The Brf and TATA-binding Protein Subunits of the RNA Polymerase III Transcription Factor IIIB Mediate Position-specific Integration of the Gypsy-like Element, Ty3*

Lynn Yieh‡§, George Kassavetis¶, E. Peter Geiduschek‖, and Suzanne B. Sandmeyer‡**

Received for publication, April 12, 2000, and in revised form, June 30, 2000
Published, JBC Papers in Press, July 5, 2000, DOI 10.1074/jbc.M003149200

Ty3 integrates into the transcription initiation sites of genes transcribed by RNA polymerase III. It is known that transcription factors (TF) IIIB and IIIC are important for recruiting Ty3 to its sites of integration upstream of tRNA genes, but that RNA polymerase III is not required. In order to investigate the respective roles of TFIIIB and TFIIIC, we have developed an in vitro integration assay in which Ty3 is targeted to the U6 small nuclear RNA gene, SNR6. Because TFIIIB can bind to the TATA box upstream of the U6 gene through contacts mediated by TATA-binding protein (TBP), TFIIIC is dispensable for in vitro transcription. Thus, this system offers an opportunity to test the role of TFIIIB independent of a requirement of TFIIIC. We demonstrate that the recombinant Brf and TBP subunits of TFIIIB, which interact over the SNR6 TATA box, direct integration at the SNR6 transcription initiation site in the absence of detectable TFIIIC or TFIIIB subunit B*. These findings suggest that the minimal requirements for pol III transcription and Ty3 integration are very similar.

Integration site selection is a key step in the retroelement life cycle, potentially influencing both the effect of the insertion on the host genome and the expression of the element itself. Similar to retroviruses, yeast Ty elements transpose through reverse transcription of an almost full-length RNA copy into a full-length DNA copy, which is integrated into the host genome. Despite very similar molecular mechanisms of integration, budding yeast elements (Tys), both gypsy-like (Ty3) and copia-like (Ty1, 2, 4, and 5), differ from retroviruses in that they exhibit dramatic global integration site preferences (1–4). Ty1 elements, for example, integrate preferentially within a window of 750 bp, upstream of genes transcribed by RNA polymerase III (pol III). Analysis of the yeast genome sequence shows that Ty2 and Ty4 also occupy this region upstream of a fraction of tRNA genes. Ty5 integrates into regions of silenced DNA, including the silent mating type loci and telomeres. Hence Ty1, Ty2, Ty4, and Ty5 exhibit regional integration specificity. Despite similarities with these other elements, Ty3 differs in that it integrates within a highly defined window, one or two base pairs (bp) upstream of pol III transcription initiation sites. Targeting of integration appears to be directed by the cooperative actions of Ty3 element- and cell-encoded factors. For example, in addition to the element-encoded integrase protein, Ty3 and Ty1 targeting requires the presence of a transcriptionally competent pol III promoter (5, 6), and Ty3 targeting requires factors involved in the establishment of silent chromatin (7).

Class III genes, including plasmid-borne U6, 5S, and tRNA genes, are used in vivo for position-specific Ty3 integration. Comparison of integration sites suggests that Ty3 integration preference is not a direct function of specific local sequences. Each class of pol III-transcribed genes differs from the others in composition of promoter elements (8) and distances of common motifs from the integration site (5). Pol III promoter mutations that affect transcription factor binding at positions distant from the integration site also block Ty3 integration (5, 9). These results lead to the hypothesis that interactions with the promoter-bound pol III transcription complex determine the selectivity of Ty3 integration sites.

Pol III genes use transcription factors (TF) IIIC and IIIB to assemble pol III at the transcription initiation site (reviewed in Ref. 8). TFIIIC is composed of six subunits and interacts with the box A and box B promoter elements. TFIIIB is composed of the TATA-binding protein (TBP), a 68-kDa protein (B* or Tfc5, also referred to as TFIIIB90), and a 67-kDa protein (Brf, also called TFIIIB70). TBP and Brf are tightly associated in a complex referred to as B*, which is chromatographically separable from B'. The contributions of these transcription factors to the specific integration of Ty3 have been investigated using an in vitro integration assay. Reconstitution of specific integration into the initiation site of a tRNA gene requires Ty3 virus-like particles (VLPs), the plasmid-borne target gene, and DEAE-purified TFIIIB- and TFIIIC-containing fractions, consistent with DNA-bound TFIIIB, or TFIIIB and TFIIIC together, recruiting the Ty3 preintegration complex to its site of integration (10). Because TFIIIC is required to load TFIIIB onto DNA at the tRNA gene promoter, the respective roles of these factors could not be distinguished using the tRNA gene target.

