Pausing controls branching between productive and non-productive pathways during initial transcription in bacteria

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Transcription in bacteria is controlled by multiple molecular mechanisms that precisely regulate gene expression. It has been recently shown that initial RNA synthesis by the bacterial RNA polymerase (RNAP) is interrupted by pauses; however, the pausing determinants and the relationship of pausing with productive and abortive RNA synthesis remain poorly understood. Using single-molecule FRET and biochemical analysis, here we show that the pause encountered by RNAP after the synthesis of a 6-nt RNA (ITC6) renders the promoter escape strongly dependent on the NTP concentration. Mechanistically, the paused ITC6 acts as a checkpoint that directs RNAP to one of three competing pathways: productive transcription, abortive RNA release, or a new unscrunching/scrunching pathway. The cyclic unscrunching/scrunching of the promoter generates a long-lived, RNA-bound paused state; the abortive RNA release and DNA unscrunching are thus not as tightly linked as previously thought. Finally, our new model couples the pausing with the abortive and productive outcomes of initial transcription.

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Transcription initiation by DNA-dependent RNA polymerase (RNAP) constitutes the first and often decisive step in gene expression in bacteria. To balance the output of transcription with environmental and cellular needs, an extensive set of molecular mechanisms has evolved to regulate the efficiency and specificity of transcription initiation. The regulatory mechanisms are either directly encoded in the transcribed DNA sequence or mediated by protein transcription factors or small-molecule signals. The target of transcription initiation regulators may be the function of RNAP itself, or the accessibility or affinity of promoters for RNAP. Further regulation occurs in the elongation and termination phases of transcription.

To perform promoter-specific transcription initiation, the bacterial RNAP core associates with housekeeping $\sigma^{70}$ initiation factor (or one of the alternative $\sigma$-factors) to form an RNAP holoenzyme. The holoenzyme employs sequence-specific interactions between the $\sigma^{70}$ and the −35 and −10 promoter elements (Fig. 1a) to form an initial RNAP–DNA closed complex, and to isomerize to the catalytically competent RNAP–promoter open complex (RPO) (Fig. 1b). During initial RNA synthesis, strong interactions with the DNA hold the RNAP at the promoter, resulting in the build-up of “scrunching” of downstream DNA, a conformational change that increases the size of the DNA bubble. The eventual break-up of RNAP–promoter contacts and the escape to elongation relax the scrunched DNA. The productive promoter escape pathway competes with abortive initiation, an unproductive pathway wherein the short nascent RNA is thought to dissociate prematurely, resetting the initially transcribing complex (ITC) to RPO. Although conformational strain resulting from the DNA scrunching may promote abortive initiation, multiple other factors such as the presence of the $\sigma^{3}_2$ region (which obstructs the entry to the RNA-exit channel), strong RNAP–promoter interactions, and the initially transcribed sequence also contribute.

The step that defines the overall rate of transcription initiation varies between promoters. In many $\sigma^{70}$-dependent promoters, the rate-limiting step is attributed to the half-life of RPO or the rate of promoter escape. An extensively studied example of an escape-limited promoter is lacUV5, which produces substantial amounts of abortive products; further, transcriptional pausing was identified in the ITC formed on lac promoter after the synthesis of 6-nt RNA, in part due to the clash of the 5′-RNA end with the $\sigma^{3}_2$ region.

Recent advances in structural characterization of bacterial transcription initiation complexes have created intriguing hypotheses on how specific molecular interactions and conformational changes drive holoenzyme formation, promoter recognition, open complex formation, and initial RNA synthesis. Complementing this structural insight with detailed functional analysis is hampered, however, by the multi-step, asynchronous nature of transcription initiation pathways. Single-molecule techniques, which can provide a direct readout for several mechanistic steps and resolve co-existing reaction pathways, are well positioned to overcome the complexity of transcription initiation.

Here we combine single-molecule and biochemical analysis of initial transcription to explore the mechanistic basis of the pause encountered by ITC6 on a consensus variant of lac promoter, i.e., with consensus −35 and −10 elements, and a 17 bp spacer. We present evidence that the ITC6 pause represents a major control point where the ITCs branch to three competing downstream reaction pathways: pause exit by productive transcription; abortive-RNA release; and slow cycling between DNA conformations with different extents of scrunching but without RNA release. The partitioning between these three pathways and their kinetics depends on distinct interactions and structural elements. The rate of productive pause exit is synergistically controlled by the initial transcribed sequence and the interaction of the 5′-RNA end with $\sigma^{3}_2$ region, whereas perturbing RNAP interactions with the initially transcribed region favors the entry into the scrunching/unscreunching pathway.

**Results**

**High-resolution observation of initial transcription.** To monitor the kinetics of transcription initiation at the single-molecule level, we developed a Förster resonance energy transfer (FRET) sensor with fluorophore-labeled consensus lac promoter for real-time imaging of individual transcription-engaged RNAP–promoter complexes. Earlier studies of this consensus lac promoter derivative identified a strong pause at ITC6. We modified the original promoter design in two ways to allow in-depth biophysical analysis of the rate-limiting ITC6 pause (Fig. 1a and Supplementary Fig. 1a). First, we extended the upstream region of the promoter from −39 to −89, to enhance RPO formation and provide a more native DNA-length context for RNAP–DNA interactions. Second, we moved the acceptor dye from position +20 to +15, to obtain distinct FRET signals for different steps of the initiation pathway. With this configuration, we clearly separated and calibrated (Methods) FRET readouts for three structural states through downstream DNA scrunching: an unscrunched (US) open complex RPO ($E_{\text{FRET}} = 0.49 \pm 0.003$), a partly scrunched (PS) paused complex ITC6 ($E_{\text{FRET}} = 0.37 \pm 0.001$), and a fully scrunched (FS) pause-cleared complex at ITC11 ($E_{\text{FRET}} = 0.80 \pm 0.002$) (Fig. 1b and Supplementary Fig. 1).

