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Identification of Specific Molecular Structures of Human Immunodeficiency Virus Type 1 Tat Relevant for Its Biological Effects on Vascular Endothelial Cells

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Human immunodeficiency virus type 1 (HIV-1) Tat transactivates viral genes and is released by infected cells, acting as a soluble mediator. In endothelial cells (EC), it activates a proangiogenic program by activating vascular endothelial growth factor receptor type 2 (VEGFR-2) and integrins. A structure-activity relationship study was performed by functional analysis of Tat substitution and deletion variants to define the Tat determinants necessary for EC activation. Variants were made (i) in the basic and (ii) in the cysteine-rich domains and (iii) in the C-terminal region containing the RGD sequence required for integrin recognition. Our results led to the following conclusions. (i) Besides a high-affinity binding site corresponding to VEGFR-2, EC express low-affinity binding sites. (ii) The basic and the cysteine-rich variants bind only to the low-affinity binding sites and do not promote tyrosine phosphorylation of VEGFR-2. Furthermore, they have a reduced ability to activate EC *in vitro*, and they lack angiogenic activity. (iii) Mutants with mutations in the C-terminal region are partially defective for *in vitro* biological activities and *in vivo* angiogenesis, but they activate VEGFR-2 as Tat wild type. In conclusion, regions encoded by the first exon of *tat* are necessary and sufficient for activation of VEGFR-2. However, the C-terminal region, most probably through RGD-mediated integrin engagement, is indispensable for full activation of an *in vitro* and *in vivo* angiogenic program.

Tat is one of the regulatory proteins of human immunodeficiency virus type 1 (HIV-1). The protein is composed of 86 to 104 amino acids (aa) (according to the viral isolate) encoded by two exons. In the portion encoded by the first exon (72 amino acids) four distinct regions can be recognized (N-terminal, cysteine rich, core, and basic). The second exon encodes the C-terminal region, containing a RGD sequence (31). Tat plays an essential role in viral replication by up-regulating viral gene expression in infected cells by increasing the rates of transcriptional initiation and elongation by DNA polymerase II (31). Tat also modulates the expression of cellular genes involved in cell survival and proliferation or in coding for cytokines (11, 12, 23, 29, 37, 41, 54, 63, 66, 69). This newly acquired cell phenotype will contribute to the pathogenesis of specific diseases associate with HIV infection. Besides its intracellular effects, Tat may alter cellular behavior when it is released by infected cells in the microenvironment (10, 15). Tat easily enters different cell types contributing to the transactivation of the HIV-1 long terminal repeat (LTR) promoter in latently infected cells (20, 39). Alternatively, it acts as soluble mediator affecting the physiologic functions of cells of the immune (30, 35, 43, 49, 66) and nervous (33, 42, 48) systems. Moreover, it influences the apoptotic program in T cells (26, 36, 41, 65, 70) and in neurons (47, 59), thus favoring the progression of AIDS and the associated brain damage.

However, one of the most relevant targets for Tat is the

vascular system, where it activates a proinflammatory and angiogenic program. Tat can up-regulate the expression of endothelial cell (EC) adhesion molecules (13, 28), resulting in leukocyte extravasation, which is essential for the homing of infected lymphomononuclear cells into lymphoid organs and for the tissue injury characteristic of some features of disease progression. Alone or combined with inflammatory cytokines, Tat induces EC to proliferate, release proteolytic enzymes, and migrate and is fully angiogenic *in vivo* (1, 3–5, 18). These features could be relevant to the chronic inflammatory damages characteristic of several AIDS-associated diseases (17). Furthermore, the ability of Tat to enter EC during the cell cycle could favor HIV-1 replication in some EC areas which are virus reservoirs (44, 45). Finally, Tat participates in the progression of Kaposi's sarcoma, both as a growth factor for spindle cells which represent the core of the tumor and as a means of sustaining its vascularization (14, 16). Furthermore, Tat transgenic mice generated by using either the HIV LTR (63) or the BK polyomavirus promoter (11) develop Kaposi's sarcoma-like lesions and tumors of different histotypes, supporting the pathogenetic role of Tat in Kaposi's sarcoma and in the vascularization of neoplasms associated with AIDS.

The molecular mechanisms leading to these broad and pleiotropic activities are largely unknown. By the use of peptides spanning specific domain of the Tat structure or of functional blocking antibodies, some investigators demonstrated that Tat binding to integrin through the RGD sequence near the C terminus (7, 62) is relevant for the activation of lymphocytes (70), EC (5, 13), monocytes (6, 35), and neuronal cells (48). Through its N-terminal structure, Tat interacts with

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dipeptidyl peptidase IV, located on the T cell surface, and suppresses antigen-induced cell activation (26, 68). Additionally, Tat binds to and activates the tyrosine kinase receptors encoded by the *KDR* and *Flt-1* genes in EC and Kaposi's sarcoma cells (4, 21) and monocytes (43), respectively.

We initiated a study of the structure-activity relationship of Tat to identify functionally important domains that are responsible for the activation of the angiogenic program in vascular EC. We report here that cysteine-rich and basic domains are relevant for functional activation of VEGFR-2 whereas the C-terminal region does not directly participate in the receptor activation but is required for full cell activation.

MATERIALS AND METHODS

Cells. Human EC from umbilical cord veins, prepared and characterized as previously described (9), were grown in M199 (Gibco, Grand Island, N.Y.) supplemented with 20% fetal calf serum (FCS) (Irvine, Santa Ana, Calif.), EC growth factor (100 μ g/ml) (Sigma Chemical Co., St. Louis, Mo.), and porcine heparin (100 μ g/ml) (Sigma). They were used at passage II and grown on a plastic surface coated with porcine gelatin (Sigma), unless specified.

Tat molecules. Recombinant wild-type HIV-1 Tat of 86 (Tat₈₆) and 101 (Tat₁₀₁) amino acids were expressed in *Escherichia coli* as maltose-binding protein (MBP) or glutathione *S*-transferase (GST) fusion proteins. They are referred to below as Tat (MBP-Tat) and *Tat (GST-Tat), respectively. Mutant constructs were obtained by a recombinant PCR procedure with overlapping oligonucleotides corresponding to the mutated sequences, and the specific mutations were verified by DNA sequencing. To obtain Tat mutants, a *PsiI-BamHI* cDNA fragment of Tat₈₆ containing the coding region of both exons was subcloned in the pALTER-Ex1 vector (Promega, Madison, Wis.). Site-directed mutagenesis was carried out with the Altered Sites mutagenesis kit (Promega) by using mutant oligonucleotides to introduce specific mutations (Tat D80E, 5' CCC GAG GGG AAC CGA CAG GCC 3'; Tat R78K/D80E, 5' CCC GAG GGG AAC CGA CAG CC 3' and 5' ACC TCC CAA TCC AAA GGG GAA CCG AC 3'; Tat R49G/K50I, 5' CTC CTA TGG CGG GAT CAA GCG GAG AC 3'; Tat R49G/K50I/R52L/R53I, 5' CTC CTA TGG CGG GAT CAA GCG GAG AC and 5' CGG GAT CAA GCT AAT ACA GCG ACG AAT 3'). The mutated cDNAs (317-bp *EcoRI-BamHI* fragments) were subcloned into the pMAL-c2 vector (New England Biolabs, Beverly, Mass.) and expressed as specified by the manufacturer. Tat₈₆ and its mutants were purified to homogeneity from bacterial cell lysates by affinity chromatography on amylose resin, as specified by New England Biolabs, and used as fusion proteins.

