

Multiple Nicotinic Acetylcholine Receptor Genes Are Expressed in Goldfish Retina and Tectum

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cDNAs encoding a novel nAChR structural subunit (GF α -3) and a ligand-binding subunit (GF α -3) have been isolated from a goldfish retina cDNA library. The protein encoded by GF α -3 shares 88% amino acid similarity with that encoded by GF α -2, a structural subunit gene previously identified to be expressed in this system (Cauley et al., 1989). The ligand-binding subunit (GF α -3) is likely the goldfish homolog of the rat α -3 gene (Boulter et al., 1986). Northern blots and S1 protection experiments show that GF α -3 and GF α -3 genes are expressed in retina and brain. GF α -3 identifies multiple RNAs differing in their 3' untranslated regions. *In situ* hybridization analysis demonstrates GF α -3, GF α -2, and GF α -3 expression by cells of the retinal ganglion cell layer. Unlike GF α -2 and GF α -3, GF α -3 is expressed at highest levels by cells of the retina's inner nuclear layer. In the optic tectum, both GF α -3 and GF α -3 genes are expressed by cells of the periventricular zone, as well as more superficial layers. These results suggest the presence of multiple nAChR systems in retina and tectum. In addition, they indicate that tectal nAChRs may arise from remote (ganglion cell) as well as local (tectal cell) synthesis.

The retina is one of the most experimentally accessible regions of the brain for biological studies. We have selected the retina as a model system to study the influence of cell-cell interactions on the expression of neural nicotinic acetylcholine receptors (nAChRs). ACh and nAChRs are likely to be involved in synaptic communication within the retina and possibly between retina and brain. ACh has long been implicated as a neurotransmitter in the vertebrate retina (Ames and Pollen, 1968; see reviews by Graham, 1974, and Neal, 1976). Identification of acetylcholinesterase and choline acetyltransferase activities evidence the presence of cholinergic synapses in the retinas of several species (Francis, 1953; Ross and McDougal, 1976). These markers, together with 3 H-choline uptake studies, identify a subpopulation of retinal amacrine cells that are cholinergic (Masland and Mills, 1979). Pharmacological and electrophysiological studies indicate the existence of nicotinic cholinergic

synapses at amacrine-ganglion cell contacts (Masland and Ames, 1976; Negishi et al., 1978; Ariel and Daw, 1982). Patch-clamp recording confirms that at least some ganglion cells express functional receptors responsive to classical nicotinic agonists and antagonists (Lipton et al., 1987). Monoclonal antibody studies and cDNA cloning show the expression of nicotinic receptors by cells of the retinal ganglion cell layer (Keyser et al., 1988; Cauley et al., 1989; Sargent et al., 1989). Ganglion cells that have complex receptive fields receive a light-driven cholinergic input (Masland and Livingstone, 1976; Masland et al., 1984). This input seems to modulate the activity of some physiological classes of ganglion cells (Masland and Ames, 1976; Negishi et al., 1978; Ariel and Daw, 1982; Glickman et al., 1982). In order to determine the role nAChRs play in the retina we have begun isolating and characterizing retinal nAChR cDNA clones (Cauley et al., 1989).

Alpha-bungarotoxin (α -BTX) has traditionally been used to identify nAChRs in vertebrate skeletal muscle (Changeux, 1980). However, in the CNS this toxin has been shown to bind sometimes to sites distinct from those that bind nicotine (Clark et al., 1985) or certain nAChR antibodies (Patrick and Stallcup, 1977). Goldfish brain possesses at least 2 classes of nicotine binding sites, one of which also binds α -BTX (Henley and Oswald, 1987). One of these α -BTX binding molecules is synthesized by retinal ganglion cells and transported to the optic tectum (Henley et al., 1986a). In goldfish retina α -BTX binding localizes to the inner and outer plexiform layers, and this binding can be competed by nicotine (Yazulla and Schmidt, 1976; Schwartz and Bok, 1979). The function of these toxin binding molecules and their relationship to each other and to the other nicotinic receptor types are not known.

In order to determine the number and function of different nAChRs expressed in the visual system it is necessary to isolate and characterize these molecules. This is most easily accomplished by cDNA cloning. Using this strategy we have previously identified a novel nAChR structural subunit, GF α -2 (goldfish non-alpha 2), expressed at high levels by retinal ganglion cells (Cauley et al., 1989). Here we report the cloning and characterization of 2 more members of this gene family—GF α -3, a putative goldfish homolog of the rat α -3 gene (Boulter et al., 1986), and GF α -3, a gene encoding a new structural subunit with unexpectedly high homology with the GF α -2 protein.

Materials and Methods

Isolation of cDNA clones. Common goldfish (*Carassius auratus*) were used in these studies. A λ gt10 cDNA library was prepared from goldfish retinal RNA and screened with a mixed α -subunit probe as previously described (Cauley et al., 1989). This probe consisted of nick-translated

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(Rigby et al., 1977) cDNAs encoding the α -subunits of the *Torpedo* electric organ nAChR (Noda et al., 1982), kindly provided by Dr. Norman Davidson (California Institute of Technology), the rat muscle nAChR, and the rat neural nAChR α -4 subunit (Goldman et al., 1987). This screening resulted in the isolation of 6 cDNAs that encode 3 different goldfish neural nAChR subunits. One of these receptor subunit cDNA clones, GF α -2, has been characterized (Cauley et al., 1989).

