Correction. In the article "Location, function, and nucleotide sequence of a promotor for bacteriophage T3 RNA polymerase" by Samit Adhya, Shantanu Basu, Probir Sarkar, and Umadas Maitra, which appeared in the January 1981 issue of *Proc. Natl. Acad. Sci. USA* (78, 147-151), the authors request that the following correction be noted. In the abstract, lines 7 and 8 should be "(−)strand sequence is 5' T-A-T-T-T-A-C-C-C-T-A-C-T-3'."
Location, function, and nucleotide sequence of a promoter for bacteriophage T3 RNA polymerase

(restriction map of T3 DNA/Southern hybridization/restriction fragment transcription by T3 RNA polymerase/DNA sequencing/ RNA sequencing)

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ABSTRACT The major promoters for bacteriophage T3 RNA polymerase on the T3 genome have been mapped by DNA-RNA filter hybridization. One promoter is located in a 300-base-pair Hpa I restriction fragment near the genetic "left" end of T3 DNA. The sequence in the vicinity of the major initiation site of transcription in this region has been determined. A part of the (-)strand sequence is 5'-T-A-T-T-A-C-C-C-T-C-A-C-T-A-A-G-G-3'. Comparison of this sequence with the prototype 23-base-pair promoter sequence for bacteriophage T7 RNA polymerase shows a striking pattern of homology and divergence. Between positions -9 and -4, the sequences are virtually identical, whereas between positions -17 and -10, the sequences are quite different. It is postulated that these sequence subsets may perform different functions in transcription initiation by the phage RNA polymerases.

The development of coliphage T3 in infected cells is controlled at the transcriptional level by two distinct RNA polymerases. First, a set of "early" genes is transcribed by the host Escherichia coli RNA polymerase. Then, one of the early gene products (that of gene 1) that is itself an RNA polymerase copies the "late" T3 genes (1-4).

T3 RNA polymerase is interesting for several reasons. It is a single-subunit enzyme that, by itself, can catalyze all the partial reactions of transcription. Also, it has remarkable template specificity and efficiently transcribes only T3 DNA (2,5). Even DNA from the related bacteriophage T7 is a poor template for it. Finally, recent studies (6) have shown that the set of 5'-terminal sequences for RNA chains synthesized by T3 RNA polymerase is restricted, implying a high degree of initiation specificity.

Thus, it was of interest to determine the DNA sequences of one or more promoters for T3 RNA polymerase. In this paper, we present data for a promoter located in the early region of the T3 genome. We show that this promoter, although not recognized by T7 RNA polymerase, has striking similarities (as well as differences) to T7 prototype promoter (7-9). The implications of these results for promoter function are discussed.

MATERIALS AND METHODS

Restriction Map of T3 DNA. The cleavage sites for a number of restriction enzymes on T3 DNA have been mapped by standard methods (ref. 10, Fig. 1). A similar map has recently been published by Bailey et al. (15).

Isolation of Restriction Fragments. The 300-base-pair (bp) Hpa I-N fragment and fragments derived from it were isolated from Hpa I digests of T3 DNA by electrophoresis on 5% polyacrylamide gels, followed by elution of the ethidium bromide-stained (or 32P-labeled) band by the "crush-and-soak" method of Maxam and Gilbert (12).

Isolation of [γ-32P]CTP-Labeled T3 RNA Polymerase Transcripts. T3 RNA polymerase transcripts were prepared in reaction mixtures (0.1 ml) containing 50 mM Tris-HCl (pH 8.0); 20 mM MgCl2; 4 mM dithiothreitol; 0.4 mM each of ATP, CTP, UTP, and [γ-32P]GTP (11,000 cpm/pmol); 0.3 pmol of T3 DNA; and 1-3 pmol of T3 RNA polymerase. Incubation was for 30 min at 37°C. The reaction mixtures were digested with RNase-free DNase I (10 µg/ml) for 30 min at 0°C and then extracted with phenol. The extracts were treated with 2.5 vol of ethanol at -20°C, and the products were chromatographed on Sephadex G-50 columns to remove unincorporated nucleoside triphosphates.

Transcription of Hpa I-N Fragment. Typical transcription mixtures had the same composition as above, except that 0.5 pmol of Hpa I-N fragment was used in place of the T3 DNA and 1 pmol of T3 RNA polymerase was used per 50 pl of mixture. After 30 min of incubation at 37°C, reactions were stopped by addition of NaDodSO4 (final concentration, 0.1%) and EDTA (final concentration, 20 mM), followed by heating at 65°C for 1 min. The mixtures (or aliquots thereof) were treated with ethanol, and the pellets were rinsed once with 95% ethanol, dried, and suspended in 50 µl of 57% formamide containing xylene cyanol and bromophenol blue before loading on 5% acrylamide/8 M urea gels for electrophoretic analysis.