*Tat₈₆ and its mutated derivatives including the product of the first exon, *Tat₇₂, a nonconservative mutant with mutations in basic [*Tat R(49,52,53,55,56,57)A] and cysteine-rich [*Tat C(22,25,27)A] regions, were produced as previously described (40), as well as *Tat₁₀₁ (61). Recombinant fusion proteins were purified by glutathione-Sepharose affinity chromatography (Sigma) (53). The purified MBP and GST fusion proteins gave a unique band after sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) (10% polyacrylamide) and silver staining. Tat₈₆, *Tat₈₆, and *Tat₁₀₁ and their mutants were lipopolysaccharide free, as assessed by the *Limulus* assay (Sigma). Tat and *Tat were able to induce transcriptional activation of the HIV-1 LTR in HL3T1 cells that contain the bacterial gene of chloramphenicol acetyltransferase (CAT) directed by the HIV-1 LTR (67). Tat₈₆ and *Tat₁₀₁ dose dependently stimulated CAT expression. Briefly, Tat molecules were added to confluent HL3T1 cells in a 100-mm-diameter dish containing prewarmed phosphate-buffered saline (PBS). Cells were immediately scraped from the plastic surface, resuspended in fresh medium, and centrifuged. The cells were again plated in a CO₂ incubator, and a CAT assay was performed after 6 h as described previously (67). Under our experimental conditions, just scraping of the cells in absence of Tat molecules had no effect on LTR-directed CAT gene expression (125 \pm 56 cpm of [³H]acetylated chloramphenicol [*n* = 3]). However, CAT gene expression was markedly elevated in cells that received Tat₈₆ at 0.5 μ g/ml (423 \pm 86 cpm of [³H]acetylated chloramphenicol), 1 μ g/ml (2,345 \pm 167 cpm of [³H]acetylated chloramphenicol), or 5 μ g/ml (6,543 \pm 567 cpm of [³H]acetylated chloramphenicol) or *Tat₈₆ at 0.5 μ g/ml (512 \pm 34 cpm of [³H]acetylated chloramphenicol), 1 μ g/ml (3,145 \pm 343 cpm of [³H]acetylated chloramphenicol), or 5 μ g/ml (7,009 \pm 671 cpm of [³H]acetylated chloramphenicol).

Tat molecules were stored at -80°C in aliquots of 5 μ g/10 μ l of PBS containing 0.1% human serum albumin (HSA; Farma Biagini, Lucca, Italy) and 1 mM dithiothreitol (Sigma).

Iodination of Tat molecules and binding studies. MBP, GST, Tat₈₆, *Tat₈₆, Tat R78K/D80E, Tat R49G/K50I/R52L/R53I, or *Tat C(22,25,27)A (2- μ g samples) were dissolved in 200 μ l of 20 mM sodium phosphate buffer (pH 7.4) without dithiothreitol and transferred in iodogen-coated tubes (50 μ g/ml) (Pierce Europe B.V., Oud Beijerland, The Netherlands), where proteins were iodinated (5 min at 4°C) with 0.2 mCi of ¹²⁵I (Amersham Pharmacia Biotech, Little Chalfont, United Kingdom). A 20- μ l volume of 20 mM phosphate buffer (pH 7.2) containing 1% HSA, 0.4 M NaCl, and 0.1% 3-(3-cholamidopropyl)-

dimethylammonio]-1-propanesulfonate (CHAPS; Pierce) was added, and the reaction products were separated on Sephadex-G10. The specific activities of the tracers were as follows: MBP, 1 μ Ci/118 fmol; GST, 1 μ Ci/134 fmol; Tat₈₆, 1 μ Ci/108 fmol; *Tat₈₆, 1 μ Ci/100 fmol; Tat R78K/D80E, 1 μ Ci/128 fmol; Tat R49G/K50I/R52L/R53I, 1 μ Ci/112 fmol; and *Tat C(22,25,27)A, 1 μ Ci/103 fmol. [¹²⁵I]Tat₈₆ and [¹²⁵I]*Tat₈₆ retained their biological activity on Kaposi's sarcoma cells (8).

For binding studies, adherent EC on 24-well plates were incubated for 90 min at 22°C in 200 μ l of M199 containing 20 mM HEPES (pH 7.4), 0.1% HSA, 0.2 U of heparin, 100 μ g of soybean trypsin inhibitor per ml, bacitracin (binding buffer), and increasing concentrations of iodinated Tat molecules or control proteins in the presence of 100-fold excess of unlabeled proteins. After washes in buffer binding, the cells were extracted with 2% SDS in PBS. Specific binding (calculated by subtracting from the total the cpm bound after incubation with a 100-excess of unlabelled ligand) was approximately 80%. Curve displacement binding was obtained by incubating cells with 0.05 nM [¹²⁵I]Tat and processed as described above. Kinetic parameters were estimated with the Ligand program (Elsevier-Biosoft, Cambridge, United Kingdom).

Immunoprecipitation and immunoblotting. Confluent EC (10⁷ cells/150-cm² dish) were made quiescent by 20 h of starvation in M199 containing 0.5% FCS and 0.1% HSA, preincubated for 15 min at 37°C with 1 mM Na₃VO₄, and then stimulated as detailed in Results in the presence of heparin (1 U/ml). The cells were lysed in a 50 mM Tris-HCl buffer (pH 7.4) containing 150 mM NaCl, 1% Triton X-100, and protease and phosphatase inhibitors (pepstatin, 50 μ g/ml; leupeptin, 50 μ g/ml; aprotinin, 10 μ g/ml; phenylmethylsulfonyl fluoride, 1 mM; soybean trypsin inhibitor, 500 μ g/ml; ZnCl₂, 100 μ M, Na₃VO₄, 1 mM [Sigma]). After centrifugation (20 min at 10,000 \times g), supernatants were precleared by incubation for 1 h with protein A-Sepharose or with anti-mouse immunoglobulin-agarose (Sigma). Samples (1 mg of protein) were incubated with rabbit anti-VEGFR-2 polyclonal antibody (no. C-1158; Santa Cruz Biotechnology, Inc., Santa Cruz, Calif.) or antiphosphotyrosine monoclonal antibody (MAb) (clone G410; Upstate Biotechnology Inc., Lake Placid, N.Y.) (5 to 10 μ g/ml) for 1 h at 4°C, and immune complexes were recovered on protein A-Sepharose or anti-mouse Ig-agarose. Immunoprecipitates were washed four times with lysis buffer, twice with the same buffer without Triton X-100, and once with Tris-buffered saline. Proteins were solubilized under reducing conditions, separated by SDS-PAGE (8 or 10% polyacrylamide), transferred to Immobilon-P sheets (Millipore, Bedford, Mass.), and probed with antiphosphotyrosine MAb or with anti-VEGFR-2 antibody. The enhanced chemiluminescence technique (Amersham Pharmacia Biotech) was used for detection.

