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Molecular mimicry and immunomodulation by the HRES-1 endogenous retrovirus in SLE

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Abstract

Genetic and environmental factors are believed to influence development of systemic lupus erythematosus (SLE). Endogenous retroviruses (ERV) correspond to the integrated proviral form of infectious retroviruses, which are trapped within the genome due to mutations. ERV represent a key molecular link between the host genome and infectious viral particles. ERV-encoded proteins are recognized by antiviral immune responses and become targets of autoreactivity. Alternatively, ERV protein may influence cellular processes and the life cycle of infectious viruses. As examples, the HRES-1 human ERV encodes a 28-kDa nuclear autoantigen and a 24-kDa small GTP-ase, termed HRES-1/Rab4. HRES-1/p28 is a nuclear autoantigen recognized by crossreactive antiviral antibodies, while HRES-1/Rab4 regulates surface expression of CD4 and the transferrin receptor (TFR) through endosome recycling. Expression of HRES-1/Rab4 is induced by the tat gene of HIV-1, which in turn down-regulates expression of CD4 and susceptibility to reinfection by HIV-1. CD4 and the TFR play essential roles in formation of the immunological synapse (IS) during normal T-cell activation by a cognate MHC class II peptide complex. The key intracellular transducer of T-cell activation, Lck, is brought to the IS via binding to CD4. T-cell receptor ζ (TCR ζ) chain binds to the TFR. Abnormal T-cell responses in SLE have been associated with reduced lck and TCRζ chain levels. HRES-1 is centrally located on chromosome 1 at q42 relative to lupus-linked microsatellite markers and polymorphic HRES-1 alleles have been linked to the development of SLE. 1q42 is one of the three most common fragile sites in the human genome, and is inducible by DNA demethylation, a known mechanism of retroviral gene activation. Molecular mimicry and immunomodulation by a ERV, such as HRES-1, may contribute to self-reactivity and abnormal Tand B-cell functions in SLE.

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Keywords

Systemic lupus erythematosus; cross-reactivity; HRES; endogenous retroviral sequences; immunodulation; receptor recycling

Genetic and environmental factors in SLE

Systemic lupus erythematosus (SLE) is a chronic inflammatory disease characterized by dysfunction of T and B lymphocytes and autoantibody production. Independent lines of evidence have implicated genetic and environmental factors in the causation of lupus [1]. On the one hand, significant familial aggregation of SLE was demonstrated by epidemiologic studies [2]. The disease occurs in relatives of SLE patients with a frequency between 0.4 and 5%, several 100-fold greater than in the general population [3]. The concordance rate of SLE among monozygotic twins may be as high as 25–60% [3,4]. On the other hand, discordance rates of SLE are as high as 70% among monozygotic twins [3], suggesting a significant role for exogenous factors. Initially, findings of virion-like tubuloreticular structures in endothelial cells and lymphocytes as well as demonstration of elevated serum levels of type I interferon (IFN) raised the possibility of a viral etiology in lupus [5]. An increased prevalence of the nearly ubiquitous Epstein-Barr virus (EBV) has been demonstrated in adolescent lupus patients [6] which could contribute to disease pathogenesis via B-cell activation and triggering of antinuclear antibodies [7]. Retroviruses were implicated by detection of retroviral p30 gag protein in renal glomeruli and serum reactivities towards p30 gag antigen in patients with SLE [8]. Indeed, many features of human retroviral infections caused by HTLV-I and HIV-1 resemble those of SLE, and viral proteins have profound effects on both antigen presentation and effector functions of the immune system [9]. Dysregulation of programmed cell death has been documented in HIV-infected [10] and lupus patients as well [11–13]. Similar to SLE, anemia [14], leukopenia [15], thrombocytopenia [16], polymyositis [17] and vasculitis have been widely reported in patients with AIDS [18]. Direct virus isolation attempts from tissues of SLE patients have not been successful [19]. Nevertheless, it is possible that a (retro)virus, responsible for provoking an immune response cross-reactive with self-antigens, has been cleared from the host, so the absence of lupus-specific viral particles is not conclusive. An alternative (retro) viral etiology, i.e. activation of endogenous retroviral sequences (ERS) was initially proposed by a study of the New Zealand mouse model of SLE [20]. Endogenous retroviral envelope glycoprotein, gp70, was found in immunecomplex deposits of autoimmune lupusprone NZB/NZW mice [20]. Abnormal expression of an ERS was noted in the thymus of lupusprone mouse strains [21,22]. More recently, expression and autoantigenicity of human ERS has been demonstrated in patients with SLE [23–27].

