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RbpA relaxes promoter selectivity of *M. tuberculosis* RNA polymerase

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ABSTRACT

The transcriptional activator RbpA associates with *Mycobacterium tuberculosis* RNA polymerase (*MtbrNAP*) during transcription initiation, and stimulates formation of the *MtbrNAP*-promoter open complex (RPo). Here, we explored the influence of promoter motifs on RbpA-mediated activation of *MtbrNAP* containing the stress-response \(\sigma^B\) subunit. We show that both the ‘extended −10’ promoter motif (T\(_{-17}\)G\(_{16}\)T\(_{-15}\)G\(_{14}\)) and RbpA stabilized RPo and allowed promoter opening at suboptimal temperatures. Furthermore, in the presence of the T\(_{-17}\)G\(_{16}\)T\(_{-15}\)G\(_{14}\) motif, RbpA was dispensable for RNA synthesis initiation, while exerting a stabilization effect on RPo. On the other hand, RbpA compensated for the lack of sequence-specific interactions of domains 3 and 4 of \(\sigma^B\) with the extended −10 and the −35 motifs, respectively. Mutations of the positively charged residues K73, K74 and R79 in RbpA basic linker (BL) had little effect on RPo formation, but affected *MtbrNAP* capacity for de novo transcription initiation. We propose that RbpA stimulates transcription by strengthening the non-specific interaction of the \(\sigma\) subunit with promoter DNA upstream of the −10 element, and by indirectly optimizing *MtbrNAP* interaction with initiation substrates. Consequently, RbpA renders *MtbrNAP* promiscuous in promoter selection, thus compensating for the weak conservation of the −35 motif in mycobacteria.

INTRODUCTION

In bacteria, transcription is performed by the multi-subunit DNA-dependent RNA polymerase (RNAP) that is composed of the catalytic core (E, subunits 2αββ′\(ω\)) and the \(\sigma\) subunit, required for promoter-specific initiation of RNA synthesis (reviewed in (1,2)). During exponential growth, expression of most genes is controlled by the housekeeping (principal) \(\sigma\) subunit (\(\sigma^70\) in *Escherichia coli*, and \(\sigma^A\) in *Mycobacterium tuberculosis*) that belongs to the Group 1 \(\sigma\) subunits. Alternative Group 2 \(\sigma\) subunits (\(\sigma^5\) in *E. coli*, and \(\sigma^B\) in *M. tuberculosis*) are the most similar to the principal \(\sigma\) subunit, and are responsible for the expression of specialized genes in response to stress, during the stationary growth phase and dormancy (3,4).

Most bacterial promoters recognized by Group 1 and 2 \(\sigma\) subunits belong to the −10/−35 class and contain two consensus elements: the −10 element (*E. coli* consensus motif: T\(_{12}\)A\(_{11}\)T\(_{-10}\)A\(_{9}\)A\(_{8}\)T\(_{7}\)) and the −35 element (*E. coli* consensus motif: T\(_{-35}\)T\(_{34}\)G\(_{33}\)A\(_{32}\)C\(_{31}\)A\(_{30}\)). These motifs are recognized by domain 2 (\(\sigma^2\)) and 4 (\(\sigma^4\)) of the \(\sigma\) subunit, respectively. The ‘extended −10’ class of promoters contains the extended −10 motif (T\(_{17}\)R\(_{16}\)T\(_{-15}\)G\(_{14}\); \(R = \text{purine}\)) that is located one nucleotide upstream of the −10 element (5–7) and is recognized by domain 3 of the \(\sigma\) subunit (\(\sigma^3\)). It has been shown that the extended −10 motif bypasses the requirement of the \(\sigma^4\)-35 element interaction (8,9). The percentage of promoters containing at least the downstream part of the extended −10 motif (T\(_{-15}\)G\(_{14}\)) varies among bacteria, from ∼18\% in *E. coli* to ∼45\% in *Bacillus subtilis* (6,7,10).

During transcription initiation, RNAP binds to the promoter and forms an unstable ‘closed complex’ (RPe) that isomerizes spontaneously into a transcriptionally competent ‘open complex’ (RPo) through the formation of several intermediate complexes (RPI) (11–13). The concerted action of the RNAP core and \(\sigma\) subunit triggers the opening of ∼13 bp of the promoter DNA around the transcription start site, and makes the single-stranded DNA template available for initiation of RNA synthesis (14–16).

*M. tuberculosis* RNAP (*MtbrNAP*) differs from the extensively studied *E. coli* RNAP because it requires auxiliary factors (CarD and RbpA) to form stable RPo on house-
keeping gene promoters (17,18). RbpA is a global transcriptional activator essential for *M. tuberculosis* growth, and could be implicated in the control of its physiological state (19–22). RbpA selectively binds to the σ^B^ and σ^A^ subunits of *Mtb*RNAP and stimulates RPo formation (19,23,24). It has been shown that the stress-response σ^B^-*Mtb*RNAP displays stronger dependence on RbpA than σ^A^-*Mtb*RNAP (24).

