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The isolation of ecdysterone inducible genes by hybridization subtraction chromatography

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ABSTRACT

We have developed a procedure for selectively enriching a mRNA population for inducible sequences. Other than the induced mRNA species, the population of mRNA in control cells is approximately the same as the mRNA population in induced cells. Cytoplasmic mRNA from control cells is bound to oligo (dT)-cellulose and used as a template for reverse transcriptase, the oligo (dT) serving as a primer. After removing the template mRNAs, the cDNA-cellulose column is used to hybridize a population of mRNAs from induced cells. The non-hybridized poly A⁺ RNAs are greatly enriched in the inducible sequences. We have used this technique of hybridization subtraction chromatography to select a mRNA population enriched for the mRNAs inducible by ecdysterone in Schneider's Line 2 *Drosophila* cells. This population of RNAs was used to screen a recombinant library. Preliminary results indicate that approximately 10% of the RNA in the probe population represents ecdysterone inducible sequences. Methods are described for optimizing the cDNA synthesis reaction (we obtain $\geq 30\%$ efficiency) and hybridizing RNA to the cDNA-cellulose resin. This method can be used to select induced mRNAs regardless of the way in which the induction is brought about.

INTRODUCTION

The isolation of a pure gene depends on the availability of a good probe. Gene isolation has been accomplished in a number of ways. The isolation of some mRNAs, for example globin mRNA (1,10,13,14), has been possible because the population of mRNAs in certain specific cell types is greatly enriched in the desired mRNA. Other RNAs, like ribosomal RNA, were isolated by taking advantage of their unusual base composition (3,12,17). Each of these cases has relied on some special property of the RNA to allow its isolation. Either the system was producing large amounts of a product (to make mRNA isolation feasible) or the gene had an unusual base composition.

The isolation of a particular RNA sequence comprising a very small portion of the entire cellular RNA complement has been very difficult. This is a particularly challenging problem when dealing with the phenomenon of gene induction, since the induced product is often only a minor component of

the cell's mRNA population. The technique of hybridization subtraction chromatography, described in this paper, lends itself readily to the isolation of a population of mRNAs greatly enriched in inducible mRNA sequences. In essence, the technique removes mRNAs from an induced cell's mRNA population that are also found in control cell mRNA populations. The remaining mRNAs are greatly enriched for the induced sequences. The method has broad applicability since it can select low abundance mRNA sequences from a highly complex mRNA population. This is true regardless of the mechanism employed to induce these low abundance RNAs. Further, once the cDNA-cellulose column is constructed, it can be used repeatedly without resynthesing more cDNA.

In the present work, we demonstrate the feasibility of hybridization subtraction chromatography by purifying an RNA population enriched for the mRNAs induced in Schneider Line 2 *Drosophila* cells by treatment with ecdysterone. These induced RNAs represent less than 0.2% of the cytoplasmic mRNA population of ecdysterone treated cells. Using the column purified mRNA as a probe, we have been able to select a number of recombinant clones containing DNA that hybridizes significantly to induced cell mRNAs, but not to control cell mRNAs.

MATERIALS AND METHODS

CELLS AND LABELING

Schneider's Line 2 (SL2) cells were grown in 75 cm² plastic tissue culture flasks to a density of 3.0 to 4.5 X 10⁶ cells per ml in Schneider's *Drosophila* medium (GIBCO) supplemented with 0.1 volumes of heat inactivated fetal calf serum (GIBCO). Hormone treated cultures were exposed to 1.0 μM ecdysterone (Sigma) for 4 hours and then harvested. In some experiments, RNA was labeled in vivo with 2.5 μCi per ml ³H-uridine (Amersham) for 4 hours.

RNA ISOLATION

Cells were lysed by resuspending cell pellets in lysis buffer (0.3 M sucrose, 2 mM MgAc₂, 3 mM CaCl₂, 10 mM tris (pH 7.4), 0.1% Triton X-100, 5mMDTT) containing 8 mM vanadium-adenosine complex (2), incubating for 10 minutes on ice, and homogenizing with the tight fitting A pestle in a Dounce homogenizer. Cell lysis was monitored by phase contrast microscopy until ≥ 90% of the cells had been broken. Nuclei were pelleted for 5 minutes in an HB-4 swinging bucket rotor at 10,000 RPM (7600xg). RNA from the cytoplasmic supernatant was deproteinized by repeated phenol/chloroform/isoamyl alcohol (50:49:1) extractions at room temperature and precipitated with ethanol overnight at -20°C. Poly A⁺ RNA was prepared by oligo (dT)-

cellulose chromatography (P-L Biochemical, type 7 Oligo (dT)-cellulose, ref 19). All poly A⁺ RNAs were bound to oligo (dT)-cellulose a minimum of three times before use.