Molecular biology of ERV

Endogenous retroviruses (ERV) and other retroviral elements have been found in all vertebrates investigated. They belong to the larger family of retrotransposable elements that make up as much as 40% of the human genome [28]. These elements include short interspersed nucleotide elements such as \sim 300 bp Alu repeats and \sim 1 kb transaldolase-

associated repetitive elements (TAREs), and long interspersed nucleotide elements (LINEs), such as L1. Alus and TAREs can be transcribed into nonpolyadenylated RNA by RNA polymerase III [29]. LINEs are polyadenylated and transcribed by RNA polymerase II. Their reintegration is dependent on reverse transcription. Most retroelements, Alus and truncated ERVs, lack reverse transcriptase (RT) which can be provided in-trans by other retroelements, such as L1 [30]. Occasionally, mRNA transcripts of functional genes can be reverse transcribed and reintegrated into the genome thus giving rise to retropseudogenes. These sequences lack introns and contain a poly-A tail at their 3′ end. As an example, the human genome contains an intronless and poly-adenylated transaldolase pseudogene on human chromosome 1 [31].

Human ERVs (HERVs) have the basic structures of the integrated proviral form of infectious retroviruses with long terminal repeats (LTRs) of several hundred nucleotides flanking sequences homologous to *gag*, *pol*, and *env* genes [32]. The *gag* gene codes for inner structural core proteins, such as matrix and capsid. The *pol* gene encodes RT, which copies viral RNA into DNA as well as protease and integrase allowing for integration of proviral DNA into the host genome. The *env* gene codes for transmembrane and outer envelop proteins, the latter playing key roles in binding to cell surface receptors. Sequence homologies between the *pol* genes have been used to divide ERVs into two classes: class I with homologies to mammalian type C retroviruses and class II with homologies to mammalian type A, B, and D retroviruses and avian type C retroviruses (Table I). HERVs are commonly designated as HERV followed by a single letter amino acid code corresponding to a tRNA. The 3' terminus of tRNA is predicted to initiate reverse transcription by annealing to an 18 nucleotide long primer-binding site (PBS) at the 5' LTR. HERVs have generally been found to be defective proviruses having accumulated deletions or stop codons in *gag*, *pol*, and/or *env* open reading frames (ORFs; [33]).

ERV represent a key molecular link between the host genome and infectious viral particles. ERVs may have originated from exogenous retroviruses that integrated into the genome and became trapped owing to mutations of essential genes [32]. They constitute a large reservoir of viral genes that may be activated by mutations caused by radiation or chemicals, or recombination with exogenous retroviruses. While exogenous retroviruses are infectious, with a replication cycle which requires integration of proviral DNA into host cell DNA, ERVs are transmitted genetically in a classical mendelian fashion through the germline as proviral DNA. Expression of ERVs can influence the outcome of infections in different ways both beneficial and detrimental to the host [32]. These include provision of genes for recombination with exogenous viruses, interference with virion assembly, blocking cellular receptors for viral entry, and modulation of immune responses to exogenous viruses (Figure 1). Recombination with murine ERV can expand cellular tropism of HIV-1 [34].

