

## PARTIAL cDNA SEQUENCE OF THE GAMMA SUBUNIT OF TRANSDUCIN

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A 151 bp cDNA segment that encodes the amino-terminal portion of the gamma subunit of bovine transducin was isolated from a retinal cDNA library constructed in the expression vector  $\lambda$ gt11. The base sequence of this cDNA confirms the sequence of the first 39 amino-terminal amino acids reported for the native protein (McConnell et al. (1984) Fed. Proc. 43, 1585). Northern blot analysis indicates that the complete mRNA is approximately 650 bases long and that its expression is limited to the retina.

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The GTP-binding protein transducin couples photolysis of rhodopsin to activation of cyclic GMP-phosphodiesterase in retinal rod outer segments (1). Transducin is a heterotrimer consisting of alpha, beta and gamma subunits (1). The alpha subunit contains the binding site for GTP (1) and the sites for ADP-ribosylation by cholera toxin (2) and pertussis toxin (3). The beta and gamma subunits are essential for rebinding of the alpha subunit to the membrane and rhodopsin (4) and remain tightly complexed to one another under physiological conditions.

McConnell et al. (5) recently reported the amino acid sequence for the gamma subunit of bovine transducin. Using antibodies to the beta and gamma subunits of transducin, we screened a retinal cDNA library in the expression

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vector  $\lambda$ gt11 (6) and have isolated a partial cDNA<sup>1</sup> segment that encodes the amino-terminal portion of the gamma subunit of transducin.

#### METHODS AND MATERIALS:

Preparation of antibodies. The beta-gamma subunit complex of transducin was isolated as previously described (1) and used to immunize rabbits. Serum titers to the beta-gamma subunit complex, measured by an enzyme-linked immunosorbent assay (7), were approximately 1:6000. The binding of rabbit antibody to antigen was detected with goat anti-rabbit immunoglobulin antibody coupled to horseradish peroxidase (Miles Laboratories). Prior to screening the  $\lambda$ gt11 retinal library, the antisera were pre-purified on an *E. coli* lysate (strain BNN97 (8)) coupled to cyanogen bromide-activated Sepharose 6B, in order to remove antibodies that cross-reacted with *E. coli* or phage proteins, following the protocol described by Young and Davis (8).

Construction and screening of the  $\lambda$ gt11 retinal cDNA expression library. A previously constructed retinal cDNA library inserted into the vector  $\lambda$ gt10, containing  $2.5 \times 10^5$  recombinants (9), was transferred into the expression vector  $\lambda$ gt11, permitting screening of the library with antibody probes. The  $\lambda$ gt10 library was amplified, fully digested with the restriction enzyme EcoRI, and then size-fractionated by sucrose gradient sedimentation (5-20% sucrose in 10 mM Tris-C1 pH 7.2 and 1 mM EDTA, centrifuged for 10 h at 38,000 rpm in a Beckman SW41 rotor) to separate  $\lambda$ gt10 vector arms from the cDNA inserts. Gradient fractions containing cDNA inserts ranging in size from 0.1 to 8 kb were pooled, ethanol precipitated, and then ligated into the unique EcoRI restriction site of  $\lambda$ gt11, which is located within the  $\beta$ -galactosidase gene. The ligated  $\lambda$ gt11 was then packaged and the expression library subsequently amplified. The library was then screened with antisera according to the protocol developed by Young and Davis (8).

Characterization of clones. The cDNA inserts from plaque-purified clones were transferred into EcoRI insertion sites in the plasmid pUC8 (10) and the phage M13mp10 (11). Both strands of the cDNA insert were subcloned into M13 phage and their base sequences were determined using the dideoxynucleotide method of Sanger et al. (12), as modified (13).

Northern blot. Freshly excised bovine tissues were collected at a local abattoir and immediately frozen in liquid nitrogen. Total RNA was prepared (14) and poly(A) RNA selected by chromatography on oligo(dT)cellulose (15). The poly(A) RNA was denatured and size-fractionated on 0.8% agarose-formaldehyde gels (16) and transferred to nitrocellulose (17). The pUC8 plasmid containing the 151 bp insert was nick-translated (18) using [ $\alpha$ -<sup>32</sup>P]dATP and used to probe the Northern blot (42°C, 3x SSC, 50% formamide, 1x Denhart's solution and 5% dextran sulfate).

Materials. The retinal  $\lambda$ gt10 cDNA library and a full-length rhodopsin cDNA clone were donated by J. Nathans, Stanford University. The expression vector  $\lambda$ gt11 and its host strains were donated by Dr. R. W. Davis, Stanford University. The plasmid pUC8 and its host strains were donated by Dr. J. Messing, University of Minnesota. [ $\alpha$ -<sup>32</sup>P]dATP and [ $\alpha$ -<sup>35</sup>S]dATP were purchased from Amersham Inc. The restriction enzyme EcoRI, T<sub>4</sub> DNA ligase, and the large fragment of DNA polymerase were purchased from Bethesda Research Laboratories or New England Biolabs. Packagene Lambda Packaging Extract was purchased from Promega Biotec (Madison, WI). Other reagents were obtained commercially.

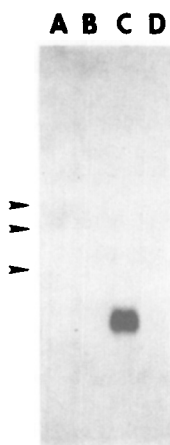
<sup>1</sup> Abbreviations: cDNA-complementary DNA, mRNA-messenger RNA, bp-base pairs.