Northern blot analysis and S1 nuclease protection experiments. Northern blots and S1 nuclease protection experiments were carried out as previously described. Briefly, RNA was isolated using a modification of the guanidinium isothiocyanate procedure (Chirgwin et al., 1979). Poly(A)+ RNA was selected over an oligo (dT) cellulose column (Aviv and Leder, 1972). For Northern blots 2.5 μ g of retinal and 5 μ g of brain poly(A)+ RNA and 10 μ g of poly(A)- RNA from each tissue were electrophoresed on denaturing agarose gels, then transferred to a Gene Screen Plus membrane. Membranes were hybridized under low-stringency conditions (\sim 40°C below the T_m) with nick-translated cDNA probes. Following hybridization, blots were washed at a stringency of \sim 40°C below the T_m and exposed to x-ray film with an intensifying screen at -80°C for 6–12 hr.

S1 nuclease digestions of heteroduplexes formed between poly (A)+ RNA and M13 subclones of GF α -3 and the GF α -3 cDNA were also carried out as previously described (Goldman et al., 1985). Retinal poly (A)+ RNA (5 μ g) was hybridized with M13 subclones containing complementary DNA corresponding to either the full-length cDNA or to subclones containing deletions at their 5' end (see Fig. 5A). Deletions were generated using T4 polymerase (Dale et al., 1985). These latter clones contained GF α -3 3' DNA extending 5' for 2498, 1918, 1658, or 950 bases. Following hybridization of these clones to the RNA, S1 nuclease was added and those hybrids surviving S1 digestion were size-fractionated by electrophoresis through a denaturing 1.2% agarose gel. Protected nucleic acids were transferred to a Gene Screen Plus membrane, hybridized with a nick-translated GF α -3 or GF α -3 probe, and washed at \sim 40°C below the T_m . Blots were exposed to x-ray film overnight at -80°C with an intensifying screen. Nick-translated probes were radiolabeled to a specific activity of \sim 10⁸ cpm/ μ g. The GF α -3 Northern blot and GF α -3 S1 nuclease protection blot autoradiograms were quantitated by densitometry using a Loats Associates Inc. image-analysis system.

Fluorescent back-labeling of retinal ganglion cells. Retinal ganglion cells were identified by fluorescence following retrograde labeling via the optic nerve using propidium iodide as a fluorescent tracer (Woolf et al., 1983; Tumosa and Stell, 1986). Propidium iodide (Sigma) was made up to 3% in 1% DMSO. Fish were anesthetized as previously described (Heacock and Agranoff, 1982), optic nerves were transected, and a small piece of propidium iodide-impregnated Gel-Foam was placed upon the proximal stump of the optic nerve. The eye was carefully repositioned and sealed with Super Glue. Three days later, retinas were removed and fixed as for *in situ* hybridization. Retinas were sectioned at 15 μ m, and back-labeled cells visualized using a Zeiss Axiophot microscope equipped with rhodamine optics.

In situ hybridization. *In situ* hybridization was performed as previously described (Cauley et al., 1989). In brief, goldfish retinas and brains were removed and fixed in ice-cold 4% paraformaldehyde in PBS (145 mM NaCl, 10 mM phosphate buffer, pH 7.4) for 2 hr. Tissues were then incubated in 20% sucrose/PBS at 4°C overnight. Sections, 15 μ m thick, were cut and mounted on gelatin-chromalum subbed, polylysine-coated slides. Prior to *in situ* hybridization, sections were digested with proteinase K (5 μ g/ml, 37°C, 5 min) and acetylated with acetic anhydride (0.25% in triethanolamine HCl, pH 8.0, 10 min, room temperature). Sections were hybridized with single-stranded ³⁵S-labeled RNA probes, prepared by run-off transcription of linearized recombinant plasmids. Hybridization solution was brought to 5 \times 10⁴ cpm/ μ l with the ³⁵S-UTP-labeled RNA probes. The GF α -3 probe was made from a Pst 1 linearized pGEM-4 vector containing the 909 bp GF α -3 cDNA inserted into the EcoR 1 site. The GF α -2 probe was made from a pGEM-4 vector harboring an EcoR 1/Dra 1 1650 bp subclone of GF α -2 (Cauley et al., 1989). This subclone contains the GF α -2 cDNA lacking its poly(A) tail and some 3' untranslated sequence. The GF α -3 probe was made from an EcoR 1 linearized pGEM-4 vector containing a 1594 bp Bgl II fragment subcloned into the BamH 1 site of pGEM-4. This fragment extends from nucleotide 107 to 1601 of the GF α -3 cDNA. Antisense probes for GF α -2 and GF α -3 were transcribed with T7 RNA polymerase and sense orientation probes with SP6 RNA polymerase (Melton et al., 1984). The GF α -3 antisense probes were tran-

scribed with SP6 RNA polymerase. Posthybridization treatments included a wash in 50% formamide, 2 \times SSC (0.15 M NaCl, 0.015 M Na citrate, pH 7.0) at 55°C (Fontaine et al., 1988) and an RNase digestion to reduce background (Cox et al., 1984). Controls for nonspecific hybridization in *in situ* hybridization experiments included the use of sense-strand probes and pretreating sections with RNase before hybridization with antisense probes. Slides were then dehydrated, dipped in Nuclear Track Emulsion NTB2, air-dried, and exposed at 4°C. Retinal sections were exposed 1–2 weeks, and brain sections were exposed 2–4 weeks. After developing, sections were stained with hematoxylin and eosin B. Low-magnification coronal brain sections were visualized using a Wild Makroskop M420 equipped with darkfield optics, and higher magnifications were visualized with a Zeiss Axiophot.

DNA sequence determination and comparison. DNA sequencing was performed using the dideoxynucleotide chain termination method (Sanger et al., 1977). cDNAs were subcloned into M13 bacteriophage vectors mp18 and mp19. Unidirectional deletions were generated with T4 DNA polymerase (Dale et al., 1985). Both strands of DNA were completely sequenced. Sequence comparisons were made with the University of Wisconsin Genetics Computer Group sequence analysis software package version 6.0. The GAP program using the algorithm of Needleman and Wunsch (1970) was used with "default" parameter settings.

