Bell1-mediated Transactivation of the Spumaretroviral Internal Promoter Is Repressed by Nuclear Factor I

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Gene expression of the internal and long terminal repeat promoters of the spuma retrovirus is specifically activated by the transactivator Bell1, the key regulator of viral gene expression. Bell1 directly binds to and activates DNA target sites of viral promoters and those of distinct cellular genes. To determine the contribution of cellular transcription factors to viral transactivation, the viral internal promoter (IP) was analyzed by transient expression, electrophoretic mobility shift assays, and supershifts. Here we report that Bell1-mediated transactivation of the full-length and shortened versions of the Bell1 response element (BRE) were repressed by nuclear factor I (NFI). Electrophoretic mobility shift assays using nuclear extracts from transfected 293T cells revealed that different DNA-protein complexes consisting of DNA target sites of NFI and Bell1 proteins were formed. The specificity of the repressor and transactivator DNA binding was shown by NFI- and Bell1-specific antibodies that led to supershifts of the different nuclear protein-oligodeoxynucleotide complexes. The specificity of the complexes was confirmed by using unlabeled, shortened, and mutated IP.BRE oligodeoxynucleotides in competition experiments with the authentic IP.BRE. Cotransfection of the infectious spuma-virus DNA genome with a human NFI-X1 expression plasmid into cell cultures greatly reduced the expression of viral structural and Bell1 proteins. These data demonstrate the relevance of NFI-mediated repression of Bell1-driven transactivation in vivo.

Foamy viruses (FV) also called spumaviruses belong to the orthoretroviruses and have exceptional properties with respect to replication, pol expression, and assembly (1, 2); for a review of the historical perspectives and the apparent apathogenicity of FV, see Refs. 3 and 4. FV are unconventional and complex retroviruses that code for transcriptional transactivators (5, 6).

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We dedicate this article to Harald zur Hausen on the occasion of his retirement as head of the German Cancer Research Center (DKFZ) with gratitude and appreciation.

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§ The abbreviations used are: FV, foamy virus; BRE, Bell1 response element; EMSA, electrophoretic mobility shift assay; HFV, human foamy virus; IP, internal promoter; luc, luciferase; NFI, nuclear factor I; HA, hemagglutinin; m, mouse; h, human; LTR, long terminal repeat; Kip2, cyclin-dependent kinase inhibitor 2.

The viral transactivators specifically recruit components of the cellular transcription machinery to viral promoters so that cellular transcription programs are specifically affected and even reprogrammed in a way favorable for viral replication (7). A key regulator of viral gene expression, the Bell1 transactivator of the human foamy virus (HFV), recently renamed primate foamy virus) binds directly to DNA target sites with no or low sequence conservation that are located in both the 5′-long terminal repeat (LTR) and the internal promoter (IP) (8–11). The IP is a strong early promoter that is crucial for viral replication and critically dependent on Bell1 (11–13). Expression of Bell1 is initiated at the IP until threshold levels of the Bell1 transactivator are reached which subsequently turn on the 5′-LTR promoter to direct synthesis of virus structural proteins (13–15). The transactivator Tas of simian foamy virus type 1 binds to corresponding proximal and distal DNA target sites directly that are not homologous to the Bell1 response element (BRE) of the IP (16). Bell1 was shown to be a nuclear protein (17, 18) that contains at least two domains, a centrally located DNA binding region and a C-terminal activation domain (19). Bell1 has a molecular size of 36 kDa (20) and can dimerize and multimerize (21). Alignments of Bell1 and Tas proteins from different species result in a remarkably low degree of homology of about 17–23% (22). The minimal IP.BRE of 27 bp is capable of directly binding Bell1 and partial transactivation in vitro compared with the full-length IP of 192 bp. High affinity DNA binding of Bell1 and full transactivation of the IP depend upon as yet unidentified cellular factors.