PI 3-kinase assay. A phosphoinositide 3-kinase (PI 3-kinase) assay was performed directly on antiphosphotyrosine immunoprecipitates exactly as described previously (58). Briefly, immunoprecipitates were incubated with 40 μ M ATP, 50 to 100 μ Ci of [γ -³²P]ATP (Amersham), and a presonicated mixture of phosphatidylinositol-4,5-bisphosphate and phosphatidylserine (final concentration of both lipids, 50 μ g/ml [Sigma]) in 25 mM HEPES (pH 7.4) and 1 mM EGTA. The reaction was stopped after a 10-min incubation at room temperature by the addition of 1 volume of 1 M HCl and 2 volumes of chloroform-methanol (1:1). The lipids in the organic phase were separated by thin-layer chromatography (Silica Gel 60; Merck, Darmstadt, Germany) in 1-propanol-2 M acetic acid (65:35, vol/vol) and visualized by autoradiography.

Migration, proliferation, and adhesion assays. EC motility was studied by using a modified Boyden chamber technique exactly as previously described (9).

To evaluate EC proliferation, 2 \times 10⁵ cells were plated in M199 containing 20% FCS in 96-well plates (Falcon, Becton Dickinson Labware, Bedford, Mass.) coated with gelatin. After 24 h, the medium was removed and replaced with M199 containing 2.5% FCS. Tat molecules were added on days 0, 2, and 4, and the cell number was estimated on day 6 as previously described (9).

To study EC adhesion to immobilized Tat molecules, 96-well polystyrene plates (Falcon) were coated overnight at 4°C with Tat molecules or control proteins (10 μ g/well), washed, and then incubated for an additional 2 h at room temperature with 1% HSA in PBS. Cells were detached in cold PBS containing 2 mM EGTA, washed twice in M199 containing 1% FCS, and plated (5 \times 10⁴/0.1 ml) in the adhesion assay. After a 1-h incubation at 37°C, the plates were extensively washed in M199 containing 1% FCS, fixed, and stained with crystal violet (9). The absorbance was read at 540 nm in a microtiter plate spectrophotometer (EL340; Bio-Tek Instruments, Highland Park, Vt.).

In vivo angiogenesis. Matrigel (Becton Dickinson) supplemented with 10 U of heparin per ml was mixed with Tat molecules or control proteins and injected (0.7 ml) into the subcutaneous tissue of BALB/c male mice (Charles River, Conago, Italy) along the peritoneal midline. After 5 days, the mice were killed and gels were processed for histology, morphometric analysis, and hemoglobin content determination measured with a Drabkin reagent kit (Sigma) as previously described (8).

Statistical methods. One-way analysis of variance (ANOVA) and the Student-Neuman-Keuls test were used to test the difference within the experimental blocks of each biological assay. Statistical analyses were performed with STATISTICA for Windows, version 4.5 (StatSoft, Tulsa, Okla.).

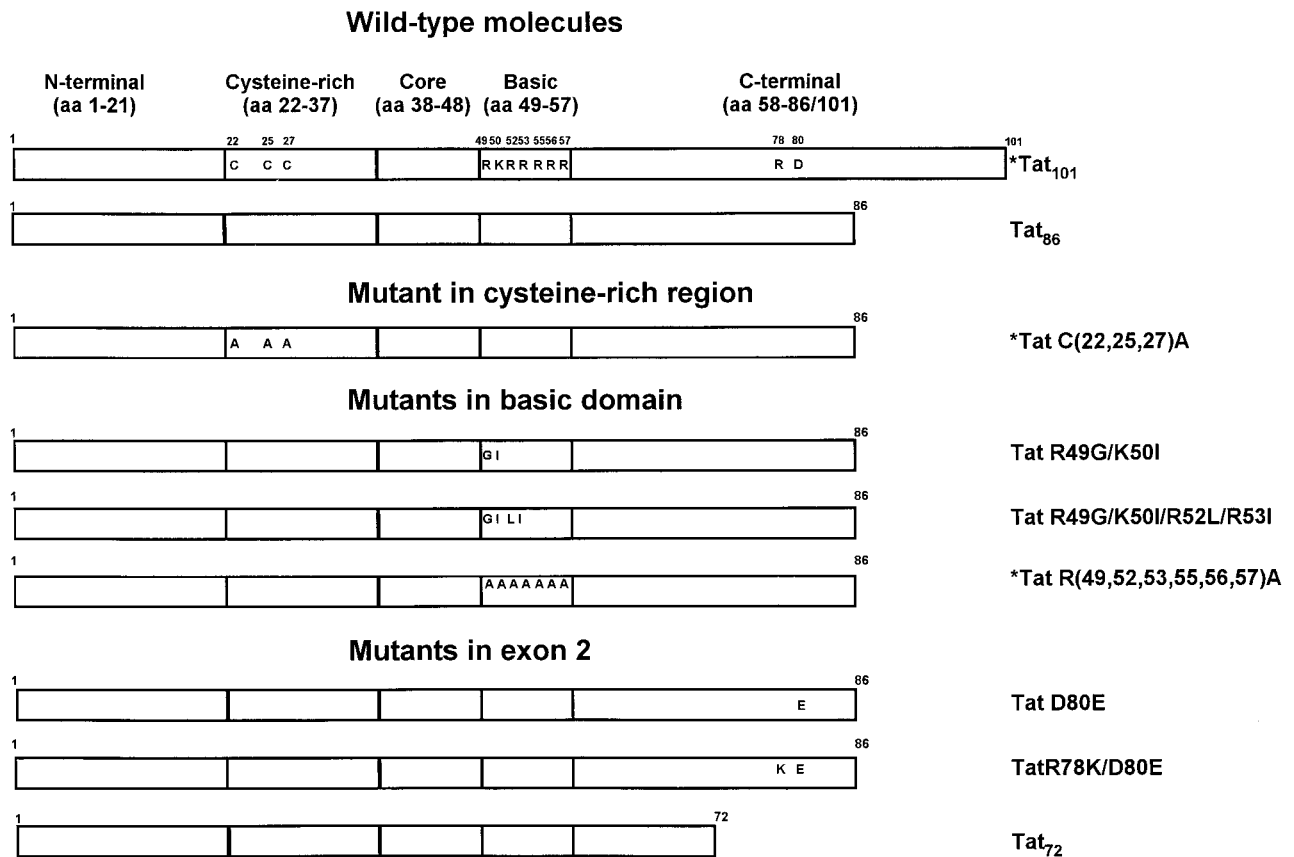


FIG. 1. Domain structure of the HIV-1 Tat protein and mutations introduced. The arbitrary domain structure is that of Kuppuswamy et al. (34). The number of mutated amino acids is indicated.

RESULTS

Effect of Tat and Tat mutants on biological functions of EC.