SYNTHESIS OF cDNA-CELLULOSE

In the standard cDNA-cellulose synthesis reaction, 600 μ g of 3 times oligo (dT)-cellulose retained cytoplasmic RNA from control cells was bound to 360 mg of oligo (dT)-cellulose in 20 ml of 50 mM Tris-HCl (pH 8.3), 20 mM dithiothreitol, 10 mM MgCl₂, 100 mM KCl, 0.6 mM dTTP, 0.4 mM each of dATP, dGTP, dCTP; 4.0 mM sodium pyrophosphate and 1.14% ethanol. Synthesis of cDNA was initiated by addition of 550 units per ml avian myeloblastosis virus reverse transcriptase (generously supplied by Dr. J. Beard, Life Sciences, St. Petersburg, FL) and 20 μ Ci per ml ³H-dGTP; synthesis was allowed to continue for 60 minutes at 37°C. The reaction was terminated by transferring the resin to a 40°C water jacketed column and washing with hybridization buffer [50% formamide (BRL), 0.1% SDS (BDH), 10 mM Tris-HCl (pH 7.6), 0.6 M NaCl, 10 mM EDTA and 20 μ g per ml polyadenylic acid (Sigma)] until the column eluate had an A₂₆₀ \leq 0.05. To denature template RNAs from their cDNA complements which are covalently linked to the cellulose matrix [through the oligo (dT) bridge], the temperature was raised to 60°C and the column washed with elution buffer [50% formamide, 0.1% SDS, 10 mM Tris-HCl (pH 7.6)] until the eluate had an A₂₆₀ \leq 0.05. RNA collected from both low and high temperature washes were ethanol precipitated. The oligo (dT)-cDNA-cellulose resin was cooled to room temperature, washed and stored in 95% ethanol at -20°C until needed.

HYBRIDIZATION OF RNA TO cDNA-CELLULOSE

(³H)-poly A⁺ cytoplasmic RNA from ecdysterone treated cells was hybridized to the cDNA-cellulose (10-fold cDNA excess) in hybridization buffer for 48 hours at 40°C with 60 strokes per minute agitation. The reaction volume was 10 μ l per mg of cDNA-cellulose resin. After the hybridization was complete, the entire mixture was poured into a 40°C water jacketed column, allowed to settle for 1 to 2 hours, and then washed with hybridization buffer (at 40°C) to remove the non-hybridized RNAs until the eluate was \leq 100 CPM per ml above background. Hybridized RNAs were then released from the column by heating to 60°C and washing with 60°C elution buffer. The hybridization/washing procedure was repeated twice more on the "non-bound" RNA fraction from the first hybridization reaction. The RNA that did not bind to the column after three cycles of hybridization was then applied to an oligo (dT)-cellulose column as described above. The poly A⁺ RNA obtained from this last column

was used to screen the recombinant library.

SCREENING THE RECOMBINANT LIBRARY

A portion of the putative ecdysterone induced RNA probe was labeled with ^{125}I by a modification of the method of Schrader and O'Malley (11) and used to screen a complete *Drosophila* genomic recombinant library obtained through the generosity of E.A. Craig (4), Dept. of Physiological Chemistry, University of Wisconsin. This library contains partial Hind III digested *Drosophila* DNA inserts of 8.8 Kb average size in pBR322. Filters containing plasmid DNAs with *Drosophila* inserts were prepared according to the method of Grunstein and Hogness (5) and hybridized to the ^{125}I labeled RNA probe. Hybridization was performed (1.5 ml per filter) in 0.02% each of Ficoll, poly vinyl pyrrolidone, and bovine serum albumin; 2 μg per ml *E. coli* RNA, 50% formamide, 1 mg per ml polyadenylic acid and 5XSSC (1 X SSC = 0.15 M NaCl, 0.015 M Na Citrate, pH 7.0) for 22 hours at 37°C. After hybridization, the filters were washed 10 minutes in 6XSSC, three more times in 2XSSC, air dried and exposed to Kodak XR-5 X-ray film for 24 hours at -70°C with Cronex Lightning Plus (DuPont) intensifying screens.