Structural studies demonstrated that RbpA C-terminal domain interacts with σ^2^ via its σ-interacting domain (SID), whereas RbpA basic linker (BL) interacts with promoter sequences upstream of the −10 element (25,26). RbpA seems not to recognize any DNA motif, although its requirement for transcription has been shown to be promoter sequence-dependent (18,24). Indeed, RbpA is required for the stable binding of σ^B^-*Mtb*RNAP at promoters of the −10/−35 (rrnAP3, sigAP, lacUV5) and extended −10 class (galP1icons) (24). However, it is dispensable for RPo formation at the extended −10 class sinP3 promoter of *B. subtilis* (24). Recently, we demonstrated that RbpA stabilizes the ‘open’ conformation of the σ^B^ subunit in *Mtb*RNAP. This is optimal for recognition of the −10/−35 promoters, but is dispensable for recognition of the extended −10 promoters (27).

Here, to better understand the molecular basis of this promoter specificity, we explored the effect of mutations in σ^B^ and RbpA on *Mtb*RNAP activity at promoter variants that harbor different combinations of the extended −10 and −35 motifs. We found that interaction between domain 3 of σ^B^ and the extended −10 motif strongly influences *Mtb*RNAP activity, but has no effect on its ability to respond to RbpA activation. Furthermore, we found that RbpA modulates *Mtb*RNAP selectivity for nucleotide substrates.

**MATERIALS AND METHODS**

*Proteins and DNA fragments*  
*Mtb*RNAP, the σ^B^ subunit and RbpA were expressed and purified as described before (24). Mutations in σ^B^ and RbpA were introduced using the Agilent Quick Change Lightning Site-directed Mutagenesis Kit, following the manufacturer’s protocol. Variants of the sigAP promoter were prepared by annealing two oligonucleotides followed by primer extension and PCR amplification with Pfu using fluorescent primers (Table S1). The amplified promoter DNA fragments were resolved by 5% native PAGE and extracted using the Nucleospin® Gel and PCR Clean-up Kit (Macherey Nagel). The sigAP-TGTG promoter labeled with Cy3 at the +2 position was purified through 6% PAGE after primer extension.

**EMSA and KMnO₄ probing**

Core *Mtb*RNAP (100 nM) was mixed with σ^B^ (300 nM) and RbpA (300 nM) in transcription buffer (TB, 40 mM HEPES pH 8.0, 50 mM NaCl, 5 mM MgCl₂, and 5% glycerol) and incubated at 37°C for 10 min. Then, fluorescein-labeled promoter DNA (50 nM) was added and samples were incubated at 37°C for 10 min. The competitor poly(dA-dT) was added to a final concentration of 20 ng/μl and incubated at 37°C for 5 min. Samples were resolved on 6% native PAGE in 1x TBE buffer. Gels were scanned with an Amersham Imager 600 (GE Healthcare) and quantified using the ImageQuant software. For KMnO₄ probing experiments, 5 mM KMnO₄ was added to the reaction mixtures formed at the indicated temperatures for 30 s, and quenched by addition of 1 M β-mercaptoethanol, 1.5 M Na(CH₃COO) pH 7.0. Reactions were incubated with 0.5 M piperidine at 90°C for 15 min, and DNA fragments were precipitated by adding 1/10 volume of 5 M LiCl and 4 volumes of ice-cold ethanol. Precipitated DNA fragments were washed with 80% ethanol, vacuum-dried, dissolved in 90% formamide and analyzed on 8% sequencing gels. Gels were scanned with a Typhoon 9400 Imager (GE Healthcare) and quantified using the ImageQuant software. Graphs were plotted using the Graphpad7 and Grace-5.1.23 software (http://plasma-gate.weizmann.ac.il/Grace/) software. The apparent dissociation constants (K_d) were calculated from equation:  
\[
RP = A_0[RNAP]/(\{RNAP\} + K_d),
\]
where RP is the RNAP fraction bound to DNA.

**Transcription assays**

Multiple-round transcription assays were performed in 10 μl of TB with 50 μM each of ATP, GTP, CTP, 5 μM of UTP and 0.5 μM of [α^32P]-UTP at 37°C for 5 min. The GpC primer (Eurogentec) was added to 100 μM, when indicated.

Single-round transcription assays, to monitor RPo formation, were performed in 10 μl of TB. First, 180 nM *Mtb*RNAP core, 590 nM σ^B^ and 590 nM RbpA were mixed and incubated at 37°C for 5 min. After addition of 50 nM of promoter DNA, samples were incubated at 37°C for 1, 2, 3, 5 and 10 min. Transcription was initiated by adding 50 μM each of ATP, GTP, CTP, 10 μM of UTP, 0.5 μM of [α^32P]-UTP and poly(dI-dC) (0.1 mg/ml final concentration) and performed at 37°C for 3 min. Single-round transcription assays, to monitor promoter escape, were performed using the same conditions as for RPo formation. *Mtb*RNAP-promoter complexes were incubated at 37°C for 15 min (longer incubation at 37°C resulted in *Mtb*RNAP inactivation). Then, after addition of the NTPs/poly(dI-dC) mixture, transcription was performed for 0.5, 1, 2, 5 and 10 min. Abortive transcription assays using the lacUV5 bubble template (28) were performed in 10 μl of TB. First, 180 nM *Mtb*RNAP core was mixed with 590 nM σ^B^ or 1 μM σ^B^Δ4 and incubated at 37°C for 5 min. Then, 50 nM bubble DNA was added and incubated at room temperature (RT; 22°C) for 15 min. After addition of 0.5 mM ApA, 100 μM GTP, and 0.5 μM of [α^32P]-UTP, samples were incubated at RT for 10 min, and then reactions were stopped by addition of an equal volume of 7M urea/100 mM EDTA solution. RNA transcripts were analyzed on denaturing 18% PAGE/7M urea gels. Gels were scanned with a Molecular Dynamics STORM Imager. Bands were quantified using the ImageQuant software. For kinetics experiments, raw data were fitted in Grace-5.1.23 using the mono-exponential function  
\[
A_t = A_\infty + A_0 \cdot \exp(-k \cdot t),
\]
where  \(A_t\) is the radioactive RNA signal at the time point  \(t\). The  \(A_\infty\) values determined from the fits were used for data normalization in each experimental set. Normalized data were used to calculate the mean and standard error (SE) values shown in...
Fluorescent assay to determine the dissociation kinetics