Results

Isolation of goldfish neural nAChR cDNAs

The vertebrate retina expresses both nicotine and α -BTX binding molecules (Masland and Ames, 1976; Vogel and Nirenberg, 1976; Betz and Müller, 1981). In goldfish, members of these classes of molecules are found in the inner and outer plexiform layers of the retina (Yazulla and Schmidt, 1976; Schwartz and Bok, 1979), along the optic nerve (Schwartz et al., 1980), and throughout regions of the optic tectum where retinal afferents synapse (Henley et al., 1986b). We are using cDNA cloning to identify these molecules (Cauley et al., 1989).

A goldfish retinal cDNA library was screened with a radiolabeled mixed receptor probe (see Materials and Methods). Screening 5 \times 10⁵ recombinants resulted in the purification of 6 cDNAs representing 3 classes of molecules. One class representing a new nAChR subunit, GF α -2, has been characterized (Cauley et al., 1989). The other 2 classes are represented by clones GF α -3 (goldfish non-alpha 3) and by GF α -3 (goldfish alpha 3), and are characterized in this study.

GF α -3

Clone GF α -3 is 2698 nucleotides in length, with an open reading frame of 1398 bp (Fig. 1). This open reading frame begins with an initiator ATG at position -84 and ends with a stop codon, TAA, at position 1315. The 5' and 3' ends of the clone contain 144 and 1156 bases of untranslated sequence, respectively. There are 4 short open reading frames in the 5' untranslated sequence, with initiator ATGs at positions -193, -158, -131, and -113, which may influence the translatability of this transcript (Kozak, 1989). Based on comparison of the deduced amino acid sequence of GF α -3 with other nAChR subunit sequences (Fig. 2), and hydrophobicity analysis (Kyte and Doolittle, 1982), and taking into account the sequence patterns around the signal cleavage sight (Perlman and Halvorson, 1983; von Heijne, 1983), we have designated the amino terminus of the mature GF α -3 protein to be an alanine residue. This results in the identification of the first 28 residues as comprising a leader peptide. The mature protein is 438 amino acids and has a predicted molecular weight of 53,783. Four potential poly (A) addition signal sequences are found within the 3' untranslated sequence (underlined in Fig. 1; Proudfoot and Brownlee, 1976; Birnstiel et al., 1985).