The roles of TFIIIB and TFIIIC in pol III transcription have been examined in detail. In vivo, TFIIIC recruits TFIIIB to the region upstream of the transcription initiation site of all yeast (Saccharomyces cerevisiae) pol III genes (11, 12). TFIIIB then recruits pol III for initiation of transcription (13, 14). Two sets of observations show that TFIIIC is the central initiation factor...
of pol III: 1) TFIIIC can be removed from tRNA genes after TFIIIB is assembled at the promoter without loss of transcription activity (13). 2) SNR6, which does not require TFIIIC for loading TFIIIB in vitro, can be transcribed by pol III in the presence of TFIIIB only (15, 16); TFIIIB components have been demonstrated to contact pol III subunits directly (17–21).

The ability to bind TFIIIB directly to the SNR6 gene in the absence of TFIIIC provides an in vitro system in which TFIIIB-bound DNA can be tested for TFIIIC-independent Ty3 targeting. In the experiments that are presented here, distinct roles for TFIIIB and TFIIIC in Ty3-specific integration have been investigated by developing a variation of a previously devised in vitro integration assay. The use of the three recombinant TFIIIB subunits, TBP, Brf, and B′ (22), allows a precise definition of the minimal protein requirements for specific integration of Ty3. We demonstrate that TFIIIB recruits the Ty3 preintegration complex to its site of integration. Recombinant B′ (i.e., TBP + Brf) is sufficient to direct specific integration of Ty3 in vitro and B′ contributes strongly to the efficiency of integration, conceivably through the DNA distortion that it generates near the integration site. TFIIIC contributes to targeting specificity and selection by determining the orientation of TFIIIB on the promoter.

EXPERIMENTAL PROCEDURES

Strains and Plasmid Constructions—Standard methods were used for culturing and transforming *Escherichia coli* and *S. cerevisiae* and for recombinant DNA constructions (23). All plasmids were amplified in and prepared from, *E. coli* HB101. Single-stranded DNA for site-directed oligonucleotide mutagenesis was prepared from *E. coli* RI2032. Plasmid pU6LboxB (24) was the pol III transcription template and target for Ty3 integration in vitro. Plasmids pDLC370 (5) and pLY1842 served as PCR controls for integration into r-U6 and l-U6, respectively. Plasmid pDLC370 has a Ty3 insertion with Ty3 sequence beginning at position –5 relative to the transcription start site r-U6. Plasmid L1842 was constructed by cloning a PCR fragment generated with primers 242 and 411 (see below) and pU6LboxB containing a Ty3 target insertion at bp –2 relative to the l-U6 TATA transcription start site (Fig. 2A) into pCRII-TOPO. The pLY1855 plasmid was generated from the 6 TATA box from pU6LboxB by site-directed mutagenesis using an oligonucleotide sequence 5′-GAAACAGATCGCGATGC-3′ with 5′-GAAACAGATCGCGATGC-3′ of DNA (50 ng) as a template. TFIIIC was supplied either as a DEAE column fraction or as a crude pol III, previously shown to inhibit Ty3 integration (33), was omitted. TFIIIB was also present, it was preincubated with DNA for 30 min before adding TFIIIB components. Samples contained 10.5 nm TFIIIC for the experiment shown in Fig. 3. For Fig. 4, samples contained the noted multiples of 0.5 nm TFIIIC. For Fig. 5A, factors were preincubated with DNA for 1 h at 23 °C prior to adding VLPs. For Fig. 5B, B′-DNA complexes were allowed to form for 30 min prior to an additional 15-min incubation with subsequently added B′. Reactions were stopped by adding phenol-K, SDS, and EDTA, pH 8.0, to final concentrations of 0.2 mg/ml, 0.2% (v/v), and 20 mM, respectively, and incubating at 37 °C for 30 min. Reaction products were extracted with phenol/chloroform, and DNA was precipitated and redissolved in 10 mM Tris-HCl, pH 8.0, 1 mM EDTA.