It has been reported that soluble Tat induces the activation of vascular endothelium and of Kaposi's sarcoma cells through the engagement of VEGFR-2 (4, 21) and the integrin system (5, 13, 16). Furthermore, Tat mimics the extracellular matrix protein and favors cell adhesion through the amino acid sequence RGD (7) or the basic domain (62, 64). To examine the Tat regions involved in EC activation, a set of Tat mutants was constructed (Fig. 1), expressed as fusion proteins in *E. coli*, and studied for their ability to induce cell migration, proliferation, and adhesion.

First we studied the effect of mutations in the basic region. Tat R49G/K50I, Tat R49G/K50I/R52L/R53I, and *Tat R(49,52,53,55,56,57)A had a reduced effect in terms of migration in the Boyden chamber (Fig. 2) and proliferation (Fig. 3) of human EC compared to wild-type molecules (Tat₈₆ or *Tat₁₀₁) ($P < 0.005$), with Tat R49G/K50I being more active than Tat R49G/K50I/R52L/R53I and *Tat R(49,52,53,55,56,57)A ($P < 0.005$). Finally, the adhesion of EC to Tat R49G/K50I/R52L/R53I and *Tat R(49,52,53,55,56,57)A was markedly reduced with respect to the adhesion to Tat₈₆ or Tat R49G/K50I ($P < 0.005$) (Fig. 4). These data suggest that the basic domain is relevant for all the EC biological activities considered.

Analysis of the mutants with mutations in the RGD sequence indicated that this sequence is also necessary for full activation of the migration (Fig. 2) and proliferation (Fig. 3) of EC and is required for the adhesion process (Fig. 4). Tat

R78K/D80E showed reduced proliferation and migration activities compared to Tat₈₆ ($P < 0.005$). Tat D80E had an effect similar to Tat₈₆, indicating that a unique mutation is insufficient to impair the activities of Tat₈₆ on EC. Deletion of the sequence encoded by exon 2 (*Tat₇₂) resulted in a molecule with biological activities (migration and proliferation) similar to those of Tat R78K/D80E (Fig. 2 and 3). Similarly, *Tat₇₂ and Tat R78K/D80E were not permissive for EC adhesion (Fig. 4).

*Tat C(22,25,27)A, the mutant with the mutation in the cysteine-rich region, was a weak activator of EC migration and proliferation and showed little impairment of the adhesive property (Fig. 2 to 4). This suggests that the cysteine-rich region of Tat is required for migration and proliferation of EC rather than for their adhesion to the extracellular matrix.

In an effort to better define the activation of EC by the different Tat domains, the migration of EC was triggered by different concentrations of Tat₈₆, Tat R49G/K50I/R52L/R53I, Tat R78K/D80E, and *Tat C(22,25,27)A. All concentrations of the mutants tested (5 to 100 ng/ml) showed a reduced activity compared to Tat₈₆. However, the highest concentrations of Tat R78K/D80E (50 to 100 ng/ml) tended to reach the activity of Tat₈₆ (Fig. 5).

MBP and GST, the two proteins fused to the different Tat molecules used, did not promote migration, proliferation, or adhesion at any concentration tested (0.1 to 200 ng/ml) (Fig. 2 to 4).

In vivo effect of Tat and Tat mutants in an angiogenesis model. The capacity of Tat to induce migration and prolifera-

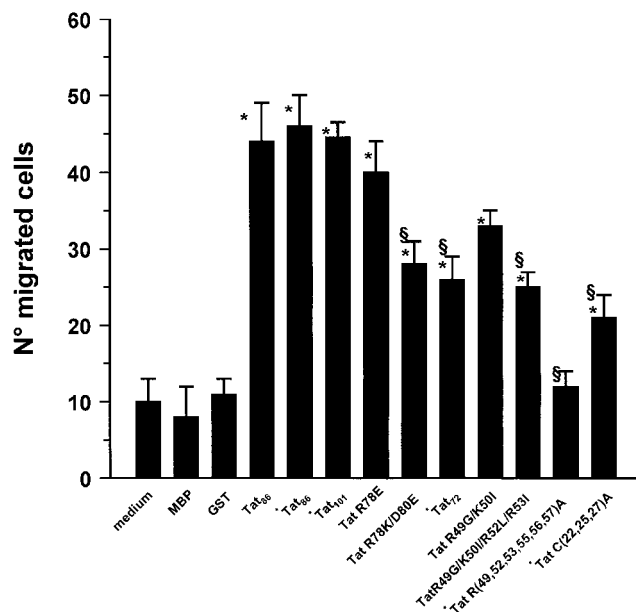


FIG. 2. Effect of Tat molecules on the migration of EC. The migration of EC across a 5- μ m-pore-size polycarbonate filter in response to Tat molecules (20 ng/ml) or vehicle was evaluated by using a Boyden chamber. At the end of the incubation (37°C for 6 h), the filters were removed and stained and five high-power oil immersion fields were counted (400 \times magnification). Results (mean and standard deviation) of one experiment (performed in triplicate) representative of at least three independent experiments are shown. Data were analyzed by ANOVA ($F = 41.11$) and the Student-Newman-Keuls test. * indicates $P < 0.05$ within Tat-stimulated EC and unstimulated or control protein-stimulated cells; § indicates $P < 0.005$ within wild-type Tat molecule-stimulated EC and Tat mutant-stimulated cells.

tion of EC has as in vivo counterpart, i.e., the formation of new blood vessels in rabbit and mouse models (3, 4). Analysis of the effects of Tat mutants in a murine angiogenesis assay is reported in Table 1. Progressive mutations in the basic region or in the RGD sequence were associated with an increasing loss of angiogenic activity compared to the effect of wild-type molecules (Tat₈₆ or *Tat₁₀₁). The deletion of the amino acids encoded by exon 2 of *tat* led to negligible angiogenic activity. Also, the mutation in the cysteine-rich region did not promote angiogenesis. Overall, the in vivo data clearly indicate that the angiogenic program elicited by Tat is dependent on the molecular integrity of its basic and cysteine-rich domains as well as that of the exon 2 product.

Binding of Tat and Tat mutants to EC. We have previously demonstrated that EC express high-affinity binding sites for Tat, identified as VEGFR-2 (4). In this study we used a large amount of [¹²⁵I]Tat₈₆ with high specific activity, which permitted us to study also the presence of low-affinity binding sites on EC. The binding of Tat was evaluated by using saturation binding curves and by competitive displacement of [¹²⁵I]Tat₈₆. The direct ligand binding curves suggested that Tat binding approached saturability without reaching full saturation. Scatchard analysis suggested the presence of two classes of binding sites. Besides a high-affinity binding site ($K_d = 15.7 \pm 5.3$ pM; $B_{max} = 31.9 \pm 7.2$ fmol [$n = 3$]), a low-affinity binding site ($K_d = 8.5 \pm 3.2$ nM; $B_{max} = 2.6 \pm 1.4$ pmol [$n = 3$]) and high-capacity binding site was also observed (Fig. 6; Table 2). The competitive displacement experiments of [¹²⁵I]Tat₈₆ with increasing amounts of cold ligand confirmed the presence of two binding sites (Table 2).

