

# Aphidicolin inhibits DNA polymerase II of *Escherichia coli*, an alpha-like DNA polymerase

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The *polB* gene of *E. coli* encodes DNA polymerase II. We have reported the cloning (1, 2) and sequencing of the *polB* gene (3) (GenBank Accession number M35371). DNA polymerase II appears to be a non-essential function since the *polB* gene is missing from some widely used strains (3). Several sub-families of DNA polymerases have been identified (4). In this communication, we demonstrate that DNA polymerase II of *E. coli* is an  $\alpha$ -like DNA polymerase by amino acid sequence conservation and inhibition by aphidicolin.

A search of the MBCRR Protein Pattern Library indicated significant similarity (6.3 standard deviations above the mean of comparisons with a negative control set) to only a single pattern (pattern 156) generated from a set of  $\alpha$ -like polymerases (Fig. 1). DNA polymerase II has the highest overall similarity to human DNA polymerase  $\alpha$  and phage T4 DNA polymerase. The entire length of DNA polymerase II is similar to a subregion of both polymerases and within this region the sequences are both approximately 22% identical. There are three sequence motifs characteristic of the  $\alpha$ -like family (regions I, II, III) (4, 5). The H region shown in Figure 1 corresponds to region I characterized by the presence of 5–7 contiguous conserved amino acids (YGDTS). The E region corresponds to region II. In addition to a central conserved sequence of 5–10 residues (DSLWPS), there are additional sequence identities on both sides of the conserved center. Regions F and G correspond to region III with invariant residues at five positions. These three regions are in the same linear arrangement (II-III-I) as other DNA polymerases in this family and the relative distances between the regions are similar.

The N-terminal region (residues 1–301) of DNA polymerase II has significant similarity to only a subset of the  $\alpha$ -like DNA polymerases (human  $\alpha$ , phage T4, yeast polIII, Epstein-Barr virus, and *Autographa californica* nuclear polyhedrosis virus [A-

CNPV]). The regions of the six polymerases having the highest mutual similarity were aligned (shaded boxes in Figure 1). Region A in other  $\alpha$ -like polymerases has 3'–5' exonuclease activity.

Human DNA polymerase  $\alpha$  is inhibited by the drug aphidicolin. We found that aphidicolin also inhibited DNA polymerase II ( $K_i = 50 \mu\text{M}$ ). The peculiar aphidicolin sensitivity of DNA polymerase II offered an opportunity to assess its possible role in DNA replication. Toluene-treated *E. coli* cells offer a convenient means of assessing the effect of compounds on the elongation phase of DNA replication, since the permeable cells eliminate problems of transport (6). We found no significant effect of aphidicolin on the level of ATP-dependent synthesis in seven different strains of *E. coli*, including two strains apparently lacking the *polB* gene (3), MC1061 and MC1000. We conclude that there is no detectable role of DNA polymerase II in the elongation phase of DNA replication.