Upon addition of NTPs to RPO complexes (either a NTP subset sufficient to reach the ITC11 complex or all NTPs), the FRET signal showed an almost instant transition from the US to the PS state (Fig. 1c, Supplementary Fig. 1b and Supplementary Fig. 1c), suggesting that the transcription complexes synthesized 6-mer RNA and paused. After the pause, the ITCs split into two main populations: the first population comprised “productive” ITCs that resumed transcription and progressed from the PS to the FS state by synthesizing an 11-mer (Fig. 1c). The second population comprised ITCs that returned from the PS to the US state (Fig. 1d); notably, such complexes could cycle multiple times (e.g., at ~100 s and ~200 s in Fig. 1d) between PS and US states until they eventually reached the FS state (e.g., at ~500 s in Fig. 1d).

**Determination of the lifetime of the ITC6 pause.** Two elements appear to contribute to RNAP pausing at ITC6: (i) the clash of the 5′-RNA end with the $\sigma^{3}_2$ region (Fig. 1b), which blocks entry to the RNA-exit channel of RNA; and (ii) a specific sequence motif (a non-template Y+6G+7 in the transcribed DNA strand) akin to that causing sequence-specific pausing in elongation. We dissected the contributions of these two elements to the ITC6 pause using our single-molecule FRET assay.

To explore the steric-clash hypothesis, we modified the 5′-RNA end of the nascent transcript (and thus its interaction with $\sigma^{3}_2$) by initiating transcription either using a synthetic dinucleotide (ApA) or using ATP, which adds a 5′-triphosphate tail to the 5′-RNA end. To evaluate the effect of the pause sequence motif on the detailed dynamics of initial transcription, we replaced the sequence T+6G+7 (non-template DNA) with G+P+T+7, creating a “ΔP promoter” (Supplementary Fig. 1a) that increased the overall rate of initial transcription by shortening the ITC6 pause. In all experiments, the initiating ATP or ApA were held at 500 µM, a level significantly above the $K_M$ of the RPO for initiating nucleotides and dinucleotide primers; we also varied the concentration of remaining NTPs (1–500 µM).
We first analyzed the effects of the pause elements on the pause duration at ITC6 ($\Delta t_{ITC6}$) by focusing on the subpopulation of molecules displaying the US $\rightarrow$ PS $\rightarrow$ FS scrunching sequence (as in Fig. 1c). The dwell-time distribution for the ITC6 pause was well described by a single exponential (Fig.2a; see Methods for analysis procedure), where the exit rate $k_{ITC6}$ was ~1.5-fold lower for the wild-type (WT) promoter compared with the $\Delta P$ promoter using ApA (Fig. 2b). When we replaced ApA with ATP as the starting substrate and employed the remaining NTPs at above 30 µM, the ITC6 pause exit rate increased from 0.07 ± 0.01 to 0.26 ± 0.06 s$^{-1}$ for the $\Delta P$ promoter and from 0.04 ± 0.01 to 0.11 ± 0.03 s$^{-1}$ for the WT promoter, i.e., 2.5-fold enhancement in $k_{ITC6}$ in the absence of the pause motif (Fig.2b). These experiments demonstrate that the ITC6 pause duration is controlled both by the transcribed sequence and by the structure of the RNA 5′-end, which interacts with $\sigma_{3.2}$.

We also noted that the NTP concentration did not influence significantly the $k_{ITC6}$ (no more than 1.5-fold) for the WT promoter with either ApA or ATP as the starting substrate, or for the $\Delta P$ promoter with ApA as the starting substrate (Fig.2b). The rate-limiting step in all these cases is thus neither the intrinsic

Fig. 1 Initial transcription monitored at the single-molecule level. a Representation of the premelted (turquoise font) WT DNA promoter used in the single-molecule experiments (Supplementary Fig.1a). The –35 and –10 elements are represented in red. The promoter was donor labeled at –15 position (green sphere) of the non-template DNA strand and acceptor labeled in +15 (red sphere) position of the template DNA strand. An arrow above the base in orange font indicates the +1 position. All the promoters used in the study are described in Supplementary Fig.1a. b Schematic of the initial transcription experiment (Methods). Above: using TIRFM-based smFRET, we monitored the E$_{FRET}$ variations of the donor–acceptor pair upon NTP addition. The RNAP fluctuates between RP$_D$, ITC6, and ITC > 6, to eventually escape the initiation phase toward the elongation phase, or to release the nascent RNA; below: cartoon that magnifies the interactions between the 5′-RNA end and $\sigma_{3.2}$ and the position of the 5′-RNA end. c Fluctuations in the donor (green) and acceptor (red) dyes intensities (above) and the resulting E$_{FRET}$ (below, blue), showing the variation of E$_{FRET}$ from an Unscrunched (US) FRET state, followed by the Partly Scrunched (PS) FRET state upon NTP addition, and ending in the Fully Scrunched (FS) FRET state. Experimental conditions: 200 ms time points (100 ms ALEX, Methods), 500 µM ApA, and 80 µM All NTP. d Similar experiment conducted as described in c, with the RP failing multiple times before reaching the FS FRET state. Experimental conditions: 200 ms time points, 500 µM ApA, and 30 µM of all NTPs and WT promoter. The red solid lines in the lower panels in c and d represent the FRET states extracted from hidden Markov modeling (HMM) (Methods)
catalytic activity of the transcription complex nor the binding of the incoming NTP substrate.

We next characterized the probability to exit the ITC6 pause on the first attempt (Fig. 2c). For this purpose, we counted the probability of ITC6 to proceed via the reaction path depicted in Fig. 1c (single-scrunch pathway), with or without a detectable ITC6 pause, versus the path in Fig. 1d (cyclic scrunching/unscreunching pathway). ATP-initiated ΔP promoter complexes (Fig. 2c) exited the pause on the first attempt at higher probability at all tested (5–500 μM) NTP concentration compared with the other starting substrate-promoter conditions. The pause-exit probability for the ApA-initiated ΔP promoter, and the ATP- or ApA-initiated WT promoter decreased steeply from 0.8 toward 0 at low NTP concentrations (Fig. 2c). By fitting the probability p(NTP) to exit the ITC6 pause on the first attempt with a descriptive model similar to a binding isotherm (Fig. 2c), we extracted an apparent binding constant KNTP and a maximal pause-exit probability Pmax,esc from ρ. Error bars are 1 SD extracted from the fit.

