Supplementary Discussion

Discussion of prior work on NCIN hypothesis.

An early study reported incorporation of NAD⁺ into initial products by *E. coli* RNAP *in vitro*³⁴. However, the work involved only promoter-independent transcription on the homopolymer template poly(dA-dT):poly(dA-dT), did not directly demonstrate the identity of the initial products, and did not demonstrate the ability of the initial products to be extended to yield longer products³⁴. Subsequent studies attempted, but failed, to detect the incorporation of NAD⁺, NADH, and dpCoA into RNA during transcription initiation by *E. coli* RNAP^{4,5}. However, a technical issue with assay conditions used in these studies--i.e., the use of ATP concentrations able to out-compete, and make undetectable, transcription initiation by NAD⁺, NADH, and dpCoA--may render the negative results in this study non-determinative. Here, we re-examine the NCIN hypothesis using an assay of promoter-dependent transcription, directly assessing the identity of the initial products, directly assessing the ability of the initial products to be extended to yield longer products, and using assays that do not contain ATP concentrations able to out-compete NAD⁺, NADH, and dpCoA.

Discussion of crystal structures of RPo-pppApC, RPo-NAD⁺pC, RPo-dpCoApC.

A crystal structure of a substrate complex for transcription initiation, consisting of RPo, ATP as initiating nucleotide, and CMPcPP as extending nucleotide, previously has been reported^{16,17}. However, no crystal structure of an initial product complex for transcription initiation previously has been reported. The crystal structure of the initial product complex obtained herein for initiation with ATP and CTP (RPo-pppApC) shows ordered density for all non-hydrogen atoms of pppApC (Figure 4a, left). The pppA residue of pppApC base pairs to the DNA template strand in the RNAP active-center "i-1 site" and interacts, through its α -phosphate, with the same RNAP residues that interact with the γ -phosphate of the initiating nucleotide in the substrate complex (β Q688 and β H1237; residues numbered as in *E. coli* RNAP; ^{16,17} and, through its β - and γ -phosphates, with β R529 and β K1242 (Figure 4a, right). The pC residue of pppApC base pairs with the DNA template strand in the RNAP active-center "i site," making interactions, through its sugar and phosphate, with the RNAP catalytic Mg²⁺ ion [Mg²⁺ (I)], and RNAP residues, notably β K1065 and β K1073, that are identical to those made by the sugar and α -phosphate of the initiating nucleotide in the substrate complex (Figure 4a, right; ^{16,17}. Strikingly, the organization of the RNAP active center enables the same RNAP residues (β Q688 and β H1237) to interact with the α -phosphate of the initiating nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the extending nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the initiating nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the initiating nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the initiating nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the initiating nucleotide in the substrate complex and enables the same RNAP residues (β K1065 and β K1073) to interact with the α -phosphate of the initiating nucleotide in the substrate complex.

The crystal structure of the initial product complex obtained upon initiation with NAD⁺ and CTP (RPo-NAD⁺pC) shows ordered density for all non-hydrogen atoms of NAD⁺pC (Figure 4b, left). The NAD⁺ residue of NAD⁺pC base pairs to the DNA template strand in the RNAP "i-1 site," making interactions through its base and phosphates identical to those in the product complex for initiation with ATP (Figures 4a-b, right), and making additional interactions through its nicotinamide ribonucleoside moiety with RNAP β D516 and β H1237 (Figure 4b, right). The pC residue of NAD⁺pC base pairs to the DNA template strand in the RNAP active-center "i site," making the same interactions as in the product complex for initiation with ATP (Figures 4a-b, right).

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The crystal structure of the initial product complex obtained upon initiation with dpCoA and CTP (RPo-dpCoApC) shows ordered electron density for the adenosine diphosphate moiety and two atoms of the pantetheine moiety of the dpCoA residue and for all atoms of the pC residue (Figure 4c, left). The dpCoA residue of dpCoApC base pairs to the DNA template strand in the RNAP "i-1 site," making interactions through its base and phosphates identical to those in the product complex for initiation with ATP (Figures 4a,c, right). The first two atoms of the pantetheine moiety project into a space having sufficient volume to accommodate the pantetheine moiety in multiple conformational states; terminal atoms of the pantetheine moiety are disordered, suggesting conformational heterogeneity (i.e., flexibility). The pC residue of dpCoApC base pairs to the DNA template strand in the RNAP active-center "i site," making the same interactions as in the product complex for initiation with ATP (Figures 4a,c, right).

