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# The Presence of Intervening Sequences in the $\alpha$ -Fetoprotein Gene of the Mouse\*

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Messenger RNA for the oncofetal protein  $\alpha$ -fetoprotein was isolated from yolk sacs of 16- to 18-day-old mouse embryos. This RNA was used as a template to synthesize full-length double-stranded DNA containing predominantly  $\alpha$ -fetoprotein coding sequences. Chimeric plasmids containing the double-stranded DNA were constructed in two ways. First, molecular linkers containing the recognition site for the restriction endonuclease *Hind*III were ligated to the blunted ends of the DNA, and following cleavage with *Hind*III, the recombinant molecules were ligated to the single *Hind*III site in the plasmid vehicle pBR322. Second, internal *Pst* I fragments of the double-stranded DNA were ligated to the single *Pst* I site of pBR322. Following transformation of the host *Escherichia coli*  $\chi$ 1776, colonies containing those chimeric plasmids which had incorporated  $\alpha$ -fetoprotein sequences were identified by selective hybridization and arrest translation procedures. Two cloned sequences derived from the 5' and 3' regions of the mRNA were used as hybridization probes to detect the presence of the  $\alpha$ -fetoprotein gene within a two-dimensional fingerprint of mouse genomic DNA cleaved with *Eco*RI, an enzyme which does not cleave within the messenger RNA sequence. The detection of 3 *Eco*RI fragments demonstrates that the single  $\alpha$ -fetoprotein gene must be represented discontinuously in the mouse genome, with at least two intervening sequences.

$\alpha$ -fetoprotein is a major constituent of fetal serum in all mammalian species which have been examined (1-4). During development in the mouse, AFP<sup>1</sup> is synthesized by the yolk sac and liver and secreted into the blood and amniotic fluid. After birth, the amount of AFP in serum decreases markedly in most strains of mice to a basal level which represents less than 0.01% of that in fetal serum (3, 5). This decline has recently been shown by Olsson *et al.* (5) to be inherited as an autosomal recessive trait, which they termed regulation of  $\alpha$ -fetoprotein (*raf*).

Reinitiation of  $\alpha$ -fetoprotein synthesis in the adult occurs

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<sup>1</sup> Abbreviations used are AFP,  $\alpha$ -fetoprotein; dsDNA, double-stranded DNA; SSC, 0.15 M NaCl, 0.015 M sodium citrate; bp, base pairs; kb, kilobase pairs; Hepes, *N*-(2-hydroxyethyl)-1-piperazine-ethanesulfonic acid; SDS, sodium dodecyl sulfate.

under a select number of pathological conditions: following liver injury (6, 7), in hepatocarcinomas (1, 2), and in testicular teratocarcinomas (8, 9). In addition, a number of congenital birth defects, including congenital nephrosis, severe Rh-hemolytic disease, and several open neural tube defects are associated with abnormally elevated concentrations of AFP in the maternal and fetal circulation and amniotic fluid (10-12). These striking and reproducible increases in the production of AFP in fetal abnormalities, in liver regenerative diseases, and in carcinomas of the liver and germ cells in humans has generated interest in the mechanism of control of the expression of AFP.

Recent studies by Tamaoki and his co-workers (13, 14) have used cell-free translation assays to demonstrate that the rate of synthesis of  $\alpha$ -fetoprotein in fetal and neonatal mouse liver is related to the concentration of translatable AFP mRNA. Taking this analysis one step further, Innis and Miller (15) reported the isolation of rat AFP mRNA. Complementary DNA to the AFP mRNA was used in hybridization kinetic experiments to show that the actual amount of AFP mRNA in adult liver mRNA was less than 1% of that in hepatoma cells. These studies imply that the control of AFP synthesis occurs at the level of mRNA transcription or processing, or both.

Distinguishing between these possibilities will require large amounts of specific hybridization probes to the  $\alpha$ -fetoprotein gene, as well as intimate knowledge about its structural organization in the genome. Toward this end, we have constructed chimeric plasmids containing portions of the mouse AFP mRNA sequence, and used them to identify three *Eco*RI fragments of mouse genomic DNA which encode in a discontinuous manner the single copy AFP gene.

## EXPERIMENTAL PROCEDURES

**Purification of  $\alpha$ -Fetoprotein**—Amniotic fluid, pooled from 16- to 18-day mouse fetuses, was subjected to 35 to 70% ammonium sulfate precipitation. The 70% pellet was dialyzed against 50 mM Tris-HCl (pH 7.5) and electrophoresed through a nondenaturing 7% polyacrylamide gel (16). The AFP band was identified by a comparison to fetal and adult serum protein markers, extracted and concentrated by ethanol precipitation (16). This material was used to raise antisera to AFP by bimonthly injections into a rabbit. The rabbit antisera were regularly tested for anti-AFP activity by Ouchterlony analysis (17) against purified AFP, amniotic fluid, and adult mouse serum.

