRIMCyp (Sayah et al. 2004). This recombination event occurred independently in Pig tailed (Pgt) macaques that express another variant of TRIMCyp with a distinct specificity in that PgtTRIMCyp restricts the Feline Immunodeficiency Virus (FIV), a retrovirus causing an AIDS-like syndrome in cats (Gardner and Luciw 1989), but not HIV (Virgen et al. 2008). Furthermore, TRIMCyp was discovered as restriction factor for HIV-2 infection in Rhesus macaque (Wilson et al. 2008). CypA is a ubiquitously expressed peptidylprolyl isomerase that was earlier shown to interact with the CA protein of HIV-1, but not of HIV-2 (Luban et al. 1993). Disruption of the interaction between CypA and HIV-1 CA by competitive inhibitors such as CsA, by mutations in the CA protein (G89V or P90A), or by suppression of CypA expression demonstrated that HIV-1 infection of human cells is highly dependent on CA interaction with CypA (Berthouix et al. 2005; Franke et al. 1994; Luban et al. 1993). Likely, CypA confers protection to the incoming virus from a yet unidentified restriction factor (Sokolskaja et al. 2006). In non-human primates, CypA does not bind to CA (Braaten et al. 1996; Lin and Emerman 2006); however, when CypA is fused to TRIM5, it restricts HIV-1 in the same way the B30.2 does for TRIM5 α . Thus, CypA functions in an opposite manner in non-human primate cells as compared to human cells by promoting restriction rather than replication (Luban 2007).

The role of the N-terminus RBCC domain of TRIM5 α in retroviral restriction has also been studied extensively. The RING domain of some TRIM, also found in proteins not belonging to the TRIM family, possesses an E3 ligase activity involved in the addition of ubiquitin to proteins targeting them for proteasomal degradation (Joazeiro et al. 1999; Lorick et al. 1999; Boutell and Everett 2003; Jones and Gellert 2003; Jang 2004; Vichi et al. 2005; Yamauchi et al. 2008). This observation has led to the hypothesis that the destruction of HIV-1 CA could be ubiquitin-mediated although independent studies have shown that proteasomal degradation is not required for TRIM5 α mediated restriction (Perez-Caballero et al. 2005b). Even in the case of HIV-1 restriction induced by TRIMCyp, the rapid kinetics of CA inactivation occurred independently of cytoplasmic

bodies, ubiquitin, and proteasome activity (Perez-Caballero et al. 2005b). Among the RBCC components that contribute to HIV-1 restriction, the B-box 2 plays a crucial role, since a loss of activity was caused by its deletion (Diaz-Griffero et al. 2007; Javanbakht et al. 2005; Perez-Caballero et al. 2005a). Indeed, the B-box and coiled-coil motifs have been implicated in mediating protein–protein interactions, either with the same or other proteins to form multiprotein complexes (Mische et al. 2005). Thus, the RBCC domain seems to act as a scaffold on which other cellular components of the restriction machinery assemble, possibly leading to the sequestering of incoming viral particles. The RBCC has also been implicated in the cellular localization of the TRIM proteins (Reymond et al. 2001), guiding the restriction factor into the appropriate cellular compartment utilized by the incoming virus. Hence, another role of the RBCC in restriction could be to form higher order TRIM5 α arrays that contribute to CA binding avidity, as recently suggested (Diaz-Griffero et al. 2009).

Despite the molecular characterization of the mechanism of TRIM5 restriction, the influence of human TRIM5 in the HIV-1 infection in vivo remains largely unexplored. In this regard, a recent report has shown the expression of hu TRIM5 α in the peripheral blood mononuclear cells obtained from the CAPRISA cohort study of sex workers at high risk for infection by real time PCR (Sewram et al. 2009). Notably, HIV-negative individuals had statistically significant higher levels of TRIM5 α as compared to HIV-positive individuals. In addition, these lower levels of TRIM5 α expression were most likely the result of seroconverters having significantly lower hu TRIM5 α levels at baseline (before infection), compared with nonseroconverters (Sewram et al. 2009). Consequently, the levels of expression and role of TRIM5 α and other endogenous TRIMs mediating “intrinsic immunity” to HIV will need to be thoroughly evaluated at the sexual mucosal level, a primary site of viral transmission.

TRIM22

TRIM22, previously described as “Stimulated Trans-acting Factor of 50 kDa (Staf50)”, is located on chromosome 11 adjacent to TRIM5 (Sawyer et al. 2007; Tissot et al. 1996). TRIM22 was originally identified in a screening for IFN-inducible genes in the human B lymphoblastoid Daudi cell line (Tissot and Mechti 1995). In the same study, cotransfection of COS-7 cells with a TRIM22 expression plasmid inhibited an LTR-mediated expression of a reporter gene suggesting a potential role of TRIM22 in controlling HIV transcription (Tissot and Mechti 1995). No information, however, were provided concerning its mechanism of action. During a screening of gene expression in monocytic