Positive colonies were picked, grown overnight in L broth, cloned and stored in 96 well microtiter plates (Costar). Duplicate filters were made from clones in the microtiter plates and were hybridized to mRNA from either control cells (-) or ecdysterone treated cells (+). The "+/-" screening method permitted us to identify the induced clones as those which hybridized to induced cell mRNAs but not to control cell mRNAs.

RESTRICTION DIGESTS AND GEL ELECTROPHORESIS

Plasmids were purified as described by Guevry et al. (20) and digested with Hind III restriction endonuclease under conditions recommended by the supplier (Bethesda Research Labs). Reactions were phenol extracted, the DNA ethanol precipitated and analyzed by agarose gel electrophoresis. The gel was 1% agarose in 18 mM NaCl, 20 mM NaAc, 2 mM EDTA, and 50 mM Tris·HCl (pH 8.0). Electrophoresis was carried out at 8V/cm until the bromphenol blue dye front reached the bottom of the gel.

RESULTS AND DISCUSSION

PREPARATION OF cDNA-CELLULOSE

Reverse transcriptase can be used to synthesize cDNA from an RNA template by extending from a base paired primer. In solution, typical reverse transcriptase reactions using oligo (dT) primers hydrogen bonded to poly A tails of

mRNAs synthesize 10-15 μg of cDNA for every 100 μg of mRNA in the reaction (16)- i.e., a 10-15% efficiency. Using a column bound primer often results in even lower efficiencies (15,21). Because of this potential problem, we optimized our reaction in a number of parameters.

Originally, following the conditions of Hirsch, et al. (6,7), we had little success. Switching from potassium acetate and magnesium acetate to KCl and MgCl_2 made a significant difference as shown in Table 1. Maximal cDNA synthesis occurs at 100 mM KCl which is the salt concentration used in all subsequent reactions.

The concentration of reverse transcriptase was the next factor optimized. As shown in Table 1, the enzyme optimum is 550 units of reverse transcriptase per ml of reaction mix. The plateau probably results from the saturation of all available elongation sites for the enzyme (i.e. - there are no more oligo (dT) primers hydrogen bonded to mRNAs which can serve as enzyme recognition sites).

After optimal salt and enzyme concentrations were determined, other conditions of the reaction were investigated to improve further the efficiency of our system. Actinomycin D was included in early reactions to minimize the synthesis of double stranded cDNA (9,18). However, we found that actinomycin D significantly reduced the efficiency of our reactions (perhaps by blocking the synthesis of double stranded cDNA) as shown in Table 1. An alternative is the use of sodium pyrophosphate (9) in the reactions to prevent the reverse transcriptase from recopying the cDNA. The inclusion of 4.0 mM sodium pyrophosphate provided high efficiencies while preventing synthesis of double stranded cDNA. With higher levels of synthesis, it seemed logical to increase the triphosphate and Mg concentrations (11). Increasing the dTTP concentration from 0.4 mM to 0.6 mM; dATP, and dCTP from 0.14 mM to 0.4 mM; and MgCl_2 from 6 mM to 10 mM increased the efficiency further. As shown in Table 1, the presence of some ethanol in the reaction was necessary but no significant dependence on its concentration was observed. Doubling the amount of oligo (dT)-cellulose from 0.6 mg per μg mRNA to 1.2 mg per μg mRNA results in half the amount of cDNA synthesis per mg oligo (dT)-cellulose. Doubling the amount of template mRNA in the reaction doubles the amount of cDNA synthesized. For any particular oligo (dT)-cellulose resin, there was as much as a 10-fold increase in efficiency when the resin was thoroughly washed with water. This treatment apparently removed any trace contaminants which severely inhibit reverse transcription. Also, oligo (dT)-cellulose from different suppliers or different lots from