Structural determinants of transcription pathway partitioning. Our single-molecule reaction trajectories demonstrated (Fig. 1) that the transcription complexes paused at ITC6 may either resume RNA extension or cycle between differently scrunchèd paused states. To establish the interactions contributing to the pathway partitioning, we engineered structural changes (Fig. 3a) in RNAP, σ70, and nucleic acids, and characterized the impacts on the function of ITCs.

Finally, a fully double-stranded promoter (dsWT, Supplementary Fig. 1a) did not modify the ITC6 pause exit rate both for ApA and ATP starting substrates (Supplementary Fig. 2c), whereas the probability to reach the FS state during the first attempt on this promoter was also strongly decreased in the absence of a 5′-RNA end triphosphate (14 ± 4% vs. 58 ± 5%, Supplementary Fig. 2d), suggesting again that the 5′-RNA end triphosphate assists in the ITC6 pause exit.

Fig. 2 The pause characteristics are a function of the downstream DNA promoter sequence at the +6 position and of the 5′-RNA end nature. a Probability density distribution for the ΔITC6 for the RP complexes behaving as in Fig. 1c. The dashed line is a single-exponential fit from a MLE. Inset: Log-λn representation of the same data. Experimental conditions: 500 μM ApA starting substrate, 80 μM all NTPs. b ΔITC6 lifetime extracted from single exponential MLE fit similar to a for different promoter/starting substrate conditions (as indicated in the panel), different NTP conditions, i.e., all NTPs for WT/ApA (yellow) and ITCC (Supplementary Fig. 1a) for all others, and different NTP concentrations (Supplementary Table 1). In the ATP-initiated reactions, we did not use NTP concentration below 5 μM to prevent potential misincorporations of ATP (used at 500 μM for initiation purposes)69. On the right-hand side is indicated the mean ± SD of kITC6 for each promoter/starting substrate condition. c Probability to reach the fully scrunched (FS) FRET level in a single attempt (Fig. 1c). The solid lines are fits to a binding isotherm of the form p(NTP) = Pmax,esc × [NTP] / ([NTP] + KNTP). The error bars are 95% confidence intervals. d KNTP and Pmax,esc extracted from c. Error bars are 1 SD extracted from the fit.
ITC6 toward the scrunching/unscreunching pathway. In comparison, the $\sigma_{3.2}$ region deletion has a much more severe defects in transcription initiation and strictly requires dinucleotide primers for 11-mer synthesis22,27 (Fig. 3b).

We next destabilized by D446A substitution the binding of non-template guanine in the “CRE-pocket” (Core Recognition Element-pocket) of RNAP29,37. Our results align with an earlier observation of the CRE-pocket being involved in open complex formation and transcription start-site selection40; we observed fourfold less (20 ± 5% vs. 70 ± 4%) complexes with a consensus elongation pause37,a when increasing the NTP concentration to 500 µM (Fig.3c). We also observed, similar to the consensus elongation pause37, a reduced escape rate (0.10 ± 0.01 vs. 0.06 ± 0.01 s$^{-1}$) from the ITC6 pause (Supplementary Fig. 2f). Both pauses are characterized by the presence of Y–G$^{+1}$ ntDNA motif. Our third observation reveals a potentially novel function for the CRE-pocket in helping to maintain the scrunched promoter DNA conformation; fourfold less (20 ± 5% vs. 70 ± 4%) complexes managed to escape the pause on the first attempt (Fig. 3e). In bulk transcription reactions, only a minor fraction of complexes formed by the D446A RNAP could extend RNA beyond six nucleotides, suggesting that the contacts of D446 with +7G are critically important to exit the promoted state (Fig. 3b)35.

To probe the effects of weakened interactions between $\sigma$ region 2 and the -10 promoter element, we replaced the consensus –7 thymine in the non-template DNA by an adenine (–7T/A, Supplementary Fig. 1a). The –7 thymine is inserted into a pocket of $\sigma$ in RPO$\text{O}_{29,41,42}$ However, as –7T/A substitution resulted in only small changes in the ITC6 pause exit rate and the fraction of complexes exiting the pause on the first attempt (Fig. 3c, d), –7T–$\sigma$ interaction appears to have a minor role after RNA length is ≥ 6.

**Kinetics of promoter unscreunching/scrunching.** We next analyzed the molecules whose pausing at ITC6 was followed by cyclic unscreunching/scrunching events. These molecules may cycle for tens to hundreds of seconds between the PS and US states until they reach the FS FRET level or the dyes bleached (Figs. 1d and 4a). For this cycling population, we generated probability density distributions for the dwell times in PS ($\Delta t_{PS}$) and US ($\Delta t_{US}$) states (Fig. 4b, c). Both PS and US distributions showed a similar trend, with dwell times varying from ~0.4 s to ~200 s. The distributions were fitted well by a two-exponential probability distribution (solid lines, Fig. 4b, c; dashed lines depict a single-exponential function) (Methods). The fit thus defines for the US and PS states the exit rates $k_1$ and $k_2$, as well as the probability $P(k_1)$ to exit a state with rate $k_1$ (Supplementary Fig. 2e, g).