By using Tat mutants, we examined the regions of Tat re-

quired for binding to EC. Saturation binding curves of [¹²⁵I]Tat R49G/K50I/R52L/R53I and of [¹²⁵I]*Tat C(22,25,27)A (Fig. 6) as well competitive displacement of [¹²⁵I]Tat₈₆ with the two unlabeled peptides (Table 2) indicated that these mutants bound EC only with low affinity. The number of low-affinity sites bound by [¹²⁵I]Tat R49G/K50I/R52L/R53I and [¹²⁵I]*Tat C(22,25,27)A was increased compared to that bound by [¹²⁵I]Tat₈₆ (Table 2). The same experimental approaches showed that Tat R78K/D80E bound endothelium in almost the same manner as did Tat₈₆ (Fig. 6; Table 2). [¹²⁵I]MBP and [¹²⁵I]GST did not show any specific binding to EC, and the unlabeled proteins were unable to displace [¹²⁵I]Tat (data not shown).

Effect of Tat and Tat mutants on VEGFR-2 phosphorylation and signal transduction. Figure 7 shows the tyrosine phosphorylation of VEGFR-2 immunoprecipitated from EC stimulated with Tat₈₆ and different Tat variants. Tat₈₆, *Tat₇₂, Tat R78K/D80E, and TatD80E induced the phosphorylation of VEGFR-2. Moreover, we consistently observed that Tat R78K/D80E phosphorylated the receptor more efficiently than Tat₈₆ did. In contrast, mutants with mutations in the basic domain [(Tat R49G/K50I, Tat R49G/K50I/R52L/R53I, and *Tat R(49,52,53,55,56,57)A) showed a reduced ability to phosphorylate the receptor. This feature depends on the number of basic residues mutated, with Tat R49G/K50I being more active than Tat R49G/K50I/R52L/R53I and *Tat R(49,52,53,55,56,57)A. These data confirm that the binding and activation of VEGFR-2 are mediated by the basic domain, while the RGD sequence seems to be not involved in receptor phosphorylation. Mutations in the cysteine-rich region [*Tat C(22,25,

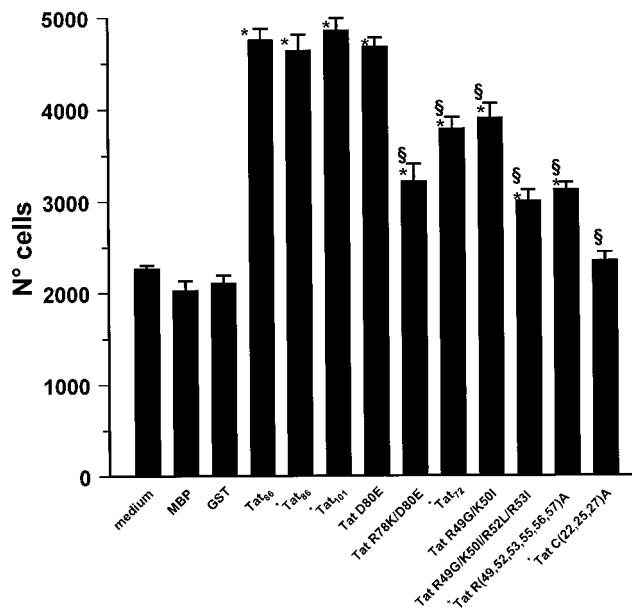


FIG. 3. Effect of Tat molecules on EC proliferation. A total of 2×10^3 EC were plated in 96-well plates and grown for 12 h in M199 containing 20% FCS. After 24 h, the medium was removed and replaced with M199 containing 2.5% FCS. Tat molecules (20 ng/ml) were added on days 0, 2, and 4, and the cell number was estimated on day 6. Cells were fixed and stained with crystal violet, and the absorbance was read at 540 nm. Results (mean and standard deviation) of one experiment (performed in quadruplicate) representative of at least four independent experiments are shown. Data were analyzed by ANOVA ($F = 86.31$) and the Student-Newman-Keuls test. * indicates $P < 0.05$ within Tat molecule-stimulated EC and unstimulated or control protein-stimulated cells; § indicates $P < 0.005$ within wild-type Tat molecule-stimulated EC and Tat mutant-stimulated cells.

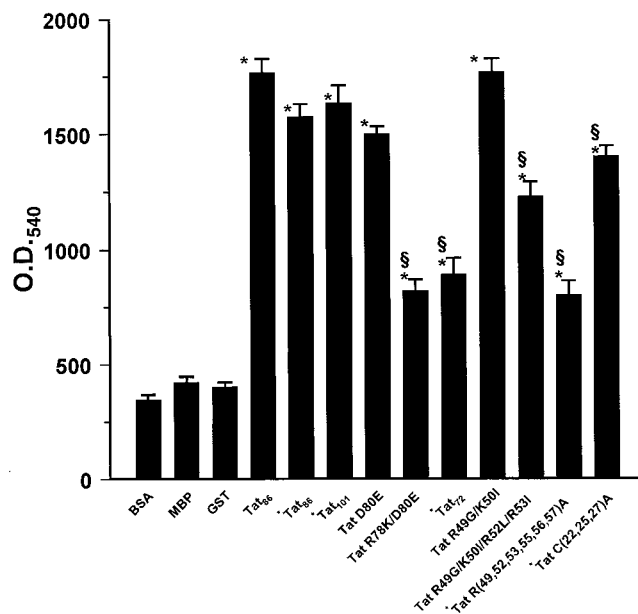


FIG. 4. Effect of immobilized Tat molecules on adhesion of endothelial cells. A plastic surface was coated overnight at 4°C with Tat molecules or control proteins (10 µg/well) and then saturated with 1% HSA. Suspended cells (5 × 10⁴/0.1 ml) were seeded, and after a 1-h incubation at 37°C, plates were extensively washed in M199 containing 1% FCS, fixed, and stained with crystal violet. The optical density (O.D.) was read at 540 nm in a microtiter plate spectrophotometer. Results (mean and standard deviation) of one experiment (performed in quadruplicate) representative of at least four independent experiments are shown. Data were analyzed by ANOVA (F = 71.16) and the Student-Newman-Keuls test. * indicates P < 0.05 within Tat molecule-stimulated EC and unstimulated or control protein-stimulated cells; \$ indicates P < 0.005 within wild-type Tat molecule-stimulated EC and Tat mutant-stimulated cells.

27)A] also abrogated the ability of Tat to promote VEGFR-2 phosphorylation. MBP and GST did not phosphorylate VEGFR-2 (Fig. 7).