Assays were performed in 60 μl of TB; 50 nM of RNAP was mixed with 5 nM of the sigA promoter fragment labeled with Cy3 at position +2 of the non-template DNA strand and incubated at 37°C for 10 min. To initiate dissociation of the MtbRNAP-promoter complexes, heparin was added to 10 ng/μl. Data were acquired using a PTI Quanta-Master spectrophotometer at room temperature. Data were fitted using the following bi-exponential equation: \( A_t = A_0 + A_1 \cdot \exp(-k_{fast} \cdot t) + A_2 \cdot \exp(-k_{slow} \cdot t) \), where \( A_t \) is the promoter DNA fraction bound to RNAP, calculated from the fluorescence fold change value \( (A_t = (F - F_0)/F_0) \), and \( k_{fast} \) and \( k_{slow} \) are the rate constants for the fast and slow phase, respectively; \( F \) is the fluorescence signal of RNAP-bound DNA, and \( F_0 \) is the fluorescence signal of free DNA. The slow phase constant \( k_{slow} \) was considered to be the rate constant \( k_d \) for RPo dissociation.

Native gel electrophoresis assay to study RbpA binding

RbpA was conjugated with the sulhydryl-reactive dye, Dylight 633 Maleimide (Thermo Scientific), as described (24). Labeled RbpA (1.6 μM) was incubated with different concentrations of the \( \sigma^B \) subunit (0.8, 1.6, and 3.2 μM) in 10 μl of TB at 37°C for 10 min. Samples were analyzed on 5–10% native native PAGE in Tris–glycine buffer. Gels were scanned with a Typhoon 9400 Imager (GE Healthcare).

RESULTS

RbpA is dispensable for transcription from promoters containing the extended –10 motif

To explore the impact of the extended –10 motif on transcription initiation by the stress-response \( \sigma^B \)-MtbRNAP holoenzyme, we used four templates derived from the housekeeping, RbpA-dependent M. tuberculosis sigA promoter (sigA-WT) (Figure 1A). The four sigA variants carried the TG motif at different positions: −15 to −14 (T-15G-14) in sigA-TG1; −16, −17 (T-17G-16) in sigA-TG2; and −14 to –12 (T-14G-16) in sigA-TG3 and in sigA-TGTC. In addition, the sigA-TGTC template carried a C nucleotide at position −13. We then tested whether \( \sigma^B \)-MtbRNAP could initiate transcription from these different sigA promoter variants using multiple-round run-off transcription assays (Figure 1B and C; Supplementary Figure S1A). In the absence of RbpA, \( \sigma^B \)-MtbRNAP was almost inactive at the sigA-WT promoter, in agreement with our previously published results (24). Introduction of any of the TG motifs stimulated transcriptional activity. Thus, the efficiency of transcription from the sigA-TGTC promoter in the absence of RbpA was similar to that observed at the sigA-WT promoter in the presence of RbpA. Introduction of a C nucleotide at position −13, which is known to stimulate promoter binding by the orthologous stress-response \( \sigma^S \) subunit from E. coli (29), had no effect on \( \sigma^B \)-MtbRNAP activity. We conclude that the T-15G-14 motif can fully abolish RbpA requirement for transcription initiation. The fact that neither the TG1 nor the TG2 motif alone was sufficient to reach the level of transcription observed with the TGTC motif suggests that DNA bases at positions −17 to −14 interact cooperatively with \( \sigma^B \). The RbpA-\( \sigma^B \)-MtbRNAP complex showed similar levels of transcription at all tested templates (Figure 1C), suggesting that RbpA makes MtbRNAP tolerant to sequence variations in the extended –10 motif.