While expression of murine ERV can lead to production of infectious virus and cause viremia, no production of infectious virion has been documented by HERV. High copy number of most ERV families makes it difficult to distinguish which members of a group are expressed. Although, no single provirus with intact LTRs and uninterrupted *gag*, *pol*, and *env* ORFs has been identified, the HERV-K ERV, as a family, has been shown to encode gag [35], RT [36], integrase [37], and rev proteins [38,39]. The HERV-K rev protein, encoded by

the LTR region, is functionally analogous to the HIV-1 rev and HTLV-I/II rex proteins. HERV-K rev binds to both the nuclear export factor Crm1 and to a cis-acting viral RNA to activate nuclear export of unspliced RNAs [39]. Alternatively, the HERV-K LTR is also recognized by HIV-1 *rev*, suggesting a potential interaction between these exogeneous and ERV.

The HERV-K class of HERV may be most potent in terms of its ability to form virions [38,40]. HERV show a characteristic pattern of tissue-specific expression. Most ERV are expressed in the placenta, teratocarcinomas, and other malignant tissues. Several ERV are expressed in normal peripheral blood lymphocytes [41–43], salivary gland [25], breast [44], and keratinocytes [45].

Mechanisms of endogenous retroviral involvement in autoimmunity

ERSs may lead to autoimmunity directly, by encoding autoantigens, or indirectly, by affecting the expression of genes regulating immune responses and tolerance [9]. Direct autoantigenicity of HRES-1 and ERV-3 has been documented in SLE (Table II). ERS, if expressed, are likely targets of cross-reactivity for virally induced immune responses. Such cross-reactivity, i.e. molecular mimicry between self-antigens and viral proteins has been proposed as a trigger of autoimmunity [46,47].

In addition to serving as cross-reactive targets of antiviral immunity, ERS may also have a direct role in regulating immune responses [9]. ERS and other retrotransposable elements possess a relatively high mobility and may cause immune dysregulation by insertional mutagenesis or cis or trans-regulation of cellular genes [48]. HERV-K10 has an integration site within the complement C2 gene [49]. Variable repeats of this element may have a role in C2 expression. Integration of a 5.3 kb ETn retrotransposon in the FasR gene locus resulted in dysruption of this apoptosis pathway in lupus prone MRL/lpr mice [50,51]. Expression of HERV-K18 is increased in juvenile rheumatoid arthritis [52]. A synthetic heptadecapeptide corresponding to the transmembrane domain of the env protein conserved among many exogenous and ERV has been shown to have potent immunosuppressive properties [53,54]. The *tat* gene of HIV-1 enhances expression of the HRES-1/Rab4 ERV protein which in turn inhibits recycling of CD4 and infection by HIV-1 [55].

Activation of ERV by DNA demethylation

Expression of HERV-E4-1 appears to be increased in patients with SLE due to DNA hypomethylation [56]. Interestingly, higher expression levels in SLE lymphocytes correlate with production of U1 snRNP [57] which includes a 70 kDa protein with a region of homology to gag antigens of infectious and ERV [24,58]. The 1q42 chromosomal region that has been associated with lupus susceptibility [59] and harbors the HRES-1 ERV [27,60] is genetically unstable [61]. 1q42 has been identified as one of the three most common fragile sites in the human genome [62,63]. In general, genomic loci harboring ERV has been associated with increased chromosomal fragility [64]. Fragility at 1q42 has shown an evolutionary conservation in man, gorilla, and chimpanzee [65], similar to the appearance of HRES-1 in old world monkeys [66]. Fragility at 1q42 can be triggered with 5-azacytidine (5AZA), a demethylating agent and relative inducer of endogenous retroviral genes in

chicken cells [64]. This mechanism is particularly interesting with regards to induction of T-cell autoreactivity by 5AZA [67] and impaired DNA methylation in T cells of patients with SLE [68].