It has been recently demonstrated that PI 3-kinase activation is associated with the signals elicited by VEGFR-2 activation

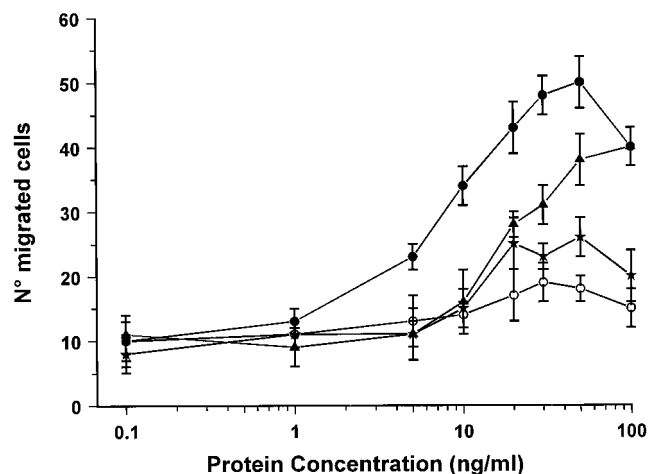


FIG. 5. Dose-dependent effect of Tat₈₆ (●), Tat R49G/K50I/R52L/R53I (★), TatR78K/D80E (▲), and *Tat C(22,25,27)A (○) on EC migration. The cell migration was studied by the Boyden chamber technique as described in the legend to Fig. 1. The data obtained with *Tat₈₆ have not been reported as superimposable on those obtained with Tat₈₆. Results (mean and standard deviation) of one experiment (performed in triplicate) of two are shown.

TABLE 1. Quantitative analysis of the angiogenic effect of Tat molecules^a

Conditions	No. of positive implants/total no. of implanted Matrigel plugs ^b	Morphometric result (% of the total Matrigel area that is vascularized) ^c
1. Control	3/13	6 ± 3
2. Tat ₈₆	10/11	56 ± 7
3. Tat ₇₂	2/7	13 ± 3
4. *Tat ₁₀₁	3/3	56 ± 13
5. Tat D80E	4/4	49 ± 8
6. Tat R78K/D80E	3/9	5 ± 3
7. Tat R49G/K50I	9/13	36 ± 9
8. Tat R49G/K50I/R52L/R53I	1/8	7 ± 8
9. *Tat C(22,25,27)A	1/5	11 ± 7
10. MBP	1/5	9 ± 7
11. GST	1/5	8 ± 3

^a Matrigel (0.5 ml) containing 10 U of heparin per ml was mixed with factors, and the angiogenic response was evaluated after 4 days by measurement of the hemoglobin content and morphometric analysis done on hematoxylin-eosin-stained histological sections (4).

^b Implants were considered positive with a hemoglobin content ≥ 0.2 g/dl. R × C tables of contingency gave a χ² of 58.66 with P < 0.05.

^c Morphometric analysis was performed on four representative implants for each group. Results are mean ± standard deviation. One-way ANOVA gave F = 39.62 with P < 0.0001. The Student-Newman-Keuls test gave a P < 0.05 in 1 versus 2, 4, 5, and 7; 2 versus 3, 6, 7, 9, 10, and 11; 3 versus 4, 5, and 7; 4 versus 6, 7, 8, 9, 10, and 11; 5 versus 6, 7, 8, 9, 10, and 11; 6 versus 7; and 7 versus 8, 9, 10, and 11.

elicited by VEGF-A and Tat₈₆ (25, 58). To support the notion that the basic domain of Tat₈₆ is involved in the signalling pathways downstream of VEGFR-2, we tested the activity of PI 3-kinase in EC stimulated with Tat R49G/K50I/R52L/R53I and Tat R78K/D80E. The results reported in Fig. 8 show that Tat R49G/K50I/R52L/R53I activated PI 3-kinase activity to a lesser extent than Tat₈₆ or Tat R78K/D80E did.

DISCUSSION

HIV-1 Tat is essential for viral replication in infected cells and acts as a soluble mediator in the microenvironment. Several studies on the structure-activity relationship of Tat have determined the domains involved in gene transcription. The basic domain (aa 49 to 57) mediates the binding of Tat to *trans*-activation element RNA (22, 27), directs it to the nucleus (27, 52), and is essential for the recruitment of the p300/CBP transcriptional coactivator (40). A cluster of acidic residues (Glu2, Asp5, and Glu9) in the proline-rich domain, the cysteine-rich domain (aa 22 to 37), and the core domains (aa 32 to 47) all contribute to LTR-directed transcriptional activation (22, 38, 51, 52, 56). More recently, it has been reported that the C-terminal domain encoded by exon 2 also makes a small contribution to viral replication (60).

In this study we have analyzed Tat mutants for binding to and activation of EC, which are among the more relevant extracellular targets for this viral protein (1, 3–5, 13, 18, 28).

In a previous work (4), we detected only a high-affinity binding site corresponding to VEGFR-2, as demonstrated by the ability of VEGF-A to displace [¹²⁵I]Tat. However, it has been recently demonstrated that Tat binds to heparan sulfate (3, 53) and to integrins (7, 62) that both have features of low-affinity, high-capacity binding sites. Therefore, we have revised these binding studies by using larger amounts of [¹²⁵I]Tat than in our previous study, labeled at high efficiency. Under these experimental conditions, we detected two binding