**Preparation of RNA**—Yolk sac and livers, obtained from 16- to 18-day-old Swiss mouse fetuses were frozen in liquid N<sub>2</sub>. Poly(A) RNA was prepared by phenol extraction of total cellular RNA (18) followed by oligo(dT)-cellulose chromatography (19). The RNA was fractionated on an 8 to 25% sucrose gradient in 2 mM EDTA, 100 mM NaCl, 10 mM Hepes (pH 7.6), which was centrifuged at 29,000 rpm for 22 h in a Beckman SW40 rotor. Individual fractions were precipitated by the addition of 2 volumes of ethanol, resuspended in H<sub>2</sub>O and tested for AFP mRNA activity using a cell-free synthesizing system derived from wheat germ (20, 21). After treatment with 200  $\mu$ g/ml of

RNase A for 30 min the [ $^{35}$ S]methionine-containing products of translation were analyzed on sodium dodecyl sulfate polyacrylamide gels (22). To identify *de novo* AFP, 25- $\mu$ l portions of each translation were incubated at 37°C for 1 h in the presence of an excess of anti-AFP sera, purified carrier AFP was added for an additional hour, and the chilled precipitate was washed by centrifugation through a discontinuous sucrose gradient (23). The pellets were resuspended in 1% SDS, 1%  $\beta$ -mercaptoethanol, 20% glycerol, 60 mM Tris-HCl (pH 6.8) and subjected to electrophoresis as before. In most experiments, RNA obtained from adult mouse liver was treated identically, and used as a negative control for the presence of AFP.

**Construction of Chimeric Plasmids Containing  $\alpha$ -Fetoprotein Sequences**—The 18 S yolk sac RNA (50  $\mu$ g/ml) was transcribed by avian myeloblastosis virus reverse transcriptase in the presence of 140 mM KCl, 500  $\mu$ M dXTP's, and 1,000 units/ml of reverse transcriptase. The second strand was synthesized in the presence of DNA polymerase I according to Wickens *et al.* (24) using 120 units/ml of DNA polymerase and 500  $\mu$ M dXTP's. The double-stranded DNA was extracted with  $\text{CHCl}_3$ , passed through a Sephadex G-100 column in  $\text{H}_2\text{O}$ , and digested for 30 min with 200 units/ml of S1 nuclease in 0.3 M NaCl, 30 mM NAOAc (pH 4.5), 3 mM  $\text{ZnCl}_2$  along with 10  $\mu$ g/ml of single-stranded fd DNA carrier. Following phenol extraction, the DNA was concentrated by ethanol precipitation in the presence of 50  $\mu$ g/ml of yeast tRNA.

In experiments where *Hind*III linkers were used to attach the dsDNA to pBR322, the procedure of Ullrich *et al.* (25) was followed, except that a 50-fold molar excess of *Hind*III linkers (Collaborative Research) over "ends" of dsDNA was used, and the excess linkers were removed after *Hind*III digestion by Sephadex G-100 chromatography. The linked dsDNA was concentrated by ethanol precipitation and ligated to the EK2 vector pBR322 which had been cleaved with *Hind*III and bacterial alkaline phosphatase (25). The ligation in 1 mM ATP, 10 mM  $\text{MgCl}_2$ , 20 mM Tris-HCl (pH 7.5) occurred at 14°C for 16 h at a pBR322 DNA concentration of 3  $\mu$ g/ml and cDNA concentration of 0.5 to 1  $\mu$ g/ml.

In experiments where internal *Pst* I fragments of AFP dsDNA were cloned, the dsDNA was cleaved before S1 nuclease treatment with *Pst* I, phenol-extracted, ethanol-precipitated, and ligated to pBR322 DNA which had been digested with *Pst* I and bacterial alkaline phosphatase as above.

**Transformation of *E. coli*  $\chi$ 1776 and Identification of  $\alpha$ -Fetoprotein-positive Colonies**—All experiments involving recombinant DNA were performed in a P3 facility using EK2 hosts and vectors in accordance with the NIH Guidelines for Research Involving Recombinant DNA.<sup>2</sup> *E. coli*  $\chi$ 1776 (100 ml) was grown to an  $A_{590}$  of 0.2 to 0.3 in LB broth supplemented with 100  $\mu$ g/ml of diaminopimelic acid and 40  $\mu$ g/ml of thymidine. The cells were centrifuged, washed in 50 ml of 100 mM NaCl, 5 mM Tris-HCl (pH 7.5), and resuspended in 50 ml of 5 mM Tris-HCl (pH 7.5), 10 mM  $\text{MgCl}_2$ , 70 mM  $\text{CaCl}_2$ . After 20 min at room temperature, the cells were concentrated by centrifugation and resuspended in 2 ml of the same buffer. Fifty microliters of the ligated mixtures, which had been dialyzed briefly against 100 mM NaCl, 5 mM Tris-HCl (pH 7.5) were mixed with 0.2 ml of cells for 60 min at 4°C, heated at 42°C for 1 min, chilled on ice for 10 min, and grown in 3 ml of LB broth supplemented with diaminopimelic acid and thymidine for 40 min. The cells were plated onto ampicillin (25  $\mu$ g/ml) or tetracycline (25  $\mu$ g/ml) LB plates for *Hind*III or *Pst* I insertion sites, respectively.