Preparation of 5' -32P-Labeled Hpa I-N Transcripts. The following procedure was used to end label the major Hpa-N transcript. Transcription reactions containing only unlabelled ribonucleoside triphosphates were prepared. The products were subjected to electrophoresis on a 5% acrylamide/8 M urea gel alongside Hpa I-N transcripts labeled with [α-32P]UTP as markers. After autoradiography, the regions in the unlabeled lanes corresponding to the 32P-labeled major transcript were excised and eluted by the "crush-and-soak" method (12). The 5'-triphasate end of the RNA was dephosphorylated with bacterial alkaline phosphatase and then labeled with [γ-32P]ATP and polynucleotide kinase as described (16). The labeled transcript was separated from unreacted ATP and any degradation products by electrophoresis on 5% acrylamide/8 M urea gels and eluted as above.

RESULTS

Mapping T3 RNA Polymerase Start Sites on T3 DNA. The first step in the determination of the structure(s) of the promoters for T3 RNA polymerase was to locate the major transcriptional start sites in the restriction fragments of known map position. To do this, use was made of the fact that T3 RNA poly-

Abbreviation: bp, base pair(s).
merase initiates solely with GTP (17). 5'-32P-labeled RNA was prepared in an in vitro reaction mixture containing T3 DNA, T3 RNA polymerase, and nucleoside triphosphates having [γ-32P]GTP as the only labeled nucleotide. This RNA was hybridized to Southern blots of denatured Hpa I and Mbo I restriction fragments of T3 DNA (18). After hybridization, excess filter-bound RNA, as well as nonhybridized portions of DNA-bound RNA, were digested with RNase A. Autoradiography of the treated filters was used to locate the bands corresponding to those DNA fragments containing internal RNA start sites (and thus protecting the 5'-32P-label of the probe). The following Hpa I bands were found to contain transcription start sites: Hpa I-A, Hpa I-B, C (not resolved by this procedure), Hpa I-E, Hpa I-G, and Hpa I-N. Mbo I fragments hybridizing to 5'-32P-labeled RNA included Mbo I-A, Mbo I-B, Mbo I-C, Mbo I-D, Mbo I-E, Mbo I-G, and Mbo I-I (Fig. 2). Under different conditions of transcription (i.e., 10 mM MgCl2/50 mM KCl), an additional Hpa I fragment—Hpa I-H—was observed to hybridize to [γ-32P]GTP-labeled T3 RNA polymerase transcripts (data not shown). Therefore, these fragments were suitable for promoter-structure analysis.

Template Activity of Hpa I-N Fragment. One of the restriction fragments found to contain a T3 RNA polymerase start site was Hpa I-N, a 300-bp fragment located about 330 bp from the genetic left end of T3 DNA [in front of the 0.3 gene for SAMase (19); see Fig. 1]. However, the hybridization assay used does not detect complete promoter elements, including sequences upstream from the start site known to be important for E. coli RNA polymerase (20–23). Furthermore, it was not possible to conclude solely on the basis of this assay whether one or more than one promoter is present in the fragment. Therefore, the promoter activity of the Hpa I-N fragment was examined by carrying out in vitro transcription reactions with T3 RNA polymerase using the fragment as template. Gel analysis of the transcription products, labeled with [α-32P]UTP, showed the presence of one major band (transcript A) and a few minor bands (Fig. 3). Transcript A is 230 ± 10 nucleotides long and represents the major promoter within the Hpa I-N DNA fragment. The other bands probably represent minor start sites for T3 RNA polymerase and are not considered further in this report.

The specificity of initiation from the major Hpa I-N promoter was examined in transcription reactions containing [γ-32P]GTP or [γ-32P]ATP as the labeled substrate. Transcript A was labeled

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**Fig. 1.** Restriction endonuclease cleavage sites on T3 DNA. (A) Sites of T3 DNA cleavage by HindIII, Xba I, Bgl II, Kpn I, Mbo I, and Hpa I nucleases. Mapping was by a combination of standard techniques, including (i) use of deletions R4 and R14 (11) in the early region for orientation with the genetic map, (ii) 5'-end labeling to identify terminal fragments (12), (iii) double and partial digestions (13), (iv) combined exonuclease III-exonuclease VII digestion for deletion of restriction sites from both ends of the DNA (13), and (v) the partial-digestion mapping method of Smith and Birnstiel (14). The horizontal scale calibrates percentage units from the genetically defined left end of T3 DNA. One T3 unit equals 380 bp. (B) Sites of cleavage by HindIII, Hae III, and Hpa II nucleases within the Hpa I-N fragment. The map was constructed from end-labeling experiments and DNA sequencing. Distances of various sites (in bp) are from the leftward Hpa I site.

