Tight Regulation, Modulation, and High-Level Expression by Vectors Containing the Arabinose P_{BAD} Promoter

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We have constructed a series of plasmid vectors (pBAD vectors) containing the P_{BAD} promoter of the *araBAD* (arabinose) operon and the gene encoding the positive and negative regulator of this promoter, *araC*. Using the *phoA* gene and *phoA* fusions to monitor expression in these vectors, we show that the ratio of induction/repression can be 1,200-fold, compared with 50-fold for P_{TAC}-based vectors. *phoA* expression can be modulated over a wide range of inducer (arabinose) concentrations and reduced to extremely low levels by the presence of glucose, which represses expression. Also, the kinetics of induction and repression are very rapid and significantly affected by the *ara* allele in the host strain. Thus, the use of this system which can be efficiently and rapidly turned on and off allows the study of important aspects of bacterial physiology in a very simple manner and without changes of temperature. We have exploited the tight regulation of the P_{BAD} promoter to study the phenotypes of null mutations of essential genes and explored the use of pBAD vectors as an expression system.

In bacterial physiology studies, it is often useful to express a cloned gene from an inducible promoter and assess the effect of the expression or depletion of the gene product in mutants lacking the chromosomal gene. In these situations, it is highly desirable to use a system that can be efficiently shut off. This is particularly the case when the phenotype caused by the absence of a protein can be obscured by leakiness from a partially repressed promoter or when even low levels of a protein are detrimental to the cell. Also, it would be desirable to modulate the expression system to achieve synthesis levels similar to those of the wild-type gene. However, the available repertoire of *Escherichia coli* expression systems usually produce high levels of the corresponding cloned gene product (4, 13, 18, 45, 48) and in many cases still produce substantial levels of synthesis in uninduced or repressed conditions (4, 13, 15, 16, 48, 49). These systems include controllable expression vectors based on the strong inducible promoters P_{LAC} (48), P_{TAC} (13), P_{TRC} (4), P_L and P_R (18), and P_{T7} (45). Some are better repressed than others, but induction of expression requires changes of temperature (18, 45) and produces very high levels of protein, resulting in conditions detrimental to cell growth and viability (17, 45).

We have been studying the function of several essential genes that encode membrane proteins involved in cell division of *E. coli* (7a, 22). To analyze their role, we have sought to deplete cells of the proteins and then examine the phenotype of cells so depleted under conditions that would minimize alterations in cell physiology. For these purposes, we wished to use a plasmid that would satisfy the following two conditions: (i) the synthesis of the proteins should be shut off rapidly and efficiently without changes of temperature, and (ii) expression before depletion should not produce very high levels of pro-

tein, which itself may give a phenotype or influence the phenotype of the depletion.

To achieve these conditions, we constructed a set of vectors (pBAD vectors) containing the P_{BAD} promoter of the arabinose operon and its regulatory gene, *araC* (28, 41). The AraC protein is both a positive and a negative regulator (6, 30). In the presence of arabinose, transcription from the P_{BAD} promoter is turned on; in its absence, transcription occurs at very low levels (28, 29). The uninduced levels can be reduced even further by growth in the presence of glucose. Glucose reduces levels of 3′,5′-cyclic AMP, thus lowering expression of the catabolite-repressed P_{BAD} promoter (32). The properties of the mechanism of expression and repression of P_{BAD} by AraC have been studied extensively, and their interactions have been dissected at the molecular level (reviewed in reference 41). Additionally, plasmids described previously in which transcriptional or translational fusions to *araB* were used to set genes under P_{BAD} and AraC control suggested that expression from this system was tightly regulated (12, 26, 38, 40).

Here, we describe the construction of pBAD vectors and the characteristics of repression, induction, and modulation of the expression of genes cloned into them. In addition, we show the application of the tight regulation of the vectors to the study of null mutations of essential genes and discuss the relevance of this and the vector's properties of expression for bacterial physiology.

MATERIALS AND METHODS

Bacterial strains and media. The *E. coli* strains used in this study were KS272 [F⁻ Δ*lacX74 galE galK thi rpsL ΔphoA* (PvuII)] (44), LMG194 (KS272 Δ*ara714 leu*::Tn*10*), DHB4 (3), LMG145 [KS272 *ftsL*::Tn*phoA*L81ΔIS*50R* (Kan^r)/pLMG180 (Amp^r)], LMG89 (LMG145 *pcnB*80 *zid1*::Tn*10*) (22), and DH5α (Bethesda Research Laboratories, Gaithersburg, Md.). The Δ*ara714* deletion in LMG194 encompasses most of the *araBAD* operon (47) and was obtained from strain JP63 (37).

The NZY rich and M63 minimal media have been described (22). The M63 medium was always supplemented with a mixture of 18 amino acids (no methionine or cysteine) at a final concentration of 50 μg/ml (22). Unless otherwise indicated, glycerol, D-glucose, and L-arabinose (Pfanstiehl Labs) were used at a concentration of 0.2%. The following antibiotics were used at the concentrations

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pBAD series

A

pBAD18s 4.6 Kb

pBAD18 4.6 Kb

pBAD24 4.5 Kb

pBAD18-Cm 6.0 Kb

pBAD18-Kan 5.4 Kb

pBAD28 5.8 Kb

pBAD30 4.9 Kb

pBAD33 5.3 Kb

pBR origin

pACYC origin

B

MCS 1

P_{BAD} ----TACCCGTTTTTTTGGAT GGAGTG aaacg ATGgcgatt gcaattgGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTT
+1
araB S.D.   NH2-AraB Met ala ile ala ile gly
SacI XmaI SmaI XbaI PstI HindIII
EcoRI KpnI BamHI SalI AccI SphI

MCS 2

P_{BAD} ----TACCCGTTTTTTTGG GCTAGCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTT
+1
NheI SacI XmaI SmaI XbaI PstI HindIII
EcoRI KpnI BamHI SalI AccI SphI

MCS 3

P_{BAD} ----TACCCGTTTTTTTGG GCTAGC AGGAGG AATTCACC ATG GTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTT
+1
S.D. Kozak NcoI XmaI SmaI XbaI Pst1 HindIII
NheI EcoRI KpnI Asp718I BamHI SalI AccI SphI

Frame

NcoI / Klenow   = CC ATG 0
Asp718I / Klenow = CC ATG, GTA, C .... +1
XmaI / Klenow   = CC ATG, GTA, CCC, GG ---- +2
          Met Val Pro Gly

shaded sites = double sites
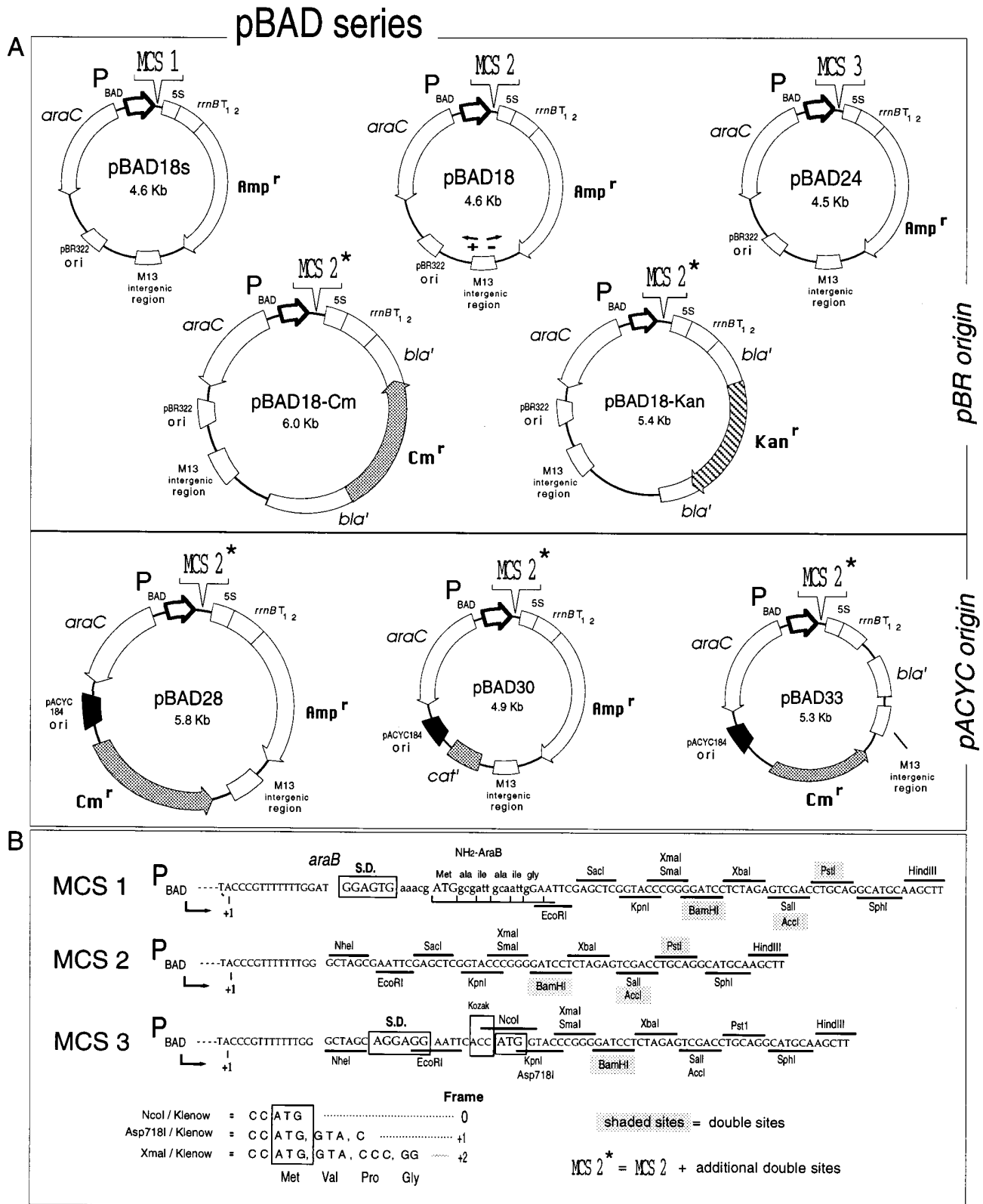
$MCS 2^*$ = MCS 2 + additional double sites