Colonies which were shown by replica plating to grow in the presence of one drug alone were grown on replica nitrocellulose filters (Millipore Corp.) for 24 h and treated according to Grunstein and Hogness (26). Identical filters were treated for 4 h in the presence of 4  $\times$  Denhardt's solution [ $1 \times$  is 0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% bovine serum albumin (27)] and 3  $\times$  SSC ( $1 \times$  is 0.15 M NaCl, 0.015 M sodium citrate) at 68°C. They were hybridized to cDNA prepared against either 18 S adult liver, fetal liver, or yolk sac RNA's. The cDNAs were prepared by incubating 50  $\mu$ g/ml of RNA in 50 mM Tris-HCl (pH 8.3), 10 mM  $\text{MgCl}_2$ , 3 mM  $\beta$ -mercaptoethanol, 40  $\mu$ g/ml of oligo(dT) (12-18) (Collaborative Research), 800  $\mu$ M dXTP's, 4 mM sodium pyrophosphate, and [ $^{32}$ P]dCTP (specific activity of 80 cpm/pg) at 60°C for 2 min. After cooling on ice, reverse transcriptase was added to 1000 units/ml and the reaction was allowed to proceed for 1 h at 41°C. The RNA template was hydrolyzed at 37°C for 4 h in 0.3 N NaOH, and after neutralization, the cDNA was recovered by chloroform extraction and Sephadex G-100 chromatography in  $\text{H}_2\text{O}$ .

The filters were hybridized at 68°C in a volume of 3 ml in the presence of 0.5 to 2.0  $\times 10^6$  cpm of cDNA, 4  $\times$  Denhardt's solution, 6  $\times$  SSC, 0.5% SDS, 100  $\mu$ g/ml of *E. coli* DNA, and 50  $\mu$ g/ml of poly(A) and yeast tRNA's. After washing the filters at 50°C in 0.1  $\times$  SSC and 0.05% SDS for several h, the filters were autoradiographed.

**Hybrid Arrest Translation**—Colonies were grown in brain heart infusion media supplemented with diaminopimelic acid and thymidine to an  $A_{590}$  of 1.2 and amplified in the presence of 50  $\mu$ g/ml of chloramphenicol. The plasmid DNA was extracted by a modification of the procedure of Meagher *et al.* (28) whereby plasmid DNA was separated from RNA using Sepharose 2B chromatography in 1 M NaCl, 50 mM Tris-HCl (pH 7.5), 10 mM EDTA. Twenty micrograms of DNA was cleaved with *Eco*RI (29), extracted with phenol and ether, and concentrated by ethanol precipitation. The arrest translation procedure of Paterson *et al.* (30) was followed. The DNA was dissolved in 20  $\mu$ l of deionized formamide and heated at 90°C for 5 min. Five microliters containing 5  $\mu$ g of poly(A) RNA, 2 M NaCl, and 50 mM 1,4-piperazinediethanesulfonic acid (pH 6.8) was added, and the mixture was incubated at 50°C for 2 h. After the addition of 200  $\mu$ l of  $\text{H}_2\text{O}$ , the solution was divided into two equal portions, one of which was heated to 90°C for 1 min before precipitation with 2 volumes of ethanol and one which was precipitated directly. The two pellets after centrifugation were dissolved in 10  $\mu$ l of  $\text{H}_2\text{O}$  and added to wheat germ lysates as before.

**Restriction Endonuclease Mapping of DNA**—Double-stranded DNA or plasmid DNA was cleaved with *Eco*RI, *Pst* I, *Hind*III, or *Bam*HI, under conditions previously described (31). The fragments were analyzed on 1 to 2% agarose gels or 5% acrylamide gels (32) by staining with 25  $\mu$ g/ml of ethidium bromide. When fragments were isolated for the preparation of radiolabeled probes, the bands were cut out, placed in a dialysis membrane with electrophoresis buffer, and submerged in a horizontal slab gel electrophoresis apparatus. After 4 to 6 h at 150 mA, the buffer was removed, filtered, and concentrated with ethanol and tRNA carrier. The DNA was labeled to specific activities of 10 to 50  $\times 10^6$  cpm/ $\mu$ g by nick translation in the presence of [ $^{32}$ P]dCTP (33).

When restriction fragments were denatured prior to gel electrophoresis, the DNA was deproteinized by phenol extraction and concentrated by ethanol precipitation. The fragments were treated with 15% glyoxal and 50% dimethyl sulfoxide in 10 mM potassium phosphate, pH 7.0 at 50°C for 45 min, and run in a 1.5% agarose gel in 10 mM potassium phosphate, pH 7.0 (34). After treatment of the gel in 50 mM NaOH, the bands were stained with ethidium bromide.

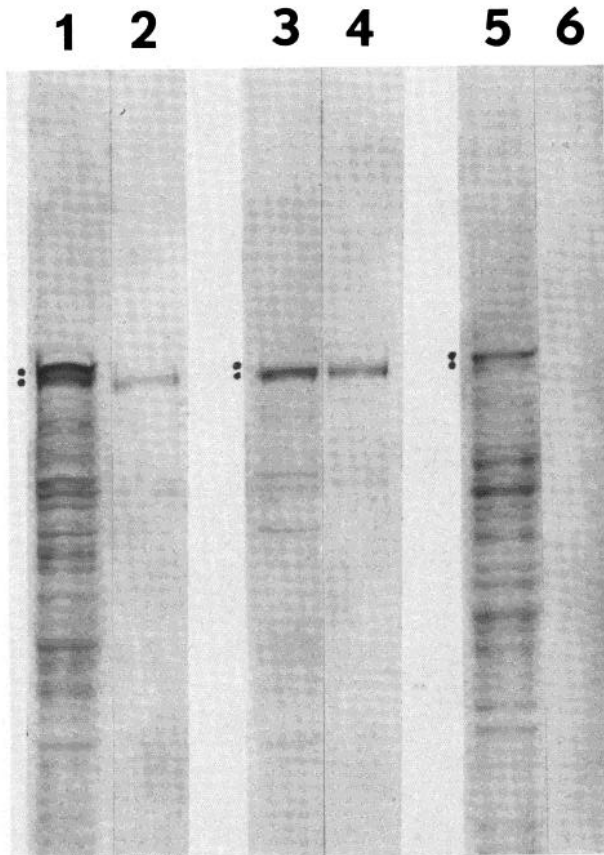
**RPC5 Chromatography and Identification of  $\alpha$ -Fetoprotein-coding *Eco*RI Fragments**—Mouse embryonic DNA was isolated (35), cleaved with *Eco*RI, and chromatographed on an RPC-5 column as previously described (36). Replica 1.0% agarose gels of 10  $\mu$ g of pooled DNA fractions were run, and the DNA was transferred to nitrocellulose filters (37). The filters were pretreated and hybridized to labeled fragments of chimeric plasmids as described in detail above, using 5 to 10  $\times 10^6$  cpm of DNA per filter in 20 ml of hybridization buffer. The filters were washed as above and exposed to Kodak XR-1 film in the presence of Dupont Lightning-plus intensifiers.