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Hum. $\alpha$	VKKSTALNQPVSWC-	KVEAMALK PDLVNVIKDVSPPL VVMAFSMKTMONAKN HONEIIAMAI VHHS FALDKAAPKPP--FQ	581	
Pol II	MNYEKRLREGVT--	-VYEA VRP PERYL MEREIT S P V W VEGDMHN GT IV N A R L KPHPDYR-PPIK W V S ID IETTRH G E Y C	78	
T4	RDW MKRMEDIGEAL	GMNDFKLAYISD TYG SE IVYDRKFV --RVA NCDIEVTGDKFPDPM KAEYEID-AITHYDS IDR FYVF D L NS MY	154	
		<b>A</b>		
Hum. $\alpha$	SHFCVVSKPKDCIFP	YAFKEVIEK---KN -VKV EVAATERTLLG FFLAKVHKIDPDIIV GAN IYGELE VILLOR I ---NV-C KAP H W	660	
Pol II	IGLEACGQRIVYMLG	PENG D-ASS---LD -FE LE Y V A S P O L L E KIN AWFAN Y P D V I I GAN V V O D L A M Q K H A ---ER-Y RLP--	154	
T4	GSVSKWD AKA LKD	C E G D -EV P Q E I L D R VIYMPFDNERDMLME Y IN L W -EQ K R E A I F T GAN I E G D V E Y I M N R V K M I L G E R S M K R F --	240	
Yst PIII		DPDV I I G Y T T M D P Y L L R A 413		
EBV		S V E I V T G A V A N T D P Y L L R A 392		
ACNPV		N P D V I L D P N G D V T D P Y L L R L 293		
		<b>B</b>		
Hum. $\alpha$	SKIGRLKRSNMPKLG	GRSGFGERNATCGRM ICD-VE ISAK-ELIR CKSYHL SELVQ OIL- KTERVVIP M E N I Q N M Y S E S S Q -L L Y L E H T	746	
Pol II	L R I G R D N S E L E W R E H	GFKNGVFFAQAKGRL IIDGIEAL-KSAFWN FSSE SLETVAQELLG EGKSIDNP W D R M D E I DRRFAEDKPA L A T Y N	243	
T4	SPI GRVKS K L I Q N M Y	G S K E --I Y S I D G V S I I D Y L D Y K K F A T N L P S E S L E S V A Q H E T --K K G K L P Y D --G P I N K L R E T N H Q R Y I S Y N	322	
Yst PIII		G R L Q D 461		
EBV		G L I P D 440		
ACNPV		Y Y I H D 335		
		<b>C</b>		
Hum. $\alpha$	W K D A K F I L Q I M C E L N	V I P L A D Q I T N I A G N I M S R T L M G R S E R N E F L L L H A F Y E N N Y I V P D K Q I F R K P Q Q K L G D E D E E I D G D T N K Y K K G R K	836	
Pol II	I K D C E L V T Q I F H K T E	I M P F I L E R A T V N G I P V D R H -G G S V A A F G H L Y F P R M H R A G Y V A P N -----	306	
T4	I I P V E S V O A I D K I R G	F I D L V I S M S Y Y A K M P F S G V --M S P I K T W D A I I F N S L K G E H K Y I P Q -----	385	
Yst PIII	I K D A Y I P P R L	525		
EBV	V Q Q S A L V M D L	504		
ACNPV	V Q Q C M L P I K L	400		
		<b>D</b>		
Hum. $\alpha$	K G A Y A G G I V L D P K V G	F Y D K F I L L D F N S I L Y P S I I Q E F N I C F -- --T T V Q R V A S E A Q K V T E D G E Q E Q I P E -- L P D P S I E M G I L P R E I R	917	
Pol II	P H A S P G G Y V U M D S R P G	LY D S -V L V L D Y K S I L Y P S I I R T F L I D P -- --V G L V E G M A Q P D P E H S T E G F L D -- A W F S R E K H C L P E I V T	382	
T4	K Q S F P G A F V F E P K P I	A R R Y -I M S F D L T S I L Y P S I I R O V N I S P E T I R G Q F K V H P I H E Y T A G T A P K P S D E Y S C S P N G W Y M D K H Q E G I I P K E I A	474	
Yst PIII	Y G A T V I E P J R G	Y D V P I A T L D F N S I L Y P S I I Q A H N I C 621		
EBV	Y G A T V I Q E L S G	F Y N S P V L V V D E A S L Y P S I I Q A H N I C 599		
ACNPV	Y K G G K V L K P R A G	I Y K N A F -S L D F N S I L Y T I M I A I C A C 545		
		<b>E</b>		
Hum. $\alpha$	K L V E R R K O V K Q I M K Q	Q D I N P D L I L Q Y D I R - -----		
Pol II	N I W H G R D E A K --	R Q G N K P L -----		
T4	K V F F O R K D W K K I M F A	E E M N A E A I -K K I I M K G A G S C S T K P E V E R Y V K F S D D F L N E L S N Y T E S V L N S L I E C E K A A T L A N T M Q L N R K I L I N S	563	
Yst PIII		Q L A L K I S A M S		