Molecular mimicry between ERV and infectious virus: Cross-reactivity of HRES-1/p28 with viral peptides and the 70 kDa protein of U1 snRNP in SLE

Immunological cross-reactivity between antigens of infectious viruses and self-proteins have long been documented (Table II). However, proving a causal role of the implicated viruses has proven challenging. EBV shows cross-reactivity to several lupus autoantigens [69,70] and appears to infect lupus patients earlier than control donors [6], yet its nearly ubiquitous presence in the normal adult population makes it difficult to prove a causal role in SLE. Nevertheless, EBV remains an attractive candidate both as an initiator of autoreactivity and stimulator of B-cell survival. Other viruses with strong cross-reactivity to self-antigens, particularly, the human retroviruses with homology to ERV-encoded antigens (Table II), are also difficult to implicate in disease pathogenesis, since these viruses rarely infect patients with SLE. Along this line, relatedness and cross-reactivity to HTLV-I and HIV 1 gag antigens, have been demonstrated [23,66]. However, HIV or HTLV-I provirus was absent in genomic DNA of lupus patients, thus, they could not have initiated immunore-activity to HRES-1/p28 [23]. Comprehensive epitope mapping with fourty-four 15 amino acid long peptides overlapping the entire protein HRES-1/p28 by 10 amino acids with antibodies of 16 HRES-1/p28 Western blot-seropositive SLE patients identified three immunodominant epitopes within residues 41-55, 121-13, and 156-170. Two newly identified immunodominant epitopes in peptides 41–55 and 156–170 showed significant homology to antigens of viruses commonly infecting humans [71]. The immunodominant HRES-1/p28 epitopes and viral peptides were synthesized on the same cellulose membrane and tested in parallel for binding by 16 HRES-1/p28 Western blot-reactive lupus sera. The highest prevalence of cross-reactivity was found with a ORF2a peptide of the newly discovered TT virus (TTV); 14/16 (87.5%) of lupus sera bound to this peptide. Further, antibodies from 11 patients recognized both HRES-1/p28 peptide 41-55 and TTV ORF2a peptide. All HRES-1/ p28-reactive sera recognized at least one TTV peptide. In parallel, sera of four HRES-1/p28seronegative lupus patients and four healthy donors failed to bind to the TTV peptides [71].

TTV is a recently discovered single-stranded circular DNA virus that has not been causally associated with any disease [72]. TTV was originally named after the initials of first patient TT, then transfusion-transmitted, and recently renamed "torque teno" virus [73]. Due to the high degree of genomic variability of the putative coding regions [74] and difficulties in expression of full-length TTV protein for antibody testing [75,76], the diagnosis of TTV infection has been dependent on PCR detection of viral DNA using primers specific for the noncoding regions [77]. TTV DNA was detected in 120/211 SLE patients and 66/199 healthy control donors (p < 0.0001). TTV DNA prevalence was also increased in SLE patients relative to RA patients (23/91; p < 0.0001). The prevalence of TTV DNA was increased in lupus patients (80/121) with respect to their first degree healthy relatives (40/78; p = 0.0184) and the prevalence of TTV DNA was also increased in first degree healthy relatives of lupus patients (40/78) with respect to unrelated healthy donors (66/199; p = 0.0001).

0.0026). Sera of all TTV PCR-positive patients recognized at least one TTV-derived peptide. HRES-1/p28 Western blot reactivity was observed in 12/23 TTV PCR-negative donors and 43/58 TTV PCR-positive lupus donors (p < 0.0281). In addition, TTV cross-reactive lupus sera showed high binding affinity to HRES-1/p28 peptide 121–135 (DRRREGPDRSPRQPP) harboring three consecutive highly charged amino acids (RRE). This RRE triplet is repeated three times in the retroviral gag-like region of 70K U1 snRNP lupus autoantigen and represent crossreactive epitopes between the two proteins [24].

HRES-1/p28 residues 41–55 (PRHRHPQDPRSPGPA) contain epitopes cross-reactive with EBV-LF3 and EBNA-3C antigens [71]. Co-infection of malignant B cells by EBV and TTV has recently been documented in nonHodgkin lymphomas and diffuse large B-cell lymphoma [78]. Expression of HRES-1/p28 is enhanced in EBV-transformed B cells [9]. These observations suggest that cooperativity between EBV and TTV may contribute to autoantigenicity of HRES-1. Thus, co-infection with EBV and TTV and molecular mimicry with immunodominant HRES-1/p28 epitopes may mediate epitope spreading to self-antigens such as the 70 kDa U1snRNP, and thus contribute to formation of antinuclear autoantibodies in SLE.