## RESULTS

**Isolation of  $\alpha$ -Fetoprotein mRNA**—In order to identify a suitable source of murine AFP mRNA, total poly(A)-containing RNA was extracted separately from 16- to 18-day-old fetal livers and yolk sacs. These were subjected to sucrose gradient centrifugation, and individual fractions were tested for AFP template activity using a wheat germ *in vitro* protein synthesis system. The products of translation were analyzed by SDS-polyacrylamide gel electrophoresis, and AFP and albumin were identified using monospecific antibodies to each protein. The AFP mRNA template activity migrated as an 18 S RNA species, which agrees with the size determinations of previous investigators for rat (15) and mouse (14) AFP mRNA, and with the molecular weight of the protein being 70,000 (38). The products of the 18 S mRNA translations are shown in Fig. 1. In *Lane 1*, two predominant bands which co-migrate with mouse albumin (*upper dot*) and AFP (*lower dot*) were synthesized by 18 S fetal liver RNA. The lower band is completely immunoprecipitable by anti-AFP sera (Fig. 1, *Lane 2*). When the total translation products derived from 18

<sup>2</sup> NIH Guidelines for Research Involving Recombinant DNA (1976) National Institutes of Health, Bethesda, Md.





**FIG. 1. *In vitro* translation of RNA and identification of AFP.** An 18 S fraction from adult liver 16- to 18-day-old fetal liver or yolk sac RNA was translated in a 50- $\mu$ l wheat germ lysate in the presence of [ $^{35}$ S]methionine. Either the total translation products (Lanes 1, 3, and 5) or the translation product precipitated with anti-AFP (Lanes 2, 4, and 6) were analyzed by electrophoresis in slab 9% SDS-polyacrylamide gels, and autoradiographed. The RNAs were: 1 and 2, fetal liver RNA; 3 and 4, yolk sac RNA; and 5 and 6, adult liver RNA. The upper and lower dots indicate the migration of authentic mouse albumin and AFP, respectively.

S yolk sac mRNA were analyzed (Fig. 1, Lane 3), there was a single predominant protein band which was completely immunoprecipitable by anti-AFP sera (Lane 4) and could be competed for by authentic AFP (data not shown).

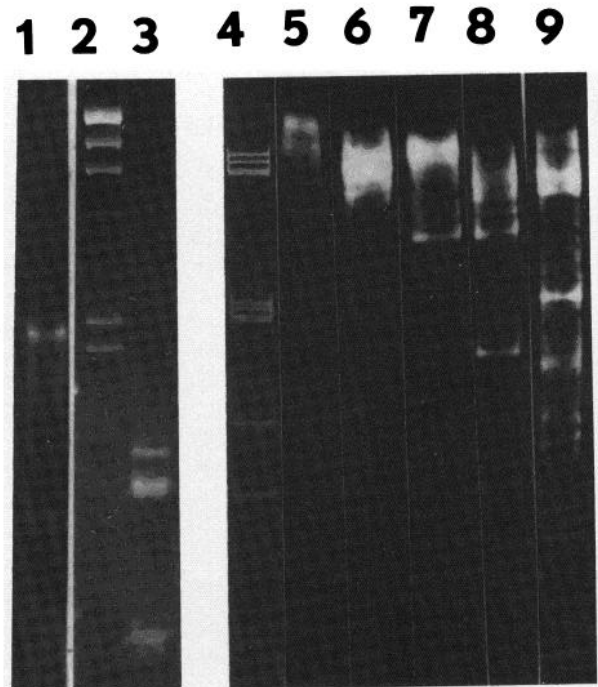
The striking predominance of  $\alpha$ -fetoprotein, the only major protein encoded by the 18 S yolk sac RNA, supports the previous observations of Wilson and Zimmerman (39), who concluded that AFP represented 40 to 60% of the protein synthesis of yolk sac, while only 20% of that in fetal liver. As a control, poly(A) RNA from adult mouse liver which should contain no AFP template activity was used to direct protein synthesis in the wheat germ system. As shown in Fig. 1, Lanes 5 and 6, no labeled protein which could be immunoprecipitated with AFP antibody was synthesized.

The relative migration of albumin and  $\alpha$ -fetoprotein in the gel buffer system used (Fig. 1) is contrary to their molecular weights of 68,000 and 70,000, respectively (38). By using a different buffer system (40), we could reverse the order of migration of both the *in vitro* products and the mature proteins, such that albumin exhibited a faster migration. We conclude that the aberrant migration observed is a result of the primary amino acid sequences of these proteins and not to any post-translational modification.