FIG. 1. Construction of pBAD vectors. (A) Maps of pBAD vectors with the relevant features of the plasmids. (B) MCSs of pBAD vectors. All sites are single, with the exception of shaded sites which are double. For MCS1 and MCS 2, the double sites are *Bam*HI, *Acc*I, and *Pst*I. In MCS 3, *Bam*HI is the only double site. The unique and double sites of MCS 2 are applicable only to pBAD18. Vectors with MCS 2* contain the same double sites as those of pBAD18 (MCS 2) and the following additional double sites: pBAD18-Cm, *Eco*RI; pBAD18-Kan, *Sma*I and *Hin*dIII (*Pst*I becomes unique); pBAD28, *Nhe*I and *Eco*RI; pBAD30, *Nhe*I; and pBAD33, *Nhe*I and *Eco*RI (*Pst*I becomes unique). (C) Steps in construction of pBAD vectors (see Materials and Methods). Abbreviations: 5S and *rrnB* T₁T₂, parts of the 5S rRNA and the strong ribosomal *rrnB* terminators, respectively; ori, origin of replication; +1, site of initiation of transcription; ATG, initiation of translation codon; *bla'* and *cat'*, truncated *bla* and *cat* genes; ER1, *Eco*RI; H3, *Hin*dIII; MCSa, MCS of M13mp10; MCSb, MCS of pUC9; T4 pol, T4 polymerase; MCS, multicloning site; SD, Shine-Dalgarno box.
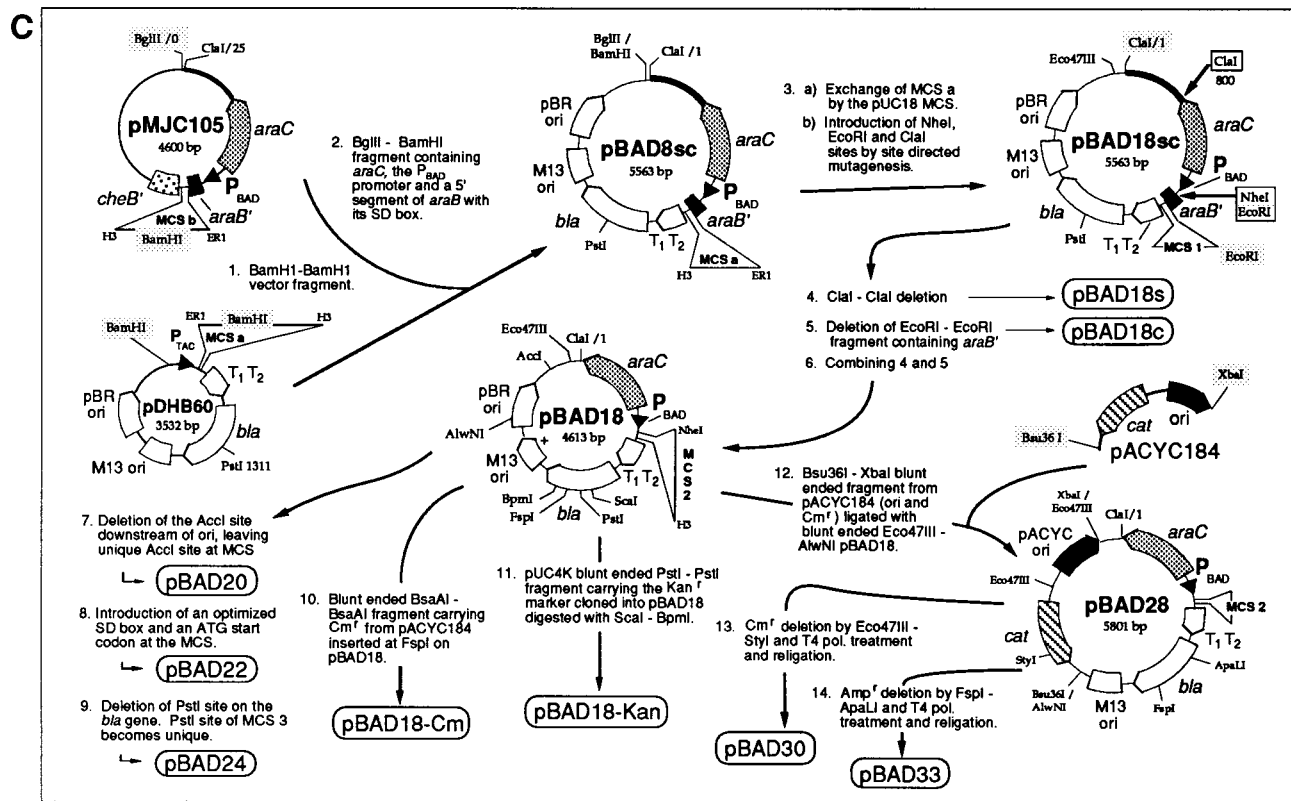
FIG. 1—*Continued.*

indicated: ampicillin, 100 µg/ml (pBR origin) and 30 µg/ml (pACYC origin and *pcnB* strains); chloramphenicol, 10 µg/ml; and kanamycin, 40 µg/ml.

Construction of pBAD vectors. The DNA region that contains the *araC* gene and the P_{BAD} promoter of pBAD vectors was derived from plasmids pRS48, pRS4, and pCR48 (38) via plasmid pPC1 (10). pRS48 and pRS4 (38) were constructed by fusion of the *araC* gene (obtained from pTB1 [8]) and the P_{BAD} promoter (obtained from pRFS4 [R. Schleif]), both of *E. coli* B/r origin, and the introduction of an *Eco*RI site six codons after the beginning of *araB*. Plasmid pPC1 consists of the *BglII-Eco*RI *araC*-P_{BAD} region from pRS4, followed by the polylinker of pUC9 (48) and several chemotaxis genes. The plasmid pMJC105 (Fig. 1) was derived from pPC1 by an *Nde*I deletion that eliminates most of the chemotaxis genes.

Plasmid pDHB60 (3) (Fig. 1C) provided the backbone for the pBAD plasmids. It was derived from the P_{TAC} expression vector pKK223-3 (Pharmacia Biotech, Inc., Piscataway, N.J.) via pDHB32 by replacement of *malF* with the M13mp10 polylinker. pDHB60 also differs from pKK223-3 in that it contains an *Sph*I-*Pvu*II deletion which truncates the *rop* gene and has the M13 intergenic region (50) inserted at the *Dra*I site (3).

To construct plasmid pBAD8sc (Fig. 1C), the P_{TAC} promoter from pDHB60 was replaced by a *BglII-Bam*HI fragment of pMJC105 that contained the *araC* gene, the P_{BAD} promoter, and a 5' region of *araB* with the *araB* Shine-Dalgarno (SD) box and the beginning of *araB*. Steps 3 through 6 in Fig. 1C led to pBAD18 in which the *araB* sequences and sequences downstream of *araC* are absent. It also contains the polylinker of pUC18 (48) with an *Nhe*I site at the beginning of it. Expression of genes cloned into the multiple cloning site (MCS) of pBAD18 do not produce any type of translational fusions and requires an SD box provided by the cloned gene. In pBAD20, the *Acc*I site present downstream of the pBR origin of replication was deleted by *Tth*111I-*Nde*I digestion and filling in with Klenow fragment. pBAD22 was constructed by PCR with a 5' primer with the sequence for an optimized SD box (42, 43), a Kozak box (25), and an ATG start codon at an *Nco*I site (Fig. 1B, MCS 3), followed by a stretch of 10 bases complementary to the MCS of pBAD20 from the *Sma*I to the *Xba*I sites. The 3' primer was complementary to sequences beyond the MCS. After amplification, the *Nhe*I-*Hin*dIII digestion product from the PCR fragment containing the new MCS (MCS 3) was used to replace the MCS of pBAD20. pBAD24 consists of pBAD22 with a single base change that alters the *Pst*I site normally present in the middle of the *bla* gene. This change was accomplished by excising the *Fsp*I-*Sca*I *bla* fragment of pBAD22 and replacing it with the corresponding fragment from pUC18, which lacks the *Pst*I site. The construction of pBAD18-Cm and pBAD18-Kan is depicted in Fig. 1C (steps 10 and 11). In both of these two

plasmids, *bla* sequences surround the chloramphenicol- and kanamycin-resistant markers. The construction of pBAD vectors with the pACYC origin of replication (9) is described in Fig. 1C (steps 12 to 14). These vectors can be used for coexistence or coexpression of genes in combination with pBR-derived plasmids.