TABLE 1
EFFICIENCY OF cDNA SYNTHESIS

KCl	MCCl ₂	dTTP	dATP dCTP dGTP	Reverse Trans- criptase	Actino- mycin D	NaPP _i	ethanol	Temp.	Relative Effi-
		μM	μM	$\mu\text{g/ml}$	$\mu\text{g/ml}$	mM	%	$^{\circ}\text{C}$	
100 mM KAc	6 mM MgAc ₂	400	140	55	36	0	1	42	0.43%
100 mM KAc	6 mM	400	140	55	36	0	1	42	0.95
100	6	400	140	55	36	0	1	42	1.10
100	6	400	140	55	0	0	1	42	1.23
100	6	400	140	55	36	0	1	42	1.10
100	6	400	140	55	72	0	1	42	0.92
100	6	400	140	55	36	0	0	42	0.75
100	6	400	140	55	36	0	1	42	1.14
100	6	400	140	55	36	0	2	42	1.29
100	10	400	400	550	36	0	1	42	2.77
100	10	400	400	550	36	0	1	37	8.85
100	6	600	140	0	36	0	1	37	0.0006
100	6	600	140	55	36	0	1	37	0.57
100	6	600	140	550	36	0	1	37	1.52
100	6	600	140	1100	36	0	1	37	1.29
100	6	600	140	1650	36	0	1	37	1.48
100	6	600	140	2200	36	0	1	37	1.02
0	6	600	140	550	36	0	1	37	3.78
50	6	600	140	550	36	0	1	37	5.81
100	6	600	140	550	36	0	1	37	7.14
150	6	600	140	550	36	0	1	37	5.99
200	6	600	140	550	36	0	1	37	4.89
100	10	600	400	550	0	4	1	37	31.3

Assays for incorporation of ³H-dGTP into cDNA were carried out by pelleting the resin after the 60' synthesis reaction, washing two times in hybridization buffer, resuspending in water, and counting the resuspended resin in a triton/toluene fluor.

the same supplier could vary by as much as two orders of magnitude in efficiency of the cDNA synthesis reaction. Lowering the incubation temperature from 42°C to 37°C also increased efficiency. These careful optimization procedures allowed us to increase our efficiency from an original 0.43% to greater than 30%.

To determine what fraction of the template RNA was actually copied into cDNA during the reaction, the oligo (dT)-cDNA-cellulose resin was washed with hybridization buffer at 40°C immediately after the synthesis reaction. This low temperature washing removes RNAs that are bound only by the A:T base pairs (between the poly A mRNA tail and the oligo (dT) of the resin), but will not release most mRNAs that are hydrogen bonded to their cDNAs. The column was then heated to 60°C and washed with elution buffer to denature the template RNAs from their cDNAs which were covalently attached to the cellulose through the oligo (dT) linker. The results showed that 322 µg (54%) of the template RNA was eluted in the low temperature wash while 278 µg (46%) of the template RNA eluted in the high temperature wash. In this reaction, the 278 µg of template RNA were copied to produce 168 µg of cDNA (as determined by ³H-dGTP incorporation). The average length of the cDNA can therefore be estimated to represent ~60% of the template RNA length. Since extension of the cDNA starts at the 3' end of the mRNA, the cDNA sequences attached to the column are likely to be enriched for sequences complementary to the 3' mRNA ends in comparison to the 5' mRNA end sequences.

RNA ENRICHED FOR ECDYSTERONE INDUCIBLE SEQUENCES

Hybridization of mRNA from ecdysterone treated cells (16 µg) was performed under conditions of cDNA excess (168 µg of cDNA attached to cellulose). After hybridization, the column was regenerated and the RNA not hybridizing the first time was re-incubated with the cDNA-cellulose. This procedure was repeated once more to yield an RNA population that had not hybridized to cDNA-cellulose after three incubations under hybridization conditions. This RNA was then applied to an oligo (dT)-cellulose column to remove RNA fragments (which may have been produced during the various manipulations) that did not contain poly A tails; these RNAs mostly represent sequences from the 5' ends of the RNAs. The non-hybridizing poly A⁺ RNA was enriched in ecdysterone inducible sequences. In typical purifications, about 1.5% of the RNA remains in the last fraction which represents a 67-fold enrichment, although this value was ranged from 0.6% to 7.0%. The RNA purified in this manner was subsequently used as a probe to screen the recombinant DNA library.