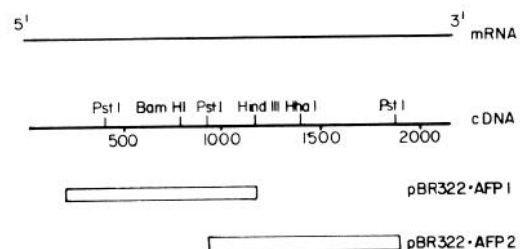
**Insertion of  $\alpha$ -Fetoprotein mRNA Sequences into a Plasmid Vehicle**—The 18 S poly(A) mRNA preparation from yolk sac should contain greater than 50% AFP mRNA, ensuring that at least one in two hybrid plasmids contain AFP se-

quences. The heterogeneous mRNA's were transcribed by avian myeloblastosis virus reverse transcriptase using the conditions of Wickens *et al.* (24). The second strand was synthesized using DNA polymerase and the resulting hairpin loop and single stranded tails removed by treatment with S1 nuclease from *Aspergillus oryzae*. Agarose gel electrophoresis of the double-stranded cDNA's (Fig. 2) demonstrated the presence of a predominant band migrating as 2,150 base pairs of DNA. This is the size one would predict for a full-length transcript of an 18 S mRNA.

To choose a suitable strategy for cloning the  $\alpha$ -fetoprotein cDNA, the 2,150 bp dsDNA was cleaved with *Pst* I, *Hind*III, and *Bam*HI (Fig. 2). These enzymes were chosen because they each cleave the genome of the plasmid vector pBR322



**FIG. 2. Restriction endonuclease digestion of yolk sac dsDNA.** Double-stranded DNA labeled with [ $^{32}$ P]dCTP, prepared from 18 S yolk sac RNA, was electrophoresed in a 1.5% agarose gel and autoradiography was performed (Lane 1). The markers in Lane 2 are a *Hind*III digest of  $\lambda$ cI857 DNA where the fragment sizes are, from top to bottom, 22.0, 9.4, 6.6, 4.2, 2.3, 1.9, and 0.62 kb. The markers in Lane 3 are a *Hae* III digest of ColE1 DNA where the visible fragments are 1.18, 0.95, and 0.45 kb. The double stranded DNA was digested with *Eco*RI (Lane 5), *Hind*III (Lane 6), *Bam*HI (Lane 7), *Hind*III and *Bam*HI (Lane 8), and *Pst* I (Lane 9) and electrophoresed in a 5% acrylamide gel. The markers in Lane 4 are a *Hae* III digest of ColE1 where the resolvable fragments are 1.18, 1.02, 0.95, 0.45, 0.44, 0.43, 0.247 and 0.179 kb.



**FIG. 3. Restriction endonuclease map of AFP DNA.** The 2.15-kb double stranded AFP DNA is represented in the second line with the map positions of the indicated restriction endonucleases. The first line illustrates the orientation of the 5' and 3' ends of the mRNA relative to the cDNA. At the bottom are drawn the regions of the cDNA contained within the plasmids pBR322-AFP1 and pBR322-AFP2.



once, in either the ampicillin resistance gene (*Pst* I) or the tetracycline resistance gene (*Bam*HI and *Hind*III) (41), and thus insertion into any one of these sites allows for discrimination between colonies that contain recombinant plasmids and those that contain parental plasmids. All three enzymes cut the AFP sequence, generating unique fragments detectable by autoradiography. The presence of clearly identified bands which correspond to a single species supports the previous estimate by translation that AFP is the only predominant species in the 18 S yolk sac mRNA. Both *Hind*III and *Bam*HI cleave the sequence once (Fig. 2, Lanes 6 and 7) and *Pst* I makes 3 cuts (Lane 9). In contrast, *Eco*RI (Lane 5) does not cleave within the AFP sequence. By performing a series of double digests such as the *Bam*HI-*Hind*III cleavage illustrated in Fig. 2, Lane 8, it was possible to construct a restriction map of the cDNA (Fig. 3).

The orientation of the restriction map relative to the 5' and 3' ends of the  $\alpha$ -fetoprotein mRNA, illustrated in Fig. 3, was determined using ds cDNA which had not been treated with S1 nuclease. Following cleavage of the dsDNA with *Hha* I, which recognizes one asymmetric site in the cDNA, the fragments were denatured by glyoxal and electrophoresed in a 1.5% agarose gel (34). The presence of a 700-bp denatured fragment demonstrates that *Hha* I must cleave closer to the open 3'-derived end of the dsDNA (compare Fig. 4, Lanes 2 and 3). On the other hand, denaturation of *Bam*HI fragments, derived from a cleavage at the other end of the dsDNA, produces a 1.4-kb denatured fragment (Fig. 4, Lanes 5 and 6). The fragments representing the 5' end of the mRNA are not clearly resolved in this system, due to the difficulty in completely denaturing a snap-back sequence.