Immunomodulation by ERV

In addition to providing cross-reactive targets of antiviral immunity, ERV may also have a direct role in regulating immune responses. Changes in production of cytokines similar to those in patients with SLE, a shift from a Th1 to a Th2-type cytokine profile, have been described as a result of HIV-1 infection [79]. A synthetic heptadecapeptide (CKS-17) corresponding to the transmembrane domain of the env protein conserved among many exogenous and ERV has potent immunosuppressive properties [53], possibly via suppression of Th1 type cytokine production [54]. Recently, a full-length env protein of HERV-H was found to suppress anti-tumor immunity in the mouse [80]. The env protein of HERV-W, also called syncytin [81], stimulates expression of the type D mammalian retrovirus receptor in placenta [82]. HERV-W env can function as an envelope protein, form pseudotypes with human immunodeficiency virus type 1 (HIV-1) virions and confer tropism for CD4-negative cells [83]. HERV-W env may also act as a superantigen, causing Vβ16-specific T-cell expansions [84]. In turn, ERV expression may be induced by environmental signals and activation of the immune system. Interleukin 1 (IL-1) induces expression of xenotropic ERV in pancreatic β cells of NOD mice susceptible to IDDM [85]. IL-1 and tumor necrosis factor α (TNFα) stimulate, while IFN-γ inhibits transcription of HERV-R in human vascular endothelial cells [86]. IFN-α induces expression of HERV-K18.1 env, which acting as a superantigen, causes Vβ7- [87] or Vβ13-specific T-cell expansions [88]. Steroids have long been known to induce expression and virion formation from ERV in the mouse [89]. Promoter of HERV-K can be induced by treatment with estradiol and progesteron [90]. Unlike related mouse mammary tumor viruses, HERV-K is not sensitive to stimulation by dexamethasone. Expression of RRHERV-I [91] and HERV-R is enhanced by retinoic acid [92]. HERV-R can also be induced by vitamin D3, IFN- γ , and phorbol esters [92]. Transcription of ERV family members HERV-K, HERV-L, and ERV-9 was increased in ultraviolet B light (UVB)-irradiated skin and skin biopsies of lupus patients [45]. Expression of HRES-1/Rab4 is enhanced by the tat gene of HIV through trans-activation of the HRES-1

LTR [55]. In turn, HRES-1/Rab4 regulates expression of CD4, the cellular receptor of HIV, via endocytic recycling (Figure 1).

HRES-1/Rab4 regulates HIV infection via recycling of CD4

Several ORFs have been identified both in the sense and antisense strands of HRES-1.The 6 kb "sense" transcript encodes a 28 kDa nuclear protein, HRES-1/p28, which is expressed in T-cell lines, placenta, and epithelial cells but not in PBL [23,25,66]. We cloned a novel 2986 base long cDNA (Genbank accession number: AY585832) corresponding to the antisense strand of the HRES-1 locus [55]. This cDNA sequence has considerable homology to the 735 base long Rab4a gene (Genbank accession number: M28211.gb_pr1) and was termed HRES-1/Rab4. The 5' and 3' untranslated regions in the HRES-1/Rab4 cDNA were markedly different from those of Rab4a [55].

HRES-1/Rab4 codes for five additional amino acids and two discordant residues, $163 \ (D \rightarrow N)$ and $209 \ (T \rightarrow A)$ [55]. Since, the HRES-1 is a single copy sequence in the haploid genome [60], the previously identified Rab4a may originate from another chromosomal locus or correspond to an alternative translation product of the polymorphic HRES-1/Rab4 genomic locus. HRES-1 was previously mapped to human chromosome $1q42 \ [60]$. All eight coding exons of the HRES-1/Rab4 cDNA were localized within contig NT 031728.1 mapped to the 1q42 genomic locus [55]. Bidirectional transcription has been previously documented at several genomic loci [93,94], including another ERS, HERV-H [95] and the 1q42 locus harboring HRES-1 [96].