RbpA activates transcription by stimulating MtbRNAP capacity to form RPo (24). To assess whether the TG motif makes RbpA dispensable for transcription initiation through stimulation of RPo formation, we performed KMnO4 probing of RNAP-promoter complexes formed at equilibrium. The template DNA strand thymines at positions −11, −9, −8 of the sigA promoter were KMnO4-reactive in RPo formed by the RbpA-\( \sigma^B \)-MtbRNAP complex (Figure 1D). In agreement with the result of the transcription assay, \( \sigma^B \)-MtbRNAP was able to open the sigA-TGTG promoter even in the absence of RbpA. However, the amount of RPo was ~30% of that formed in the presence of RbpA, suggesting that RbpA stimulates RPo formation even at extended –10 promoters. In the absence of RbpA, sigA-TG1 promoter opening was barely detectable (Figure 1D), in striking contrast with the significant transcription activity of \( \sigma^B \)-MtbRNAP observed in the transcription assay (Figure 1B). This discrepancy likely indicates that RPo complexes were active but unstable (see below). We conclude that sequence-specific interaction of \( \sigma^B \)-MtbRNAP with the bases between −17 to −16 of the extended –10 motif is an essential determinant of promoter opening in the absence of RbpA.

Based on the observation that RbpA was not required for transcription from the perfect extended –10 consensus sinP3 promoter (24) and from the sigA promoter variants harboring TG motifs (24), we predict that any promoter harboring the extended –10 motif should be active in the absence of RbpA. To estimate the number of such presumably RbpA-independent or weakly RbpA-dependent gene promoters in M. tuberculosis, we performed a bioinformatic analysis using the set of 1658 promoters containing the \( \sigma^{\text{inv}} \)-type –10 motifs (nAnnnT) (30). These promoters were reported to be active during exponential growth (30). The analysis demonstrated that 338 of 1668 promoters contained a partial or full-length extended –10 motif (Figure 1E). Specifically, 173 (10.4%) promoters contained the T-15G-14 and 135 (8.1%) the T-17G-16 motif and therefore, they expected to be loosely RbpA-dependent. Only 30 (1.8%) promoters contained the T-17G-16T-15G-14 motif and therefore, they are expected to be constitutive. Accordingly, the majority of \( \sigma^B \)-dependent genes in M. tuberculosis are expected to be under the control of RbpA.

The extended –10 motif stabilizes MtbRNAP-promoter complexes in the absence of RbpA

Next, we used electrophoretic mobility shift assays (EMSA) to test whether \( \sigma^B \)-MtbRNAP can form stable RPo at sigA promoter variants in non-equilibrium conditions, in the presence of competitor poly(dI-dC) (Figure 2A and B). EMSA showed that in the absence of RbpA, the full-length extended –10 motif (T-17G-16T-15G-14) and the downstream transcription.
Figure 1. RbpA is dispensable for transcription from promoters containing the extended −10 motif. (A) Schematic representation of the sigAP promoter and its derivatives. Mutated bases are underlined. (B) Representative gel of the run-off [32P]-RNA products synthesized in the multiple-round transcription assay using sigAP-WT and the indicated derivatives in the absence and presence of RbpA. (C) Quantification of the run-off [32P]-RNA products obtained in the transcription assay shown in panel B (mean values ± SE of three experiments except of TGTGC values which are from one experiment). All shown products were used for quantification. Values were normalized to the value obtained with the sigAP-WT promoter in the presence of RbpA. (D) KMNq4 probing of the open complexes formed at the sigAP-WT promoter and the indicated derivatives. Promoter DNA was fluorescin-labeled on the template strand. Traces of the gel lanes are shown at the bottom (E) Number and percentage of promoters harboring the indicated extended −10 motif variants in a subset of M. tuberculosis promoters active during the exponential phase (promoters from Cortez et al. (30)). The bioinformatic analysis was performed using the UniproUgene software (49).
Figure 2. RbpA stabilizes open promoter complexes at the extended −10 promoter. (A) EMSA analysis of the promoter complex formation using αB-MtbRNAP and fluorescein-labeled sigAP promoter variants. Complexes were resolved using native 5% PAGE. (B) Quantification of the EMSA results (mean values ± SE of three experiments). (C) Effect of RbpA on sigAP-TGTG promoter binding measured by MtbRNAP titration in EMSA assays. (D) Quantification of the results shown in panel E. (E) Time-course of RPo formation monitored in a single-round run-off transcription assay. αB-MtbRNAP was incubated with the sigAP-WT and sigAP-TGTG promoters for the indicated times and then supplemented with NTPs and competitor poly(dI-dC). Representative gel showing the run-off [32P]-RNA products produced during 3 min of transcription. (F) Time-course of promoter escape measured in a single-round transcription assay. NTPs and competitor poly(dI-dC) were added to pre-formed RPo complexes and transcription was performed for the indicated times. Representative gel showing the run-off [32P]-RNA products used for quantification. (G) Quantification of the experiments shown in panel G. (H) Fluorescence fold-change during dissociation of the complexes formed by MtbRNAP at the sigAP-TGTG promoter with and without RbpA. E, MtbRNAP core enzyme (red); Eαα, αB-MtbRNAP (blue); Eαα + RbpA, RbpA-αB-MtbRNAP (black). The graph represents the average of three independent experiments. (J) Apparent kinetic and thermodynamic constants calculated from the data presented in panels D and I. The half-times of RPo formation and of promoter escape were determined from the plots shown in panel G. (I) Fluorescence fold-change during dissociation of the complexes formed by MtbRNAP at the sigAP-TGTG promoter with and without RbpA. E, MtbRNAP core enzyme (red); Eαα, αB-MtbRNAP (blue); Eαα + RbpA, RbpA-αB-MtbRNAP (black). 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The graph represents the average of three independent experiments. (J) Apparent kinetic and thermodynamic constants calculated from the data presented in panels D and I. The half-times of RPo formation and of promoter escape were determined from the plots shown in panel G.
RbpA stabilizes open promoter complexes formed at the sigAP-TGTG promoter