ISOLATION OF RECOMBINANT CLONES COMPLIMENTARY TO ECDYSTERONE INDUCED RNAs

The probe obtained by hybridization subtraction chromatography was iodinated *in vitro* with ^{125}I and used to screen a recombinant library. Due to the small amounts of probe available, the library was screened in several steps. Twelve microtiter plates (96 wells in each) were set up with each well containing 22 individually picked recombinants. These plates were grown to saturation and then stored at -20°C after addition of an equal volume of 80% glycerol to each well. Using a homemade transfer device, recombinants from each microtiter plate were transferred in an ordered array to agar/ampicillin petri dishes and grown overnight. Nitrocellulose filters made by the method of Grunstein and Hogness (5) were hybridized to ^{125}I probe RNA. Approximately 25,000 recombinants were screened, corresponding to 1.2 times the *Drosophila* haploid genome length. After autoradiography, 35 positive colonies were evident, representing 3% of the microtiter wells screened. These first generation positives were picked, grown overnight, appropriately diluted and spread on 10 cm agar/ampicillin to a density of 200 to 250 colonies per dish. Again, Grunstein and Hogness screening was employed to select individual positive clones. Second generation positive clones were picked and grown to saturation in microtiter wells for further examination. A third and final screen determined which of the probe selected clones actually represented ecdysterone inducible sequences. The "+/-" method was employed on duplicate filters prepared from microtiter plate clones. One filter was hybridized to mRNA from control cells (-), and the other to mRNA from ecdysterone treated cells (+). Positives were scored if they hybridized to a significantly greater extent with induced cell mRNA than with control cell mRNA. The results of our preliminary "+/-" screen are shown in Figure 1.

Of the 192 second generation positives, 20 were shown to be inducible sequences by the "+/-" procedure. These 20 third generation positives correspond to 10 of the 35 first generation positive wells detected in the initial screen. Therefore, we estimate that 20/192 or 10.4% of the probe prepared by hybridization subtraction chromatography represented ecdysterone inducible sequences.

Seven of these clones were then chosen at random and analyzed by digestion with Hind III and agarose gel electrophoresis. As shown in figure 2, there are six distinctly different patterns of DNA fragments for the seven clones, which implies that these clones originated from different regions of the genome. Thus, our procedure has given us a set of clones,