PCR was performed essentially as described (28), with the following changes to make detection specific to the SNR6 target: primer 242 (5′-GGAACAGATCGCGATGC-3′) (200 ng) and primer 411 (5′-CGAACACAGAACCAACC-3′) (164 ng) were used for amplification of 40 ng (18 fmol) of DNA from the integration reactions (first incubation for 2.5 min at 95 °C, followed by 40 cycles of denaturation at 94 °C for 1 min and renaturation/extension at 65 °C for 1 min, followed by 5 min at 72 °C). The standard amplification reactions in a total of 40 ng of target plasmid DNA yielded products equivalent to those of reactions containing 1.6 to 8 fg of Ty3-positive target plasmid in a total of 40 ng of target plasmid. Thus, the products are highly specific to positive plasmid templates. To control for consistent DNA recovery from the integration reaction and for consistent operation of the above PCR, primers 679 (5′-ACTCCCGTCTGTTAGATAATGC-3′) and 680 (5′-AAGCCTATCAAAACGAG-A-3′) were used to amplify the target plasmid. PCR amplification of 100 pg of DNA (5 μl of 1:200 reaction dilution) was performed using 200 ng of each primer (first denaturation for 2.5 min at 95 °C, followed by 18 cycles of denaturation at 94 °C for 45 s, renaturation at 55 °C for 30 s, and extension at 72°C for 30 s, with a final 5 min at 72°C). PCR products were resolved by electrophoresis on nondenaturing, 8% polyacrylamide gels and visualized by staining with ethidium bromide. The fluorescence video image was quantified using a gel documentation program.

Cloning of Specific Integration Products—PCR fragments representing specific integrations were separated as described above. Bands containing specific fragments were excised from the gel, DNA was eluted, ligated into the vector pCRII-TOPO according to the supplier’s instructions, and transformed into *E. coli*. Individual transformants, selected on LB + ampicillin, were picked for analysis. DNA was prepared from five transformants per band and sequenced with oligonucleotide 242 primer.

RESULTS

Ty3 in Vitro Integration Upstream of the SNR6 Gene Is Detectable by PCR Amplification—In order to investigate whether TFIIIB suffices for Ty3 position-specific integration, a previously used *in vitro* tRNA gene integration assay (10) was modified to utilize SNR6 as a target. Integration reactions contained Ty3 VLPs, the *S. cerevisiae* SNR6 gene in plasmid pU6LboxB (24), and combinations of TFIIIB and TFIIIC. Pol III, previously shown to inhibit Ty3 integration (33), was omitted. TFIIIC was supplied either as a DEAE column fraction or as highly purified protein (27); TFIIIB was added either as a DEAE fraction or as recombinant protein (35).

Integration of Ty3 into the target plasmid was detected using a polynucleotide chain reaction (PCR)-based assay (Fig. 1A). One PCR primer anneals to the SNR6 gene and the other to a unique sequence in Ty3. A diagnostic PCR template sequence is created when Ty3 integrates into the SNR6 target in one of the two possible orientations, and the length of the corresponding PCR-amplified fragment specifies the position of integration.

This assay differs from the previously described tRNA gene assay (10) in that the target primer does not overlap with the
Ty3 insertion, so that detection of integration is not limited to a single location; additional rounds of PCR are used to increase assay sensitivity.

The integration assay uses the plasmid pU6LboxB, which contains a modified SNR6 gene with altered flanking DNA sequence (24) as its Ty3 target. A duplication of the SNR6 transcriptional start site and terminator in pU6LboxB allows TFIIIB-DNA complexes oriented to promote transcription from leftward to rightward (Fig. 1A) on this template. In constructing pU6LboxB, the SNR6 TATA box was inverted to preferentially orient TFIIIB for leftward transcription, and the boxB promoter element was moved closer to the natural SNR6 boxA promoter element in order to optimize the ability of TFIIIC to direct TFIIIB binding at the SNR6 TATA box. TFIIIC shifts the preferred direction of transcription from leftward to rightward (Fig. 1B) on this template. In constructing pU6LboxB, genomic sequence upstream of the SNR6 TATA box containing a Ty1 LTR (or δ element) was deleted, positioning a second TATA box (which originally flanked the SNR6 gene-distal end of the δ element) between the SNR6 TATA box and the terminator for leftward transcription. This “δ TATA box” (identical in sequence and orientation to the SNR6 TATA box in pU6LboxB) generates its own pair of divergent transcription units. Thus, TFIIIB binding autonomously to either TATA box of pU6LboxB in either orientation generates four primary transcripts (l-U6, r-U6, l-δ, and r-δ in Fig. 1B). By selecting the site and orientation of TFIIIB binding, TFIIIC favors the formation of the r-U6 transcript and restricts the formation of the others (Ref. 24 and data not shown).