The cleavage of  $\alpha$ -fetoprotein cDNA with *Pst* I generated

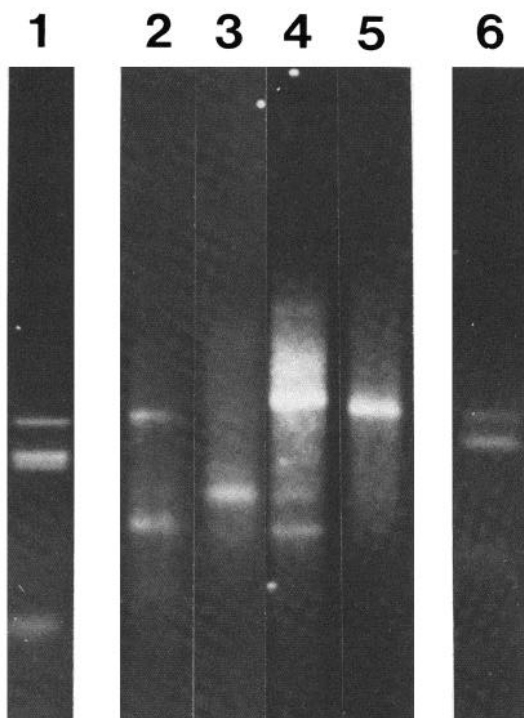
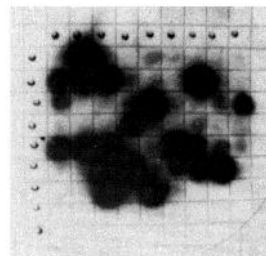


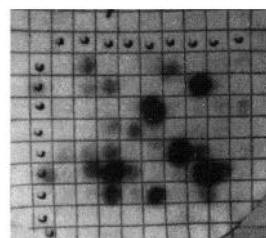
FIG. 4. **Orientation of AFP DNA.** Double-stranded AFP DNA, untreated with S1 nuclease, was digested with *Hha* I or *Bam*HI, and the resulting fragments electrophoresed before or after denaturation by glyoxal. Lane 1, ColE1-*Hae* III native; Lane 2, AFP dsDNA-*Hha* I native; Lane 3, AFP dsDNA-*Hha* I denatured; Lane 4, AFP dsDNA-*Bam*HI native; Lane 5, AFP dsDNA-*Bam*HI denatured; Lane 6, ColE1-*Hae* III denatured. The visible ColE1 fragments in Lanes 1 and 6 are 1.12, 1.02 to 0.95, and 0.45 kb. Lanes 2 to 5 are autoradiographs.

## Probe:

yolk sac  
cDNA



fetal liver  
cDNA



adult liver  
cDNA

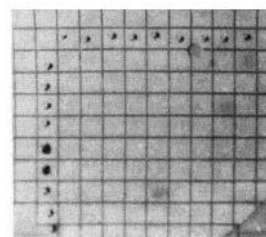


FIG. 5. **Screening of colony filters with specific cDNA's.** Replica filters on which colonies had been grown were hybridized to the cDNA probes as indicated. The filters were autoradiographed, and the autoradiographs were overlaid on the filters for photography.

two internal fragments, 520 and 900 bp in length (Fig. 3). These fragments were ligated directly to pBR322, which had been digested with *Pst* I and treated with bacterial alkaline phosphatase (25) to reduce the number of parental colonies. After the ligated mixture was used to transform  $\text{CaCl}_2$ -treated  $\chi$ 1776 cells, hybrid colonies were identified and screened by the method of Grunstein and Hogness (26). Replica filters were hybridized separately to [ $^{32}\text{P}$ ]cDNA's prepared from 18 S mRNA's of yolk sac, 18-day fetal liver and adult liver (Fig. 5). Thus, colonies which hybridized strongly to the cDNA from yolk sac and fetal liver mRNA's, but not to adult liver cDNA's, would be expected to contain  $\alpha$ -fetoprotein sequences and were selected for analysis. The plasmids were isolated by the procedure of Meager *et al.* (28) and digested with *Pst* I. Those containing the 520- and 900-bp (or both) *Pst* I fragments were thus identified.

To clone those portions of the  $\alpha$ -fetoprotein cDNA sequence which were outside the two *Pst* I internal fragments, we used the method of Ullrich *et al.* (25) which required attaching 10-bp molecular linkers to the ends of ds cDNA. *Hind*III linkers were ligated to the 2,150-kb AFP cDNA and the resulting molecules cleaved with a vast excess of *Hind*III to destroy excess linkers and create ligatable ends. In this way, the dsDNA would also be cleaved internally at the *Hind*III site. The dsDNA fragments were ligated to pBR322 cut by *Hind*III and transformants were generated and selected by hybridization. Several clones, all derived from the 5' end of the AFP mRNA were identified.

**Characterization of pBR322-AFP1 and pBR322-AFP2—**Two recombinant plasmids, termed pBR322-AFP1 and pBR322-AFP2, were selected for further characterization.