**Fig. 2.** Hybridization of [γ-32P]GTP-labeled T3 RNA polymerase transcripts to T3 restriction fragments. Restriction digests of T3 DNA and Hpa I (A) or Mbo I (B) were subjected to electrophoresis on 1% agarose gels alongside 32P-labeled markers (not shown). The separated fragments were denatured with alkali, transferred to nitrocellulose filters by the technique of Southern (18), and hybridized for 15 hr at 60°C in 1 ml of 0.3 M NaCl/0.03 M sodium citrate/0.1% NaDodSO4/100 μg of E. coli tRNA/225,000 cpm of [γ-32P]GTP-labeled T3 RNA polymerase products. The filters were then washed with 0.3 M NaCl/0.03 M sodium citrate, incubated in the same mixture with RNase A (19 μg/ml) for 30 min at room temperature, washed again, dried, and autoradiographed. Hpa I and Mbo I fragments hybridizing to the probe are indicated.
ATP at the following enzymes: lane d, T3 RNA polymerase at 16 units (1 pmol); lane e, T7 RNA polymerase at 3 units; and lane f, E. coli RNA polymerase at 6.5 units. (C) T3 RNA polymerase (1 pmol) was used to transcribe 0.5 pmol of Hpa I-N (lane g) or 0.5 pmol Hpa I-N digested with Hae III [i.e., a mixture of Hpa I/Hae III (175 bp) and Hae III/Hpa I (115 bp); see Fig. 1] (lane h). [α-32P]UTP at 1700 cpn/pmol was used as the labeled substrate. All reactions were processed as described and run on 6% acrylamide/8 M urea gels for 5 hr at 110 V. Lane M, denatured 32P-labeled DNA molecular-length markers. Sizes (in nucleotide residues) are indicated at the left of each panel. The high molecular weight smear in lane b probably represents an aggregate of [γ-32P]GTP with reaction components.

When [γ-32P]GTP was present but not in the presence of [γ-32P]ATP. These observations are consistent with the reported specificity of T3 RNA polymerase for GTP as the initiating nucleotide (17).

We also determined whether the major Hpa I-N promoter was recognized by RNA polymerases other than the T3 enzyme. In vitro transcription reactions containing E. coli RNA polymerase, no band corresponding to transcript A was detected, although other bands were present. Furthermore, T7 RNA polymerase was completely inactive in the reaction. These results confirm the unique specificity of the T3 promoter for its cognate (T3) RNA polymerase.

The direction of transcription from the major promoter was deduced as follows. Hpa I-N was digested with Hae III to generate two fragments, Hpa I/Hae III (175 bp) and Hae III/Hpa I (115 bp), and the mixture was then used as template for T3 RNA polymerase. Under these conditions, the size of the major transcript A was reduced from 230 to 115 nucleotides, as expected if transcription proceeds from left to right as shown in Fig. 1—i.e., the same as the general direction of T3 RNA polymerase transcription on T3 DNA.

**DNA Sequence of the Promoter Region.** To sequence the promoter region in Hpa I-N, the restriction fragment was labeled at its 5'-ends by using [γ-32P]ATP and T4 polynucleotide kinase (12). The labeled fragment was then recut with Hae III, HinfI, or Hpa I to generate fragments labeled at a single 5'-end (see Fig. 1B). Fragments Hpa I/HinfI (210 bp), HinfI/Hpa I (92 bp), Hpa I/Hae III (175 bp), and Hae III/Hpa I (115 bp) were subjected to DNA sequencing by the Maxam-Gilbert method (12) to obtain the entire sequence of Hpa I-N DNA fragment.

The DNA sequence of a portion of Hpa I/Hae III (175 bp) fragment is shown in Figs. 4 and 5. The start point for transcription from the major promoter was deduced as follows. Knowing the size of transcript A (230 ± 10 nucleotides) and assuming that transcription continues to the end of the Hpa I-N fragment in the left-to-right direction, we can tentatively assign the start site to 70 ± 10 bp from the left (Hpa I site) end of the Hpa I/Hae III (175 bp) fragment. The DNA sequence in this region showed the presence of two identical octameric sequences, 5'-G-G-G-A-A-U-A-A-3', starting at positions 63 and 87, respectively. The hexamer 5'-G-G-G-A-A-U-A-3' has been shown to be one of the
major 5'-terminal RNA sequences for T3 RNA polymerase. Thus, one, or both, of the octameric sequences could represent the start site for T3 RNA polymerase in the Hpa I-N fragment. To decide which start site was used by the polymerase, the sequence near the 5' end of the major Hpa I-N transcript was determined.