We applied this data analysis to WT promoter reactions initiated with ApA or ATP, and the $\Delta P$ promoter initiated with ApA (Fig. 2b). We did not include ATP-initiated $\Delta P$ promoter results because most complexes exited the ITC6 pause directly to the FS state (Fig. 2c). We first noted that the exit rates $k_1$ and $k_2$, as well as the $P(k_1)$ probabilities of PS and US states, remained fairly constant in all used NTP concentrations (Supplementary Fig. 2h, j). We observed a single exception with the ITC on the ApA-initiated WT promoter, which showed a decreased probability $P(k_1, \text{PS})$ at higher NTP concentrations (right panel, Supplementary Fig. 2h). We observed, in average that the US and
concentration (Supplementary Fig.2e-g) of the double exponential MLE parameters \( (k_1, k_2, P) \) for each FRET level. Experimental condition: WT DNA promoter; NTP start: ApA; NTP: U/G/ATP 80 \( \mu \)M. \( a \) Probability density distribution of the dwell times \( \Delta t \) for each FRET level. \( b \) Typical \( E_{FRET} \) trace where the RP alternates between unscrunched (US) and partly scrunched (PS) DNA promoter FRET levels. The red solid line represents the FRET levels extracted from empirical Bayesian probability hidden Markov model. We collect the dwell times \( \Delta t \) for each FRET level. Experimental condition: WT DNA promoter; NTP start: ApA; NTP: U/G/ATP 80 \( \mu \)M. \( b \) Probability density distribution of the dwell times \( \Delta t \) for each FRET level. Experimental condition: WT DNA promoter; NTP start: ApA; NTP: U/G/ATP 80 \( \mu \)M. \( c \) Probability density distribution of the dwell times \( \Delta t \) for each FRET level. Experimental condition: WT DNA promoter; NTP start: ApA; NTP: U/G/ATP 80 \( \mu \)M. \( d \) Average for all the NTP concentration (Supplementary Fig. 2e-g) of the double exponential MLE parameters \( (k_1, k_2, P) \) respectively (Supplementary Table1). The US/PS and US/PS/FS subpopulations likely represent the ITCs, which at the moment of first cycling for ~ 10 s with ITC11 (Fig.5e, g) or ITC7 (Supplementary Fig. 3a) NTP subsets, (ii) the surface was extensively rinsed to remove NTPs, (iii) surface-bound complexes were re-imaged. To our surprise, 28 ± 4% (ApA, ITC11) extensively unscrunched/scrunched also in the absence of NTPs (Fig. 5d). The fraction of unscrunched/scrunched molecules was comparable to those observed in the continuous presence of NTPs (27 ± 3%, ApA starting substrate; 42 ± 4% ATP) (Fig. 5d). Scrunching/unscrunching by the NTP-depleted complexes lasted for hundreds of seconds, being only limited by dye bleaching (Fig. 5e, g). Consistent with the maximal RNA length, complexes pulsed with ITC7 NTPs sampled only US and PS states (Supplementary Fig. 3a), whereas complexes pulsed with ITC11 NTPs could additionally occupy the FS state (Fig. 5g). This confirms that we did not observe re-synthesis of a 11mer transcript, as we observed earlier that the complex could not escape the ITC6 pause at low NTP concentration (Fig. 5c). Our results clearly demonstrate that the extended cycling in different scrunching states does thus not require active RNA synthesis.

Analysis of the complexes pulsed with ITC11 NTPs identified two types of unscrunched/scrunched molecules: the first cycled between US and PS FRET levels only (Fig. 5f), whereas the second cycled between US, PS, and FS FRET levels (Fig. 5g). The US/PS subpopulation included 48 ± 6% (ApA starting substrate) or 39 ± 5% (ATP starting substrate) of all cycling molecules, respectively (Supplementary Table1). The US/PS and US/PS/FS subpopulations likely represent the ITCs, which at the moment of NTP withdrawal had synthesized 6- and 11-nt RNAs, respectively. The US/PS subpopulation showed similar unscrunched/scrunched kinetics to what was observed with NTPs, i.e., \( k_1 = 0.16 \pm 0.07 \text{ s}^{-1} \), \( k_2 = 0.02 \pm 0.004 \text{ s}^{-1} \), and \( P(k_1) = 0.57 \pm 0.05 \) (Fig. 5f). The US/PS/FS subpopulation instead sampled all scrunching states almost an order of magnitude faster compared to the US/PS subpopulation (i.e., \( k_1 = 0.96 \pm 0.04 \text{ s}^{-1} \), \( k_2 = 0.07 \pm 0.01 \text{ s}^{-1} \), and \( P(k_1) = 0.79 \pm 0.07 \) for US, Fig. 5h), independently of using ATP or ApA for initiation (Fig. 5f, h).

Promoter unscrunching and RNA release. The discovery of extensive unscrunching/scrunching cycling raises intriguing questions about its relationship with abortive initiation. Is the nascent RNA released or retained in unscrunching event, and is the subsequent re-scrunching driven by the synthesis of a new RNA (Fig. 5a)? To address the questions, we devised a three-step assay (Fig. 5b) in several conditions (Fig. 5c): (i) RNA synthesis was triggered for ~ 10 s with ITC11 (Fig. 5e, g) or ITC7 (Supplementary Fig. 3a) NTP subsets, (ii) the surface was extensively rinsed to remove NTPs, (iii) surface-bound complexes were re-imaged. To our surprise, 28 ± 4% (ApA, ITC11) and 18 ± 2% (ATP, ITC11) of initially active complexes cyclically unscrunched/scrunched also in the absence of NTPs (Fig. 5d). The fraction of unscrunched/scrunched molecules was comparable to those observed in the continuous presence of NTPs (27 ± 3%, ApA starting substrate; 42 ± 4% ATP) (Fig. 5d). Scrunching/unscrunching by the NTP-depleted complexes lasted for hundreds of seconds, being only limited by dye bleaching (Fig. 5e, g). Consistent with the maximal RNA length, complexes pulsed with ITC7 NTPs sampled only US and PS states (Supplementary Fig. 3a), whereas complexes pulsed with ITC11 NTPs could additionally occupy the FS state (Fig. 5g). This confirms that we did not observe re-synthesis of a 11mer transcript, as we observed earlier that the complex could not escape the ITC6 pause at low NTP concentration (Fig. 5c). Our results clearly demonstrate that the extended cycling in different scrunching states does thus not require active RNA synthesis.
Close inspection of the trajectories belonging to the US/PS/FS subpopulation revealed that the two most frequently encountered state transitions were FS→US and its reversal US→FS (Fig. 5i and Supplementary Fig. 3f); this was also the case in the continuous presence of NTP (Supplementary Fig. 3g). The US→PS and PS→US transitions were about 4-fold less frequent, whereas PS→FS or FS→PS transitions were only rarely observed. This data clearly indicate that RPs engaged in the unscrunching/scrunching pathway do not share the same linear US→PS→FS reaction coordinate of ITCs engaged in productive transcription (Fig. 5j).