The complete sequences of pBAD18 and pBAD24 were obtained by sequencing the MCSs, their neighboring regions (including the P_{BAD} promoter, the beginning of *araC*, and the *rrnB* T_1T_2 terminators), and all mutagenized sites and surrounding regions. These sequenced regions were joined with overlapping data bank sequences of pKK223-3, *araC*, the P_{BAD} promoter, and the M13 intergenic region (50), with the appropriate modifications incorporated (details are provided in the databases under the sequence accession numbers). Sequencing of genes cloned into the MCS of pBAD vectors has been done with a 5' primer (5'-CTGTTTCTCCATACCCGTT) and one of two 3' primers (5'-CTCATC CGCCAAAACAG or 5'-GGCTGAAAATCTTCTCT). The 5' primer lies from 27 to 8 bp upstream of the *Nhe*I site, and the 3' primers are complementary to sequences from 2 to 19 bp and 17 to 33 bp downstream of the *Hin*dIII site.

DNA manipulations were performed as described in established protocols (39) and recommendations of the restriction enzyme manufacturer (New England Biolabs, Beverly, Mass.). Double-stranded dideoxy chain sequencing was determined by use of Sequenase (U.S. Biochemical Corporation, Cleveland, Ohio) and PCRs with Vent polymerase (New England Biolabs).

Other plasmids. Plasmid pLMG161 was constructed by cloning a 900-bp *Eco*RI-(*Kpn*I)-*Kpn*I fragment from plasmid pMJC103 (7a) into the same sites of pBAD18 (unpublished results). This fragment carries the complete *ftsQ* gene, including the poorly efficient *ftsQ* SD box (33), and an additional 12 bp that precede the *Eco*RI site. pLMG163 was obtained by inserting a 5,250-bp *Kpn*I-*Kpn*I fragment from plasmid pZQ::Tn*phoA91* (7a) into the internal *Kpn*I site of *ftsQ* from plasmid pLMG161. This cloning resulted in replacement of the 3' end of the *ftsQ* gene by the *ftsQ-phoA91* fusion with the rest of the IS*R50*-deleted Tn*phoA* (7a) and expression of the fusion from the P_{BAD} promoter. pLMG160 was constructed in the same manner as pLMG161 but cloned into pBAD18s instead of pBAD18 (unpublished results). Also, the *ftsQ-phoA91* fusion was cloned into pLMG160 to yield pLMG162, as was done with the pLMG163 plasmid. The resulting *phoA* fusion in pLMG162 contains the SD box and the first 5 residues of the *araB* gene located before the *Eco*RI site of the pBAD18s vector (Fig. 1B, MCS 1), followed by the SD box of *ftsQ* and the *ftsQpho*Δ*91* coding sequence. The expression of the *ftsQ-phoA91* fusion from pBAD18s is higher than that obtained from pBAD18; however, no AraB fusion protein is produced since the 5' end of *araB* is fused out of frame with respect to *ftsQ*. Similarly, higher levels of alkaline phosphatase (AP) activity were observed when
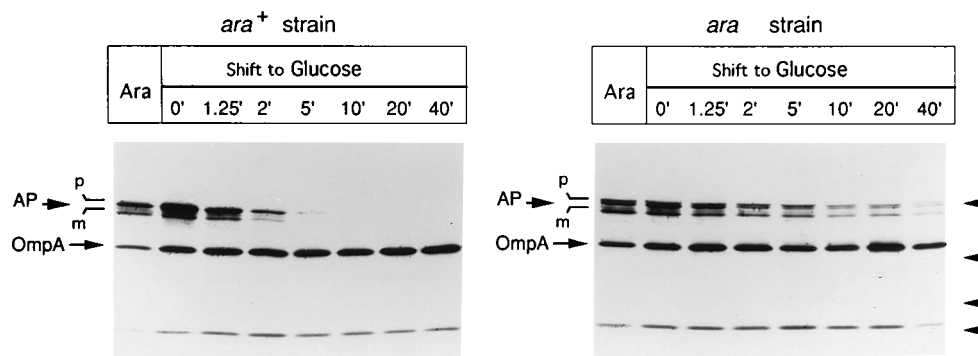
FIG. 2. Synthetic rate of wild-type AP production from P$_{BAD}$: kinetics of repression by glucose. Cultures of *ara*$^+$ and *ara* mutant strains with plasmid pDB3 (wild-type AP cloned into pBAD22) were grown at 37°C in glycerol-minimal medium supplemented with 0.02% arabinose. When cultures reached the mid-log phase of growth, 0.5-ml aliquots were taken and pulse-labeled for 1 min with 20 μCi of ^{35}S-methionine per ml (Ara lanes). Subsequently, 4 ml of the cultures was washed once with glycerol minimal medium containing 0.2% glucose by a brief centrifugation of 2 min. After resuspension of the cultures in the same glucose-containing medium, they were returned to the initial culturing conditions, and 0.5-ml fractions were pulse-labeled immediately (0′) and at the indicated times (in minutes). Labeled cultures were arrested by the addition of 0.05% unlabeled methionine, subsequently immunoprecipitated with anti-AP and anti-OmpA antibodies, and analyzed by 10% polyacrylamide gel electrophoresis and fluorography as described previously (22, 44). The positions of precursor (p) and mature (m) AP and OmpA are indicated. Induction of plasmid pDB3, which expresses wild-type AP very efficiently, seems to cause some difficulty for the export of AP as judged by the elevated amount of AP precursor. Arrows on the right indicate molecular mass markers for ovalbumin (43,000 Da), carbonic anhydrase (29,000 Da), β-lactoglobulin (18,400 Da), and lysozyme (14,300 Da). The band at the bottom corresponds to the dye front.

other *ftsQ-phoA* fusions (7a) were expressed in pBAD18s than when they were expressed in pBAD18. Thus, it is possible that the presence of the second, more-efficient *araB* SD box increases the efficiency of translation of the *ftsQ-phoA91* fusion by an unknown mechanism. The plasmid pLMG281 was constructed by subcloning the *ftsQ EcoRI-HindIII* fragment from pLMG163 into pDHB60 (Fig. 1) and then inserting the *ftsQ-phoA91* fusion between *KpnI* sites. This plasmid, which places the *ftsQ-phoA91* fusion under the control of P$_{TAC}$, is otherwise identical to the pLMG163 plasmid. Finally, pDB3 consists of the wild-type *phoA* gene lacking its SD box and cloned at the *NcoI* site of pBAD22. This vector provides an optimized SD box and promotes high levels of expression of *phoA* (Table 1).

AP assays. AP enzymatic activity was measured from duplicate cultures of cells grown to the mid-logarithmic phase (optical density of 600, ~0.5) at 37°C in the appropriate medium and by determining the rate of *p*-nitrophenyl phosphate hydrolysis with washed, permeabilized cells incubated at 28°C as described previously (22).

Nucleotide sequence accession numbers. The complete sequences of pBAD18 and pBAD24 were submitted to the EMBL/GenBank/DDBJ databases under accession numbers X81837 and X81838.

RESULTS

Construction and characteristics of the vectors. Details on the construction of pBAD vectors are shown in Fig. 1C and Materials and Methods. In steps 1 to 6 (Fig. 1C), four plasmids were constructed by several steps of cloning and site-directed mutagenesis to eliminate a 5′ fragment from *araB* and avoid production of any *araB* fusions, to eliminate downstream sequences from *araC*, and to exchange polylinkers among pUC vectors. The resulting 4.6-kb pBAD18 plasmid (Fig. 1) contains the *araC* gene and the P$_{BAD}$ promoter followed by an MCS (MCS 2) which can be used to clone any gene containing translation initiation sequences. Immediately downstream of the MCS are the strong *rrnB* transcription terminators. The plasmid also carries a ColE1 origin of replication, an M13 intragenic region for phage packaging and production of single-stranded DNA, and an ampicillin resistance gene. pBAD18-Cm (Fig. 1) is a Cm^r Ap^s derivative of pBAD18 that contains the chloramphenicol-resistant gene from pACYC184 (9) inserted into the ampicillin gene, whereas pBAD18-Kan (Fig. 1) has a kanamycin resistance gene from pUC4K (Pharmacia Biotech) inserted in the same fashion. As with pBAD18, these last two plasmids should be used to clone genes that contain their own SD box. Also, in both of these two plasmids (pBAD18-Cm and -Kan), the chloramphenicol- and kanamycin-resistant markers are surrounded by *bla* sequences which could promote

recombination when these plasmids are used in combination with other compatible ampicillin-resistant plasmids. Recombination can be avoided by the use of *recA* strains; however, this recombination can also be useful to intentionally exchange markers among the plasmids. This is also applicable to pBAD30 and pBAD33 (Fig. 1).