Comparison of the deduced amino acid sequence of clone

| | | |
|------|---|------|
| -228 | TGA TCG TTT TCC AAA ACG GCC CGG TTT CCA GCC ATA TGA ATA AAA AAA CAA TAT ACC CCG | -169 |
| -168 | TTT TTT GTC GAT GAC AGG GAC TCG CTA TTC AAC CAG CAT GAA ATA ATT CTA TTG CAT GAA | -109 |
| -108 | GGA ATT GGA GCC GGG AAA GAC AGC <u>Met Lys Leu Gln Ile Ser Gly Leu Leu Leu Val Thr</u> | -49 |
| | <u>ATG AAG TTA CAA ATC TCC GGT CTT TTG CTC GTA ACT</u> | |
| | <u>1</u> | |
| -48 | GCA GTA GCC TAT GCA ACG ATA GAA GCT CCT GAG GAG TTT GTC TCA CTG GCT GAG ATG GAG | 12 |
| 13 | Asp Thr Leu Leu Arg Asn Leu Phe Arg Gly Tyr Gln Lys Trp Val Arg Pro Ile Leu His | 72 |
| | GAC ACG TTG TTG AGG AAT CTG TTT CGG GGC TAT CAG AAG TGG GTG AGA CCT ATC CTT CAC | |
| 73 | Ala Asn Asp Thr Ile Thr Val Arg Phe Gly Leu Lys Ile Ser Gln Leu Val Asp Val Asp | 132 |
| | GCC AAC GAC ACG ATT ACC GTT CGC TTT GGT CTG AAG ATC TCG CAG CTG GTG GAT GTG GAT | |
| 133 | Glu Lys Asn His Leu Met Thr Thr Asn Val Trp Leu Trp Gln Glu Trp Thr Asp Tyr Lys | 192 |
| | GAA AAG AAT CAC CTA ATG ACG ACA AAT GTC TGG TTG TGG CAG GAG TGG ACA GAC TAT AAG | |
| 193 | Leu Arg Trp Asn Pro Glu Asp Tyr Gly Gly Ile Thr Ser Ile Arg Val Pro Ser Glu Thr | 252 |
| | CTT CGG TGG AAT CCG GAA GAT TAC GGT GGA ATC ACA TCC ATC AGA GTG CCC TCA GAA ACC | |
| 253 | Ile Trp Leu Pro Asp Ile Val Leu Tyr Glu Asn Ala Asp Gly Arg Phe Glu Gly Ser Leu | 312 |
| | ATC TGG CTA CCA GAC ATT GTC CTT TAC GAG AAT GCT GAT GGC CGA TTT GAG GGC TCT CTG | |
| 313 | Met Thr Lys Ala Ile Val Arg Phe Asn Gly Thr Ile Met Trp Thr Pro Pro Ala Ser Tyr | 372 |
| | ATG ACC AAA GCC ATT GTA AGG TTT AAT GGT ACC ATC ATG TGC ACT CCT CCT GCC AGC TAT | |
| 373 | Lys Ser Ser Cys Thr Met Asp Val Thr Phe Phe Pro Phe Asp Arg Gln Asn Cys Ser Met | 432 |
| | AAA TCC TCC TGT ACC ATG GAT GTC ACC TTT TTC CCC TTC GAC AGG CAG AAC TGC TCG ATG | |
| 433 | Lys Phe Gly Ser Trp Thr Tyr Asp Gly Thr Met Val Asp Leu Thr Leu Leu Asp Ala Tyr | 492 |
| | AAG TTT GGA TCG TGG ACG TAC GAT GGC ACT ATG GTG GAC CTG ACT CTG TTA GAC GCA TAT | |
| 493 | Val Asp Arg Lys Asp Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Thr Gly Gln | 552 |
| | GTA GAC CGT AAA GAC TTC TTT GAC AAT GGC GAA TGG GAA ATA CTC AAC ACC GCC ACC GCG CAG | |
| 553 | Arg Gly Ser Arg Arg Asp Gly Ile Tyr Ser Tyr Pro Tyr Val Thr Tyr Ser Phe Ile Leu | 612 |
| | AGG GGA AGT CGG CGT GAC GGC ATT TAC TCT TAT CCT TAC GTC ACA TAT TCG TTC ATT CTG | |
| 613 | Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Leu Gly Leu Ser Phe | 672 |
| | AAA CGT CTT CCT CTG TTT TAC ACA CTC TTT CTC ATC ATC CCA TGT CTG GGT CTG TCG TTT | |
| 673 | Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Asp Glu Gly Glu Lys Leu Leu Leu Ser Thr | 732 |
| | CTC ACG GTT CTG GTC TTC TAC CTC CCC TCG GAT GAA GGA GAA AAG CTG CTC CTC TCC ACC | |
| 733 | Ser Val Leu Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser Ser | 792 |
| | TCC GTC CTT GTG TCT CTC ACT GTG TTT CTT CTT GTC ATC GAA GAG ATC ATT CCA TCT TCC | |
| 793 | Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met Ile Phe Val Thr Phe | 852 |
| | TCT AAA GTC ATT CCT TTG ATT GGA GAC TAT CTG CTT TTT ATC ATG ATC TTC TCT ACA TTC | |
| 853 | Ser Ile Ile Val Thr Leu Phe Val Ile Asn Val His His Arg Ser Ser Ala Thr Tyr His | 912 |
| | TCG ATC ATC GTG ACT TTG TTC GTC ATC AAC GTC CAT CAT CGT TCT TCT GCC ACG TAC CAT | |
| 913 | Pro Met Ala Pro Trp Val Lys Ser Leu Phe Leu Gln Arg Leu Pro Arg Leu Leu Cys Met | 972 |
| | CCA ATG GCG CCG TGG GTT AAG AGT CTT TTC CTT CAG AGA TTA CCC AGA CTG CTC TGC ATG | |
| 973 | Arg Gly His Thr Asp Arg Tyr Gln Tyr Pro Asp Ile Glu Leu Arg Ser Pro Glu Leu Lys | 1032 |
| | AGG GGA CAT ACT GAT CGC TAT CAG TAC CCA GAC ATC GAG CTG CCG AGC CCA GAG CTA AAA | |
| 1033 | Arg Gly Met Lys Lys Gly Gln Gln Lys Ser Ala Gly Gly Gly Arg Gly Gly Leu Lys Glu | 1092 |
| | CGA GGG ATG AAG AAA GGG CAA CAG AAG AGT GCC GGA GGA GGG CGA GGA GGG TTA AAG GAA | |
| 1093 | Asp Glu Asn Gln Ala Trp Ile Ala Leu Leu Glu Lys Ala Thr His Ser Val His Tyr Ile | 1152 |
| | GAT GAG AAT CAG GCC TGG ATT GCT CTG TTG GAG AAA GCC ACT CAC TCA GTG CAC TAC ATT | |
| 1153 | Ser Arg His Ile Lys Lys Glu His Phe Ile Arg Glu Val Val Gln Asp Trp Lys Phe Val | 1212 |
| | TCC AGA CAC ATC AAG AAG GAA CAC TTC ATC AGA GAG GTT GTT Gln Asp TGG AAG TTT GTG | |
| 1213 | Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Val Phe Leu Thr Ala Ser Val Leu Gly Thr | 1272 |
| | GCT CAG GTA TTG GAC CGG ATC TTC CTC TGG GTC TTT CTT ACA GCT TCT GTG CTT GGG ACC | |
| 1273 | Ile Leu Ile Phe Thr Pro Ala Leu His Met Tyr Leu Ser Thr End | 1332 |
| | ATC CTC ATC TTC ACC CCA GCT CTG CAC ATG TAC CTC AGC ACA TAA AAA AAA ACA GCC TAC | |
| 1333 | CAA ATC TCC TTT ACC CTC GAC AAC ATT CTT ATG ACC CCT TTG <u>AAA TAT ATA</u> GTT CCC ACA | 1392 |
| 1393 | ATA TCA CAG GAA TCC TTC TAA ACG TAT TTC TGA CCT AGC ATA TCT GTA ATC CTC CTA AAA | 1452 |
| 1453 | TTC CAG TCT CCT AGC TCT CCT TTC AGC TCT GAA AAA AAG TCA AAC TTT CAA AAC ATT TTC | 1512 |
| 1513 | AAC CCG TTT AAC ACA TAA CTA AGA ATC TTA TGA AGT TGG TGT TGT TTG GAT TTG TGT | 1572 |
| 1573 | AAT CTC TCC AAA TGG GTC ATG GGT TTA AAG ATC TTC <u>AAT AAT</u> TTG ACT TTA ATC ACT | 1632 |
| 1633 | ACT GTG ATG TAA AAG GTG AAC CAC ATC TTT CAT GCC TCT TAT TTC ACT TGG TAT CAT TCA | 1692 |
| 1693 | TTC CTG TAT TTA TGT ATT TAT TTA TTT AGG GTG GGT AAA AAT TGT GTC AGT GTT CAT TTA | 1752 |
| 1753 | AGT AAT ATT TTA CAG TAA TAT TTT ATC ATT CCG GTC ATT AGG AAA CAA ACC TAT TCA ATA | 1812 |
| 1813 | GAT TAA AAT TCC ATC TGT ATG CAA TAA ATA TTA ATT TTT TAC ACT ATA CAG ATA TTA CTT | 1872 |
| 1873 | CTG GAT GAT GAT AGC ATG GAG AAC ATT ACT AGA TTT GAT ACT AAT TAT ATG AAA TTA TAA | 1932 |
| 1933 | CAG TAT CTC TAT TAT TGG GAA AGG TTC CTT ACT GTA CAG TCT TGC ATA TAT TGT CCT AGT | 1992 |
| 1993 | TTT TAG TAC TGT TAA ATG CAT GTA GTA TCA TGC CTT TGG ATG ACA GTA TGC ATA TGT AAA | 2052 |
| 2053 | TGT TAT GCA GAT GAG GCC ATG CAT AAT ACA AAG TGC ATG TGT ATG TAT CTA CAA TCT TCC | 2112 |
| 2113 | ACA ATC TGG GAT TTA TAA AAA AAG ACA TTT ACA CAG ATG CAT ATA CTG TAT GGT GCA TAT | 2172 |
| 2173 | ATG GAT TTA TAA ATC TCA ATA TCT CCC ATT TGT GCT TAT AGG ATG AAG TCT ACA CCA CAT | 2232 |
| 2233 | GTT AAA CAT TCT TAT CCC TAA ATC CTT GGA GAT ATT GTC GCT GAT TCA AGT GGG ACA GAT | 2292 |
| 2293 | TAC TTG ATC ACA GCT TGT GTT TGG CAT AAT AAG CAA GGA CTT TAT TAT CAT ATC CAT CTT | 2352 |
| 2353 | TAT TTC TGT TCA TTC ACA CTG GTC <u>AGT AAA</u> TGG AAA TGT CAT TGT ATC AGT TTT TTG TTG | 2412 |
| 2413 | TTT GAA TGT CTA ACA TGT GTT TCA TGT <u>AAA TAA</u> CCT TGT AAG TGA TCT AAA AAA AAA A. '3' | 2470 |