Cleavage of pBR322·AFP1 with *Hind*III and electrophoresis in an acrylamide gel yielded the parental 4.3-kb fragment and a 960-bp *Hind*III insert (Fig. 6, Lane 2). On the basis of digests with combinations of *Hind*III and *Pst* I or *Bam*HI (Fig. 6,

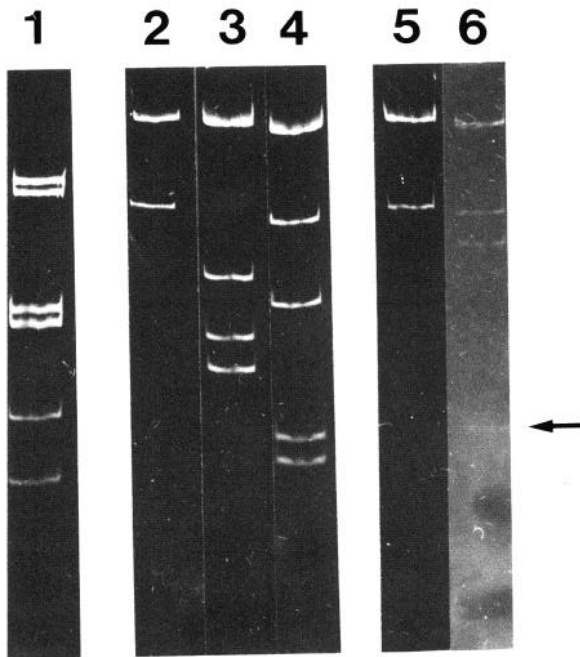


FIG. 6. Restriction endonuclease digestion of chimeric plasmids. The plasmids pBR322·AFP1 and pBR322·AFP2 were digested with the following restriction endonucleases and electrophoresed on a 5% acrylamide gel: Lane 1, *Hae* III digest of *ColE1* as in Fig. 2; Lanes 2 to 4, *Hind*III, *Hind*III and *Pst* I, *Hind*III and *Bam*HI of pBR322·AFP1; Lanes 5 and 6, *Pst* I and *Pst* I and *Hind*III of pBR322·AFP2.

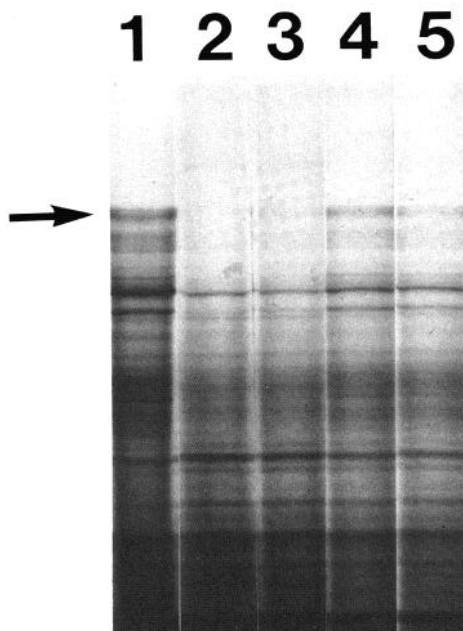


FIG. 7. Arrest translation of pBR322·AFP1. The following RNA and RNA-DNA hybrids were translated in a wheat germ lysate in the presence of [ $^{35}$ S]methionine. The products were electrophoresed in a 9% polyacrylamide gel and autoradiographed. Lane 1, total poly(A) RNA from yolk sac; Lane 2, yolk sac RNA hybridized to pBR322·AFP1; Lane 3, yolk sac RNA hybridized to pBR322·AFP1 and heated before translation; Lane 4, yolk sac RNA hybridized to pBR322; and Lane 5, yolk sac RNA hybridized to pBR322 and heated before translation. The arrow indicates the migration of authentic AFP.

Lanes 3 and 4), it was possible to map the insert to the 5' end of the  $\alpha$ -fetoprotein dsDNA sequence, as shown in Fig. 3. Likewise, pBR322·AFP2 was shown by a series of digests with *Pst* I (Fig. 6, Lane 5) and *Pst* I plus *Hind*III (Lane 6) to contain the 900-bp *Pst* I fragment of AFP dsDNA derived from the 3' end of AFP mRNA. The two inserts overlapped each other by approximately 200 bp, within a common *Pst* I-*Hind*III fragment (Fig. 6, arrow).

As further evidence that the two cloned DNA's contained AFP sequences, the hybrid arrest procedure of Paterson *et al.* (30) was used. Total pBR322·AFP1 DNA was hybridized to poly(A)-containing yolk sac RNA under conditions favoring RNA-DNA hybrids (30), and the mixture was translated in a wheat germ extract. The translation products from the control RNA are shown in Fig. 7, Lane 1, and the migration of authentic  $\alpha$ -fetoprotein is indicated by the arrow. When the pre-hybridized RNA is translated, the AFP band preferentially disappears (Lane 2). If the hybrids are dissociated by heating, the AFP template activity is recovered (Lane 3). When parental pBR322 DNA is used to form hybrids instead of pBR322·AFP1 DNA, there is no preferential loss of AFP mRNA activity (Lanes 4 and 5). Similar results were obtained with pBR322·AFP2 (data not shown). The specific arrest of AFP translation from a yolk sac RNA population demonstrates that these clones contain AFP mRNA sequences.

**Detection of  $\alpha$ -Fetoprotein mRNA Sequences within Mouse Genomic DNA**—With the availability of monoclonal hybridization probes to the AFP mRNA sequence, it was possible to visualize the genomic sequences in mouse DNA which encode the AFP gene(s). Thus, a two-dimensional "fingerprint" of *Eco*RI-digested genomic DNA was prepared by chromatography on an RPC-5 ion exchange column followed by agarose gel electrophoresis of individual column fractions. The DNA was transferred to Millipore filters (37), and hybridized to labeled DNA probes derived from specific regions of the AFP mRNA sequence. The ethidium bromide stain of a gel is shown at the top of Fig. 8. The insert from pBR322·AFP1, which contains sequences derived from the 5' end of the AFP mRNA, hybridized to two *Eco*RI fragments, 6.0 and 3.0 kb in size. On the other hand, the pBR322·AFP2 insert, derived from the 3' end of the AFP mRNA, and overlapping the pBR322·AFP1 by approximately 200 bp (see Fig. 3), detected the 3.0 kb fragment, along with a different 5.2 kb fragment,