Previously, a Kip2-BRE DNA element located within the second exon of the human p57Kip2 gene was identified that mediates a specific Bell1 transactivation (23). It is worth noting that the Kip2-BRE primarily consists of direct repeats of three 14mers that partially overlap with the G base pattern conserved in both the IP.BRE and Kip2-BRE (10, 23). The Kip2-BRE was bound by proteins in nuclear extracts from 293T cells that had been transfected with Bell1 as shown by EMSA and supershift experiments. A purified glutathione S-transferase-Bell fusion protein was bound specifically to Kip2-BRE, and the formation of the Bell1-Kip2-BRE complexes was effectively blocked by the minimal viral IP.BRE oligonucleotide (10, 23). Cotransfection with Sp1 expression plasmids enhanced the Bell1-specific transactivation of Kip2-BRE to a limited extent.2

In the present study we aimed to identify cellular transcription factors and their DNA targets that either repress or activate Bell1-mediated transactivation of the viral internal promoter. We analyzed the ability of cellular transcription factors to affect the level of Bell1-driven transactivation with the clear focus on the core IP element from −166 to −116. Our investi-

oxynucleotides, heat-denatured, annealed, and inserted into EclB1 described below. The probes used for EMSAs included the IP.BRE (Fig. 160 to H11002
/GATTGAGCTTTGAGCCACGACTGCCAA-3/H11032
/pGL3-pro-IP.BRE preincubated for 5 min at room temperature in a volume of 40 μg of nuclear extracts that were transfected into 293T cells grown in 6-cm Petri dishes. The human fibrosarcoma cell line HT-1080 (ATCC number CCL-121) was propagated as described by the supplier and transfected using LipfectAMINE plus (Invitrogen).

Construction of Eukaryotic IP-based luc Reporter Plasmids—Reporter constructs containing the HFV internal promoter were constructed by PCR-mediated amplification of the defined promoter fragments. Sense primer was: IPs (−192 to −173), 5′-CGCATGCTGTTGGAG-TCTGACG-3′; the antisense primer was: IPs (−1 to −22), 5′-GATA-GATTTGCAGTTGCTTCTGCAAACGTCG-3′. PCR reactions using sense primer IPs and antisense primer IPs were done with Pfu polymerase (Stratagene) and pHSRV13 (12). PCR reactions were carried out with the buffer recommended by supplier supplemented for 1 min at 94 °C, 1 min at 56 °C, 2 min at 72 °C for 35 cycles. The resulting blunt-ended PCR amplicon was digested with BglII and inserted into the BglII- and EcoRI-digested reporter plasmid pGL3 basic (Promega). The resulting reporter construct was designated pGL3-basic-HFV-IP. Separately, pGL3-promoter plasmids were constructed. The core IP.BRE (−166 to −116), 5′-AGGCCACTGGTGTCGGGAAAGGA-GATTGAGCTTTGAGCCACGACTGCCAA-3′ (or the IP.BRE from −166 to −140) was mixed with the corresponding antisense oligodeoxynucleotides, heat-denatured, annealed, and inserted into EcoRI-digested luc reporter plasmid pGL3-promoter in the sense orientation. These plasmids were designated pGL3-promoter (136II-digested reporter plasmid pGL3 basic (Promega).

RESULTS

Characterization of the Repressive Effects of Different NFI Family Members on the Full-length Viral Internal Promoter—The minimal HFV IP has been reported to comprise 27 bp but longer promoter regions showed higher activities when assayed by transient expression assays. In the first step of our analysis, we decided to use a longer IP that extends from −192 to −116 of 27 bp is marked by underlining, and the IP.NFI from −142 to −116 by solid underlining; six predicted NFI half-sites are marked by vertical bars and are numbered; NFI half-sites s1, s2, and s7 (identified here) are boxed and were analyzed in more detail (see “Results”). Locations of the TATA box and cap site are shown; the rectangular arrow indicates the direction of Bel1 transcription. N nucleotide sequences of oligodeoxynucleotides representing NFI half-sites (underlined) and IP.BRE mutants used; mutated bases in NFI sites are boxed and in italics. Double-stranded oligodeoxynucleotide FIB2.6 was taken from (31).
Nuclear Factor I Represses Foamy Virus Bel1-driven Transactivation

Fig. 2. Repression of Bel1-mediated transactivation by different NFI plasmids as determined by luc reporter assays. 