EBV		Q L A L K I C H A		
ACNPV		Q N S V E R T A N S		
		<b>F</b>		
Hum. $\alpha$	Y G Y G Y G S Y S R F Y A K	P L A A V T Y K G R -- --E I L M H T K E M V Q K M N L E -V I Y G D T D S I M I --N T N S T N L E E V F K I G N K V K S E V N --	1031	
Pol II	F Y G V I G T T A C R F F D P	R L A S S I T M R G H -- --Q I M R Q T K A L I E A Q G Y D -V I Y G D T D S T F V --W L K G A H S E E E A K I G R A L V Q H V N A W W	488	
T4	L Y G A L G N I H F R Y Y D L	R N A T A I T I F G Q V G I Q W I A R K I N E Y L N K V C G T N D E D F I A G D T D S V Y C V D K V I E K V G L D R F K E Q N D L V E F M N Q F G	653	
Yst PIII	V Y G F T G 709	I S S I T A Y G R 729	V V Y G D T D S V M Y 765	
EBV	V Y G F T G 692	I A F T T L G R 712	V I Y G D T D S L E I 761	
ACNPV	V Y G Y Y G 617	L A V Y T R V G R 632	V V X G D T D S T F V 674	
		<b>G</b>		
Hum. $\alpha$	--K Y K L L E I D I D G V E K S L L --	--L K K K K Y A A L V V E P T S D G N Y V T K Q E L K G L D I V R P D W C D L A K D T G N F V I G Q I L S	1102	
Pol II	A E T L Q K Q R L T S A L E L	E Y E T H E C R F I M P T I R G A --D T G S K K R Y A G L I Q E G D K -- --Q R M V F K G L E T V R T D W T P L A Q Q F Q Q E L Y L R I F R	569	
T4	K K K M E P M I D V A Y R E L	C D Y M M N R E H L M H M D R E A I S C P P I G S K G -V G G F W K A K R -- --Y A L N V Y D M E D K R F A E P H L K I M G E T --Q Q S S T	735	
		<b>H</b>		
Hum. $\alpha$	D Q S R D T I V E N I Q K R L	I E I G E N V L N G S V P Y S Q F E I N K A L T K D P Q D Y P D K K S L P H V H V A L W I N S Q --G G R K V K A G D T V S Y V I C Q D G S N -L T A	1189	
Pol II	N E P Y Q E Y V R E T I D K L	M A -G E --L D A R L -V Y R K R L R R P L S E Y Q R N V P --P H V R A A R I A D E E N Q K --R G R P L Q Y Q N R G T I K Y V W T T G -P E P	650	
T4	P K A V Q E A L E E S I R R I	L Q E G E --E S V Q -E Y Y K N F E R E Y R Q L D Y K V I A E V K T A N D I A K Y D D K G W P G F K C P F H I R G V L T Y R R A V S G I G V A P I	821	
		<b>I</b>		
Hum. $\alpha$	S Q R A Y A P E Q L Q K Q D N	L T I D T Q Y Y L A Q Q I H		
Pol II	P G L P T F T T G L R T L S D	P P A T R G G G N T P F Y		
T4	L D G N K V M V L P L R E G N	P F G D K C I A W P S G T E		

**Figure 1.** Composite of several pairwise and multiple alignments between  $\alpha$ -like DNA polymerases. This figure shows the alignments of selected regions of the following polymerases (reference or SWISS-PROT ID, or GenPept Locus): *E. coli* DNA polymerase II, human alpha (DPOA\$HUMAN), T4 (DPOL\$BPT4), yeast polIII large subunit (DPO3\$YEAST), Epstein-Barr virus (DPOL\$EBV), *Autographa californica* nuclear polyhedrosis virus (Gen-Pept Locus: NPADNAPMA 1). Human alpha and T4 polymerases were aligned pairwise with DNA polymerase II and the composite of the two alignments is summarized in the figure. Selected regions of all six polymerases were aligned using the multiple alignment method of Smith and Smith (7). These regions are shaded in the figure. Amino acids present in one-half or more of the sequences in any region are underlined. Positions proposed to be invariant in all polymerases (5) are indicated with an arrow. Position coordinates are the number of amino acids from the N-terminal amino acid as given in the indicated data base entry.