The pBAD24 vector (Fig. 1) is used to clone genes which lack sequences for initiation of translation. This vector contains an optimized SD sequence (42, 43) between the *NheI* and *EcoRI* sites of the MCS as well as a translation start codon (ATG) at the *NcoI* site. A Kozak sequence, relevant for expression in eukaryotic cells (25), is also present before the ATG. If this start codon is to be used, the desired frame can be obtained by digesting with the appropriate enzyme and filling in with Klenow fragment as depicted in Fig. 1B. Besides the sequences for translation initiation, the only other difference between pBAD24 and pBAD18 is that in the former, the *AccI* and *PstI* sites of the MCS are unique in the plasmid. The complete sequences of these two plasmids have been deposited in the EMBL/GenBank/DDBJ databases (see Materials and Methods).

pBAD28 (Ap^r Cm^r), pBAD30 (Ap^r), and pBAD33 (Cm^r) (Fig. 1) are derivatives of pBAD18 that contain the pBR322-compatible p15A origin of replication from the pACYC184 vector (9). These plasmids can be used to reduce gene expression (due to lower copy number) or, in conjunction with pBAD18 or pBAD24, to stably coexpress different genes.

Repression from P$_{BAD}$ is rapid and efficient. In Fig. 2, we show that the P$_{BAD}$ promoter is turned off rapidly and efficiently. Cultures of strains KS272 (*ara*$^+$) and LMG194 (*ara*) carrying the wild-type AP enzyme cloned into pBAD22 were grown in minimal medium supplemented with arabinose and glycerol and subsequently shifted to glucose-containing medium. At the indicated times, samples were pulse-labeled with ^{35}S-methionine, immunoprecipitated with anti-AP and anti-OmpA (internal control) antibodies, and analyzed by fluorography. In the cultures of the repressed *ara*$^+$ strain, the amount of pulse-labeled AP protein decreased rapidly in the first minutes, became negligible by 5 min, and was below detection at subsequent times. In the *ara* strain cultures, repression of AP synthesis was slower and did not decrease significantly until 20
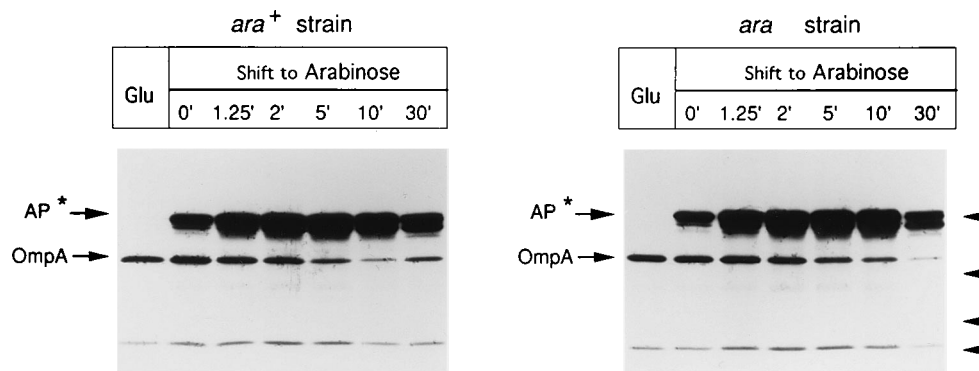
FIG. 3. Synthetic rate of wild-type AP production from P_{BAD}: kinetics of induction by arabinose. The details of the experiment illustrated by this figure are the same as those described in the legend to Fig. 2, with the exception that cultures were first grown under repressing conditions (glycerol-minimal medium supplemented with 0.2% glucose) and subsequently shifted to inducing conditions (glycerol-minimal medium supplemented with 0.05% arabinose).

to 40 min. Nondetectable levels of AP synthesis were then maintained for at least 2 h (see Fig. 3, Glu lanes) for both strains. Thus, P_{BAD} is rapidly and efficiently repressed, particularly in ara^+ strains. A likely explanation for the difference in repression kinetics between the two strains is that ara^+ strains lower the concentration of inducer as they grow since they can metabolize arabinose and use it as a carbon source. In contrast, in ara mutant strains, the intracellular concentration of inducer remains elevated since arabinose cannot be degraded. This is particularly relevant in this experiment where submaximal concentrations of arabinose were used for induction (see also Fig. 4B). We also point out that ara mutant strains that are $araD$ alone must be avoided since arabinose is toxic for these strains (19).

The P_{BAD} promoter has a very fast induction rate. The converse time course labeling experiment to the one shown in Fig. 2 was performed to determined how fast the P_{BAD} promoter is induced (Fig. 3). Here, cultures of strains were grown under repressing conditions for several hours and then shifted to inducing conditions. Upon induction, samples were pulse-labeled and analyzed by immunoprecipitation and fluorography. First, it is evident that after several hours of growth in repressing conditions, just prior to induction (Fig. 3, Glu lanes), the expression of AP is totally repressed. Subsequently, as early as 1 min after the addition of arabinose, significant amounts of labeled AP, which continued to increase over the following 2 to 4 min, were observed. Induction was maintained at a high level as judged by the total amount of AP and the AP/OmpA protein ratio (ara^+ strain). After 10 min of induction, the ara mutant strain displayed a tendency to decrease the rate of AP synthesis, probably as a result of the deleterious effects of high-level AP expression. The timing of the induction is only approximated since it can be observed that samples in lanes 0′ show significant amounts of AP due to induction of the promoter during the 2-min wash and resuspension, in which case induction still occurs very soon after the addition of arabinose. Thus, these results indicate that the P_{BAD} promoter has a very fast rate of induction.

Ratio of induction/repression from pBAD vectors. To estimate the levels of expression from the $araC$-P_{BAD} promoter system in induced and repressed states, we determined the enzymatic activity of an FtsQ fusion to AP (FtsQ–AP-91) as well as that of wild-type AP cloned into pBAD vectors. FtsQ is an *E. coli* cell division membrane protein that is normally expressed at very low levels (7a, 33). AP fusions to the periplasmic domain of the protein exhibit normal specific activities of

AP, which make them suitable to estimate the levels of expression (7a). Plasmids pLMG162 and pLMG163 express the *ftsQ–phoA-91* fusion, which retains the *ftsQ* SD box, from the P_{BAD} promoter of vectors pBAD18s and pBAD18 (see Materials and Methods). The only difference between the two constructs is that in pLMG162, the pBAD18s vector provides an additional SD box and 5 residues from the *araB* gene, and this plasmid produces higher levels of the FtsQ–AP-91 fusion than those produced by pLMG163. The mechanism of translation of the fusion in pLMG162 is not known. pDB3 contains the wild-type *phoA* gene devoid of its SD box, expressed from the P_{BAD} promoter, and an optimized SD box provided by pBAD22. This plasmid produces high levels of AP and in conjunction with pLMG162 and pLMG163, which produce medium and low AP activity levels, respectively, allows a careful assessment of the ratio of induction/repression of the P_{BAD} promoter.

Table 1 shows that the ratio of induction/repression for wild-type AP under the control of $araC$-P_{BAD} was about 250-fold in rich medium and about 1,300-fold in minimal medium. Similarly, the induction/repression ratios for the FtsQ–AP-91 fusion on plasmid pLMG162 ranged from about 280-fold in rich medium to 1,000-fold in minimal medium. Therefore, the efficiency of repression from the P_{BAD} promoter can be from 2 to even 3 orders of magnitude. In strains carrying the plasmid pLMG163, the induction/repression ratios varied from the overall lowest (118-fold) to the overall highest (1,855-fold). These estimates are probably inaccurate because of the low expression of the *ftsQ–phoA-91* fusion from the weak SD box-containing pLMG163 plasmid, which resulted in low levels of AP activity at maximum induction and repression levels very close to those of the negative control strain that carries the pBAD22 vector. The *ftsQ–phoA-91* fusion was also expressed from the P_{TAC} promoter in the vector pDHB60, which differs from pBAD vectors only in the promoter region (Fig. 1C). This P_{TAC}-derived plasmid, pLMG281, is directly comparable to pLMG163. The P_{TAC} promoter was maintained in a repressed state by the *lacI*q gene provided by the DHB4 strain (3) and was induced by isopropyl-β-D-thiogalactopyranoside (IPTG) at concentrations that provide maximum induction. pLMG281 (P_{TAC}) produced higher levels of AP activity than those of pLMG163 (P_{BAD}) after induction and in the repressed state. The highest induction/repression ratio for this P_{TAC}-derived plasmid was 50-fold (Table 1). Thus, the efficiency of repression from P_{BAD}, which is about 12- to 40-fold greater than that

TABLE 1. Induction/repression ratios of expression of AP fusions and wild-type enzyme from the P_{BAD} promoter

Plasmid	Strain	Rich medium[a]			Minimal medium[a]		
		AP activity (U)		Induction/ repression[b]	AP activity (U)		Induction/ repression[b]
		Inducing[b]	Repressing[b]		Inducing[b]	Repressing[b]	
pBAD22	KS272 (ara^+)	0.33			0.41		
	LMG194 (ara)	0.36			0.41		
pLMG163 = pBAD18/ FtsQ–AP-91	KS272 (ara^+)[c]	47.3	0.40	118	229	0.57	402
	LMG194 (ara)[c]	71.2	0.52	136	593	0.32	1,855
pLMG162 = pBAD18s/ FtsQ–AP-91	KS272 (ara^+)	427	1.80	237	1,593	1.65	965
	LMG194 (ara)	580	1.73	335	1,363	1.18	1,155
pDB3 = pBAD22/wt AP[d]	KS272 (ara^+)[e]	2,382	10.32	231	5,851	4.37	1,338
	LMG194 (ara)[e]	2,430	9.30	261	5,782	4.20	1,376
pLMG281 = pDHB60 (P_{TAC})/FtsQ–AP-91	DHB4 ($lacI^q$)[c,f]	270	5.73	47	1,029	20.82	49

[a] Diluted cultures were grown for four to six generations to the mid-logarithmic phase in NZY (rich) medium or glycerol-minimal medium supplemented with either 0.2% glucose or 0.2% arabinose to ensure maximum induction. AP enzymatic activity was determined in these cultures as indicated in Materials and Methods. The rich NZY medium is very similar to LB medium (39). The only difference is that in NZY, NZ amine is used instead of tryptone. Enzyme levels from pBAD vectors are comparable in both media. However, LB medium may give higher expression levels than NZY medium does from the uninduced P_{TAC} promoter, depending on the tryptone batch.