A, the pGL3-basic HFV-full-length internal promoter (HFV-IP from −192 to −1, see Fig. 1) was cotransfected with plasmids pbel1s into 293 T cells with and without human NFI-X1 (32). B, four different murine NFI plasmids were separately cotransfected with pbel1s; luciferase activity was determined as described previously (23). The data represent the mean ± S.D. for three experiments shown by error bars.

To assess expression levels of the Bel1 and NFI proteins, aliquots of nuclear extracts from transfected 293T cells were analyzed on Western blots. The results of immunoblotting showed that the expression levels of the four mouse NFI genes. The results shown in Fig. 2B indicated that the four different NFI proteins, NFI-A1, -B2, -C2, and -X2, each inhibited the Bel1-mediated transactivation of the full-length promoter 4- to 6-fold (lower panel, Fig. 2B). In contrast, transfection of the four different NFI family members separately or alone did not affect the basal activity of the full-length IP.BRE (upper panel, Fig. 2B).

To determine more precisely the region of the IP that is responsible for the NFI-repressive effects, shorter regions of the internal promoter, two IP.BRE DNA fragments from positions −166 to −140 and −166 to −116 were cloned into the corresponding luc reporter plasmid pGL3-pro (Fig. 1A, broken and solid underlining, respectively). When the IP.BRE was shortened to the internal promoter, two IP.BRE DNA fragments from positions −166 to −140 and −166 to −116 were cloned into the corresponding luc reporter plasmid pGL3-pro (Fig. 1A, broken and solid underlining, respectively). When the IP.BRE was shortened to the internal promoter, two IP.BRE DNA fragments from positions −166 to −140 and −166 to −116 were cloned into the corresponding luc reporter plasmid pGL3-pro (Fig. 1A, broken and solid underlining, respectively). 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Fig. 4. EMSA of nuclear proteins from NFI- and Bel1-transfected 293T cells that bind to DNA target sites of the core IP.BRE from −166 to −116. A, the core IP.BRE oligonucleotide from −166 to −116 (see Fig. 1) was used. EM-SAs were carried out with nuclear extracts from 293T cells transfected with the Bel1 expression plasmid pbel1s or cotransfected with one of five different NFI plasmids as indicated. The oligonucleotide IP.BRE probe was labeled with \(^{32}\)P-ATP and incubated with 2 µg of nuclear extract and 25 ng/µl poly(dA-dT) and processed as described under “Experimental Procedures.” Arrows in lanes 3, 5, 7, 9, 11, and 13 mark the Bel1 protein-DNA complexes at distinct positions. B, supershift EMSA of the DNA protein complexes reacted with either the monoclonal antibody (anti-HA 5 ng/µl) against the HA-tagged NFI or polyclonal antiserum against Bel1 at 1:80 dilution. The core IP.BRE oligodeoxynucleotide from −166 to −116 (see Fig. 1) was used. Conditions were as described in panel A. Minus signs indicate absence of pbel1s or NFI-plasmids. Inset presents enlargement of upper part of lanes 9–11. C, the \(^{32}\)P-labeled FIB2.6 oligonucleotide was used as probe. Nuclear extracts from cotransfected cells were used as described in A and supershifts were done as described in B.
expression plasmid (Fig. 4A, lanes 4, 6, 8, and 12 marked by vertical arrows marked A1, B2, C2, X2, and X1). After cotransfection with pbel1s, the four individual NFI protein-DNA complexes gave rise to an additional set of complexes with lower mobility (vertical arrows in Fig. 4A, marked A1+Bel1, C2+Bel1, X2+Bel1, and X1+Bel1). The partial shifts were concomitant with a slight decrease in intensity of the DNA-Bel1 complexes. The Bel1-DNA-NFI-X2 and -X1 complexes migrated as comparatively intense bands (lanes 11 and 13). In contrast, the NFI-B2-DNA complex became detectable only after longer exposure; however, a band corresponding to a Bel1-DNA-NFI-B2 complex was not observed (lane 7). Two additional bands observed in nuclear extracts from transfected cells are considered to be unspecific (lane 2) as reported previously (10, 23). These results indicate that the different NFI-A1, -C2, -X2, and -X1 proteins bound the core Bel1-IP.BRE DNA (−166 to −116) together with Bel1. To assess the presence of other potential protein-IP.BRE complexes, different conditions with varying buffers and copolymers were used. No evidence for any other complexes than those detected before and shown in Fig. 4A was found.