To quantitatively characterize the impact of RbpA on RPo formation at extended −10 promoters, we studied the dissociation kinetics of MtbRNAP-sigAP-TGTG promoter complexes using a fluorescence-based assay (31,32). We incubated the sigAP-TGTG promoter, labeled with Cy3 at position +2 of the non-template DNA strand, with MtbRNAP (E; control), $\sigma^B$-MtbRNAP (E$\sigma^B$) or the RbpA-$\sigma^B$-MtbRNAP complex (E$\sigma^B$ + RbpA). Then, we monitored the fluorescence intensity change before and after addition of the competitor heparin that neutralizes free RNAP (Figure 2I). Binding of E$\sigma^B$-MtbRNAP or RbpA-$\sigma^B$-MtbRNAP to the promoter DNA induced a 2-fold and 2.5-fold change in fluorescence intensity, respectively. The MtbRNAP core enzyme also induced a ~1.8-fold increase in fluorescence, possibly due to non-specific binding and the high sensitivity of Cy3 fluorescence to the environment (33). Indeed, the core-specific signal decayed according to the single exponential decay model in $<$4 s after heparin addition (Figure 2I and J). As the MtbRNAP core enzyme, which cannot bind specifically to the promoter, also produced a significant change in fluorescence, we conclude that this assay can detect not only RPo, but also RPc and RPi. This result also suggests that the fluorescence signal increase observed in the presence of the holoenzyme could arise in part from non-specific binding. Indeed, after heparin addition to the complexes formed by the $\sigma^B$-MtbRNAP holoenzyme or RbpA-$\sigma^B$-MtbRNAP, we observed a first rapid fluorescence decrease (few seconds), followed by a slow decay (Figure 2I and J). Based on the results obtained with the MtbRNAP core enzyme, we attributed the first signal decrease to the dissociation of non-specific complexes (e.g., formed upon MtbRNAP binding to the DNA fragment ends), and the subsequent slow decay phase (fitted by a single exponential) to dissociation of the specific promoter-RNAP complexes. Considering the three-step model of open complex formation (Figure 2I), RNAP dissociation rate from the promoter (RPo $\rightarrow$ RPi $\rightarrow$ RPc $\rightarrow$ undetectable species) is determined mainly by the slow isomerization of RPo to RPc, and is characterized by the dissociation rate constant $k_d$ ($k_d = k_2/(1+K_2)$) which is determined from the exponential fit of the slow decay phase (see Methods section) (34,35). Because the RPo complex formed without RbpA dissociated ~50-fold faster than the complex formed in its presence (Figure 2J), we conclude that RbpA acts on the isomerization step and may stabilize the final ‘open’ state of DNA in RPo (24,25).

The synergy between RbpA and the extended −10 motif allows promoter opening at 0°C

Promoter melting by E. coli RNAP containing the $\sigma^{70}$ subunit is strictly temperature-dependent (11,36). This feature reflects RNAP capacity to undergo temperature-dependent isomerization, leading to the formation of a stable transcription bubble. To assess the effect of RbpA and the extended −10 motif on bubble formation, we performed KMnO$_4$ probing of MtbRNAP complexes at the sigAP-WT and sigAP-TGTG promoters at increasing temperatures, from 0 to 37°C (Figure 3). RPo formation by RbpA-MtbRNAP at the sigAP-WT promoter displayed weak temperature dependence. Furthermore, RbpA-MtbRNAP could open the sigAP-WT promoter even at 0°C (Figure 3C). At the sigAP-TGTG template, DNA melting was detected at temperatures as low as 16°C even without RbpA. RbpA boosted MtbRNAP capacity to open the promoter, thus rendering it temperature-independent (Figure 3D). Indeed, the amounts of RPo formed at 0 and at 37°C were quite similar. This result suggests that MtbRNAP interaction with either RbpA or TGTG decreases the thermal energy requirement for RPo formation, while interaction with both leads to a strong cooperative effect.

The $\sigma^{166A}$ mutant abolishes MtbRNAP-promoter interaction at the extended −10 motif