The transcription start site of HRES-1/Rab4 was mapped to HRES-1 position 1611 [55]. HRES-1 (nucleotides 2151–1606) exhibited strong promoter activity when oriented in the direction of HRES-1/Rab4 transcription. The HRES-1 LTR enhanced the promoter activity in HeLa cells transfected with HIV-1 tat (HeLa-tat), while it diminished promoter activity in control HeLa cells. Moreover, HRES-1/Rab4 protein levels were elevated in HeLa-tat, Jurkat-tat, and HIV-infected H9 human T cells. Thus, HIV tat can increase expression of HRES-1/Rab4 via trans-activation of HRES-1 LTR [55]. Interestingly, higher expression levels of HRES-1/Rab4 abrogated production of HIV-1 gag p24 as determined by Western blot analysis and reduced the percentage of HIV-1-infected cells by flow cytometry of intracellular gag p24 staining and diminished HIV-induced apoptosis. HRES-1/Rab4S27N had the opposite effects [55].

Rab4a has been shown to regulate recycling of early endosomes carrying the TFR in epithelial cells [97] or GLUT4 in adipocytes [98]. Therefore, we examined whether the impact of HRES-1/Rab4 on HIV infection was mediated via recycling and expression of surface receptors. Expression of CD4 was markedly reduced on the surface of cells over-producing HRES-1/Rab4. By contrast, surface expression of CD4 was enhanced by dominant-negative HRES-1/Rab4S27N. As controls, HIV co-receptor fusin/CXCR4 and CD45RO were not influenced by HRES-1/Rab4 [55]. Coordinate suppression by HRES-1/Rab4 and upregulation by HRES-1/Rab4S27N indicated a specific role for HRES-1/Rab4 in regulation of CD4 expression.

CD4 undergoes protein kinase C (PKC)-mediated endocytosis following T-cell activation [99]. Thus, CD4 internalization was induced by activation of PKC with the phorbol ester PDBu (100 nM) for 1 h at 37°C. Surface expression and recycling of CD4 was profoundly reduced in cells overexpressing HRES-1/Rab4, while baseline expression and recycling of CD4 was markedly enhanced by HRES-1/Rab4^{S27N} [55]. Following PDBu-induced internalization, CD4 co-localized with HRES-1/Rab4 to intracellular blebs [55]. CD4 recycled to the membrane of control and HRES-1/Rab4^{S27N}-expressing cells and displayed a uniform ring pattern. CD4 failed to evenly recycle to the cell membrane and remained confined to discrete foci in cells overproducing HRES-1/Rab4. Interestingly, lysosomal inhibitors chloroquine and NH₄Cl normalized CD4 levels diminished by HRES-1/Rab4. The abrogation of CD4 expression by HRES-1/Rab4 resulted from inhibition of endocytic recycling and from targeting of CD4 for lysosomal degradation [55].

Potential impact of HRES-1/Rab4 on immunological synapse formation and T-cell signaling in SLE

The role of receptor recycling and endosomal trafficking in the immune system is largely unknown, although, its likely to be significant based on a few established models. A dominant-negative form of Rab4, Rab4N121I, inhibited antigen-presentation by a B-cell line to a T-cell hybridoma [100]. In T cells, CD3-induced Ca²⁺ fluxing and proliferation are enhanced in transgenic mice expressing dominant-negative Rab5 [101]. Rab27, which is involved in granule exocytosis [102], is over-expressed 3-fold in effector memory T cells [103]. Patients with Griscelli syndrome and *ashen* mice exhibit albinism and hemophagocytosis due to macrophage and T-cell dysfunction. They carry inactivating mutations of Rab27 resulting in impaired melanosome transport melanocytes and defective T-cell cytotoxicity due to blocked cytotoxic granule exocytosis [102,104].