To confirm the specificity of the IP.BRE interaction with Bel1 and NFI proteins, a polyclonal Bel1-specific antibody and a monoclonal directed against the HA epitope of the four mNFI proteins was used in supershift assays (Fig. 4B). The intense bands of the Bel1-DNA complexes are marked by short arrows in lanes 3, 4, 9, and 10. The HA and Bel1 antibodies unrelated to each other served as specificity controls (lanes 4 and 8). The EMSAs shown in Fig. 4B indicate that in the presence of nuclear extracts from 293T cells transfected with Bel1, the two Bel1-oligonucleotide complexes reacted with antibody directed against Bel1 that resulted in a complete supershift to three bands (lanes 5, short arrows marked Bel1+aBel1, Fig. 4B) as reported previously (10, 23). Incubation with antibody against the HA epitope located at the N terminus of the NFI-X2 protein resulted in a supershift of the original NFI-X2-oligonucleotide complex to positions marked by the long arrow NFI-X2+aHA (lane 7, inset, lane 9 versus 10).

The mobilities of the NFI-X2-DNA complexes (lanes 6, 8, and 9) were slightly slower than the Bel1-DNA complexes in lanes 3, 4, 9, and 10. In contrast, the NFI-X2-DNA complex resulted in a partial shift to a new position after cotransfection of the Bel1 expression plasmid (inset, lane 9). Clearly, the ternary NFI-X2-DNA-Bel1 complexes were shifted by addition of either anti-HA or anti-Bel1 antibodies (inset, lanes 9, 10, and 11). Thus, we defined the upper band (lane 9) as a Bel1-DNA-NFI-X2 complex. The uppermost band in lane 11 likely presents a DNA complex of NFI-X2 and Bel1-anti-Bel1 that migrated more slowly than the DNA complex of anti-HA-NFI-X2 and Bel1 (lane 10).

Similar EMSA evidence of NFI-Bel1-DNA ternary complexes was obtained when the mNFI-C2 expression was used for transfection instead of mNFI-X2 (data not shown).

To confirm the specificity of the EMSA assay and anti-HA and antiBel1 antibody supershifts, we carried out EMSA and supershift experiments with a 32P-labeled FIB2.6 oligodeoxynucleotide. FIB 2.6 was reported to bind specifically to NFI proteins with very high affinity (31). The results of the binding assays in Fig. 4C clearly show that with nuclear extracts from 293 cells cotransfected with Bel1 alone, FIB2.6 was incapable of binding to Bel1 (lanes 3–5). Expression of Bel1 did not lead to any new band (lanes 9–11) even after reaction with Bel1-specific antibodies (lane 11). Both proteins, mNFI-X2 and Bel1, were expressed as confirmed by Western blotting (data not shown). The absence of any band shift in lanes 9 and 11 indicates that direct NFI-Bel1 protein interactions are not detected.

**Competition EMSAs of Nuclear Extracts from NFI- and Bel1-transfected Cells Reacted with Various Double-stranded Oligodeoxynucleotides as Competitors for Binding to the Core IP.BRE**—To determine whether distinct oligonucleotides were able to act as competitors for the formation of the different nuclear protein-IP.BRE complexes, the following oligonucleotides were used: unlabeled core IP.BRE (−166 to −116), FIB2.6 (Fig. 1B) shown previously to strongly bind NFI in vitro (31) and an unrelated AP-1 oligonucleotide (lanes 6, 10, and 14). Arrows mark the different DNA-nuclear protein complexes. B, The IP.BRE oligonucleotide from −166 to −116 was labeled with γ-32P]ATP and used as probe. Nuclear extracts from mNFI-X2-transfected 293T cells were treated as described in A and incubated with excess of various unlabeled oligonucleotides as competitors as indicated (sequences in Fig. 1B).
core IP.BRE (−166 to −116) functioned as effective competitor for both the major and minor DNA-Bel1 complexes (lanes 4 and 12) almost as well as for the DNA-NFI-X2 complexes (lanes 8 and 12). It is noteworthy that the unlabeled 26-bp FIB2.6 oligonucleotide effectively competed for the NFI-X2-DNA complex (lanes 9 and 13) but not for Bel1-DNA complex (lane 5).