**RESULTS:**

Using serum from a rabbit immunized with the beta-gamma subunit complex of transducin, we screened  $7 \times 10^5$  recombinant plaques from the  $\lambda$ gt11 retinal cDNA library, and identified five cDNA clones that reacted most strongly with anti-beta-gamma antibody. Serum from a second rabbit immunized with the beta-gamma subunits also reacted with these clones. The protein expressed by these cDNA clones did not react with sera from rabbits that had been immunized with the alpha subunit of transducin; (anti-alpha subunit titers of these sera were approximately 1:6000, as measured by enzyme-linked immunosorbent assay). The three clones that gave the strongest signals during screening were characterized further. Both strands of the insert were subcloned into the phage M13mp10 (11) and sequenced. The base sequences of these three cDNA inserts were identical, with a length of 151 bp (Fig. 1).

		[-10]									
1	glu phe gly lys gln phe ala tyr arg gln										
	GAA TTC GGC AAA CAG TTT GCT TAC AGG CAG										
		[1]									
31	lys met pro val ile asn ile glu asp leu										
	AAG ATG CCA GTG ATC AAT ATT GAG GAC CTG										
		[10]									
61	thr glu lys asp lys leu lys met glu val										
	ACA GAA AAG GAC AAA TTG AAG ATG GAA GTC										
		[20]									
91	asp gln leu lys lys glu val thr leu glu										
	GAC CAG CTC AAG AAA GAA GTG ACG CTG GAA										
		[30]									
121	arg met leu val ser lys cys cys glu glu										
	AGA ATG CTG GTG TCC AAA TGT TGT GAA GAA										
		[40]									
151	phe arg asp tyr val glu glu arg ser gly										
	TTC										
		[50]									
	glu asp pro leu val lys gly ile pro glu										
		[60]									
	asp lys his pro phe lys glu leu lys gly										
		gly									

**Figure 1.** Nucleotide sequence of the cDNA for the gamma subunit of bovine retinal transducin and the corresponding amino acid sequence. Nucleotides are numbered in the 5' to 3' direction, beginning with the EcoRI restriction site. Numbers in brackets indicate the amino acid position relative to the amino-terminal proline determined by McConnell et al. (5). The overline indicates the 39-residue amino acid sequence encoded by bases 37-151 of the cDNA fragment.



**Figure 2.** Autoradiogram of poly(A)<sup>+</sup> mRNA from bovine tissues hybridized to <sup>32</sup>P-labelled  $\gamma$ -cDNA probe. Lanes contained 1.5  $\mu$ g poly(A)<sup>+</sup> mRNA from heart (A), brain (B), retina (C), and liver (D). Arrows indicate positions of markers, including 28S rRNA (4.7 kb), rhodopsin mRNA (2.65 kb), and 18S rRNA (1.7 kb).

The correct reading frame of the insert is indicated by the reading frame of the  $\beta$ -galactosidase gene at the EcoRI insertion site of  $\lambda$ gt11 (6). Because the insert did not contain a poly(A)<sup>+</sup> segment at either end, the coding strand was determined by comparing the deduced amino acid sequence from both strands with the previously published amino acid sequence of the gamma subunit of transducin (5). The 5' and 3' ends of the cDNA fragment correspond to the occurrence of EcoRI restriction sites in the cDNA.

A Northern blot of poly(A)<sup>+</sup> mRNA prepared from bovine retina, brain, heart and liver, probed with the 151 bp fragment, showed only one band, which was unique to the retina (Fig. 2). This RNA was approximately 650 bases in length.

#### DISCUSSION:

We have isolated a partial cDNA that encodes the gamma subunit of bovine transducin. This cDNA hybridizes with a mRNA that is unique to the retina (Fig. 2). Because 650 bases, the approximate length of the mRNA, is too short to encode both the beta ( $M_r$ -35,000) and gamma ( $M_r$ -8,000) subunits, we conclude that the beta and gamma subunits of transducin are synthesized separately, and not as a precursor protein that undergoes post-translational cleavage to yield the individual peptides.

The base sequence of the cDNA fragment confirms the amino-terminal amino acid sequence of the gamma subunit of transducin (5). An AUG codon occurs immediately 5' to the amino-terminal proline. Following analysis of 211 eukaryotic mRNA's, Kozak (19) concluded that: 1) Translation begins at the 5'-proximal AUG triplet in 95% of cases, and 2) There is a strong preference for a purine (usually adenosine) at the -3 position preceding the AUG triplets that serve as initiator codons. In addition, site-directed mutagenesis has confirmed the importance of the purine in position -3 (20). The AUG codon that immediately precedes the amino-terminal proline in the cDNA we sequenced could thus serve as the initiator codon for the gamma subunit. However, because we do not know the sequence of the bases that are 5' to the cDNA fragment, we cannot exclude the occurrence of an AUG codon further upstream. Furthermore, the pattern of codon utilization for amino acid residues predicted from bases 1-33 of our cDNA fragment is in close accord with the pattern determined for nucleic acid sequences that encode mammalian proteins (21); therefore, it is possible that this sequence encodes part of a precursor polypeptide. In conclusion, the base sequence indicates that post-translational modification of the amino-terminus does occur, and involves removal of either a methionine or a larger peptide.

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