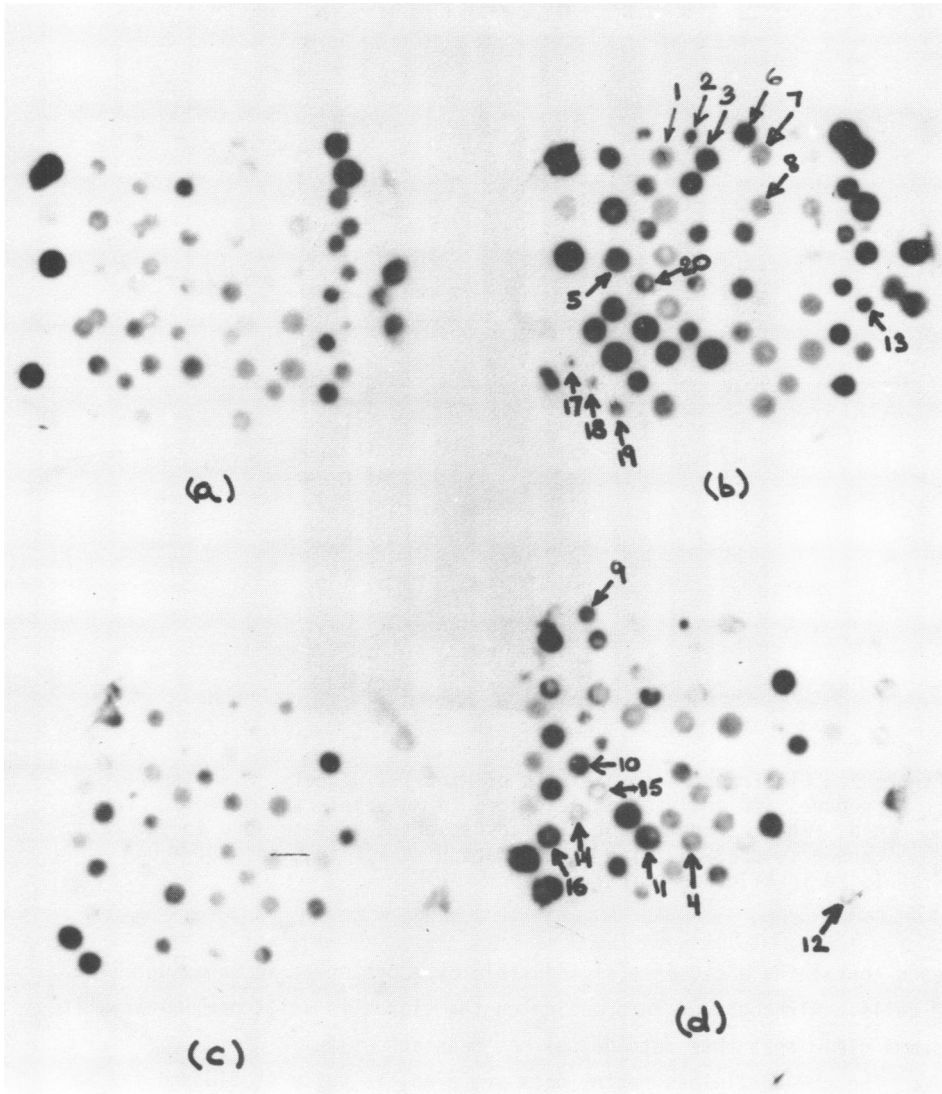


Figure 1. +/- Screening of Candidate Clones. A total of 192 candidate clones were screened (96 in each of two microtiter plates - a/b and c/d) by hybridization with mRNA from ecdysterone treated cells (b and d) or mRNA from control cells (a and c). The clones in (b) are the same as those in (a), and the clones in (d) are the same as those in (c). Colonies 1-4 hybridize with induced cell mRNA but show no detectable hybridization with control cell mRNA. Colonies 5-20 show quantitative differences only, in that they hybridize very weakly with control cell mRNA but strongly with induced cell mRNA.

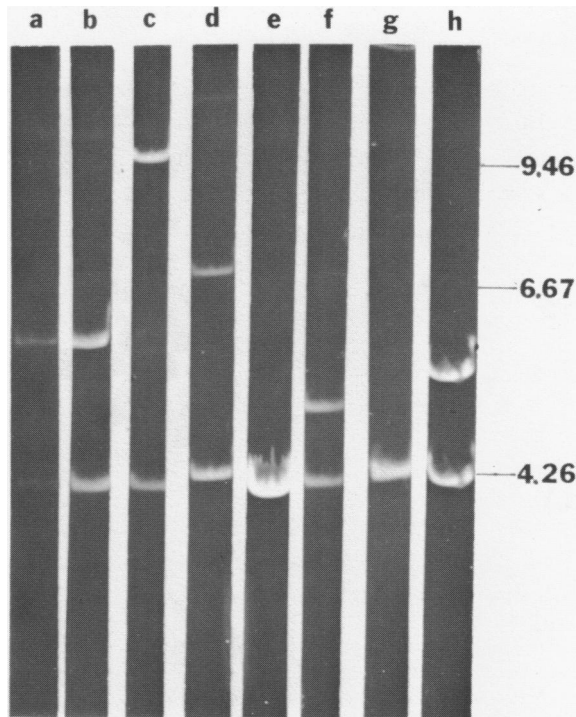


Figure 2. Electrophoretic Analysis of Hind III Digests. Samples were prepared and analyzed as described in materials and methods. Lanes a-d, f-h are recombinant plasmids selected as described in the text. Lane e is pBR322. Size markers are Hind III fragments of λ DNA (size in kilobase pairs).

each containing a sequence(s) inducible by ecdysterone in Schneider line 2 cells. Although our information on the clones is still preliminary, it seems clear that this methodology has been successful.

The cDNA-cellulose resin, once prepared, is quite stable and may be used many times. The resin, containing cDNAs to control cell mRNAs, can be used to purify any inducible sequence regardless of how the mRNA is induced. If some genes expressed in control cells are inhibited by hormone treatment, isolation of those genes may be accomplished by synthesizing cDNA-cellulose using induced mRNAs as template and hybridizing control mRNAs to that cDNA-cellulose. We hope to use our cDNA-cellulose resin to isolate juvenile hormone induced genes, another hormone involved in insect development (8).

Unlike previous techniques, induced mRNAs do not have to be present in

high abundance to be purified. We estimate that the ecdysteroid inducible mRNAs represent less than 0.2% of cytoplasmic mRNAs ($1.5\% \times 10.44\% = 0.16\%$). The enriched mRNA population obtained is approximately 10% ecdysterone inducible sequences. In addition, the technique allows for the isolation of a set of genes, all of which are subject to coordinate induction. The availability of a number of coordinately regulated genes should facilitate the elucidation of molecular control events.

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