5'-Terminal Sequence of Major Hpa I-N Transcript. The major Hpa I-N transcript, isolated from Hpa I-N DNA-directed T3 RNA polymerase reactions, was enzymatically labeled at its 5' end by using a combination of bacterial alkaline phosphatase and polynucleotide kinase. The end-labeled RNA was then sequenced by the technique of Donis-Keller et al. (16), involving partial digestion with RNases that possess defined specificities. The autoradiogram of the products showed the sequence of the RNA to be 5' G-G-G-A-ApyA-A-A-GpyG-G-ApyA . . . . 3' (Fig. 6). This suggests that the precise start for T3 RNA polymerase transcription is located at nucleotide 63 of the Hpa I-N [or Hpa I/Hae III (175-bp)] DNA fragment (see Figs. 4 and 5).

DISCUSSION

We have presented data showing the locations of the T3 RNA polymerase start sites on T3 DNA and determined the nucleotide sequence of one of these promoter regions. The promoter chosen is located in the 300-bp Hpa I-N DNA fragment, which is on the left of the SAMase gene (0.3) in the early region of the T3 genome (19). The presence of a T3 RNA polymerase start site in this region, as shown by the filter hybridization studies, corroborates previous reports (3, 24) of the production of the SAMase enzyme in vitro translation systems directed by in vitro T3 RNA polymerase products as well as by in vivo late T3 RNA. In this respect, T3 differs from T7 and other related phages that lack either a SAMase gene or, as far as is known, a promoter so far to the left of the early DNA region. The physiological significance of this promoter is unknown. It may be that during the late phase of T3 infection (when the host RNA polymerase is inactive), continued SAMase production under the control of T3 RNA polymerase is necessary to maintain host restriction (11). Alternatively, if the promoter serves as an initiation site for class II mRNAs (derived by uninterrupted transcription into the late region), its location before the SAMase gene may be purely coincidental. Our hybridization studies have also shown the presence of other potential class II promoters in the early region (see Fig. 2).
As the first step toward identification of the sequences necessary and sufficient for promoter recognition by T3 RNA polymerase, we have determined the DNA sequence around the major transcriptional start site in the $Hpa\ I$-$N$ DNA fragment. Similar studies of a number of other promoter regions of T3 DNA will be necessary, however, before a common (consensus) sequence can be identified, although our results enable us to compare this system with that of the related phage T7. If the T3 and T7 sequences are aligned with the transcription start-points in register and, we assume that, in T3 as in T7, the 23-bp stretch from position $-17$ to position $+5$ (see Fig. 5) defines the promoter sequence, we find a striking pattern of sequence homology and divergence. Between positions $-9$ and $+4$, the T7 and T3 sequences are identical except for the single base pair at position $-2$. Upstream from this 13-bp stretch, the sequences diverge, corresponding at only 3 out of 8 positions (between $-10$ and $-17$). It is tempting to postulate that these two sets of sequences constitute the different elements required for transcription initiation in T3 and T7 systems.

The sequence between positions $-9$ and $+4$ may serve a basic function for initiation—e.g. helix unwinding by the RNA polymerase. It is interesting that, for the two E. coli promoters, $lac\ UV5$ and T7A3, similar stretches of DNA, located at similar positions (between $-9$ and +3 and between $-9$ and +2, respectively), are apparently unwound within the promoter complex (25). On the other hand, the sequence between $-17$ and $-10$ (or part thereof) could serve as a specificity element at which the polymerase initially binds. This would explain the lack of T3 promoter recognition by T7 RNA polymerase and vice versa (refs. 2 and 5; this report).

The presence of two functionally different subsets of DNA sequence in T3 and T7 promoters would imply a similar dichotomy at the level of the respective RNA polymerases. Distinct domains of the protein may interact, perhaps cooperatively, with the two subsets of the promoter. Homologous polymerase-promoter interaction would then be a result of binding of the specificity domain of the protein to the specificity element (between positions $-17$ and $-10$) of the promoter sequence. This model is supported by studies with T3-T7 hybrid RNA polymerases that show that a restricted region near the COOH-terminal end of the gene 1 protein determines its preference for T3 or T7 DNA as a template (26).

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