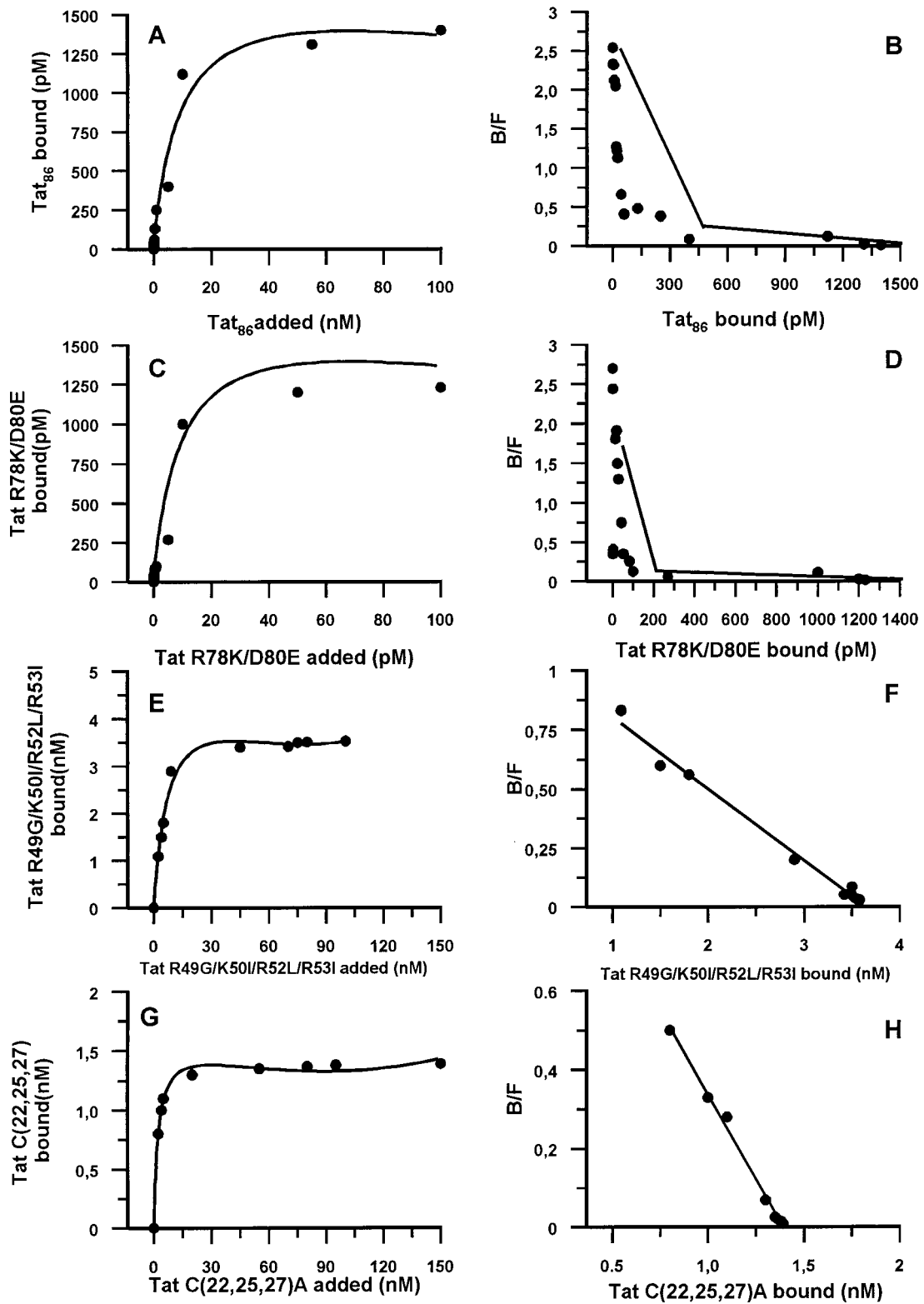


FIG. 6. Specific binding at equilibrium and Scatchard plot of [^{125}I]Tat₈₆ (A and B), [^{125}I]Tat R78K/D80E (C and D), [^{125}I] Tat R49G/K50I/R52L/R53I (E and F), and [^{125}I] Tat C(22,25,27)A (G and H) to EC. Monolayers (10^5 cells) were incubated for 90 min at 22°C with the indicated concentrations of iodinated molecules in the presence of a 100-fold excess of cold ligands. Results of one experiment of three are shown. Tat₈₆: K_d (site 1) = 12.9 pM; B_{max} (site 1) = 28.9 fmol; K_d (site 2) = 4.21 nM; B_{max} (site 2) = 1.32 pmol. Tat R78K/D80E: K_d (site 1) = 23.8 pM; B_{max} (site 1) = 38.4 fmol; K_d (site 2) = 13.2 nM; B_{max} (site 2) = 1.50 pmol. Tat R49G/K50I/R52L/R53I: K_d (site 1) = 4.58 nM; B_{max} (site 1) = 3.51 pmol. *Tat C(22,25,27)A: K_d (site 1) = 1.15 nM; B_{max} (site 1) = 1.39 pmol.

TABLE 2. Binding affinity of Tat molecules to EC

Protein	High-affinity sites ^a			Low-affinity sites ^a		
	K_d^b (pM)	B_{max}^b (fmol)	IC_{50}^c (pM)	K_d^b (nM)	B_{max}^b (pmol)	IC_{50}^c (nM)
Tat ₈₆	15.7 ± 7.3	31.9 ± 7.2	12.3 ± 7.1	8.5 ± 3.2	2.6 ± 1.4	17.0 ± 6.2
Tat R78K/D80E	25.6 ± 1.6	4.6 ± 1.2	10.2 ± 4.1	11.2 ± 4.3	4.3 ± 2.1	8.5 ± 3.2
Tat R49G/K50I/R52L/R53I	ND ^d	ND	ND	5.6 ± 2.1	5.5 ± 2.4	12.3 ± 6.3
*Tat C(22,25,27)A	ND	ND	ND	4.8 ± 2.8	3.1 ± 0.2	10.7 ± 3.5

^a Mean ± standard deviation of three experiments.

^b Calculated from binding-affinity curves.

^c Calculated from displacement binding curves.

^d ND, not done.

sites for Tat on the surface of EC. The presence of MBP did not interfere with the binding, because it did not show any specific binding to the cells and did not displace [¹²⁵I]Tat. The K_d of the first was in the picomolar range, and that of the second was in the nanomolar range. We can hypothesize that this low-affinity site reflects the binding of Tat to membrane glycosaminoglycans and/or to integrins.

To elucidate the functional importance of the basic domain of Tat, two, four, or six nonconservative mutations were made. Variants with a double mutations exhibited only a slightly reduced activity compared to Tat₈₆ or Tat₁₀₁ in term of migration, proliferation, and adhesion of EC and of angiogenesis induction. However, the variants with four or six substitutions showed a marked decrease in the activities studied. Because Tat signals inside the cells through the tyrosine kinase VEGFR-2 (4, 21, 58), we investigated the tyrosine phosphorylation of VEGFR-2. Tat R49G/K50I/R52L/R53I and *Tat R(49,52,53,55,56,57)A failed to activate the receptor. Tat R49G/K50I induced VEGFR-2 phosphorylation but to a lesser extent. The variants with two or four mutations did not activate PI 3-kinase, which is downstream of Tat₈₆ and VEGF-A-activated VEGFR-2 (58). These results are in agreement with the similar observations obtained with a peptide encompassing the basic domain, which mimics the effect of Tat₈₆ on VEGFR-2 (4, 21). The variant with four mutations did not retain the ability to bind to the high-affinity sites on EC, which correspond to VEGFR-2 (4). Taken together with the previous data, this suggests that the Tat basic domain is crucial for the binding and activation of VEGFR-2. The relevance of the positively charged amino acids in performing these functions is consistent with the observation that the charged residues R82, K84,

and H86 of VEGF-A are important for VEGFR-2 recognition (32).

To ascertain whether the RGD sequence is required for Tat binding or activity, mutants with single (D80E) and double (R78K/D80E) mutations and a variant truncated after the residue 72 (Tat₇₂) were obtained. Tat R78K/D80E and Tat₇₂ had reduced biological activity in vitro and in vivo, which is consistent with previous reports showing that $\alpha_v\beta_3$ -, $\alpha_v\beta_5$ -, and $\alpha_5\beta_1$ -integrin participate in Tat-induced activation of EC (5, 13) as well as of other cell types (6, 7, 35, 48, 62, 70). Moreover, the RGD sequence and the C-terminal domain are not required for VEGFR-2 activation, as shown by the ability of Tat R78K/D80E and Tat₇₂ to induce VEGFR-2 phosphorylation. Furthermore, the variant with the double mutations activated PI 3-kinase activity and retained the ability to bind both low- and high-affinity Tat binding sites on the EC membrane. In our experiments, we have observed that the activity of Tat R78K/D80E on VEGFR-2 phosphorylation was greater than that elicited by Tat₈₆. The explanation of this result is lacking, but it will be interesting to determine the role of VEGFR-2 regulatory pathways associated with integrins. For instance, we have recently shown that β_3 -integrin is associated with VEGF-