[b] Induction/repression ratios were calculated by dividing the number of units of AP activity obtained from inducing conditions (medium plus arabinose for strains containing plasmids pBAD, pLMG163, pLMG162, and pDB3 and medium plus IPTG for the strain with plasmid pLMG281) by that obtained from repressing conditions (medium plus glucose for strains containing plasmids pBAD22, pLMG163, pLMG162, and pDB3 and medium without IPTG for the strain with plasmid pLMG281). The average ratios for pBAD plasmid-containing strains grown in rich and minimal media were 220 ± 74 and 1,182 ± 441, respectively.

[c] The difference in induction and repression levels between the P_{BAD} and P_{TAC} promoters was calculated by comparing the average levels from ara^+ and ara strains with pLMG163 with the levels of strain DHB4 with pLMG281. Accordingly, P_{TAC} has 4.5-fold (rich medium) and 2.5-fold (minimal medium) higher levels of induction than P_{BAD} and 12.4-fold (rich medium) and 46.7-fold (minimal medium) less repressed than P_{BAD}.

[d] wt, wild type.

[e] Cultures of strains containing pDB3 were first grown in rich or minimal medium with only glycerol as the carbon source to the beginning of the log phase, and then arabinose or glucose was added and growth was continued for about four generations before determination of AP activity.

[f] For this strain, rich NZY medium or 0.2% glucose minimal medium was used in inducing or repression conditions. For induction, 5 mM IPTG was used, and for repression, cultures were grown in the absence of inducer.

of P_{TAC} (Table 1), is due primarily to lower uninduced levels from the P_{BAD} promoter.

These results indicate that the repression of the P_{BAD} promoter is very efficient and that, under some conditions, it can yield striking levels of repression. However, this tight control does not mean that the protein levels in the repressed state are always zero, since the levels of expression in repressed states are relative to the levels of expression at maximum induction. Thus, as shown in Table 1, the P_{BAD} promoter is turned off to levels close to zero only when the expression of the gene at maximum induction is not too high (pLMG163). When levels of expression are high, the repressed promoter can produce as much as 11 U of AP activity (pDB3). Induction and repression levels do not appear to be consistently different between ara^+ and ara strains for all plasmids. pLMG163-containing strains gave different levels of induction, while in pDB3-containing strains, similar levels were observed. However, these results were obtained at maximum induction. It is possible that at lower concentrations of arabinose, all ara^+ strains would yield lower induction levels than ara mutant strains would (see Fig. 4B). Also, results shown in Table 1 indicate that the P_{BAD} promoter is expressed more efficiently in minimal medium than in rich medium.

These observations are of particular importance for studies of null mutations in essential genes in which the complementing P_{BAD}-driven gene expression is required to be shut off as efficiently as possible. If such complementing, arabinose-induced expression gives high levels of the protein, enough protein could be produced in the repressed state to complement the null mutation and its phenotypic effect would not be observed. This problem could be circumvented by lowering the overall expression of the gene from the pBAD-derived plasmid, for instance, by making initiation of translation less efficient (use of a nonoptimal SD box) (42, 43), by using pACYC derivatives or *pcnB* mutant strains to decrease the plasmid copy number (31), or, when possible, by recombining the P_{BAD}-driven gene into the chromosome.

The *araC*-P_{BAD} promoter system can be modulated. A useful property of a controllable expression system is the possibility to obtain different levels of expression by partial induction of the promoter. Thus, we assessed the susceptibility to modulation of pBAD vectors by measuring the extent of induction from P_{BAD} at different concentrations of inducer. Figure 4A shows a plot of the amount of AP enzymatic activity produced by cultures of strain DHB4 (ara/pBAD22-*phoA*) as a function of induction at different arabinose concentrations. A linear relationship between induction and expression is clearly observed for arabinose concentrations that extend over 2 logarithms. There is virtually no induction at concentrations equal to 1.33 μM (8 U of AP activity) or lower, and the curve plateaus between 133 (2,000 U of AP activity) and 1,330 μM. A comparison of this latter value with the levels of AP produced by the cultures repressed with glucose (6 U of AP activity) shows that the ratio of induction/repression is about 300-fold. Based on estimates that correlate the enzymatic activity of *phoA* fusions with the number of molecules per cell (7a), the observed ratio of induction/repression, in this particular case 6/2,000, would correspond to (60 ± 15)/(20,000 ± 5,000) molecules per cell.

These results indicate that the expression from the *araC*-P_{BAD} promoter system can be modulated over a wide range of inducer concentrations, starting with conditions that yield effective repression of expression. Similar results were obtained with strains carrying the pLMG162 and pLMG163 plasmids with the FtsQ–AP-91 fusion (Fig. 4), although the curves are displaced down as a result of the lower overall efficiency of expression of these fusions with respect to that of wild-type AP. Figure 4B shows a comparison of the induction curves of ara^+
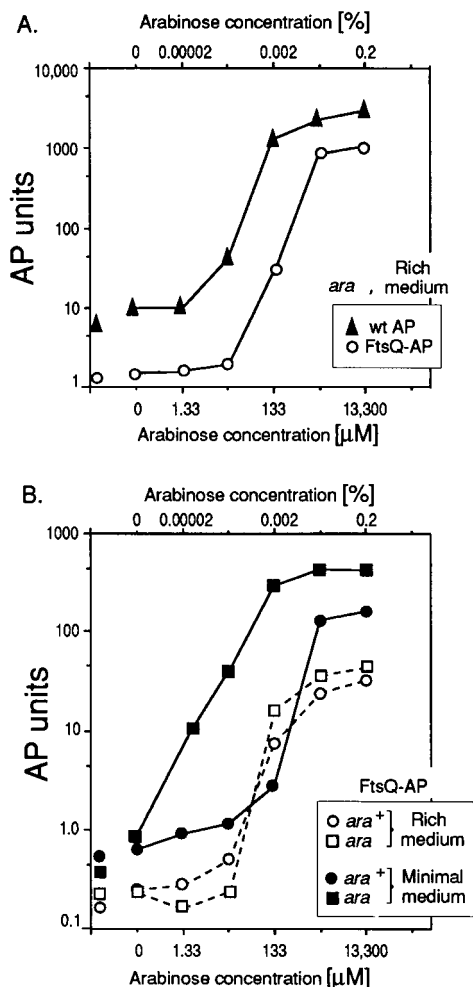
FIG. 4. Modulation of expression from the $araC$-P_{BAD} system. Overnight cultures of ara^+ and ara strains carrying pDB3 (pBAD22/wt AP), pLMG162 (pBAD18s/FtsQ–AP-91), or pLMG163 (pBAD18/FtsQ–AP-91) were diluted to 10^{-2} and grown at 37°C in glycerol-minimal medium or rich medium supplemented with 0.2% glucose or with arabinose at the indicated concentrations. When cultures reached the mid-log phase, they were transferred to 4°C and assayed for AP enzymatic activity as indicated in Materials and Methods. (A) Strains DHB4 (ara)/pDB3 (wt AP) and LMG194 (ara)/pLMG162 (FtsQ-AP) were grown in rich medium. (B) The ara^+ strain is KS272/pLMG163, and the ara mutant strain is LMG194/pLMG163. Growth in rich or minimal medium is indicated. Unconnected points at the beginning of the curves, before 0, indicate values obtained under repressing conditions with glucose.