The ability to reconstitute specific integration of Ty3 upstream of SNR6 in vitro was first tested using DEAE column fractions enriched for TFIIIB and TFIIIC. Plasmid pDLC370 (“Experimental Procedures”), which contains a Ty3 insertion, was used as a template for primers 411 and 242 in PCR to amplify a 442-bp fragment that served as a positive control for integration into the r-U6 initiation site (9). As a control for the quantity of DNA in each reaction, primers 679 and 680 were also used to amplify the β-lactamase gene on pU6LboxB. PCR products were separated by non-denaturing polyacrylamide gel electrophoresis. Reconstitution of integration at the SNR6 gene in these preliminary trials (data not shown) depended on the presence of Ty3 VLPs, as PCR amplification of reactions lacking VLPs was equivalent to amplification of the target plasmid alone. Integration reactions performed with TFIIIB and TFIIIC generated a predominant PCR product, whose length was consistent with specific integration close to the r-U6 transcription initiation site (Fig. 2A). A random (or at least complex and dispersed) pattern of integration was observed with Ty3 VLPs alone (Fig. 2B). Comprehensive TFIIIB Directs Specific Integration of Ty3 in Vitro—The advantage of the relatively complex pU6LboxB construct is that it permits a determination of whether TFIIIB alone suffices to mediate Ty3-specific integration, while also examining whether TFIIIC exerts an effect on integration site selection. The binding of rTFIIIB to the target plasmid was verified by its ability to direct transcription by pol III in vitro. The four expected transcription products were generated, with preferential production of the l-U6 transcript, as expected (data not shown). Integration at the four transcription initiation sites is predicted to produce four different classes of PCR products (Fig. 2A). Integrations were performed under conditions tested for transcription activity, and with comparable concentrations and proportions of rTFIIIB and plasmid DNA (Fig. 2B and data not shown). The combination of rTFIIIB and TFIIIC yielded a single PCR-amplified integration product (Fig. 2B, lane 3). Integration in the presence of rTFIIIB alone generated three major PCR products (lane 4) each consistent in size with integration at one of the four transcription initiation sites (Fig. 2A); the size of the smallest PCR fragment corresponded with an integration event near the initiation site of r-U6 transcription (Fig. 2B, compare lane 4 to lanes 3 and 5). The sizes of the remaining products corresponded to PCR templates generated by specific integration very close to the l-δ (lane 4, largest fragment, ~552 bp), and r-δ and l-U6 (middle size fragment, ~492 and ~501 bp) transcription initiation sites, respectively.

To determine whether these PCR products indeed report specific integration events, DNA fragments contained in the bands marked at the side of Fig. 2B were recovered from a gel (cf. Fig. 2B, lane 4) and cloned into the vector pCRII-TOPO. Sequences were determined for the Ty3-SNR6 junction in five clones from each fragment preparation using the SNR6 internal PCR primer (Fig. 2A). Sequencing of these clones demonstrated that the smallest fragment corresponds to Ty3 sequence beginning at positions −6 and −7 relative to the r-U6 transcription start site (Fig. 2C). Because Ty3 integrates by means of a staggered strand transfer that is repaired, resulting in repeats of the intervening sequence on either end of the Ty3, this corresponds to a gene-proximal strand transfer between positions 1 and −1 and between −1 and −2, respectively, relative to the start site of transcription. The middle fragment appears to represent integration events at the l-U6 and/or r-δ transcription initiation sites. The identified integration sites in this region showed Ty3 sequence positioned at −2 and +5...
with a Ty3 insertion at the r-U6 start site was used as the PCR template. The patterned arrowheads indicate the correspondence with positions of insertion shown in A, C, fragments indicated by arrowheads in B were cloned, sequenced determined, and Ty3 insertion sites deduced. Dots indicate the first base of Ty3 sequence in sequence primed with the wild-type and mutated targets. Addition of TFIIIC changed the pattern of integration into the reference target, as already noted (Fig. 2B), but left the pattern of Ty3 integration into the C56 G mutant target essentially unchanged from integration mediated by TFIIIB alone (Fig. 3, lanes 2–4) and its mutated derivative in pU6LboxB-G56 (lanes 6–8) were compared. Similar patterns of specific integration mediated by rTFIIIB (compare lanes 3 and 7) and of nonspecific integration in the absence of TFIIIC (compare lanes 2 and 6) were seen with the wild-type and mutated targets. Addition of TFIIIC changed the pattern of integration into the reference target, as already noted (Fig. 2B), but left the pattern of Ty3 integration into the C56 G mutant target essentially unchanged from integration mediated by TFIIIB alone (Fig. 3, compare lane 8 with lanes 3 and 7). If sufficient TFIIIC had been present in Ty3 VLPs to affect integration of Ty3 into the wild-type target, then the pattern of integration in the presence (lane 4) and absence (lane 3) of additional TFIIIC should have been similar, and the patterns of integration into the reference and C56 G mutant DNA (lanes 3 and 7, respectively) should have been entirely different. In each instance, the observed pattern was entirely consistent with the conclusion that TFIIIC was not significantly contributed by the VLP fraction.