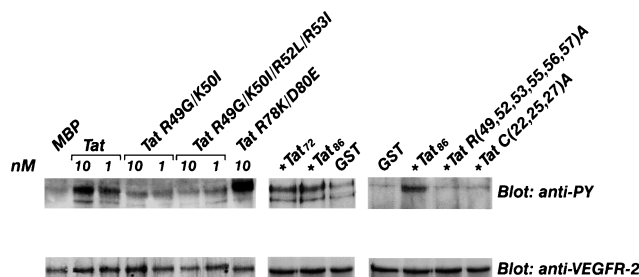


FIG. 7. Effect of Tat molecules on tyrosine phosphorylation of VEGFR-2. Quiescent, confluent EC were preincubated for 15 min at 37°C with 1 mM Na_3VO_4 and then stimulated with Tat molecules (20 ng/ml) for 10 min. The cells were lysed and immunoprecipitated with anti-VEGFR-2 antibody. The immunoprecipitate was analyzed by SDS-PAGE followed by immunoblotting with antiphosphotyrosine MAb. Subsequently, the blots were reprobated with anti-VEGFR-2 antibody. Immunoreactive bands were detected by enhanced chemiluminescence. The results are representative of three similar experiments.

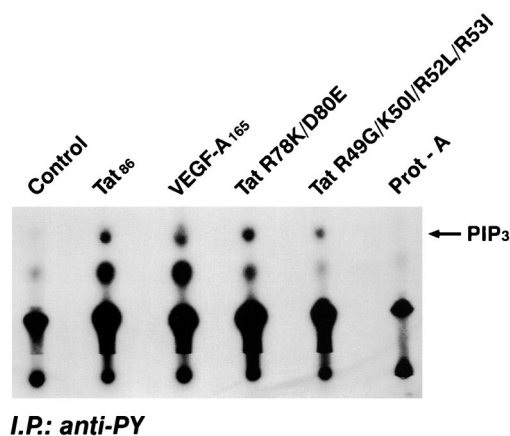


FIG. 8. Effect of Tat molecules on PI 3-kinase in endothelial cells. Quiescent, confluent ECs were stimulated with Tat molecules (20 ng/ml) for 15 min at 37°C. The PI 3-kinase assay was performed on immune complexes done with MAb antiphosphotyrosine (anti-PY) antibodies from lysates of EC in the presence of 40 μ M ATP, 50 μ Ci of [γ -³²P]ATP, and 50 μ g of a presonicated mixture of phosphatidylinositol-4,5-bisphosphate and phosphatidylserine per ml in 25 mM HEPES (pH 7.4)–1 mM EGTA. The extracted lipids were separated by thin-layer chromatography and visualized by autoradiography. PIP₃, phosphatidylinositol-3,4-bisphosphate; Prot-A, a PI 3-kinase assay done on protein A alone. Spots corresponding to PIP₃ were recovered and counted ($n = 3$): control, 420 ± 132 cpm; Tat₈₆, 1,342 ± 231; Tat R78K/D80E, 1,280 ± 280; Tat R49G/K50I/R52L/R53I, 750 ± 201. I.P., immunoprecipitate.

A-stimulated VEGFR-2 and that a MAb against this integrin inhibits the activation of the receptor (58). Alternatively, this variant can assume a spatial conformation more favorable for receptor activation, independent of the interaction with integrins. Therefore, the activation of the biological activities of EC related to angiogenesis most probably requires the engagement of VEGFR-2 as well as integrins by two specific molecular determinants of Tat: the basic domain and the product of exon 2 containing the RGD motif. Many of the integrin-induced signalling pathways are also normally activated by binding of soluble growth factors to their receptors, which suggests the existence of coordinate mechanisms between integrins and growth factors in the control of cell functions, and there is increasing evidence that growth factors can induce an appropriate cellular response only when the target cells express defined sets of integrins (24, 55). Normally, growth factors do not directly bind to and activate integrin. The data reported here and those showing that anti- $\alpha_v\beta_3$ or anti-VEGFR-2 neutralizing antibodies (4, 5, 58) inhibit the EC response to Tat suggest that this viral protein is a unique example of a molecule which turns on intracellular signals by direct activation of both receptor and integrin systems. Furthermore, besides playing a direct role in integrin activation, the C terminus region of Tat could regulate VEGFR-2 through the presence of other determinants relevant for the engagement of neuropilin-1, a coreceptor of this tyrosine kinase receptor (57).

*Tat C(22,25,27)A was used to study the role of the cysteine-rich region of Tat in EC activation. This variant was less potent than Tat₈₆ or Tat₁₀₁ in terms of migration, proliferation, adhesion, and in vivo angiogenesis, bound only the low-affinity binding site, and showed low efficiency in VEGFR-2 phosphorylation. Because it has been suggested that Tat forms a dimer bridging cysteine-rich regions from each monomer (19) and that two cysteine residues are pivotal for the VEGF-A dimerization and the subsequent binding to and activation of endothelium (46, 50), it could be hypothesized that the active form of Tat on the endothelium has a dimeric structure. The relevance of this domain has also been emphasized by Albini et al., who demonstrated its role in the migration of monocytes (2).

Except for Tat D80E, all mutants studied showed a reduced ability to activate EC functions, but their effects are only partially overlapping. For example, mutants with mutations in the RGD sequence have reduced biological activities but fully activated VEGFR-2 phosphorylation. Tat R49G/K50I promoted cell adhesion as Tat₈₆, but its migratory and proliferative capacities were consistently lower than those of Tat₈₆. Mutants with mutations in basic and in cysteine-rich domains had similar kinetic binding parameters, which differed from those of TatR78K/E80D. Furthermore, Tat E80D was similar to Tat₈₆ or *Tat₁₀₁ in all assays performed. Taken together, these observations exclude the possibility that the effects of the Tat mutants are caused merely by an unfolded protein, as also reported for other studies performed with Tat mutants (22, 27, 38, 40, 51, 52, 56, 60).

In conclusion, this study demonstrates that the product of the first exon of *tat* is crucial for the activation of VEGFR-2 and for induction of the activation of an angiogenic program in EC. However, to obtain full activation of this program, Tat also requires the C-terminal region containing the RGD sequence. The C-terminal region could influence the VEGFR-2 response by interacting with integrin subunits or with neuropilin-1 (57), which modulate the functions of this tyrosine kinase receptor, or with other unidentified coreceptors. Further studies of the hypothesized role of Tat dimerization by intermolecular cysteine bridge formation should make it possible to define the receptor-ligand interaction more precisely.

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ADDENDUM IN PROOF

Boykins et al. (R. A. Boykins, R. Mahieux, U. T. Shankavaram, Y. S. Gho, S. F. Lee, I. K. Hewlett, L. M. Wahl, H. K. Kleiman, J. N. Brady, K. M. Yamada, and S. Dhawan, *J. Immunol.* **163**:15–20, 1999) recently reported that a peptide containing six cysteine residues (from amino acids 21 to 40 of the Tat molecule) is angiogenic in chicken chorioallantoic membranes.

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