and ara strains with pLMG163, in rich and minimal media, at different arabinose concentrations. Similar to results shown in Table 1, pLMG163-driven expression in minimal medium is more efficient than that in rich medium, and ara mutant strains produce higher levels of synthesis than ara^+ strains do. Additionally, modulation is similar in ara^+ and ara backgrounds in rich medium but is significantly different in minimal medium. At low concentrations of arabinose, ara strains are induced more efficiently and give a linear response, whereas ara^+ strains yield lower AP activities in a nonlinear fashion. At high concentrations of inducer, the strains behave similarly. This is probably expected since at low arabinose concentrations in minimal medium, ara^+ strains will rapidly and effectively decrease the intracellular concentration of arabinose and induction becomes less efficient. Thus, modulation is more effective and reproducible in ara strains than in ara^+ strains.
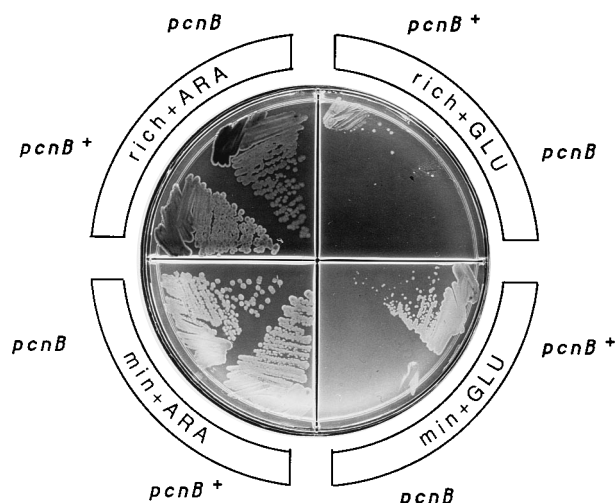

FIG. 5. Essentiality of the $ftsL$ gene in $pcnB^+$ and $pcnB$ mutant strains. Strains LMG145 ($pcnB^+$) and LMG89 ($pcnB$), both containing the chromosomal insertion $ftsL$::Tn$phoA$ L81ΔIS$R50$ complemented by the plasmid pLMG180 (wild-type $ftsL$ cloned into pBAD18 [22]) were grown on plates containing rich or minimal medium supplemented with 0.2% arabinose, ampicillin (30 μg/ml), kanamycin (20 μg/ml), and 5-bromo-5-chloro-3-indolyl phosphate (XP). Single colonies from both strains were streaked on plates with four divisions, each containing a different medium as indicated. Colonies were first streaked on minimal medium sections and incubated at 37°C for several hours. Later, colonies were streaked on sections containing rich medium and incubated for an additional 12 to 16 h at the same temperature. Medium abbreviations: rich+ARA, NZY medium supplemented with 0.2% L-arabinose, ampicillin (30 μg/ml), and XP (40 μg/ml); rich+GLU, same as rich+ARA but supplemented with 0.2% D-glucose instead of arabinose; min+ARA, M63 minimal medium supplemented with 0.2% L-arabinose, 0.2% glycerol, ampicillin (30 μg/ml), and XP (40 μg/ml); rich+GLU, same as min+ARA but supplemented with 0.2% D-glucose instead of arabinose.

Application of pBAD vectors to the study of null mutations of essential genes. We have exploited the tight regulation of the $araC$-P_{BAD} promoter system to determine the essentiality of the $ftsQ$ and $ftsL$ cell division genes and to study the phenotype of their null mutations (7a, 22). In these experiments, chromosomal $ftsQ$ or $ftsL$ null mutations were complemented by pBAD18 plasmids containing the $ftsL$ or $ftsQ$ genes. The viability of the mutants depends on the presence of arabinose to induce the expression of the corresponding genes. $ftsQ$ and $ftsL$ encode bitopic membrane proteins present in 25 to 50 copies per cell (7a, 22). Thus, the $araC$-P_{BAD} promoter system provided efficient repression of $ftsQ$ or $ftsL$ in glucose such that it failed to produce enough copies of the proteins to complement the chromosomal null mutation. Moreover, depletion experiments in which the expression of the genes was shut off by the addition of glucose allowed us to examine the null mutant phenotype, which was a fast and efficient block in cell division and septum formation that produced multinucleate aseptate filaments (7a, 22).

It was also previously observed that depletion of FtsL in minimal medium was not very effective and varied with different culture conditions (22). This was attributed to a less-efficient shutoff of the P_{BAD} promoter in this medium as compared with that in rich medium. However, similar to the case shown in Table 1 for $ftsQ$ fusions, the expression of $ftsL$-$phoA$ fusions cloned into pBAD18 is repressed very efficiently and at about the same levels in rich and minimal media but induced to much higher levels in the latter (data not shown). Thus, it is likely that reducing the total amount of the complementing wild-type FtsL would permit observation of the null phenotype

in minimal medium. In Fig. 5, the essentiality of *ftsL* was tested in *ftsL* null mutant strains complemented by a pBAD-*ftsL* plasmid on rich and minimal medium plates containing arabinose or glucose. One of the null mutants harbored a mutation in the *pcnB* gene in addition to the *ftsL* mutation. The *pcnB* mutants (31) have a significantly lower copy number of pBR origin-containing plasmids and make them unstable, resulting in a mixture of low-copy-plasmid and plasmidless cells in the culture. Essentiality was then inferred from the ability of the strains to form colonies after streaking on the plates. It is shown that both strains grew in arabinose-containing media and failed to grow in rich medium with glucose. However, in glucose minimal medium, the *pcnB* mutant strain did not grow, while the *pcnB*$^+$ strain grew well. These observations indicate that the *ftsL* gene is indeed essential in both media and that lowering the gene dosage of the complementing *ftsL* gene in a *pcnB* mutant strain allowed the observation of the null phenotype in glucose minimal medium. It seems possible that the effect of lowering the gene dosage could also be achieved with careful modulation of the P_{BAD} promoter. These results also indicate that in addition to the very good repression provided by the P_{BAD} promoter, it is important to avoid protein overproduction prior to depletion since, after repression, the observation of the depletion phenotype will depend on how much of the already existent protein is diluted and turned over through growth and subsequent cell divisions. Consistently, one of the best conditions for depletion in broth occurs when stationary, saturated, induced cultures of Ara$^+$ strains (where arabinose has been partially or totally depleted) are diluted into medium containing 0.2% glucose.

Additional evidence for the usefulness of the pBAD vectors in the characterization of null phenotypes of essential genes has been provided by studies with the *ffh* gene (36), *ftsI* (7), and the protein secretion genes *secE* (34), *secD* (37), and *secF* (37).

High levels of expression from pBAD vectors. The results shown in Table 1 and Fig. 3 and 4 indicate that high levels of expression can be obtained when genes are cloned under *araC*-P_{BAD} control, particularly when the gene possesses a good natural SD sequence or when an optimized one is provided by pBAD22 or pBAD24. Thus, the FtsQ–AP-91 fusion produces 47 to 593 U of AP activity when the system contains the wild-type *ftsQ* SD sequence (Table 1), which deviates from the SD consensus sequence (33, 43). When the system is provided with an additional SD box from the *araB* gene, which better fits the SD consensus, 427 to 1,363 U of AP activity is produced. More than 5,000 U of AP activity can be obtained after maximal induction when wild-type *phoA* is expressed from the P_{BAD} promoter and uses the optimized SD sequence present in pBAD22 (Table 1 and Fig. 4). In previous studies, Johnston et al. (24) used the *araC*-P_{BAD} promoter system from *Salmonella typhimurium* for high-level expression of proteins in *E. coli* cells. They obtained overproduction levels corresponding to almost 15% of the total protein, which provided an abundant source for purification and direct visualization. Also, the P_{BAD} promoter system present in pBAD18 has been used as an expression system for peptide libraries (11).

Comparison of the expression of the FtsQ–AP-91 fusion from the P_{BAD} or P_{TAC} promoters (Table 1, pLMG163 versus pLMG281) indicates that P_{TAC} is 2.5- to 4.5-fold stronger than the P_{BAD} promoter. Therefore, promoters based on P_{LAC} (i.e., P_{TAC}, P_{LACuv5}, and P_{TRC}) (4, 13, 48) may be more suitable for hyperexpression purposes than P_{BAD}. However, problems that arise from massive overproduction of some proteins from these promoters (1, 16) can be relieved by the use of the P_{BAD} promoter, while reasonably high yields of protein can still be obtained. For instance, expression of the *malF* gene and a truncated *malG* gene from the P_{BAD} promoter at maximum induction is slightly deleterious to the cells, although growth is close to normal. However, when the same genes are expressed from the P_{TAC} promoter on the comparable vector pDHB60 (Fig. 1), fully induced by IPTG, expression is lethal (data not shown).

Other problems that result from hyperproduction of certain proteins, such as the formation of inclusion bodies, have also been relieved by expression from the P_{BAD} promoter. This was the case for the IS*911* transposase, which formed inclusion bodies when produced from P_{TAC}. When the protein was produced from the pBAD18 vector, inclusion bodies were no longer observed and high quantities of the soluble transposase from IS*911* could be purified (37a).

DISCUSSION

We have constructed a series of vectors based on the P_{BAD} promoter and its regulator *araC* that provide versatile features for genetic engineering techniques and for expression purposes. The most important characteristics of this system are that it can be used to (i) achieve very low levels of uninduced expression, (ii) obtain moderately high levels of expression in the presence of inducer, and (iii) modulate expression over a wide range of inducer concentrations.