Previous experiments showed that TFIIIC loads TFIIIB in the rightward orientation on the U6 promoter (24). In pU6LboxB, TFIIIB alone binds the TATA box preferentially in the absence of TFIIIC, because of a 5-base offset in the initiating, staggered two-strand attack from the TATA box. Induced. B in Fig. 2B, lanes 3 and 4) because the l-\( \delta \) integration site is over 120 bp away from boxA. Nevertheless, the possible dependence of integration on TFIIIC contributed by the Ty3 VLP fraction was addressed by introducing a C56 G mutation into the boxB sequence of pU6LboxB to create plasmid pU6LboxB-G56. The boxB element is the primary, high affinity TFIIIC-binding site of pol III-transcribed genes, and the C56 G mutation has been shown to abrogate TFIIIC binding to tRNA and U6 gene promoters (34–36). Thus, TFIIIC-dependent integration into pU6LboxB should be decreased by the C56 G mutation, but TFIIIC-independent integration should not be affected.

Integration into the reference target in pU6LboxB (Fig. 3, lanes 2–4) and its mutated derivative in pU6LboxB-G56 (lanes 6–8) were compared. Similar patterns of specific integration mediated by rTFIIIB (compare lanes 3 and 7) and of nonspecific integration in the absence of TFIIIC (compare lanes 2 and 6) were seen with the wild-type and mutated targets. Addition of TFIIIC changed the pattern of integration into the reference target, as already noted (Fig. 2B), but left the pattern of Ty3 integration into the C56 G mutant target essentially unchanged from integration mediated by TFIIIB alone (Fig. 3, compare lane 8 with lanes 3 and 7). If sufficient TFIIIC had been present in Ty3 VLPs to affect integration of Ty3 into the wild-type target, then the pattern of integration in the presence (lane 4) and absence (lane 3) of additional TFIIIC should have been similar, and the patterns of integration into the reference and C56 G mutant DNA (lanes 3 and 7, respectively) should have been entirely different. In each instance, the observed pattern was entirely consistent with the conclusion that TFIIIC was not significantly contributed by the VLP fraction.

Previous experiments showed that TFIIIC loads TFIIIB in the rightward orientation on the U6 promoter (24). In pU6LboxB, TFIIIB alone binds the TATA box preferentially in

**FIG. 2.** Recombinant TFIIIB mediates specific integration in the absence of TFIIIC. A, Ty3 integration into pU6LboxB. Four positions of specific Ty3 integration mediated by rTFIIIB are indicated with triangles and labeled according to the transcription start site used as a target. The location of the Ty3 PCR primer that was used to amplify each of these integration events (in one orientation only) is represented by a pattern-filled arrow. The common primer in the U6 sequence is shown by a dashed line. The predicted sizes of PCR products reporting each integration event are indicated. B, determination of integration sites in pU6LboxB by analysis of PCR products. Products of integration reactions were used to template PCR; input proteins are indicated. The patterned arrowheads indicate the correspondence with positions of insertion shown in A, C, fragments indicated by arrowheads in B were cloned, sequenced determined, and Ty3 insertion sites deduced. Dots indicate the first base of Ty3 sequence in sequence primed with the wild-type and mutated targets. Addition of TFIIIC changed the pattern of integration into the reference target, as already noted (Fig. 2B), but left the pattern of Ty3 integration into the C56 G mutant target essentially unchanged from integration mediated by TFIIIB alone (Fig. 3, compare lane 8 with lanes 3 and 7). If sufficient TFIIIC had been present in Ty3 VLPs to affect integration of Ty3 into the wild-type target, then the pattern of integration in the presence (lane 4) and absence (lane 3) of additional TFIIIC should have been similar, and the patterns of integration into the reference and C56 G mutant DNA (lanes 3 and 7, respectively) should have been entirely different. In each instance, the observed pattern was entirely consistent with the conclusion that TFIIIC was not significantly contributed by the VLP fraction.

Previous experiments showed that TFIIIC loads TFIIIB in the rightward orientation on the U6 promoter (24). In pU6LboxB, TFIIIB alone binds the TATA box preferentially in
the orientation that directs leftward transcription. TFIIIC stabilizes TFIIIB binding in the opposite orientation, and transcription preference switches accordingly. The results shown in Fig. 3 suggest that, although TFIIIC is not absolutely required for Ty3 integration into DNA, it influences Ty3 integration site preference. In order to better assess this effect, highly purified TFIIIC was titrated into integration reactions performed at one concentration of rTFIIIB. In the presence of TFIIIB only, integration was seen to be distributed among the transcription initiation sites with a preference for integration at I-U6 (and/or r-U6) (Fig. 4, lane 3). Increasing amounts of TFIIIC (lanes 4–7) progressively shifted integration preference to the r-U6 transcription initiation region; specific integration was dependent on the presence of rTFIIIB (compare lanes 2 and 8 with lanes 3–7). The change in integration pattern observed in Fig. 4 correlated directly with TFIIIC-dependent changes in transcription (data not shown, but see Ref. 37). Thus, TFIIIC affects Ty3 integration in vitro, by dictating the location and polarity of TFIIIB binding at a pol III promoter.