Interestingly, the proposed ternary NFI-X2-Bel1-DNA complex was effectively competed out by FIB2.6 (Fig. 5A, lane 13 versus lane 11). FIB2.6 partially blocked the formation of the minor IP.BRE-Bel1 complex (lanes 5 and 13). These results indicate that most or all of the upper band in lane 11 contained a NFI protein. By analogy, the modest decrease in intensity of the slowest migrating DNA-Bel1* complex suggests that an endogenous NFI protein may be part of this complex (lanes 5 and 13 compared with lanes 3 and 6). These data are in agreement with the results obtained in the supershift assay (Fig. 4B, lane 10). The unrelated AP-1 oligonucleotide did not act as competitor for either of the nuclear protein-DNA complexes as anticipated. The data argue for a specific interaction of the NFI DNA binding sites s1 and s2 of the IP.BRE with NFI proteins.

In an effort to further delineate the contributions of individual NFI DNA binding sites to DNA-NFI complex formation, we used an unlabeled 27-bp-long IP.NFI DNA from −142 to −116 as competitor. In addition, three IP.BRE mutants, DNAs of five different NFI sites, and two IP.BREs were used to test for competition (for sequences, see Fig. 1, A and B). The core IP.BRE was used as labeled probe. As shown in Fig. 5B, lane 6, the core IP.BRE was capable of inhibiting formation of the DNA-NFI-X2 complex. In contrast, the minimal IP.BRE (−166−140), IP.BRE mutant 1, and oligonucleotides representing the NFI DNA binding sites s1−s6 did not block formation of the DNA-NFI-X2 complexes (lanes 4, 9−13 versus 3). Intriguingly, the IP.NFI (lane 8) was the more effective competitor pointing to an essential role of NFI-s2 or another site that resides in the flanking sequences. A role of NFI-s2 was revealed by the ability of IP.BRE.M2 (lane 6) to compete with the IP.BRE. IP.BRE.M2 contains a mutation in the NFI-s2, which resulted in a detectable competition although slightly less effective than that of the native core IP.BRE (Fig. 5B). To more precisely determine the roles of the potential NFI sites s2 and s7, a double mutant, IP.BRE mutant 3 that contains an additional mutation at s7, was used as competitor (Fig. 1B). It is revealing that the double mutant had almost completely lost its ability to act as competitor (Fig. 5B, lane 7) when compared with IP.BRE −166 to −116 (lane 5). We conclude that the NFI-s2 and s7 sites play more important roles than the NFI-s1 DNA binding site.

To determine the in vivo relevance of NFI-dependent repression, the infectious pHSRV13 DNA plasmid (12) was transfected with and without the hNFI-X1 expression plasmid into two different cell lines. Immunoblotting of cellular extracts revealed that pHSRV13-transfected cells expressed the viral structural proteins Gag and Pol (Fig. 6, A and B). The viral Gag proteins p70 and p68 migrated as a characteristic double band (marked by the arrow in Fig. 6A) as reported previously (11, 14), and their expression levels decreased upon cotransfection with the NFI-X1 expression plasmid. The known HFV Pol proteins p127 and p65 (11) were detected by an anti-RNase H serum (marked by two arrows in B). In extracts from cells cotransfected with hNFI-X1, the relative amounts of these Pol proteins were substantially decreased (as marked by arrows in lanes 2, 4, and 6). Importantly, the cellular lysates expressed the 36-kDa Bel1 protein after transfection with pHSRV13 as determined with an anti-Bel1/Bet serum (Fig. 6C, lanes 1 and 3).

In contrast, in cellular extracts from 293T cells cotransfected with hNFI-X1 the relative amount of Bel1 protein strongly decreased (Fig. 6C, compare lanes 1 and 3 with lanes 2 and 4). Taken together, the results indicate that in cell cultures that overexpress NFI-X1 proteins, expression of Bel1 was downregulated in agreement with our transfection data.