The tight control of expression provided by the *araC*-P_{BAD} promoter system is an important characteristic that is mostly absent in other available expression systems (4, 13, 15, 38). This feature has been indispensable in the isolation and study of null mutations in essential genes and in the evaluation of the depletion phenotype of these genes. In fact, the efficient repression available with this system is very useful in complementation studies of any null mutations, whether in essential or in nonessential genes, since leakiness can obscure results in both cases. The tight control also helps to avoid deleterious effects due to the uninduced expression of toxic genes. Additionally, we showed that the repression of expression of genes cloned into pBAD vectors is rapid and efficiently maintained for at least several hours (Fig. 2 and 3). A practical consequence of this finding, besides providing an efficient shutoff of gene expression, is that rapidity helps in the evaluation of primary effects of the depletion of a protein. If secondary effects result from depletion, they will be more likely to be observed at later times after shutoff of the gene.

In general, genes cloned under the control of the *araC*-P_{BAD} promoter system are efficiently repressed. This has been the case for the essential genes *ftsQ* (7a), *ftsL* (22) (Fig. 5), *ftsI* (7), *ffh* (36), *secD* and *secF* (37), *secE* (34), and *lepA* (12) and for the nonessential genes *dsbA* (31a), *phoA* (Fig. 2 to 4), and *malF* (data not shown). However, the levels of expression of P_{BAD}-controlled genes may not be zero in the repressed state (Table 1), and that a particular gene is not turned off efficiently is a possibility. The P_{BAD} promoter on pBAD vectors is repressed from 200- to 1,200-fold, which provides an excellent range to repress most genes.

There are several factors that contribute to an efficient repression of gene expression. These include the concentration of arabinose used in inducing conditions (the lower the better), the ability of the strain to degrade arabinose (*ara*$^+$ strains are better), and the physiological state of the culture due to the type of medium and amount and type of carbon sources present in the medium. Regarding the latter, since the *araC*-P_{BAD} promoter system is subject to catabolite repression (32), levels of cyclic AMP will have a marked influence on expression. This could be important for strains growing in minimal medium with mixtures of carbon sources. Additionally, alter-

native compounds can be used to improve and expand the levels of repression from P_{BAD}; for instance, glucose-6-phosphate, which catabolite represses more efficiently than glucose, could be used to lower further the levels of repression. Also, the nonmetabolizable analog of L-arabinose, D-fucose, antagonizes arabinose induction by AraC (2, 28) and can be added to cultures containing arabinose to inhibit induction and lower the level of expression from P_{BAD}. Thus, different mixtures of arabinose and D-fucose can be used to obtain yet another level of modulation of expression with pBAD vectors, while mixtures of glucose and D-fucose could also achieve lower levels of repression as compared with those of glucose alone (2, 29). Finally, once the P_{BAD} promoter has been repressed, the efficiency of repression depends mainly on the specific properties of posttranscriptional control of expression of each gene. For genes that yield very high levels of protein from the P_{BAD} promoter, repression may require lowering the overall expression of the gene (by lowering plasmid copy number and/or efficiency of initiation of translation).

Most of the available expression systems are not well repressed (4, 13, 15, 48). However, there are several systems that provide good repression (16, 20, 21, 35). Among them are vectors based on the lambda phage P_L promoter and its temperature-sensitive cI repressor allele, cI857 (15, 18, 35), and runaway replication plasmids (21, 23, 27). Still, the use of pBAD vectors will be advantageous in situations where (i) the high temperature required for P_L and some runaway vectors is not desired (23, 27), (ii) rapid shutoff is needed (e.g., runaway plasmids take several generations to be lost), (iii) analysis of recovery from a depleted state by turning on (very rapidly) a previously repressed promoter is desired, and (iv) modulation of expression is required.

Cagnon and coworkers (5) have also reported vectors allowing expression from the P_{BAD} promoter. However, the development of these vectors was oriented more towards biotechnological goals of high-level expression, which is in contrast to ours which were developed for physiological studies.

Using wild-type *phoA* and *phoA* fusions, we have estimated that the induction/repression ratio from the P_{BAD} promoter is from 200- to 1,200-fold, compared with a ratio of 50-fold for the P_{TAC} promoter (Table 1). In studies of the regulation of the arabinose operon (29), it was determined that the wild-type chromosomal *araC*-P_{BAD} promoter system can be activated 1,200-fold in vivo. These measurements, which were obtained with L-arabinose isomerase assays and log-phase cultures grown in minimal medium, are very similar to the induction/repression ratios that we obtained in minimal medium under similar culture conditions (Table 1). On the other hand, we found three- to fourfold less induction in rich NZY medium than in minimal medium (Table 1). This was also observed in rich LB medium and with AP fusions to two additional cell division proteins (data not shown). Similarly, Cagnon et al. obtained induction values lower than 1,200-fold when they measured β-galactosidase activity from the P_{BAD} promoter in LB broth (5). While we do not know the basis of this effect, it could be explained as the result of properties of the rich media, such as producing lower plasmid copy number and the presence of medium-related substances that could induce partial catabolite repression or inhibition, etc. The effect of lower activation in rich media was also observed with the P_{TAC} promoter (Table 1). However, in this case, the induction/repression ratio remained constant (i.e., 50-fold) as a result of proportional increase in expression during induction and repression in minimal medium. Our results with *phoA* fusions also indicated that P_{TAC} is at least 2.5-fold stronger and 12-fold less repressed than P_{BAD}. The leakiness and high strength of

the P_{TAC} promoter has been widely observed (4, 13, 15). In fact, the higher expression from P_{TAC} is strongly supported by the observations that expression of *malF-malG'* (data not shown) and the IS*911* transposase gene (37a) from induced P_{TAC} promoter is lethal but perfectly viable when the same genes are expressed in pBAD vectors.

Finally, a great and often-overlooked disadvantage of many expression systems, including those repressed more efficiently, is that their promoters are too strong when they are induced and expression is not modulated (15, 18, 21, 23, 27, 35). In many cases, the resulting protein overproduction from these systems negates the physiological relevance of the experiments, and it becomes only useful to purify and visualize proteins. Among the two most common and drastic overproduction problems are lethality (as in the case of overproduction of membrane proteins, cytoplasmic proteins like β-galactosidase [17], some cell division proteins [14], or toxic products [16]) and formation of inclusion bodies (37a, 46). In *E. coli*, protein hyperproduction to 30% of the total protein can lead to rRNA and ribosome destruction, accumulation of heat shock proteins, and lethality (17). However, overproduction can create more subtle but nonetheless important problems. For instance, in complementation studies, a mutated gene expressed from a multicopy plasmid may complement the corresponding chromosomal mutation only when overexpressed from the plasmid. In this case, the mutated gene may encode a protein that is significantly deficient in the required function, but not totally defective, which fails to complement when expressed at levels closer to those of the wild type. However, overproduction of the mutated protein may produce enough of it, such that even though it is defective, the process can be driven to complementation. Another example is in depletion experiments, when protein overproduction before depletion (besides increasing the time needed for depletion) may be detrimental for cell growth or interfere with some processes which in turn can affect the analysis of the depletion phenotype. We have shown that moderately high expression and modulation can be achieved with pBAD vectors (Table 1 and Fig. 4). While maximum levels are high enough to permit most studies that require overproduction, they are not as high as those obtained from strong inducible promoters, and some of the detrimental effects of overproduction like lethality and formation of inclusion bodies have been alleviated by replacing the vector in use with pBAD plasmids (37a) (see Results). This is particularly the case when the excellent modulation of the P_{BAD} promoter expression is taken advantage of by inducing with arabinose concentrations that vary by as much as 2 orders of magnitude (Fig. 4).

Thus, there are many advantages in using a system that is easily modulated and contains a moderately strong promoter in conjunction with tight regulation. pBAD vectors represent a simple and useful expression system for efficient repression, modulation, and moderately high expression, which should permit more careful experimentation on biological processes in bacteria.