The H455 residue in the $\sigma^{70}$ subunit domain 3 (σ3) interacts with the −17GC base pair (C on the template strand) of the extended −10 motif (8,37). On the basis of the structure of Mycobacterium smegmatis RNAP, the homologous residue H166 in $\sigma^B$ should interact with the upstream (T-17G-16; TG2) and downstream (T-13G-14; TG1) parts of the TGTG motif in the major DNA groove (see model Figure 4A). RbpA interacts with the TGTG motif on the opposite DNA face, and could affect its interaction with σ3. To determine whether RbpA affected the σ3-TGTG interaction, we generated the $\sigma^B$ subunit containing the His→Ala substitution in position 166. In the absence of RbpA, the H166A substitution abolished run-off transcription from the sigAP promoter variants that contain the extended −10 motif (Figure 4B and D; Supplementary Figure S1B). Addition of RbpA restored the activity of $\sigma^{166A}$-MtbRNAP to a level even higher than that of the wild type holoenzyme, possibly due to increased RNAP recycling. In agreement with the result of the transcription assay, EMSA showed that the H166A substitution abolished RPo formation at the sigAP-TGTG promoter (Figure 4C). Compared with the wild type holoenzyme, $\sigma^{166A}$-RNAP formed less RPo at the sigAP-TGTG promoter also in the presence of RbpA (Figure 4C and D). Thus, we conclude that the sequence-specific interaction between the H166 residue of the $\sigma^B$ subunit and the TGTG motif is pivotal for efficient transcription initiation by $\sigma^B$-MtbRNAP at promoters of the extended −10 class. This interaction enhances RbpA capacity to stabilize RPo, but is not essential for RbpA-mediated transcription activation.

Domain $\sigma^4$ is essential for transcription initiation from extended −10 promoters

Interaction of domain 4 of $\sigma^{70}$ ($\sigma^4$) with the −35 element in the promoter is dispensable for transcription from promoters of the extended −10 class (9,38). To test whether the $\sigma^4$/−35 element interaction contributes to transcription initiation in the presence of RbpA, we introduced mutations in the −35 motif of the sigAP-WT and sigAP-TGTG promoters (Figure 5A). EMSA and multiple-round run-off transcription assays demonstrated that substitutions in the −35 element did not significantly affect promoter binding and transcription (Figure 5B; Supplementary Figure S2A).
suggesting that sequence-specific recognition of the −35 element by σ4 is dispensable for transcription initiation in the presence of RbpA or of the TGTG-motif. However, we cannot exclude that, in the absence of the perfect −35-motif, a non-specific interaction of σ4 with promoter through contacts with the DNA phosphate backbone (39) contributes to transcription initiation.

If the σ4/-35 element interaction is dispensable for transcription initiation in the presence of RbpA, σ4 deletion should not affect the activity of the MtbRNAP-RbpA complex. To test this hypothesis, we generated a σB subunit mutant in which the C-terminal residues 252–323 were deleted (σBΔ4) (Figure 4A). Using a native PAGE-based protein-protein interaction assay (24), we demonstrated that this deletion did not affect the σB subunit capacity to form a stable complex with RbpA (Figure 5F). To test whether mutant σBΔ4-MtbRNAP was catalytically active, we performed abortive transcription assay using the synthetic lacUV5 promoter harboring a heteroduplex region between position −11 and −5 (28) (Figure 5G). Initiation of transcription on lacUV5 promoter by addition of dinucleotide RNA primer, ApA, and two nucleotides (GTP and [α-32P]UTP) resulted in formation of short RNA products, up to 7nt in length (14). In these experimental conditions, wild type σB-MtbRNAP initiated transcription (with similar efficiency) both in the presence and absence of RbpA, which is in line with the fact that RbpA acts at the promoter melting step. The mutant σBΔ4-MtbRNAP displayed reduced (~18%), but detectable catalytic activity, compared with the wild type enzyme. This could be caused by defects in promoter binding, holoenzyme σBΔ4-MtbRNAP assembly, and structural disturbance in the σB region 3.2, which is implicated in transcription initiation and promoter escape (40,41). As expected, the mutant σBΔ4-MtbRNAP holoenzyme was inactive in run-off transcription assays performed with the sigAP-WT promoter in the absence and presence of RbpA (Figure 5H). Surprisingly, the mutant σBΔ4-MtbRNAP holoenzyme was also inactive at the sigAP-TGTG promoter and at the sinP3 promoter (24) that harbors the perfect extended −10 consensus motif (5′-T-GTGTATAAT-7–3′) and lacks the −35 element. Addition of RbpA partially restored σBΔ4-MtbRNAP activity at the sinP3, but not at the sigAP-TGTG promoter, possibly due to differences in promoter architectures. Because mutant MtbRNAP showed low but detectable activity on the lacUV5 bubble template, irrespective of RbpA, the lack of transcription at the sigAP promoter in the presence of RbpA and at the sigAP-TGTG in the absence of RbpA cannot be explained only by defects in initiation of RNA synthesis. Altogether, these results suggest that RbpA cannot compensate for the lack of σ4 interaction with the core enzyme or/and the promoter, and that σ4 per se is an essential component of the RbpA-mediated activation mechanism at the −10/-35 class promoters. Based on these results we hypothesize that even for promoters of the extended −10 class, interaction of the σ4 domain with the MtbRNAP core enzyme, and/or non-specific interaction with DNA contribute to transcription initiation.
Figure 4. The substitution H166A in region 3 of σB abolishes MtbRNAP interaction at the extended −10 motif. (A) Structural model of Mycobacterium smegmatis RNAP in complex with RbpA and promoter DNA (PDB code: 5TW1). Red ribbon, RbpA; green ribbon, σB subunit; gray semitransparent molecular surface, RNAP core; blue, DNA template strand; red, DNA non-template strand; orange, TG1-motif (T−15G−14); yellow, TG2-motif (T−17G−16). Residues in σB (H166) and RbpA (K73, K74, R79) that were mutated are shown in CPK rendering. Schematic representations of the RbpA and σB domains are shown at the bottom. The positions of the mutated residues are indicated. (B) Run-off [32P]-RNA products synthesized in run-off transcription assays using sigA promoter derivatives in the presence or not of RbpA. (C) EMSA analysis of promoter complex formation by σB-MtbRNAP and fluorescein-labeled sigA promoter variants. Complexes were resolved in native 5% PAGE. (D) Quantification of the experiment shown in panel C (mean values ± SE of two experiments).