Figure 1. Nucleotide and deduced amino acid sequence of cDNA clone GF α -3. Nucleotides are numbered in the 5' to 3' direction. The amino acid designated 1 (Ala) represents the putative amino-terminal residue in the mature protein. Sequences extending 5' to base 1 are designated with negative numbers and include residues encoding the putative signal peptide and 5' untranslated sequence. Polyadenylation signal sequences are underlined in the 3' untranslated region.

GF α -3 with the muscle and neural nAChR sequences shows that this clone encodes a protein that is a member of the nAChR gene family (Fig. 2, Table 1). GF α -3 is remarkably similar to GF α -2, with an overall amino acid sequence similarity of 88% (Table 1). These 2 proteins are more similar to the rat β 3 protein (Deneris et al., 1989; 85% for GF α -3, 82% for GF α -2) than to any other nAChR subunit identified to date (Table 1). In fact, no other known pair of nAChR subunits show this level of similarity.

Analysis of the GF α -3 protein sequence indicates that it contains many structural features common to all neural nAChR subunits sequenced to date (Barnard et al., 1987). These include (1) four hydrophobic putative transmembrane domains; (2) an extracellular β -loop structure occurring before the first hydrophobic domain, formed by cysteines 128 and 142, with a turn induced by the conserved proline at position 136; (3) 2 putative cytoplasmic N-linked glycosylation sites at positions 26 and 141; and (4) a hydrophilic domain situated between the third and fourth hydrophobic domains. In addition to those putative glycosylation sites mentioned above, the GF α -3 protein also has N-linked glycosylation consensus sites at amino acid positions 113 and 180.

The protein encoded by GF α -3 lacks adjacent cysteines corresponding to positions 191 and 192 of the *Torpedo* nAChR α -subunit (Noda et al., 1982). These cysteines are found in all nAChR α -subunits sequenced to date and are believed to be close to the agonist binding domain (Kao and Karlin, 1986). In this respect, GF α -3 is more similar to the structural non- α ($n\alpha$) subunits of muscle and neural nAChRs. Based on the absence of these adjacent cysteine residues in GF α -3, and the conservation of the many structural domains between this protein and all other neural nAChR subunits, we propose that GF α -3 represents a structural subunit of a novel class of neural nAChRs.

GF α -3

Since 2 novel nAChR subunit genes have been identified in goldfish (GF α -2, Cauley et al., 1989, and GF α -3, this paper), it was important to determine whether other previously identified members of the vertebrate nAChR gene family are also expressed in fish. The identification of these genes would imply that a similar gene family is expressed in fish and higher vertebrates. Clone GF α -3 represents one such gene. GF α -3 is a partial cDNA whose deduced amino acid sequence indicates that it may represent the goldfish homolog of the rat α -3 gene (Boulter et al., 1986; Fig. 3).