REFERENCES

1. **Belder, J. B., M. Nguyen-Disteche, N. Houba-Herin, J. M. Ghuysen, I. N. Maruyama, H. Hara, Y. Hirota, and M. Inouye.** 1988. Overexpression, solubilization and refolding of a genetically engineered derivative of the penicillin-binding protein 3 of Escherichia coli K12. Mol. Microbiol. **2:**519–525.
2. **Beverin, S., D. E. Sheppard, and S. S. Park.** 1971. D-Fucose as a gratuitous inducer of the L-arabinose operon in strains of Escherichia coli B/r mutant in gene araC. J. Bacteriol. **107:**79–86.
3. **Boyd, D., C. Manoil, and J. Beckwith.** 1987. Determinants of membrane protein topology. Proc. Natl. Acad. Sci. USA **84:**8525–8529.
4. **Brosius, J., M. Erfle, and J. Storella.** 1985. Spacing of the −10 and −35 regions in the tac promoter. Effect on its in vivo activity. J. Biol. Chem. **260:**3539–3541.
5. **Cagnon, C., V. Valverde, and J.-M. Masson.** 1991. A new family of sugar-inducible vectors for Escherichia coli. Protein Eng. **4:**843–847.
6. **Carra, J. H., and R. F. Schleif.** 1993. Variation of half-site organization and DNA looping by AraC protein. EMBO J. **12:**35–44.
7. **Carson, M. J.** Unpublished results.
7a. **Carson, M. J., J. J. Barondess, and J. Beckwith.** 1991. The FtsQ protein of Escherichia coli: membrane topology, abundance, and cell division phenotypes due to overproduction and insertion mutations. J. Bacteriol. **173:**2187–2195.
8. **Cass, L. G., A. H. Horwitz, and G. Wilcox.** 1981. The araI^c mutation in Escherichia coli B/r. J. Bacteriol. **146:**1098–1105.
9. **Chang, A. C. Y., and S. N. Cohen.** 1978. Construction and characterization of amplifiable multicopy DNA cloning vehicles derived from the p15A cryptic miniplasmid. J. Bacteriol. **134:**1141–1156.
10. **Conley, M. P., A. J. Wolfe, D. F. Blair, and H. C. Berg.** 1989. Both CheA and CheW are required for reconstitution of chemotactic signaling in Escherichia coli. J. Bacteriol. **171:**5190–5193.
11. **Cull, M. G., J. F. Miller, and P. J. Schatz.** 1992. Screening for receptor ligands using large libraries of peptides linked to the C terminus of the lac repressor. Proc. Natl. Acad. Sci. USA **89:**1865–1869.
12. **Dalbey, R. E., and W. Wickner.** 1985. Leader peptidase catalyzes the release of exported proteins from the outer surface of the Escherichia coli plasma membrane. J. Biol. Chem. **260:**15925–15931.
13. **de Boer, H. A., L. J. Comstock, and M. Vasser.** 1983. The tac promoter: a functional hybrid derived from the trp and lac promoters. Proc. Natl. Acad. Sci. USA **80:**21–25.
14. **de Boer, P. A. J., R. E. Crossley, and L. I. Rothfield.** 1988. Isolation and properties of minB, a complex genetic locus involved in correct placement of the division site in Escherichia coli. J. Bacteriol. **170:**2106–2112.
15. **Diederich, L., A. Roth, and W. Messer.** 1994. A versatile plasmid vector system for the regulated expression of genes in Escherichia coli. BioTechniques **16:**916–923.
16. **Doherty, A. J., B. A. Connolly, and A. F. Worrall.** 1993. Overproduction of the toxic protein, bovine pancreatic DNaseI, in Escherichia coli using a tightly controlled T7-promoter-based vector. Gene **136:**337–340.
17. **Dong, H., L. Nilsson, and C. G. Kurland.** 1995. Gratuitous overexpression of genes in Escherichia coli leads to growth inhibition and ribosome destruction. J. Bacteriol. **177:**1497–1504.
18. **Elvin, C. M., P. R. Thompson, M. E. Argall, P. Hendry, N. P. Stamford, P. E. Lilley, and N. E. Dixon.** 1990. Modified bacteriophage lambda promoter vectors for overproduction of proteins in Escherichia coli. Gene **87:**123–126.
19. **Englesberg, E., R. L. Anderson, R. Neinberg, N. Lee, P. Hoffee, G. Huttenhauer, and H. Boyer.** 1962. L-Arabinose-sensitive, L-ribulose 5-phosphate 4-epimerase-deficient mutants of Escherichia coli. J. Bacteriol. **84:**137–146.
20. **Gil, D., and J. P. Bouche.** 1991. ColE1-type vectors with fully repressible replication. Gene **105:**17–22.
21. **Giza, P. E., and R. C. Huang.** 1989. A self-inducing runaway-replication plasmid expression system utilizing the Rop protein. Gene **78:**73–84.
22. **Guzman, L.-M., J. J. Barondess, and J. Beckwith.** 1992. FtsL, an essential cytoplasmic membrane protein involved in cell division in Escherichia coli. J. Bacteriol. **174:**7716–7728.
23. **Hoffmann, I., J. Widstrom, M. Zeppezauer, and P. O. Nyman.** 1987. Overproduction and large-scale preparation of deoxyuridine triphosphate nucleotidohydrolase from Escherichia coli. Eur. J. Biochem. **164:**45–51.
24. **Johnston, S., J.-H. Lee, and S. D. Ray.** 1985. High-level expression of M13 gene II protein from an inducible polycistronic messenger RNA. Gene **34:**137–145.
25. **Kozak, M.** 1983. Comparison of initiation of protein synthesis in prokaryotes, eukaryotes and organelles. Microbiol. Rev. **47:**1–45.
26. **Kuhn, A., and W. Wickner.** 1985. Isolation of mutants in M13 coat protein that affect its synthesis, processing, and assembly into phage. J. Biol. Chem. **260:**15907–15913.
27. **Larsen, J. E. L., K. Gerdes, J. Light, and S. Molin.** 1984. Low-copy-number plasmid-cloning vectors amplifiable by derepression of an inserted foreign promoter. Gene **28:**45–54.
28. **Lee, N.** 1980. Molecular aspects of ara regulation, p. 389–410. In J. H. Miller and W. S. Reznikoff (ed.), The operon. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.
29. **Lee, N., C. Francklyn, and E. P. Hamilton.** 1987. Arabinose-induced binding of AraC protein to araI_2 activates the araBAD operon promoter. Proc. Natl. Acad. Sci. USA **84:**8814–8818.
30. **Lobell, R. B., and R. F. Schleif.** 1990. DNA looping and unlooping by AraC protein. Science **250:**528–532.
31. **Lopilato, J., S. Bortner, and J. Beckwith.** 1986. Mutations in a new chromosomal gene of Escherichia coli, pcnB, reduce plasmid copy number of pBR322 and its derivatives. Mol. Gen. Genet. **205:**285–290.
31a. **Martin, N. L.** Unpublished results.
32. **Miyada, C. G., L. Stoltzfus, and G. Wilcox.** 1984. Regulation of the araC gene of Escherichia coli: catabolite repression, autoregulation, and effect on araBAD expression. Proc. Natl. Acad. Sci. USA **81:**4120–4124.
33. **Mukherjee, A., and W. D. Donachie.** 1990. Differential translation of cell division proteins. J. Bacteriol. **172:**6106–6111.
34. **Murphy, C. K., and J. Beckwith.** 1994. Residues essential for the function of SecE, a membrane component of the Escherichia coli secretion apparatus, are located in a conserved cytoplasmic region. Proc. Natl. Acad. Sci. USA **91:**2557–2561.
35. **O'Connor, C. D., and K. N. Timmis.** 1987. Highly repressible expression system for cloning genes that specify potentially toxic proteins. J. Bacteriol. **169:**4457–4462.
36. **Phillips, G. J., and T. J. Silhavy.** 1992. The E. coli ffh gene is necessary for viability and efficient protein export. Nature (London) **359:**744–746.
37. **Pogliano, J. A., and J. Beckwith.** 1994. SecD and SecF facilitate protein export in Escherichia coli. EMBO J. **13:**554–561.
37a. **Polard, P., and M. Chandler.** Personal communication.
38. **Russell, C. B., R. C. Stewart, and F. W. Dahlquist.** 1989. Control of transducer methylation levels in Escherichia coli: investigation of components essential for modulation of methylation and demethylation reactions. J. Bacteriol. **171:**3609–3618.
39. **Sambrook, J., E. F. Fritsch, and T. Maniatis.** 1989. Molecular cloning: a laboratory manual, 2nd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.
40. **San Millan, J. L., D. Boyd, R. Dalbey, W. Wickner, and J. Beckwith.** 1989. Use of phoA fusions to study the topology of the Escherichia coli inner membrane protein leader peptidase. J. Bacteriol. **171:**5536–5541.
41. **Schleif, R. S.** 1992. DNA looping. Annu. Rev. Biochem. **61:**199–223.
42. **Shine, J., and L. Dalgarno.** 1974. The 3′-terminal sequence of E. coli 16S ribosomal RNA: complementary to nonsense triplets and ribosome binding sites. Proc. Natl. Acad. Sci. USA **71:**1342–1346.
43. **Stormo, G. D., T. D. Schneider, and T. M. Gold.** 1982. Characterization of translational initiation sites in E. coli. Nucleic Acids Res. **10:**2971–2996.
44. **Strauch, K. L., and J. Beckwith.** 1988. An Escherichia coli mutation preventing degradation of abnormal periplasmic proteins. Proc. Natl. Acad. Sci. USA **85:**1576–1580.
45. **Tabor, S., and C. C. Richardson.** 1985. A bacteriophage T7 RNA polymerase/promoter system for controlled exclusive expression of specific genes. Proc. Natl. Acad. Sci. USA **82:**1074–1078.
46. **Wagatsuma, M., N. Asami, J. Miyachi, S. Uchida, H. Watanabe, and E. Amann.** 1993. Antibody recognition of the recombinant human nuclear antigens RNP 70kD, SS-B, and Sm-D by autoimmune sera. Mol. Immunol. **30:**1491–1498.
47. **Wilcox, G., K. J. Clemetson, P. Cleary, and E. Englesberg.** 1974. Interaction of the regulatory gene product with the operator site in the L-arabinose operon of Escherichia coli. J. Mol. Biol. **85:**589–602.
48. **Yanisch-Perron, C., J. Vieira, and J. Messing.** 1985. Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors. Gene **33:**103–119.
49. **Yansura, D. G., and D. J. Henner.** 1990. Use of Escherichia coli trp promoter for direct expression of proteins. Methods Enzymol. **185:**54–60.
50. **Zagursky, R. J., and M. L. Berman.** 1984. Cloning vectors that yield high levels of single-stranded DNA for rapid DNA sequencing. Gene **27:**183–191.