**Discussion**

The present report indicates that NFI-mediated repression of Bel1-driven transactivation and gene expression involves the interaction of NFI transcription factors with the retroviral internal promoter core IP.BRE. This report is the first that describes the identification of a cellular transcription factor that negatively regulates Bel1-mediated transactivation of the core IP.BRE in vitro and in cell cultures. This promoter is transactivated by Bel1, the key regulator of viral expression (7, 11−14). In transiently transfected 293T cells, different NFI proteins specifically repressed the level of Bel1-driven transactivation as assessed by luc expression assays. The level of activation and repression was dependent on the size of the promoter region. To gain insight into the mechanism of repression, we focused on the core IP.BRE region from −166 to −116 that allowed us to define the roles of NFI and Bel1 proteins in DNA binding by carrying out EMSAs, supershifts, and competition EMSAs. Several groups have reported that Bel1 binds its target sequence directly (10, 16, 23). The minimal IP.BRE of 27 bp seems to be the one with a high DNA binding affinity compared with the corresponding LTR BRE (10). Our data show that the minimal IP.BRE of 27 bp was transactivated by Bel1 to a limited extent, but it did not efficiently bind NFI proteins. Accordingly, the levels of NFI-mediated repression were relatively low when the minimal IP.BRE was used. In
contrast, the core IP.BRE possessed both higher transactivation activity and stronger NFI binding activity as assessed by luc assays and competition EMSAs. Thus, the functional and DNA binding properties of NFI are consistent for both IP.BREs. Apparently, the minimal region for optimal NFI repressor activity resides within the core IP.BRE.

It is well known that NFI proteins can act as either activators or repressors depending on the transcriptional context. The complex roles of the NFI gene products in transcription and development have been reviewed (33, 34). Expression of NFI proteins can modulate transcription by either transactivation or repression. To account for the multiple in vivo functions of NFI proteins, several models have been put forward (33). As NFI proteins act as dimers, the models include (i) recruitment of coactivators, corepressors, or RNA polymerase components, (ii) displacement of activators, repressors, or nucleosomes, and (iii) cooperative recruitment by specific NFI isoforms of adjacent DNA binding proteins. Here we will focus the discussion on repression. NFI proteins contain a highly conserved ~200-residue N-terminal DNA binding and dimerization domain. The C-terminal domains of the proteins harbor both repression and transactivation domains including a Pro-rich domain (33).

There are multiple potential models to address the formation of the different NFI-Bel1 complexes. The first is that IP.BRE DNA binds Bel1 and NFI-X2 proteins cooperatively so that the transcriptional factors affect each other; i.e. once NFI protein is bound to its DNA target site, it then affects subsequent Bel1 binding in a way that repression of the Bel1-mediated activation is achieved. This would likely require that the two binding proteins interact directly with each other. Thus, the repressive effect of NFI would be due to affects on Bel1 protein binding. However, our data provided no evidence for any direct NFI-Bel1 interaction.

An alternative hypothesis is that the core IP.BRE DNA binds the Bel1 and dimeric NFI-X2 proteins directly but independently at distinct but partially overlapping sites leading to a partial displacement of the Bel1 activator, particularly when NFI proteins were overexpressed. The presence of three different NFI half-sites within the core IP.BRE is in agreement with this assumption as it is well known that NFI proteins binds to half-sites as either homo- or heterodimers (35). However again, our data did not indicate that NFI-X2 could displace Bel1 from the full or minimal IP. BRE. A third model would predict that NFI-X2 binds to the promoter in the presence of Bel1 and recruits corepressor molecules that abolish Bel1 activation of the promoter. This model proposes as yet unidentified corepressors that NFI-X2 might recruit to the promoter. The identification of such corepressors will be an important future task. Our data also revealed that one of the DNA-Bel1 complexes might contain unknown endogenous nuclear proteins as well as endogenous NFI proteins (Fig. 5A). In supershift assays, this complex resulted in a partial supershift to a slowly migrating NFI-DNA-Bel1 complex indicating the composite nature of the DNA complexes and the possible presence of both activator and repressor proteins. The influence of other known or unknown cellular transcription factors on Bel1 activation remains to be determined. We can, however, rule out a role for C/EBPα that neither activated nor repressed Bel1-mediated transactivation of the IP.BRE.

Further studies are needed to determine the complete complement of endogenous transcription factors that influence Bel1-mediated activation of the IP.BRE.

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