B′ (TBP and Brf) Bound to DNA Is the Minimal Target for Ty3 Integration—Since recent experiments have shown that the B′-DNA complex is sufficient to mediate pol III transcription of templates with partly preopened promoters (38) it was of interest to explore whether any TFIIIB subunit or pair of subunits can also mediate Ty3 integration. In order to simplify the analysis, the δ TATA was deleted from pU6LboxB to create the SNR6 target plasmid LY1855.

Subunits of TFIIIB bind to DNA in an ordered manner (14, 26, 39). In the absence of TFIIIC, TBP binds directly to the TATA box, Brf modestly stabilizes TBP binding (40) to form the B′-DNA complex, and B′ addition generates the hyper-stable DNA complex that mediates pol III transcription to duplex DNA and confers DNase I hypersensitivity at the transcription initiation site. Single TFIIIB subunits and pairs of subunits were tested for their ability to direct integration. At concentrations used in the standard assay, that is in the presence of the entire TFIIIB complex, specific integration was not detected (data not shown). Increased concentrations of protein were also tested, but none of the rTFIIIB components was individually able to reconstitute integration (Fig. 5A, lanes 2–4). However, the combination of TBP and Brf (B′) sufficed to mediate specific integration (lanes 5 and 6) with a preference for the I-U6 gene start site. Integration mediated by B′ required higher concentrations of TBP and Brf (compare lanes 5, 6, and 11), as well as longer times of preincubation of recombinant protein with DNA than did integration mediated by TFIIIB. Other combinations of subunits (lanes 7–10) and the individual subunits (lanes 7–10) were incapable of directing specific integration even at elevated concentrations.

B′ Increases the Efficiency of Ty3 Integration—A firm conclusion that the B′-DNA complex recruits Ty3 to its integration site requires proof that VLPs do not constitute a significant source of B′. It was necessary first to estimate the amount of B′ that would have to be contributed to generate the observed integration. Integration in the absence of added rB′ was first compared with different amounts of rB′ (Fig. 5B, lanes 6 and 7). A significant level of integration was observed with 10-fold the standard amount of rB′ (×10 = 500 fmol of TBP and 360 fmol of Brf) (Fig. 5B, lane 7). The rB′ was then assayed over the range of 1 to 0.03 times the standard amount (75–2.8 fmol) with B′ preincubated and B′ added subsequently (lanes 2–5) to correspond with the effective order of addition that would prevail if B′ were contributed by the VLP preparation. The yield of PCR products was quantified as a function of added rB′. This analysis specified that, if B′ were absolutely required for the observed Ty3 integration and contributed solely by the VLP fraction, 5 μg of VLPs (the amount in a standard assay) would have to contain 12.5 fmol of active B′. The upper limit of B′ in the VLP fraction was then established in three ways. The most direct, but least sensitive estimate was provided by immunoblot analysis. Two relatively sensitive functional and structural assays for B′ were also used.

For immunoblotting, 10-μg aliquots of VLP (twice the amount used in the standard integration reaction) were fractionated by SDS-polyacrylamide gel electrophoresis together with His-tagged rB′ (5–80 fmol) and crude fraction (BR500), containing native B′, as standards, probed with B′ antiserum and developed with 125I-protein A (Fig. 6A). Radioactivity at the position of B′ was quantified (data not shown). The 5 fmol
Fig. 6. VLPs do not contain B'. A, immunoblot analysis. To titrate the sensitivity of the immunoblot, 5, 10, 20, 40, and 80 fmol of B' (lanes 1–5, respectively) were tested as described under “Experimental Procedures.” Because rB' is His tagged and therefore has slightly reduced mobility relative to native B', BR500 was also used to provide an accurate B' size marker (lane 6). Ten μg of VLP, twice the amount present in the standard reaction, was assayed for lane 7. B, VLPs do not contribute cross-linkable B'-DNA complexes with an internally labeled oligonucleotide duplex representing SNR6 were allowed to form, followed by the addition of 40–125 fmol of B' (lanes 1–6), no additional protein (lane 7), 5 μg of VLPs (lane 8), or 5 μg of VLPs with B' (lanes 9 and 10). The probe was also reacted in the absence of B' with 5 μg of VLPs. Cross-linked B' and Brf are indicated with arrows.