We also note the absence of any temporal correlation between two successive state dwell times (\(\Delta t_n\) and \(\Delta t_{n+1}\)), independently of the scrunching state they originate from (right hand side, Supplementary Fig. 3b, c, d), supporting a memory-less transition from one state to the next.

Paused ITC may undergo abortive initiation or hold RNA. Our FRET assay monitors the conformation of the promoter DNA and thus does not provide a direct readout for the presence of RNA in the ITCs. As pulsed RNA synthesis generated ITCs that cycle for several min between scrunched states, we assumed that these ITCs retain the nascent RNA in the transcription bubble. The assumption generates two testable hypotheses: first, RNA is

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**Diagram Descriptions**

- **Diagram a** shows the abortive transcription and backtrack-recovery pathways.
- **Diagram b** illustrates the experimental setup with RPs bound to a coverslip, NTPs added, and imaging buffer.
- **Diagram c** is a table summarizing the starting substrate and NTPs with the NTPs removed.
- **Diagram d** depicts the graph with active FRET pairs and total FRET pairs.
- **Diagram e** is another graph showing the FRET over time.
- **Diagram f** illustrates the group comparisons with error bars.
- **Diagram g** is an additional graph showing the FRET distribution.
- **Diagram h** shows another bar graph for similar comparisons.
- **Diagram i** illustrates the level n transitions with events count.
- **Diagram j** depicts the level n state transitions.
- **Diagram k** is a supplementary image showing the state transitions.
slowly released from NTP-deprived ITCs; second, RNAs retained in ITCs are extendable upon NTP reintroduction.

To determine the profile and time dependence of RNA release from ITCs, we immobilized biotinylated RP O complexes to streptavidin-coated magnetic beads. The complexes were pulsed for 10 s with the ITC7 NTP subset (containing α32P-UTP), pulled down, washed, and immersed into NTP-free reaction buffer; beads and supernatant were then analyzed at specified times to obtain the time-dependent profile of retained and released RNAs (Supplementary Fig. 4a, b). Our results showed that the RNA-release kinetics was strikingly biphasic: many ITCs released their RNA within the first 2 min, the release being almost quantitative for the shortest RNAs (~95% of 3–4 mers) and less efficient for 5-, 6-, and 7-nt RNAs (45%, 80%, and 80%, respectively; Supplementary Fig. 4b). After the rapid initial phase, the amount of released 6- or 7-nt RNA increased only marginally. After 15 min, still ~20% of 6–7-nt RNA remained bound in the ITCs. This amount is two-fold lower than what we measured in similar NTP-pulsed single-molecule experiments, where most of the active ITCs were sampling the unscrunching/scrunching states for several min (Fig. 5d). We also tested the retention of short RNAs in transcription complexes formed under the ITC11 conditions and found that comparable amounts of 6-nt transcripts remained bound to RNAP even after prolonged incubation of the complexes in the absence of NTPs (Supplementary Fig. 4c). This is in agreement with the PS and FS FRET states observed in the absence of NTPs (Fig. 5c, g).

To probe whether the stalled ITCs retaining 6-nt RNA for an extended period of time can resume active transcription, we chased the immobilized and washed ITCs with the next incoming nucleotide (GTP). We observed that the 6-nt RNA became converted quantitatively to 7-nt RNA (Fig. 5k; longer products appear due to mis-incorporation), indicating that the ITCs both retain the nascent RNA in the transcription bubble, and can access the catalytically active conformation.

In summary, the biochemical analysis revealed two populations of stalled ITCs: 70–80% of ITCs that enter the abortive initiation pathway (rapidly releasing the nascent RNAs) and 20–30% of ITCs that retain 6–7-nt RNA products and catalytic competence for tens of min after NTP depletion. These results clearly show that the nascent RNA can be stably trapped within the cyclically unscrunching/scrunching RP complex, until being eventually elongated.

**Discussion**

In this study, we employed a refined, high contrast single-molecule FRET assay to quantitatively dissect the reaction pathway and kinetics of the ITCs on the consensus lac promoter. We specifically examined the role of the σ3.2 region, the nature of pausing, and pausing-related conformational changes such as scrunching/unscrunching in the presence and absence of RNA release.

The σ3.2 region has been described as a good candidate for causing pausing, and structural, biochemical and single-molecule biophysical studies have confirmed that by occluding the RNA-exit channel of RNAP the σ3.2 region forms a barrier for the elongation of the nascent transcript past 5–6 nt15,19,20,27 (Figs. 1b and 6). Consistent with these results, we recently showed that partial deletion of σ3.2 significantly diminished pausing at ITC627. However, since the same σ3.2 derivative was associated with accelerated conformational dynamics in the open complex43, a possibility existed that some of the inferred effects on pause kinetics were indirect (e.g., due to instability of the template strand conformation in the DNA binding cleft leading to increased abortive RNA release and shortening of the ITC6 pause). Our new finding that the triphosphate moiety at the 5’-RNA end, which specifically interacts with the σ3.212,20, both shortens the half-life of ITC6 pause and increases the probability of productive pause exit44, suggests that σ3.2 is a major pause determinant in initial transcription. We also demonstrated that substitution of the σ3.2 residue F522, which contacts template DNA upstream of the active site and represents a barrier for initial RNA synthesis22,29, decreases the probability of successful RNA extension beyond the PS state. Thus, competition between the RNA 5’-end and residues from the σ3.2 region is required for efficient promoter escape, likely by promoting σ3.2 extrusion.