RbpA-BL modulates σB-MtbRNAP selectivity for initiating transcription substrates

Based on the structure of RPo and RbpA-SID fragment, it was proposed that the residues R79 (in contact with nucleotides −13 and −14 of the non-template DNA strand), K73 and K74 in RbpA-BL interact with DNA at the TGTG element in the DNA minor groove (25,26). We assessed whether mutations in these residues (R79A and the double substitution K73A, K74A (KKAA)) affected RPo formation at the sigA-WT and sigA-TGTG promoters. The EMSA results showed that in agreement with previous findings (25), the R79A substitution in RbpA decreased RPo stability by ~2-fold at the sigA-WT and by ~1.5-fold at the sigA-TGTG promoter (Figure 6A and C). Conversely, the KKAA substitutions had no effect on RPo stability (Figure 6B and D). Furthermore, KMnO₄ probing demonstrated that neither the R79A nor the KKAA substitution hinders sigA-WT promoter opening (Figure 6E). Opening of the sigA-TGTG promoter was even enhanced in the presence of the RbpA mutants. This discrepancy between KMnO₄ probing and EMSA results can be explained by the formation of an unstable RPo that dissociates in the non-equilibrium conditions of EMSA, but can be detected in the equilibrium conditions of KMnO₄ probing. Thus, we conclude that R79 contributes to RPo stabilization, while K73 and K74 are dispensable.

Next, we tested whether the RbpA mutants could stimulate de novo transcription. In multiple-round transcrip-
Figure 5. Impact of σ4 and the −35 element on MtbRNAP activity. (A) Scheme showing the −35 motif of the sigAP promoter with the introduced mutations underlined. (B) Run-off [32P]-RNA products synthesized by wild type σ^4-MtbRNAP from sigAP-WT and sigAP-TGTG and the respective variants lacking the −35 element (Δ−35). (C) Quantification of the results of the experiment shown in panel B (mean values ± SE of two experiments). (D) EMSA analysis of promoter complex formation by σ^4-MtbRNAP using the sigAP-WT and sigAP-TGTG promoters and the respective variants lacking the −35 element (Δ−35). (E) Quantification of the results shown in panel D (mean values ± SE of two experiments). (F) Analysis of the RbpA-α^4 subunit interaction by native gel electrophoresis. RbpA, labeled with DyLight 633, was incubated with increasing concentrations (0.8, 1.6, 3.2 μM) of wild type MtB (WT) or the mutant in which domain 4 residues 252–323 were deleted (ΔD4). (G) Abortive transcription activity of wild type σ^4-MtbRNAP (WT) and mutant σ^4ΔD4-MtbRNAP (ΔD4) on the lacUV5-bubble template harboring a heteroduplex region. (H) Run-off [32P]-RNA products synthesized in the presence of wild type σ^4-MtbRNAP (WT) or mutant σ^4ΔD4-MtbRNAP (ΔD4) and the sigAP-WT, sigAP-TGTG or B. subtilis sinP3 promoter that lacks the −35 element.

which is complementary to the positions −1/+1 of the sigAP promoter. Addition of GpC fully rescued the transcription defect induced by RbpA_KAA. Furthermore, the run-off RNA levels in all RbpA-containing reactions were equal.

To better understand the effect of substitutions in RbpA on RPo formation and promoter escape, we performed single-round transcription assays as described above (Figure 7). The half-time of RPo formation in the presence of RbpA was ~4-fold higher than without RbpA (compare Figure 2G, H and Figure 7C, D). The half-time of promoter escape was also 2-fold greater in the presence of RbpA (Figure 7, Table S2), suggesting that RbpA regulates not only
promoter melting but also the initial transcription. We detected no effect of the R79A substitution on RPo activation and escape rates, at least in the time resolution range of our assay. Therefore, we cannot presently explain why this substitution affects the yield of run-off RNA in multiple-round transcription assays. In agreement with the result of the multiple-round transcription assays, the KKAA substitutions led to a 2-3-fold decrease in escape rate (t1/2 = 2.8 min), while addition of GpC stimulated promoter escape. Based on our results and on the recent structure of the MtbRNAP-RbpA complex (42), we propose that RbpA, can indirectly modulate MtbRNAP selectivity for the priming substrates (NTPs and short RNAs) through contact with the σ3.2 finger (42) which controls transition from initial transcription to productive elongation (28,40,41).