Adaptive immune responses by T lymphocytes are mediated by interaction of the TCR with a specific peptide/major histocompatibility antigen complex on the antigen-presenting cell. The outcome of TCR engagement depends on concomitant signaling through the CD4 or CD8 co-receptor and costimulatory molecules (CD8, CD28, CD40L, LFA-1, CD2) and cytokines [105]. Intracellular signal transduction is mediated via protein tyrosine kinases (Lck, Syk) and phosphatases (CD45, SHP-1, phospholipase Cg1) leading to cleavage of phosphatidylinositol diphosphate (PIP₂), and Ca²⁺ mobilization. Then, a secondary cascade of kinases, PKC and protein kinase A activate transcription factors, nuclear factor of activated T cells (NFAT), NF κ B, activated protein 1 (AP-1), c-jun N-terminal kinase (JNK), Extracelluar signal-related kinase (ERK) and initiate cell proliferation and cytokine production [106].

Communication between TCR engagement by the peptide MHC complex and the intracellular machinery occurs via the TCR-associated CD3 chains. Each CD3 chain contains immune receptor tyrosine-based activation motifs (ITAMs) one each in γ , δ , and ϵ and three in ζ . Phosphorylation of ITAM by the Src-family kinase Lck is a critical event for initiating TCR signaling [106,107]. It has become increasingly clear that the macromolecular organization of the TCR, CD4, and signaling molecules with sphingolipid-rich membrane microdomains (lipid rafts) and formation of an IS, which has been also

referred to as the central supramolecular activation complex (SMAC), plays an important role in determining functional outcomes of T-cell activation [108]. The central SMAC (cSMAC) harbors the TCR, adaptor proteins, CD4, and PKCθ, surrounded by a peripheral ring (pSMAC) of adhesion factors, such as LFA-1, and a distal ring (dSMAC) containing the tyrosine phoshatases CD148 and CD45 [108]. CD4 is critical for formation of the IS/SMAC. Because, a portion of Lck is constitutively associated with the CD4 co-receptor within GM1 ganglioside-positive lipid rafts [109], the peptide–MHC-induced co-localization of TCR with CD4 results in an increased local concentration of Lck around the TCR [110].

Abnormal T-cell responses in SLE have been associated with alterations in composition and dynamics of the IS [111–114]. The TCR ζ chain and Lck levels are reduced [111] and replaced by the Fce receptor type I γ chain and Syk in lipid rafts which may contribute to enhanced CD3-initiated Ca fluxing [112]. Interestingly, the TCR ζ chain binds to the TFR [115]. While the plasma membrane-associated Lck is bound to CD4, an intracellular pool of Lck is associated with TFR-positive recycling endosomes [116,117]. Based on its homology to Rab4a, HRES-1/Rab4 is likely to be activated by p85-PI3K [118] and its GTP-bound active form associates with the CD2 adaptor protein [119] and the ubiquitin ligase Cbl [120] which are key components of the IS [108,121]. The existing data on direct binding of Rab4 to p85-PI3K and CD2 adaptor protein and regulation of CD4 and TFR recycling strongly suggest that HRES-1/Rab4 is involved in abnormal assembly and signaling through the IS. Polymorphic HRES-1 alleles have been associated with SLE [27,122] and HRES-1/Rab4 appears to be a prime candidate gene for conferring disease susceptibility at 1q42 [59,60,123–126].

Conclusions

ERV represent a key molecular link between the environmental and genetic factors that govern the development of SLE. HRES-1 is a transcriptionally active HERV that encodes a 28 kDa nuclear autoantigen, HRES-1/p28 and a small GTP-ase, HRES-1/Rab4. Autoantibodies to HRES-1/p28, which are found in half of the patients with SLE [23–27], are cross-reactive with antigens of viruses infecting patients with SLE, such as TTV and EBV [71] and the 70 kDa component of U1 snRNP [24] and may thus contribute to epitope spreading and development of anti-nuclear antibody (ANA). In turn, HRES-1/Rab4 regulates the recycling of CD4, a key component of the IS, which is abnormally assembled in T cells of patients with SLE. HRES-1 is centrally located relative to lupus-linked microsatellite markers on chromosome 1 at q42. Molecular mimicry and immunomodulation by HRES-1-encoded proteins support a role for this ERV in the pathogenesis of SLE.