The 80–90% probability to enter the pause may reflect the presence of transcriptionally non-permissive (pausing RPs) and permissive (non-pausing RPs) σ3.2 conformations present in different ITC6 complexes. Based on the structural considerations12,20 and the stage of initial transcription (ref. 27), this study, the clash between σ3.2 and RNA 5’-end may hamper the movement of the template DNA and/or RNA to the post-translocated register, and therefore stabilize the pre-translocated state27,35. We provide an additional evidence in favor of this hypothesis by showing that βD446A RNAP (which de-stabilizes the post-translocated37) displayed twofold decreased ITC6 pause exit rate. However, because the pause exit rate did not strongly depend on the NTP concentration, the pause is not directly controlled by the thermodynamic equilibrium between the pre- and post-translocated states of ITC6. By similar reasoning, the pause is also not controlled by the catalytic rate of post-translocated ITC6. We thus postulate that the pause-controlling step is kinetic and involves relatively slow repositioning of the σ3.2 tip in a way that the barrier to forward translocation is removed. The highest observed pause exit rate on the promoter variant lacking the consensus pause motif (0.3 s−1 for the ΔP promoter, Fig. 2b) may reflect the rate of ITC6 pre→post translocation that we suggest to...
be controlled by \( \sigma_{3.2} \) repositioning, increasing dramatically the lifetime of the pre-translocated state in comparison to transcription elongation \(^{44} \) (~265-fold: 2.3 s vs. 8.7 ms). Importantly, several studies of pausing during transcription elongation have shown the predisposition of the pre-translocated RNAP to isomerize into a catalytically inactive off-pathway state, known as the elemental pause \(^{37,38,45} \). The \( \sigma_{3.2} \)-dependent translocation barrier encountered during initial transcription may thus act, by accumulating the pre-translocated ITC6, to increase the probability to isomerize into an elemental pause-like state (Fig. 6).

We further noticed that the pyrimidine/guanine [(Y)/G] motif, first identified in elongation consensus pauses \(^{37,38} \), also affects pausing during transcription initiation (ref. \(^{35} \) and this study). According to our current data the pause exit rate during initiation (~0.3 s\(^{-1} \)) is similar to that during elongation (~0.5 s\(^{-1} \)). The substitution of the motif increased both the pause exit rate and the probability to exit the pause. In contrast, substitution D446A in the CRE-pocket, which was previously shown to increase consensus pausing \(^{37} \), also impaired RNA extension in the ITC6. Overall, it appears that the first events leading to a pause during initiation and elongation phases of transcription are similar: an energetic (transcribed sequence in elongation) or physical (\( \sigma_{3.2} \) in initial transcription) barrier to translocation delays RNAP in the pre-translocated register \(^{35} \) from where the protein can, with sequence-dependent efficiency, branch-off to a catalytically inactive elemental pause state (Fig. 6).

Although the entry of ITC6 into the elemental pause was nearly obligatory (80–90% of trajectories showed the pause, Supplementary Fig. 2b), a significant fraction (~20% at saturating NTP concentration, Fig. 2d) of the RNAP complexes did not exit this pause on the first attempt, but instead embarked on another reaction pathway involving cyclic unscrunching/scrunching events. Unscrunching mechanistically resembles backtracking and leads to the displacement of 3'-RNA end from the pre-translocated register (predominant in PS state) towards the NTP-entry channel in US state. The net effect is a long-duration catalytic inactivation of ITC6 (Fig. 4). Interestingly, though promoter scrunching has been associated with intermediate stressed states, we did not observe a different lifetime for US, PS, and FS states (Fig. 5h), suggesting that the transitions connecting the scrunch states are not dominated energetically by the possible intermediate stressed states. Backtracking during initial transcription was also observed using magnetic tweezers \(^{28} \) (see Supplementary Discussion). The probability to enter the unscrunching/scrunching pathway inversely correlated with NTP concentration (Fig. 2c); at periods of low cellular NTP pool, the unscrunching/scrunching mechanism may thus efficiently inhibit promoter escape and transcript levels. Furthermore, perturbation of RNAP interactions with the DNA template and RNA transcript, e.g., by \( \sigma_{3.2} \)-FS22A or \( \beta \)D446A substitutions, favored the partitioning of ITC6 into the unscrunching/scrunching pathway (Fig. 3d and Supplementary Fig. 2g). This finding may further imply that native promoter and initially transcribed sequences encode efficient promoter-escape kinetics because they disfavor ITC partitioning into the non-productive unscrunching/scrunching pathway. Consistently, Record and colleagues \(^{46} \) recently reported the correlation of stronger holoenzyme–discriminator (promoter sequence between the ~10 element and transcription start site) interaction with the production of longer abortive RNAs, while producing a higher yield of promoter escape.

Previous single-molecule studies assumed a direct link between unscrunching and abortive transcription \(^{11,17,27,28} \). However, those studies focused on the DNA conformation and did not evaluate the retention of RNA in the transcription complexes. Our data demonstrated that brief pulsing of open complexes with NTPs resulted in a population of ITCs that kept on cycling between US/PS/FS states for an extended period of time (Fig. 5),

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**Fig. 6** Model for initial bacterial transcription. The progress of initial transcription is illustrated by depicting RNAP (yellow block) at key points of the inferred mechanism. The mechanism includes three competing reaction pathways, which the ITC can embark on. Productive Transcription pathway (highlighted in green) results in promoter escape and synthesis of full-length RNA. Abortive Initiation pathway (highlighted in red) leads to the synthesis and dissociation of short RNA products. Futile Cycling (highlighted in blue) temporarily traps the ITC6 into catalytically inactive interconverting pre-translocated and backtracked states, respectively. Purple finger shows the different conformations of \( \sigma_{3.2} \). Green triangle marks the template base for the next incoming nucleotide in the active site of RNAP. Red and black strands represent the nascent RNA and template DNA, respectively. The multi-timescale transitions between PS and US in Fig. 5j have here been broken up to suggest a simple composition that would give rise to the two timescales observed in Fig. 4b, c. The numeration (1, 2, and 3) indicates the three significant molecular mechanisms described by the model: the initial barrier imposed by \( \sigma_{3.2} \) to the transcription elongation, the subsequent loss of catalytic conformation and the RNA-dependent reversible backtracking, respectively. The US, PS, and FS FRET levels observed during the experiments are indicated at the bottom of the schematic.