of B' standard was barely detectable above background, and 10 fmol was readily detected. Significant cross-reactive protein in the VLP fraction (lane 7) migrated faster than the native B' (lane 6). The PhosphorImager profile of lane 7 did not display a peak above background that would be predicted for the presence of ≥10 fmol of native B', limiting the B' contribution from the VLPs in the integration assay to <5 fmol. Nevertheless, because the detection limit of the immunoblot analysis was close to the possible B' threshold set by the Fig. 5 experiment, two further tests for the presence of B' were devised.

The first test was based on the fact that entry of B' into the B'-DNA complex generates a heparin-resistant TFIIIB-DNA complex that can be sensitively detected by electrophoretic mobility shift assay with a labeled TATA box-containing DNA probe (41). Addition of as little as 2.8 fmol of B' to pre-formed B'-DNA complexes generated readily detectable heparin-resistant TFIIIB-DNA complexes, and preincubation of B' with VLPs did not prevent formation of these complexes. Addition of twice the amount of VLPs used in the integration assays to B'-DNA complexes failed to generate any heparin-resistant TFIIIB-DNA complexes, signifying that 5 μg of VLPs could at most contribute 1.4 fmol of complex-forming B' (data not shown).

The second test detected B' in the TFIIIB-DNA complex by site-specific photochemical cross-linking (32, 42, 43). B' lies proximal to the major groove at bp −39 and −38 of the SNR6 gene (31) such that incorporation of the photoactive nucleotide 5′-[N-(p-azidobenzoyl)-3-aminoallyl]dUMP at these positions with an adjacent radioactively labeled nucleotide readily detects 1.25 fmol of B' upon TFIIIB-DNA complex formation, UV irradiation, nuclease digestion (transferring the radioactive DNA label to the cross-linked protein), and SDS-polyacrylamide gel electrophoresis (Fig. 6B, lane 6). Because the DNA-binding reaction mixtures contained only low levels of a non-specific DNA carrier, the binding of 5 μg of VLPs alone to this DNA probe yielded cross-linking to four proteins (lane 11), one of which migrated slightly more slowly than recombinant B' and one slightly faster than Brf. These cross-linking signals did not increase in the presence of B'-DNA or TFIIIB-DNA complexes (compare lane 11 with lanes 8 and 10). Addition of 5 μg of VLPs to the B'-DNA complex generated a very weak signal at the position of the B' band, corresponding in intensity (by PhosphorImager analysis) to less than 0.3 fmol of B' (lane 8). However, summation of the PhosphorImager signals of the B'-alone (lane 7) and VLP-alone (lane 11) samples indicated that even this very weak apparent B' signal derived solely from the B'-DNA complex and that it was made perceptible by the background density contributed by VLPs (analysis not shown). The VLP-dependent increase in cross-linking signal at the Brf band in lane 8 derived from the same cause. Additional analysis of the extremely weak signal overlapping the B' band in lane 7 indicated that it was an extraneous, multicross-link product, highly sensitive to TBP concentration and UV dosage. Since preincubation of B' with VLPs did not prevent B'-cross-linking (lanes 9 and 10), this analysis established that 5 μg of VLPs (conservatively) contained less than 0.3 fmol of B'. This is at most 40-fold less B' than required to account for the Ty3 integration observed in Fig. 5B as a B'-requiring process. We conclude that specific Ty3 integration is not absolutely dependent on the B' component of TFIIIB.

However, B' does increase the level of Ty3 integration and it can also change the distribution of integration sites. Preincubating B' and B' together with DNA before adding VLPs favored integration at the r-U6 site (Fig. 5A, compare lanes 6 and 12), which would be created by TBP bound in its less favored orientation. This is reminiscent of previous demonstrations that B' can freeze the orientation of B' (TBP + Brf) on DNA in non-equilibrium distributions (44). An order-of-addition experiment (based on Fig. 5B) was designed to determine whether the changes in the distribution of Ty3 integration events upon addition of B' could be explained similarly. Integration reactions were performed using target pLY1855, constant B', and varying quantities of B'. In one-half of the experiment, B' was preincubated with the target DNA before addition of B' (Fig. 5B, lanes 2–5). In the other half, B' was added simultaneously with B'. The pattern of integration did depend on the order of addition: preincubating B' with DNA before adding B' favored integration into the l-U6 region (lanes 2–5); when B' was not preincubated with DNA, integration occurred equivalently at the l- and r-U6 regions (Fig. 5A, lanes 11 and 12 and data not shown). In all cases, higher levels of B' generated more integration.