GF α -3 is 909 bp in length containing an open reading frame coding for a 303 amino acid polypeptide (Fig. 3). GF α -3 represents the 5' end of the gene coding for amino acids -21 through 281, based on the rat α -3 sequence (Boulter et al., 1986). This region includes the 2 cysteine residues at positions 192 and 193 that are presumed to be close to the ligand-binding domain. GF α -3 possesses cysteines 128 and 142, common to all known nAChR subunits. The putative glycosylation sites at amino acid positions 23 and 141, common to the neural nAChR subunits, are also present. Comparison of the deduced GF α -3 amino acid sequence with known nAChR subunits shows GF α -3 to be most similar to the neural α -3 subunit [89% similarity with rat α -3 (Fig. 3) and 93% similarity with chicken α -3 (Nef et al., 1988)]. This degree of homology is higher than that of any of the rat subunits with each other and is most consistent with GF α -3 representing the goldfish homolog of the rat and chicken α -3 gene.

Table 1. Percentage of amino acid similarity between non-alpha nAChR subunits

| Subunit | GF α -3 | GF α -2 | Rat β -3 | Rat β -2 | Rat β -4 | ARDn α |
|----------------|----------------|----------------|----------------|----------------|----------------|---------------|
| GF α -3 | 100 | | | | | |
| GF α -2 | 88 | 100 | | | | |
| Rat β -3 | 85 | 82 | 100 | | | |
| Rat β -2 | 62 | 64 | 64 | 100 | | |
| Rat β -4 | 57 | 56 | 59 | 67 | 100 | |
| ARDn α | 63 | 61 | 63 | 61 | 55 | 100 |

Similarity was determined using University of Wisconsin Genetics Computer Group Gap program. Amino acid sequences are GF α -3 (this report), GF α -2 (Cauley et al., 1989), Rat β -3 (Deneris et al., 1989), Rat β -2 (Deneris et al., 1988), Rat β -4 (clone SCG 3, Isenberg and Meyer, 1989), and ARDn α (Hermans-Borgmeyer et al., 1986).

nAChR gene expression in goldfish retina and brain

GF α -3 identifies multiple RNAs expressed in retina and brain

The level of expression of RNAs homologous to the GF α -3 cDNA was assayed by Northern blot (Fig. 4). This experiment showed GF α -3 to hybridize to several different RNAs in retina and brain, with the majority of hybridization at 2.7 kb in both tissues. Densitometric integration of the autoradiogram showed that retina has about a 12-fold higher level of GF α -3 expression per microgram of RNA than brain.

S1 nuclease protection experiments were used to determine if any of the RNAs seen hybridizing with the GF α -3 probe on Northern blots contained regions that were identical or very similar to the GF α -3 cDNA. This experiment resulted in the protection of 4 different retinal RNAs of approximately 2.7, 1.9, 1.7, and 0.8 kb (Fig. 5B, lane 2698+). An identical pattern was seen when this experiment was performed using brain RNA, although the ~800 nucleotide band was not always visible (data not shown).

To map the regions of the GF α -3 sequence responsible for protection of these RNAs, subclones were generated in M13mp19 that lacked various amounts of GF α -3 5' DNA (Fig. 5A). One predicts that S1 nuclease digestion of heteroduplexes formed between RNA and any of these deleted clones will result in a smaller S1 protected fragment than when a full-length clone is used, if the RNA overlaps with the deleted region. When this experiment was carried out, all 3 larger protected bands decreased in size in proportion to the extent of the 5' deletion, indicating that these RNAs all span the 5' end of GF α -3 and therefore must differ at their 3' ends (Fig. 5B). The largest (~2.7 kb) band represents full-length protection of the GF α -3 sequence. The bands at 1.9 and 1.7 kb represent either (1) GF α -3 gene products whose RNA transcripts contain shorter 3' untranslated regions than GF α -3 or (2) sequences which diverge from the GF α -3 sequence at their 3' ends. Consistent with the former possibility one finds 4 putative poly (A)-tail addition signal sequences in the GF α -3 3' untranslated region (underlined in Fig. 1). These sites occur at nucleotides 1378, 1610, 2379, and 2444. If each of these sites were used during RNA processing, one predicts protected fragments of 2698, 2633, 1838, and 1606 nucleotides to result from the S1 experiment. The 2 largest fragments, differing by 65 nucleotides, would probably not be resolved on the agarose gel, making it difficult to determine if one of these sites is used preferentially. Nonetheless, the sizes of the protected fragments determined experimentally (Fig. 5B) agree fairly well with that predicted from alternative use of

GF α -3 MKLQISGLLL VTAVAYATIE APEEFVSL AEMEDTLRLN LFRGYQKWVR PILHANDTIT VRFGLKISQL VDVDEKNHLM
GF α -2 MTLAVIGLF TLFTSIIAIT PAREFVSL AEREDALLRE LFQGYQRWVR PVQHANHSVK VRFGLKISQL VDVDEKNQLM
Rat β -3 MTGFLRVFLVL SATLSGSWVT LTATAGLSSV AEHEDALLRH LFQGYQKWVR PVLNSSDIK VYFGLKISQL VDVDEKNQLM
Rat β -2 MLACMAGHSN SMALFSFSL WLCSGVLGTD TEERLVEHLL DPSRYNKLIR PATNGSELVT VQLMVSQAQL ISVHEREQIM
Rat β -4 DARLFDCSGVL PDKGPAGLTV RFPGDCLAN AEEKLMDDL NKTRYNNLIR PATSSSQLIS IRLELSLSQL ISVNEREQIM
ARDna MESSCK SWLLCSILVL VAFSLVSASE DEERLVRDL .FRGYNKLIR PVQNMTPQVG VRFGLAFVQL INVNEKNQVM
* * * * *