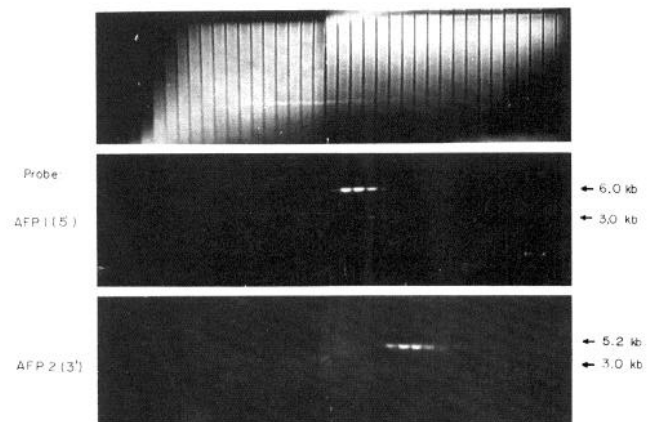


FIG. 8. Detection of AFP mRNA sequences in mouse genomic DNA. *Eco*RI-digested DNA was chromatographed on an RPC5 column and individual fractions were electrophoresed in a 1% agarose gel. The top panel illustrates an ethidium bromide stain of a gel. The middle panel shows the hybridization of the *Eco*RI fragments transferred to a Millipore filter to labeled AFP1 DNA. The bottom panel shows the hybridization of *Eco*RI fragments to labeled AFP2 DNA. The sizes of the detectable fragments are indicated on the right.

but not the 6.0 kb fragment. That the two probes recognized nonidentical fragments argues that the number of *EcoRI* fragments which hybridize to AFP sequences cannot be explained on the basis of multiple AFP gene copies. Rather, the differential hybridization pattern supports the conclusion that there is a single copy of the gene, represented in at least three *EcoRI* fragments. The absence of any *EcoRI* cleavage site in the entire AFP cDNA sequence (Fig. 2), further suggests that the two detectable *EcoRI* sites in the genomic sequence are contained within intervening sequences in the gene. The Southern blots also establish the orientation of the three fragments with respect to the AFP mRNA, with the 6.0-kb fragment representing the 5' end of the mRNA, the 3.0-kb fragment representing a portion of the mRNA which includes the region overlapped by the two probes, and the 5.2-kb fragment representing the 3' end of the mRNA.

#### DISCUSSION

We have constructed several chimeric plasmids which contain specific regions of the  $\alpha$ -fetoprotein mRNA sequence. The plasmids were detected initially by differential hybridization of the cloned sequences, derived from yolk sac RNA, to fetal and adult liver RNAs. Second, restriction endonuclease mapping of the enriched cDNA, containing predominantly AFP cDNA, permitted rapid confirmation of the identity of the cloned sequences by detection of specific cleavage sites. Finally, the specific arrest in the translation of  $\alpha$ -fetoprotein mRNA following hybridization of the plasmid DNA to total yolk sac RNA confirmed the identity of pBR322-AFP1 and pBR322-AFP2.

These plasmids, when labeled and used as hybridization probes to visualize the  $\alpha$ -fetoprotein gene within the complexity of total mouse genome DNA, were able to detect three separate *EcoRI* fragments, containing AFP mRNA sequences. The absence of an *EcoRI* site in the entire mRNA sequence, and the total size of the three fragments, 14.2 kb, argue that the  $\alpha$ -fetoprotein gene must be represented discontinuously in the genome, with at least two intervening sequences at the two *EcoRI* sites. Thus, the AFP gene appears to be encoded in a manner analogous to the rabbit (42) and mouse (31, 42)  $\beta$ -globin genes and the chick ovalbumin gene (43-47). These unique genes, along with tRNA genes from yeast (48, 49), ribosomal genes in *Drosophila* (50-52), adenovirus 2 (53-56), and SV40 genes (57, 58) have been shown in the last year to be interrupted at one or more positions in the coding sequence by noncoding DNA, which is transcribed into RNA (59) and removed during RNA processing (60, 61).

Two other important facts can be drawn from Fig. 8. First, the  $\alpha$ -fetoprotein gene must be represented only once in the genome, as the two probes recognize different *EcoRI* fragments. Second, the order of the fragments, relative to the 5' and 3' ends of the mRNA is established as 6.0, 3.0, and 5.2 kb.

The hybridization probes used in Fig. 8 are missing approximately 150 bp of DNA at the 5' and 3' ends of the cDNA sequences. Therefore, we cannot know whether the entire AFP gene is contained within the three *EcoRI* fragments. In addition, this analysis would not detect *EcoRI* fragments which contain intervening sequence DNA alone, or less than 50 bp of coding sequence. To counteract these uncertainties, and to define in greater detail the organization of the AFP gene, we have recently cloned the three *EcoRI* fragments<sup>3</sup> and intend to use them to select for DNA fragments derived from a mouse embryonic DNA library, by the methods recently described by Maniatis *et al.* (62). In this way, an accurate map

of the entire region containing and surrounding the mouse AFP gene can be drawn.

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**The presence of intervening sequences in the alpha-fetoprotein gene of the mouse.**

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