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and that the transcripts could remain stably attached to the ITC for at least 45 min (Supplementary Fig. 4). Backtracking to the US state shortens the template DNA–RNA hybrid to ≤ 5 bp, and should reduce the hybrid lifetime. However, the possibility of a short hybrid that locks the transcript into the DNA-binding cleft is supported by the observation of a 4-nt RNA bound to a bacterial open promoter complex in crystals. Furthermore, the backtracked RNA potentially forms interactions in the NTP-entry channel, as observed in the yeast RNAP II. Taken together, the stability of the short hybrid within the complex and the positive interactions between the RNA and the NTP entrance channel may support transcript retention upon promoter unscrunching.

Recent work has also noted that RP complexes on λPr and T7A1 promoters were divided into two populations upon NTP addition: a first population (30–45% of all complexes) that rapidly (within 10 sec) synthesized long RNA (ITC < 10), and that released RNA slowly, similarly to moribund complexes. We propose that these two populations, i.e., the population producing quickly long RNAs and the moribund complexes, are consistent with the two populations of complexes described here, i.e., the RP complexes that exited the ITC6 pause on the first attempt (Fig. 1c), and the population that entered the cyclic unscrunching/scrunching state from the ITC6 pause (Fig. 1d), respectively (Supplementary Discussion).

Our new findings are summarized in a kinetic model of the transition to productive transcription (Fig. 6 and Supplementary Discussion).

The dependence of entry and recovery from the pause states implies wide variation in the kinetics of initial transcription across the bacterial promoter sequence space. On the consensus lac and similar promoters, the molecular mechanism of pausing sensitizes the efficiency of promoter escape to NTP concentration, potentially trapping the RNAP to the promoter in a “ready-to-fire” or “poised” mode until improved growth conditions lead to the rephasing of cellular NTP pools. The trapping of poised RNAPs at or near the promoter thus emerges as a common transcription regulation strategy achievable by different molecular mechanisms. For example, the σ54 RNAP holoenzyme forms an inactive, stable closed complex in bacteria, whereas negative elongation factors cause RNAP to stall within 20–60 bases downstream of the transcription start site in many metazoan genes. In all cases, inhibited RNAPs are ready-to-fire when activating signals arrive from relevant signal–transduction cascades thus avoiding promoter search, binding, melting, and activation.

Methods

Glass coverslips preparation for single-molecule experiments. Borosilicate glass coverslips (1.5 MenzelGäbler, Germany) were sonicated for 30 min in a 2% (V/V) solution of Hellmanex III (Helma Analytics, Germany)/deionized water. After being thoroughly rinsed with deionized water, the coverslips were stored at 4 °C up to 2 weeks before use.

Protein immobilization protocol. The pegylated coverslips were incubated for ~10 min with a solution 0.5 mg/ml of Neutravidin (31059, Sigma Aldrich) in 0.5 × PBS and subsequently rinsed with 1 × PBS. Preceding observation on the microscope, the coverslips were incubated for ten min with a 3% (V/V) solution of Penta-His biotin conjugate antibody (34440, QIAGEN, UK) in reaction buffer (40 mM HEPES buffer pH 7.3 (ThermoFisher Scientific, UK), 100 mM potassium glutamate, 10 mM MgCl2, 1 mM diethyldithiocarb (DTT), 1 mM cysteamine hydrochloride, 1% (V/V) glycerol (V/V), 0.5% (V/V) bovine serum albumin, 0.05% (V/V) Tween 20, and subsequently rinsed with reaction buffer. After adjusting the coverslips on the microscope, 100 pM of His-tagged protein–DNA complex, e.g., RP, was incubated in the observed well until the desired density of molecules on the coverslips surface was reached, followed by one-step rinsing with reaction buffer.

Core RNAP and σ70 preparation. The expression and purification of the core bacterial RNAP have previously been described in ref. 34. The expression and purification of the WT σ70 have been previously described in ref. 21.

Holo-RNAP and RPα assembly. Core RNAP (0.5 μM) was mixed with 0.6 μM of σ70 in 20 mM Tris–HCl pH 7.9, 150 mM NaCl, 0.1 mM EDTA, 50% (V/V) glycerol, and 0.1 mM DTT, and incubated at 30 °C for 30 min. The resulting holo-RNAP was stored at 20 °C.

Holo-RNAP and RPα assembly was mixed with 2.5 nM of DNA promoter in reaction buffer and incubated for 10 min at 37 °C to form the RP complex.

DNA constructs preparation. The DNA constructs preparation is described in detail in the Supplementary Methods.

Microscope and single-molecule experiments. The single-molecule TIRF microscope for FRET experiments has been previously described in ref. 39. Shortly, the 532 nm and the 642 nm wavelength laser beams (donor laser excitation and acceptor laser excitation, respectively) were focused in the back focal plane of an oil immersion objective (Olympus, N.A. 1.4) and illuminate alternatively the field of view, i.e., ALEX mode. The TIRF-reflected beams were directed toward a position sensor to control the objective focal plane distance to the sample at a fixed position (MS-2000 stage, ASI, OR, USA). The photons resulting from the de-excitation of the donor molecules, i.e., fluorescence, were separated from the excitation laser beams with a dichroic mirror and spectrally split in two channels, e.g., donor and acceptor that are imaged on the same electron-modifying charge-coupled device camera (iXon, Andor, Irlande). For 100 ms ALEX illumination, i.e., 200 ms frame time acquisition, the laser power measured preceding the dichroic mirror is ~0.4 mW for donor excitation laser and ~0.09 mW for the acceptor excitation laser. For 40 ms ALEX illumination (only used to acquire the data with the ΔP promoter and ATP starting substrate experimental condition), i.e., 80 ms frame time, the laser power measured preceding the dichroic mirror is ~1 mW for donor excitation laser and ~0.25 mW for the acceptor excitation laser.