<-----SIGNAL PEPTIDE----->

GF α -3 TTNVWLWQEW TDYKLRWNE DYGGITSIRV PSEIWLDPDI VLYENADGRF EGSLMTKAIV RFNGTIMWTP PASYKSSCTM
GF α -2 TTNVWLWQEW LDYKLRWNE NYGGITSIRV PSEIWLDPDI VLYENADGRF EGSLMTKAIV RYNGMITWTP PASYKSACTM
RAT β -3 TTNVWLKQEW TDOKLRWNE EYGGINSIKV PSESLWLDPDI VLFENADGRF EGSLMTKAIV KSSGTVSWTP PASYKSSCTM
Rat β -2 TTNVWLKQEW EDYRLTWKPE DFDNMKKVRL PSKHIWLDPV VLYNNADGRF EVSFYNAVW SYDGSIFWLP PAIYKSACKI
Rat β -4 TTSIWLKQEW TDYRLAWNSS CYEGVNILRI PAKRVWLDPDI VLYNNADGRF EVSVTYNVIV RSNQSIQWLP PAIYKSACKI
ARDna KSNVWLRLVW YDYQLQWDEA DYGGIGVLRV PPKVWKPDI VLFNNADGRF EVRYKSNVLI YPTGEVLVWP PAIYQSCTI
* * * * *

GF α -3 DVTFFPFDRQ NCSMKFGSWT YDGTMVDLTL .LDAYVDRK DFFDNGEWI LNATGQRGSR RDGIYS..YP YVTYSFILKR
GF α -2 DVTFFPFDRQ NCSMKFGSWT YDGNMVKLV .INQVDRS DFFDNGEWI LSATGVKGRS QDSHLS..YP YVTYSFILKR
Rat β -3 DVTFFPFDRQ NCSMKFGSWT YDGTMVDLTL .INENVDRK DFFDNGEWI LNAKGMKGNR REGFYS..YP FVTYSFVLR
Rat β -2 EVKHFPFDQ NCTMKFRSWT YDRTEIDLVL .KSDVASLD DFTPSGEWDI IALPGRRENEN PDDST..YV DITYDFIIRR
Rat β -4 EVKHFPFDQ NCTMKFRSWT YDHTIDMVL KSPTAID DFTPSGEWDI VALPGRRTVN PQDPS YV DITYDFIIRR
ARDna DVTYFPFDQ TCIMKFGSWT FNGDQVSLAL YNNKNFVLS DYWKSGTWDI IEVPAYLVNV EGDNSHPTET DITYFIIIRR
* * * * *

GF α -3 LPLFYTLFLI IPCGLSFLT VLVFYLPSDE GEKLLSTSV LVSLTVFLLV IEEIIPSSK VIPLIGEYLL FIMIFVTFSI
GF α -2 LPLFYTLFLI IPCGLSFLT VLVFYLPSDE GEKVLSTSV LVSLTVFLLV IEEIIPSSK VIPLIGEYLL FIMIFVLSI
Rat β -3 LPLFYTLFLI IPCGLSFLT VLVFYLPSDE GEKLSLSTSV LVSLTVFLLV IEEIIPSSK VIPLIGEYLL FIMIFVLSI
Rat β -2 KPLFYTINLI IPCVLITSLA ILVFYLPSC GEKMTLCISV LLALTVFLLL ISKIVPPTSL DVPLVGYKYM FTMVLVTFSI
Rat β -4 NALFYTINLI IPCVLITSLA ILVFYLPSC GEKMTLCISV LLALTVFLLL ISKIVP L NIPLIGKYLL FTMVLVTFSI
ARDna KTLFYTVNLI LPTVLISFLC VLVFYLPAEA GEKVTLGISI LLSLVVFLLV VSKILPPTSL VLPLIAKYLL FTFIMTVSI
* * * * *

<-----TMD 1-----> - -+ <-----TMD 2----->+ +<-----TMD 3----->

GF α -3 IVTLFVINVH HRSSATYHPM APWVKSFLQ RLPRLLCMRG HTDRYQYPI ELRSPELKRK MKKGQKQKSG GGRGGLKEDE
GF α -2 IVTIFVINVH HRSSATYHPM SPWVRSFLQ RLPRLLCMRG NTDHYHYPEL EPHSPDLKPR NKGPPGPEG EGQALIN..
Rat β -3 IVTVFVINVH HRSSATYHPM APWVKRFLQ RLPRLLCMRG PMDRFSFDPG KESDTAVRGK VSGKRKQTPA SDGERVLVAF
Rat β -2 VTSVCLNVH HRSPTT.HTM APWVKVVFLE KLPTLLFLQ PRHRCARQL RLRRRQRE GEAVFFREGP AADPCTCFVN
Rat β -4 VTTVCLNVH HRSPTT.HTM ASWVKECFH KLPTFLMFR PGLEVSLVRV PHPSQLHAT ADTAATSALG PTSPSNLYGS
ARDna LVTVIIINVH FRGPRT.HRM PMYIRSIFLH YLPAFLMFR PRKTRLRMM EMPGMSMPAH PHPSYGSAPAE LPKHISAIGG
* * * * *

-----> <-----CYTOPLASMIC DOMAIN----->

GF α -3 NQAWIA.... LLEKATHSVH YISRHIKKEH FIREVVQDWK
GF α -2 LLEQATNSVR YISRHIKKEH FIREVVQDWK
Rat β -3LEKASESIR YISRHVKKEH FISQVQDWK
Rat β -2 PASVQLAGA FRAEPTAAGP GRSVGPCSC. GLREAVDGVV FIADHMRSED DDQSVREDWK
Rat β -4 SMYFVNVPVA APKSAVSSHT AGLPRDARLR SSGRFRE... DLQEALEGVS FIAQHLESDD RDQSVIEDWK
ARDna KQSKMEVMEL SDLHHPNCKI NRKVNSSGEL GLGDGCRRES ESSDSILLSP EASKATEAVE FIAEHLRNEED LYIQTRREDWK
* * * * *