These results suggest that the left-right integration site selection of Ty3 reflects the bias in orientation of TBP on DNA. B' does not influence the direction of B' binding per se; rather, it stabilizes the B' complex on DNA regardless of orientation. Parallel observations have been made on transcription polarity. Part of the enhanced efficiency of Ty3 integration that is contributed by B' may be attributable to more efficient DNA complex formation, but it is likely that B' also makes a direct structural contribution to Ty3 integration, as discussed below.

DISCUSSION

Ty3 transposition targets the pol III transcription machinery. In this work, we precisely define this connection by showing that TFIIIB is the essential cellular factor of Ty3 transposition. TFIIIC is dispensable for position-specific integration in vitro into a U6 RNA gene target, presented as bare duplex DNA.

In order to identify the contributions of components of the TFIIIB-DNA complex to Ty3 targeting, the abilities of individ-
ual and pairwise combinations of the transcription factor subunits to mediate integration have been tested. TBP and Brf constitute the B′ component of TFIIIB and bind DNA as a complex. Together with VLPs, the B′-DNA complex generates a modest level of integration. The possibility that contamination of the VLP complex with B′ contributes to this basal activity has been excluded. It has been shown recently that specifically initiating, B′-independent pol III transcription occurs on SNR6 templates containing a partially preopened promoter (made by creating a short heteroduplex loop upstream of the transcription initiation site) (38). These results argue that similar targeting interactions are central to position-specific Ty3 integration and pol III transcription.

The locations of transcription factor components on DNA and their protein-protein interactions provide clues to potential interactions between TFIIIB subunits and the Ty3 preintegration complex. Brf contacts DNA near the site of Ty3 integration (26, 42). The primary contacts between TFIIIB and pol III are mediated by Brf (17–19, 21). Within TFIIIB Brf is oriented so that a conserved C-terminal region interacts with TBP. The N-proximal TFIIIB-like half of Brf interacts with the C34 and C17 subunits of pol III (17, 19, 26, 45). The C-terminal half of Brf also contacts C34 (19). Although there is no striking similarity between the sequences of Ty3 reverse transcriptase or integrase and C17 or C34 (analysis not shown), pol III inhibits Ty3 integration in vitro (33). A direct competition between the Ty3 preintegration complex and pol III for overlapping sites in the N-terminal region of Brf could help to explain this inhibitory effect of pol III.

The increased sensitivity developed for detecting Ty3 integration into the SNR6 target has also made it possible to demonstrate that Ty3 VLPs produce integration products when incubated together with naked DNA. These products differ significantly from the specific integration products observed in the presence of pol III transcription factors. Thus, the Ty3 preintegration complex apparently retains the ability to target a range of sites in naked DNA. This is a characteristic of nonspecific retroelements.

Although B′ is not absolutely required for in vitro integration, it does strongly affect the efficiency of the integration reaction. Significant conformational changes occur upon addition of B′ to the B′-DNA complex, including the introduction of an additional bend between the TATA box and the transcriptional start site (46). B′ also generates increased DNase I sensitivity at the transcriptional start site, suggesting a role for B′ in facilitating promoter opening (31). Melting of duplex DNA at the start site appears to require interactions between Brf and B′, since mutations in either subunit can cause deficiencies in promoter opening (31). Ty3 introduces its strand transfers at few base pairs downstream of the start site of transcription (46). B′ may also induce a structure that is conductive to Ty3 integration. The contributions of protein docking domains and DNA structure to Ty3 targeting can now be dissected, using the SNR6 integration assay and characterized Brf and TBP mutants in conjunction with TFIIIB-independent DNA structures.

Acknowledgments—We thank Charles Connolly for helpful discussions that contributed to development of the integration assay. Garth Lettsa for additional photographic cross-linking analyses, and Michael Aye for communication of results prior to publication.

REFERENCES


2 M. Aye, personal communication.
The Brf and TATA-binding Protein Subunits of the RNA Polymerase III Transcription Factor IIB Mediate Position-specific Integration of the Gypsy-like Element, Ty3

Lynn Yieh, George Kassavetis, E. Peter Geiduschek and Suzanne B. Sandmeyer

doi: 10.1074/jbc.M003149200 originally published online July 5, 2000

Access the most updated version of this article at doi: 10.1074/jbc.M003149200

Alerts:
• When this article is cited
• When a correction for this article is posted

Click here to choose from all of JBC's e-mail alerts

This article cites 51 references, 35 of which can be accessed free at http://www.jbc.org/content/275/38/29800.full.html#ref-list-1