Discussion of structural basis of specificity at promoter position -1.

The crystal structures of product complexes in Figure 4 demonstrate NCIN-mediated initiation but do not explain the specificity of NAD⁺-mediated initiation for an A:T base pair at promoter position -1. A definitive explanation for the specificity at promoter position -1 must await determination of an NAD⁺-containing substrate complexes (i.e., RPo-NAD⁺-NTP). However, model building suggests that, in an NAD⁺-containing substrate complex, the NAD⁺ nicotinamide moiety can be positioned to form a "pseudo-base pair" with template-strand T at position -1, forming two H-bonds with Watson-Crick H-bonding atoms of the template-strand thymine base at position -1 and stacking on the NAD⁺ adenine base.

Supplementary Table 1. Oligonucleotides used to generate templates for transcription assays.

Name	Description	Sequence (5' to 3')
JB 221	For cloning NudC- XbaI forward	CAATTCCCCTCTAGAAATAATTTTGTTTAAC
	primer	TTTAAGAAGGAGATATAATGGATCGTATAA
		TTGAAAAATTAGATCACGGC
JB 222	For cloning NudC- NotI reverse	GTGCTCGAGTGCGGCCGCGCGCGCGCGCGG
	primer	CACCAGCTCATACTCTGCCCGACACATCGCC
		ACCGT
JB 224	gadY template (-65 to +35) oligo	AGCGTATAGCTTATGTTTATAAAAAAATGGC
	used in Figures 1b, 2a and 2b	TGATCTTATTTCCAGTAAAAGTTATATTTAA
		CTTACTGAGAGCACAAAGTTTCCCGTGCCAA
JB 228	Forward primer for amplification of	GATTAATTTAAAATTTATCAAAAAGAGTATT
ID 220	<i>T/A1</i> template	GAC
JB 229	Reverse primer for amplification of	ICGIIGGGAIGGCIA
ID 220	<i>I/AI</i> template	
JB 230	Forward primer for amplification of	AGCGIAIAGCIIAIG
ID 221	<i>gau1</i> template	
JD 231	and V tomplate	CICCIOIIOCACOODAAAC
IB 232	N25 template (65 to +35) oligo	ΑΤΟΟ ΑΤΟ ΑΛΟΥΤΑΛΑΛΑΛΑΤΤΑΤΤ
JD 232	used in Figure 2b	TGCTTTCAGGAAAATTTTTCTGTATAATAGA
	used in Figure 20	TTCATAAATTTGAGAGAGGAGTTTAAATATG
		GCTGGTT
JB 233	Forward primer for amplification of	ATCCGTCGAGGGAAATCATAAAAAATTTATT
	N25 template	TGC
JB 234	Reverse primer for amplification of	AACCAGCCATATTTAAACTCCTC
	N25 template	
JB 235	T7A1(+2C,+3T) template (-65 to	GATTAATTTAAAATTTATCAAAAAGAGTATT
	+35) oligo used in Figure 2b	GACTTAAAGTCTAACCTATAGGATACTTACA
		GCCaCTGAGAGGGACACGGCGAATAGCCAT
		CCCAACGA
JB 244	gadY(+1G) template (-65 to +35)	AGCGTATAGCTTATGTTTATAAAAAAATGGC
	oligo used in Figure 2a	TGATCTTATTTCCAGTAAAAGTTATATTTAA
		CTTGCTGAGAGCACAAAGTTTCCCGTGCCAA
ID 201		
JB 281	Forward primer for amplification of	CGAGGTATGTAGGCGGTGCTACAG
	<i>rnal</i> templates in Figures 1b, 2a	
ID 200	and 20	
JB 288	r_{nal} template (-05 to +112, A-less)	
	+35) and (-65 to $+112$) templates	
	in Figures 1b, 2a and 2b	TGCCTGTTTCCTCGGTTCTTTGTGTTGGTTGC
	11111gures 10, 20 and 20	TCTGTGTTCCTTCGTTTTTCCGCCCTGCTTGG
		CGGTTTTTTCGTTTTCTGTGC
JB 251	Reverse primer (+112) for	GCACAGAAAACGAAAAAACCGCCAAGCAG
	amplification of rnal (-65 to $+112$)	G
	A-less template used in Figure 1b	