The imaging buffer contained the reaction buffer completed with 1 mM Trolox, 1 mM COT, 1% (w/V) glucose, 0.4 μg/ml of catalase, and 1 mg/ml of glucose oxidase (Sigma Aldrich). The catalase and the glucose oxidase were pre-mixed together in a solution of 50 mM KCl and 50 mM Tris–OAc buffer pH 7.3 at 100 × concentration.

The data were acquired after immobilization of the RP complex to the surface. After ~200 frames (~20 s), the imaging buffer is spiked with a 12.5 × NTP solution and the reaction is observed for the remaining ~5000 frames (total time: 10 min).

For the post-RNA synthesis rinsing experiments, the RPα was incubated with NTPs in the reaction buffer for 10 s before the reaction buffer was exchanged twice with the imaging buffer, followed by the start of the acquisition. The buffer exchange procedure takes ~40 sec to be completed before the start of the acquisition.

All single-molecule FRET experiments were performed at 22 °C.

Single-molecule data analysis. FRET pair localization and detection: The movies recorded on the camera were offline analyzed using the home-built Matlab routine Twotone-ALEX to extract the intensities of co-localized donor and acceptor, i.e., FRET pair. The following parameters from Twotone-ALEX were used to select only the FRET pairs formed by a single ATTO647N acceptor dye and a single Cy3b donor dye: channel filter as DexDem&8AExAem&8DexAem (colocalization of the donor dye signal upon donor laser excitation, the acceptor dye signal upon acceptor laser excitation, and the acceptor dye signal upon donor laser excitation), a width limit between the donors and acceptor between 1 and 2 pixels, a nearest-neighbor limit of 6 pixels, and a maximal ellipticity of 0.6 (ellipticity is defined as the ratio of the minor and the major axis of the ellipse). The traces extracted from the Twotone-ALEX analysis were then sorted to remove all the traces that displayed extensive blinking or multisteps photobleaching, i.e., that contain more than one donor or acceptor dye in the same diffraction limited intensity spot.

Calibration of the FRET sensor. We calibrated the FRET sensor by measuring the FRET level for initial transcription complexes in the presence of different subsets of nucleotides that allowed maximal transcript lengths of 6, 7, or 11 nucleotides, and compared their FRET profiles with RPα. These experiments allowed unambiguous assignment of the RPα and ITC11 FRET levels (FRETα) as ~0.5 and ~0.76, respectively (Fig. 1c; see also Fig. 3a, Supplementary Fig. 1). For clarity, we define these FRET states as “US” and “FS”, respectively. Although it is commonly accepted that RNAP escapes lac promoters after synthesizing an 11-mer, the HIF high signal...
after forming a 11-nt long transcript (Fig. 1c) is consistent with extended transcription past the 6-7-mer RNA and that ITFs do not pause again until reaching the position +12 of the DNA template used here.67

FRET efficiency and hidden Markov modeling. The FRET efficiency dynamics for each FRET pair was calculated with the standard formula \( E = \frac{I_{\text{donor}}}{I_{\text{donor}} + I_{\text{acceptor}}} \), with \( I_{\text{donor}} \) and \( I_{\text{acceptor}} \) being respectively the intensity of the acceptor and of the donor upon donor excitation.63 The traces were analyzed through a modified version of the hidden Markov model eFRET software from ref. 65 (the modified code is available from the corresponding authors on reasonable request), where only steps longer than two frames and separated from the subsequent step by more than twice the Allan deviation estimated at five frames were conserved to be assembled into dwell time. The first dwell time, i.e., preceding NTP addition, and the last dwell time, i.e., preceding photobleaching or transition to FS FRET state, of each trace were removed from the dwell time distribution.

Characterization of the dwell time distributions. A detailed analysis of the dwell time distributions is provided in ref. 65. Shortly, the distribution of \( \tau \) is described by a probability distribution function with \( m \) exponentials:

\[
p(\tau) = \sum_{n=1}^{m} k_n \cdot \tau^{
-1} \cdot e^{-\tau/k_n},
\]

where \( k_n \) and \( p_n \) are the characteristic rate of the \( n \)th exponential and its probability, respectively. The minimum number of exponential to fit the distributions was determined for each distribution by using the Bayes Schwarz Information Criterion.67 We calculate the maximum likelihood estimate of the parameters (MLE) by maximizing

\[
L = \prod_{i=1}^{N} \ln[p(\tau_i)]
\]

over the parameter set. Here, the \( \tau_i \) are the experimentally measured dwell times and \( N \) is the number of collected dwell times \( \tau_i \). The error bars for each fitting parameters are one standard deviation extracted from 1000 bootstrap procedures.69 The eFRET software65 was also used to extract the peak positions of each FRET level, subsequently fitted with a Gaussian function, with the peak center and the SD as free parameters (Supplementary Figs. 1d and 3a-d).

Data availability. The data sets generated and analyzed during the current study are available from the corresponding author on reasonable request.

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**Author contributions**
D.D. and A.N.K. designed the research. D.D. designed, performed, and analyzed the single-molecule experiments. M.K. made the DNA promoter constructs. D.D. and J.J.W.B. designed and implemented the custom analysis routines. D.L.V.B. and I.P. performed and analyzed the gel electrophoresis experiments. Z.M. and K.B. provided the σ70 mutant. D.D., A.M.M., A.K., and A.N.K. discussed the data. D.D., A.M.M., and M.D. discussed the model. D.D., A.M.M., and A.N.K. wrote the article.

**Additional information**

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