DISCUSSION

Transcription initiation from most of the bacterial promoters requires simultaneous binding of the RNAP σ subunit to the −10 and −35 elements. The weak conservation of the −35 element in M. tuberculosis promoters (30) predicts the existence of compensatory mechanisms. Here, we found that RbpA abolishes the requirement of sequence-specific interactions between the domains 3 and 4 of the σ subunit and promoter DNA upstream of the −10 element. Therefore it converts MtbRNAP into a hyperactive enzyme with promiscuous promoter selection. Moreover, the presence of the T-17G-16T-15G-14 motif fully abolishes RbpA requirement for transcription initiation, suggesting that mycobacterial promoters bearing the extended −10 motif are constitutive. Our estimation is that at least 2% of the known M. tuberculosis promoters belong to this group. Moreover, ~14% of M. tuberculosis promoters contain the T-15G-14 motif (43), and thus should be loosely dependent on RbpA, or hyperactive in the presence of RbpA. Based on the similarities between the effects of RbpA and of the TGTG motif on transcription, we propose that RbpA could strengthen the interaction of the σ subunit domains 3 and 4 with promoter DNA upstream of the −10 element. This hypothesis
Figure 7. Effect of mutations in RbpA-BL on the kinetics of RPo formation and promoter escape. (A) RPo formation was monitored in single-round run-off transcription assays. (B) Promoter escape was monitored in single-round run-off transcription assays. Representative gels showing run-off [32P]-RNA products synthesized from the sigA P-WT promoter by \( \textit{H}9268 \) B-\( \textit{Mtb} \) RNAP in the presence of the indicated RbpA variants. (C) Quantification of the experiments shown in A and B (mean values ± SE of three experiments). All shown RNA products were used for quantification. (D) The half-times of RPo formation and promoter escape were determined from the plots shown in panel C.

is supported by our smFRET study showing that \( \sigma^B \) in the \( \textit{MtbRNAP} \) holoenzyme adopts a conformation incompatible with binding to \(-10/-35\) promoters and that RbpA stabilizes \( \sigma^B \) in a conformation compatible with binding (27). The finding that \( \sigma^4 \) was still required for transcription initiation in the context of the extended \(-10\) \( \textit{sin} \)P3 and sigAP-TGTG promoters even in the presence of RbpA suggests that \( \sigma^4 \) may have additional roles in initiation, probably in organizing RNAP clamp or \( \beta \) subunit flap domains for RPo formation, as proposed for \( \textit{E. coli} \) \( \sigma^{70} \) (44). The \( \sigma^4/\beta\)-flap contact may be essential for correct positioning of \( \sigma^3 \) (e.g., region 3.2) in RPo, which in turn affects RPo stability and RNA synthesis initiation (28,40).

We observed that RbpA increases \( \textit{MtbRNAP} \) affinity for promoters bearing the extended \(-10\) motif (~3 fold decrease in apparent \( K_d \)) and stabilizes RPo (~50-fold decrease in \( k_d \)). Thus, we propose that RbpA acts on two initiation steps: promoter binding (RPc formation), and RPc isomerization to RPo. Our result differs from a previous study reporting no effect of RbpA on the \( k_d \) (45). The \( \sigma^4/\beta\)-flap contact may be essential for promoting correct positioning of \( \sigma^3 \) (e.g., region 3.2) in RPo, which in turn affects RPo stability and RNA synthesis initiation (28,40).

Role of the extended \(-10\) motif in promoter melting at suboptimal temperatures

Studies on the \( \textit{E. coli} \) \( \sigma^{70} \)-RNAP and \( \textit{B. subtilis} \) \( \sigma^A \)-RNAP holoenzymes demonstrated that the extended \(-10\) motif stabilizes RPo and allows promoter melting triggered by RNAP at low (6 and 10°C), suboptimal temperatures (46,47). Also it has been proposed that the \( T_{15}G_{14} \) motif can decrease the thermal energy requirement for promoter formation by \( \textit{MtbRNAP} \) (48). Our results demonstrate that the identity of the nucleotides at positions \(-17\) to \(-16\) is critical for melting of promoters of the extended \(-10\) class. The combination of TGTG motif and RbpA strongly decreased the thermal energy requirement for promoter formation in \( \textit{MtbRNAP} \) (28,40). We speculate that interaction at the TGTG motif could promote DNA bending around RNAP. This will direct promoter DNA to the downstream channel in RNAP, thus facilitating distor-
tion of the –10 element DNA by the region 2 of σ and then formation of the transcription bubble.

Role of RbpA-BL in transcription initiation

Previous studies on σ^A-MtbRNAp suggested that interaction of the residue R79 in RbpA-Bl with promoter DNA at positions −13, −14 is critical for RbpA function in vitro and in vivo (25,26). We observed a moderate effect of this mutation on RPo stability and no effect on promoter opening and on transcriptional activity. Furthermore, the RbpA^R79A mutant was even more active than wild type RbpA in multiple-round transcription assays without a 2-mer RNA primer. This discrepancy indicates that the σ^A-MtbRNAp and σ^B-MtbRNAp holoenzymes respond differently to RbpA. Indeed, differently from σ^B-MtbRNAp, the σ^A-MtbRNAp holoenzyme cannot form stable RPo at the extended −10 site^P3 promoter without RbpA and at the σ^4P promoter in the presence of RbpA (18,24). The molecular basis of these differences, lying in the abovementioned structural properties of σ^A and σ^B, is an intriguing subject for future studies.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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