cell lines, type I and II IFN and other stimuli, in particular, bacterial lipopolysaccharide (LPS) also induced TRIM22 (Bouazzaoui et al. 2006). Indeed, overexpression of TRIM22 inhibited HIV-1 infection and replication in primary human monocyte-derived macrophages (MDM), a relevant target of HIV-1 infection, although no precise mechanism of action was defined in this study (Bouazzaoui et al. 2006). Interference of TRIM22 on late steps of the HIV life cycle has also been proposed based on the observation that p24 Gag antigen levels were decreased in the supernatant of infected MDM after either transient transfection or transduction with TRIM22 expressing vectors (Bouazzaoui et al. 2006). In support of this hypothesis, a subsequent study showed that IFN-induction of TRIM22 interferes with the late steps of the HIV life cycle at the levels of virion assembly and release thereby inhibiting the accumulation of viral particles in the supernatant of various cell lines such as HOS, U2OS 143B and HeLa cells (Barr et al. 2008). In particular, an inhibitory effect on Gag synthesis was clearly shown in U2OS and 143B cell lines although not in HeLa cells (Barr et al. 2008), suggesting a role of TRIM22 in the assembly and release of virions rather than interference with Gag synthesis or viral transcription. The same study showed evidence of a direct interaction of TRIM22 with Gag polyprotein while a double mutant substituting the 2 cysteines at position 15 and 18 with alanine in the RING domain abolished TRIM22 effect on HIV particle release; however, the interaction between Gag and TRIM22 did not affect Gag protein stability and no ubiquitination of Gag was reported by effect of TRIM22 (Barr et al. 2008). Thus far, the substrate(s) of TRIM22 remains unknown in contrast to other members of the TRIM family, such as TRIM21 and TRIM25 that function as E3 ubiquitin ligase for “IFN regulating factor 8 (IRF-8)” and “Retinoic acid inducible gene I (RIG-I)”, respectively (Oshiumi et al. 2009; Yoshimi et al. 2009). The mechanism of TRIM22 restriction on the late events of the HIV life cycle remains undefined and, nonetheless, it should be related to TRIM22 subcellular localization. In this regard, TRIM22 has been reported to reside either in the cytoplasm (Herr et al. 2009; Meroni and Diez-Roux 2005) or in the nucleus (Gao et al. 2009; Sivaramakrishnan et al. 2009a, b) likely accomplishing diverse biological effects. When TRIM22 was coupled to the green fluorescence protein (GFP), its presence was localized in cytoplasmic bodies in the U2OS cells (Meroni and Diez-Roux 2005) whereas an independent study of TRIM22-GFP fusion protein described a diffuse accumulation surrounding the nucleus of COS-7 cells (Herr et al. 2009). The same localization was observed in HeLa cells expressing endogenous TRIM22 (Herr et al. 2009). In contrast, a c-myc-tagged protein product linked to TRIM22 coding sequence amplified from human peripheral blood mononuclear cells localized TRIM22 exclusively in the

nucleus (Duan et al. 2008). Furthermore, recent reports have shown that endogenous expression of TRIM22 occurred selectively in the nucleus of HeLa cells (Sivaramakrishnan et al. 2009a, b).

The formation of the nuclear bodies is dependent on TRIM22 B30.2/SPRY domain, although it has been reported that both a deletion mutant of the RING domain and a cysteine mutant in position 15 of the RING domain disrupt the nuclear bodies in HepG2 cells (Gao et al. 2009). Interestingly, nuclear bodies undergo dynamic changes during cell cycle progression (Sivaramakrishnan et al. 2009b) and TRIM22 forms nuclear bodies in G₀/G₁-phase in HeLa cells evolving into speckle-like structures during the S and probably G₂/M-phases (Sivaramakrishnan et al. 2009b).

In addition to HIV-1, TRIM22 has been shown to have suppressive activities on other viruses. In particular, the TRIM22 ubiquitin ligase activity seems to be required for the anti-viral activity against the encephalomyocarditis virus, a picornavirus that causes disease in mice (Eldin et al. 2009). More recently, TRIM22 has been shown to inhibit the replication of Hepatitis B virus (HBV) by interference with the HBV core promoter (Gao et al. 2009).

Beyond its anti-viral effects, TRIM22 has been involved in cell proliferation and survival and is a target of p53 (Obad et al. 2004). In this regard, promonocytic U937 cells devoid of endogenous p53 expression were electroporated with an expression vector encoding TRIM22 and the interference with cell clonogenic growth was monitored by colony formation in soft agar. TRIM22 reduced the capacity of these U937 cells to form colonies in soft agar consequently to their proliferation arrest and apoptosis (Obad et al. 2004). The same authors observed a differentiation stage-specific inverse correlation between the levels of TRIM22 expression and erythroid or granulocytic differentiation in CD34(+) human bone marrow progenitor cells (Obad et al. 2007).

Conclusions

The TRIM family is made by a list of 72 genes among which only a few have been studied in detail. The discovery of TRIM5 α restriction of HIV-1 replication in monkey cells has shed light on the identification of restriction factors described 50 years ago. Several questions, however, remain open and the exact mechanism of TRIM5 α or TRIM22 block of infectivity has not been defined. The identification of the precise viral and cellular partners will guide to the discovery of drugs that either mimic or enhance the effects of these restriction factors. Several other questions still remain open, particularly in regard with expression levels and inducibility of TRIM

family members in HIV-infected individuals during HIV disease progression and in response to antiretroviral agents.

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