JB 287	<i>rnaI</i> (+1G) template (-65 to +112,	CGAGGTATGTAGGCGGTGCTACAGAGTTCTT
	A-less) oligo used to make <i>rnal</i>	GAAGTGGTGGCCTAACTACGGCTACACTAG
	(+1G) (-65 to +35) template used in	AAGAGCTTGTTTTGGTGTCTGCGCTCCTCCT
	Figure 2a	TGCCTGTTTCCTCGGTTCTTTGTGTTGGTTGC
		TCTGTGTTCCTTCGTTTTTCCGCCCTGCTTGG
		CGGTTTTTTCGTTTTCTGTGC
JB 269	Reverse primer to amplify <i>rnal</i> (-65	AACAGGCAAGGAGGAGCGCAG
	to +35) and <i>rnal</i> (+1G) (-65 to +35)	
	templates used in Figures 2a and 2b	
JB 270	N25 (+2C, +3T) template (-65 to	ATCCGTCGAGGGAAATCATAAAAAATTTATT
	+35) oligo used in Figure 2b	TGCTTTCAGGAAAATTTTTCTGTATAATAGA
		TTCACTAATTTGAGAGAGGAGTTTAAATATG
		GCTGGTT
CK01639	Bubble template, template strand	TGAAGTCTTGTGTGGTCCTGAGAAAGTGTTG
	1 7 1	AGATCCATGACAGAAAGATTAATAATTGTA
		TGACTATTTATACGCGTCCTGT
CK01621	Bubble template, non-template	Biotin/ACAGGACGCGTATAAATAGTCATACA
CIKOTOZI	strand (carries 5' biotin)	ATTATTAATCTTTCACGATCTTTCCTCAACAC
	, , , , , , , , , , , , , , , , , , ,	TTTCTCAGGACCACACAAGACTTCA
JB 293	P _{rnal} forward primer to amplify	GCCAGTCTAGACGAGGTATGTAGGCGGTGC
52 275	JB313 for cloning pJB89	TACAG
JB 303	MazF-mt3 cut site reverse cloning	CTATTCGGATCCAAGGAACG
	primer for cloning pJB89 and	
	pJB91	
JB 313	P _{rnal} (+43 MazF-mt3 cut site) PCR	CGAGGTATGTAGGCGGTGCTACAGAGTTCTT
	template for cloning pJB89	GAAGTGGTGGCCTAACTACGGCTACACTAG
		AAGAACAGTATTTGGTATCTGCGCTCTGCAC
		GATGGGTTAATTCGTTCCTTGGATCCGAATA
		G
JB 306	P _{T7A1} forward primer to amplify	GCCAGTCTAGAGATTAATTTAAAATTTATCA
	JB315 for cloning pJB91	AAAAGAGTATTGAC
JB 315	P _{T7A1} (+43 MazF-mt3 cut site) PCR	GATTAATTTAAAATTTATCAAAAAGAGTATT
	template for cloning pJB91	GACTTAAAGTCTAACCTATAGGATACTTACA
		GCCACAGTATTTGGTATCTGCGCTCTGCACG
		ATGGGTTAATTCGTTCCTTGGATCCGAATAG
JB 367	<i>rnal (-1C)</i> template (-65 to +112,	CGAGGTATGTAGGCGGTGCTACAGAGTTCTT
	A-less) oligo used to make <i>rnal</i>	GAAGTGGTGGCCTAACTACGGCTACACTAG
	(-1C) (-65 to +35) template used in	AAGCACTTGTTTTGGTGTCTGCGCTCCTCCTT
	Figure 2c	GCCTGTTTCCTCGGTTCTTTGTGTTGGTTGCT
		CTGTGTTCCTTCGTTTTTCCGCCCTGCTTGGC
		GGTTTTTTCGTTTTCTGTGC