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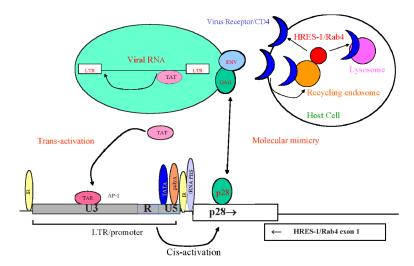


Figure 1.

Effect of ERVon viral immunity and autoimmunity via molecular mimicry, trans-activation, and receptor recycling. As an example, the HRES-1 LTR contains TATA nucleotide sequence-containing motif recognized by the RSA polymerase II transcription machinery (TATA) box, poly-adenylation (polyA) site, tRNA PBS, an HIV-1 trans-activation region, and inverted repeats at typical locations [66]. Transcription from the HRES-1 LTR may be stimulated by trans-acting factors, e.g. *tat* of HIV-1. ERV proteins may interfere with virion assembly or recycling of cell surface receptors, such as CD4, thus effecting replication, infectivity, and pathogenicity of exogenous viruses. Proteins encoded by an ERV may serve as cross-reactive targets of viral immune responses or may directly regulate signaling within the immune system, such as assembly of the IS via receptor recycling.

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Table I

ERV families in the human genome.

Designation	Organization	Length (kb)	Copy number *	Reference
Class I				
HERV-E	LTR-gag-pol-env-LTR	8.8	35–85	[32,127]
HERV-F	LTR-gag-pol-env	7.1	1	[128]
HERV-H	LTR-gag-pol-env-LTR	8.7	660	[129,130]
HERV-I	LTR-gag-pol-env-LTR	9.0	25–85	[32,130]
HERV-P	LTR-gag-pol-env-LTR	8.2	20-100	[32,131]
HERV-R	LTR-gag-pol-env-LTR	9.9	10–15	[130,132]
HERV-W	LTR-gag-pol-env-LTR	7.6	15–115	[81,130,133]
ERV-1	gag-pol-env-LTR	3–4	1–15	[134]{1358}
ERV-9	LTR-gag-pol-env-LTR	9.6	40-70	[32,130,135]
HRES-1	LTR-gag- pol	6	1	[32]
RRHERV-I	LTR-gag- pol-LTR	3.3	15–20	[32,91]
S71	gag- pol-env-LTR	5.4	1–20	[32,136,137]
Class II				
HERV-K	LTR-gag-pol-env-LTR	9.2	170	[32,130,138]
HERV-L	LTR-gag-pol- LTR	6.5	200-575	[130,139]
HERV.HML6	LTR-gag- pol-env-LTR	7.5	30–45	[130,140]

 $^{{}^{\}ast}$ Approximation based on hybridizations and frequency in the human genome sequence.

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Table II

Molecular mimicry between viral proteins and autoantigens in patients with SLE.

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Autoantigen	Prevalence * (%)	Viral protein		Reference
70k/U1 snRNP	30	gag	MoMLV, HRES-1	[24,58]
HRES-1/p28	21–52	gagp24	HTLV-I	[23–27]
HRES-1/p28	21–52	ORF2a, capsid 1	TTV	[71]
La	15	gag	FSV	[141]
Sm B/B =	30	gagp24	HIV-1	[142]
C/U1 snRNP	30	ICP4	HHV-1	[143]
Sm D	36	Epstein-Barr virus nuclear antigen (EBNA)-1	EBV	[7]
p542	10-50	EBNA-1	EBV	[144,145]
ERV-3	32	env	MoMLV	[146]

^{*} Prevalence of antibodies in patients with SLE.