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GF α -3 FVAQVLDRIE LWVFLTASVL GTILIFTPAL HMYLST....
GF α -2 FVAQVLDRIE LWTFLTVSVL GTILIFTPAL KMFLRTPPPSP.....
Rat β -3 FVAQVLDRIE LWLFLIASVL GSILIFIPAL KMWIHRFH..
Rat β -2 YVAMVIDRLF LWLVFVCFV GTVGMFLQPL FQNYTATTFE HPDHSAPSSK
Rat β -4 FVAMVDRLE LWVFLVFCIL GRTMGLFLPP LFQIHAPSKD S
ARDna YVAMVIDRLF LYIFFIVTTA GTVGILMDAP HIFEYVQDR IIEIYRKG..
* * * * *

<-----TMD 4----->

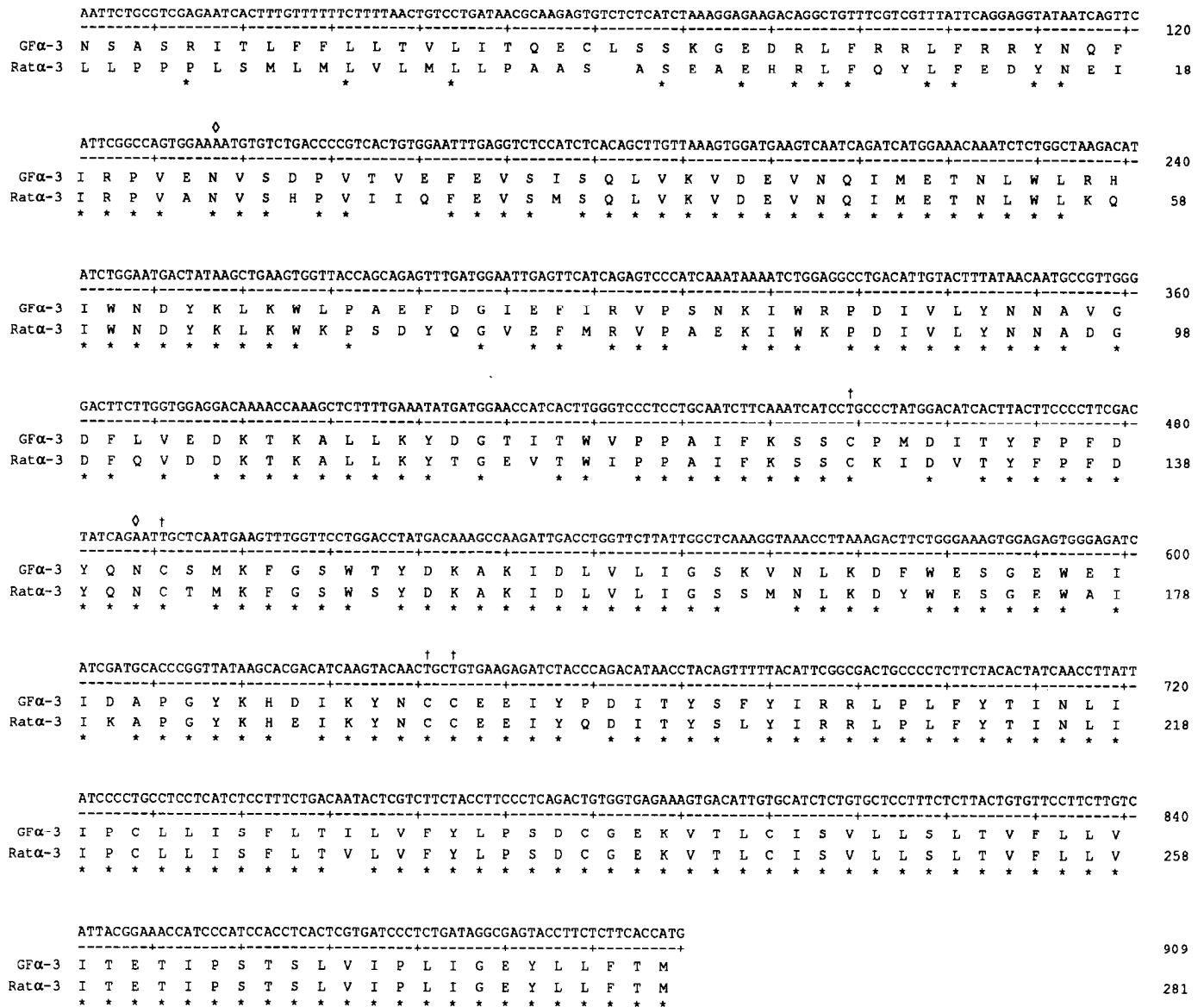


Figure 3. Nucleotide and deduced amino acid sequence of cDNA clone GF α -3, aligned with the rat α -3 amino acid sequence (Boulter et al., 1986). Amino acids conserved in both subunits are indicated by an asterisk. Diamonds indicate potential glycosylation sites and daggers indicate conserved cysteine residues.

poly(A) addition sites based on DNA sequence analysis (Figs. 1, 5C). Since Northern blots only detected hybridizing RNA at about 2.7 kb, it is likely that these smaller S1 nuclease-resistant fragments have longer 5' ends than clone GF α -3.

The smallest fragment observed in these S1 nuclease protection experiments was approximately 0.8 kb. Its intensity and appearance was heterogeneous, appearing clearly in 2 out of 5 experiments. S1 nuclease protection experiments using sense and antisense single-stranded DNAs from GF α -2 and GF α -3 cDNAs show that this ~800 bp fragment does not result from

hybridization between these very similar gene products. Therefore, this fragment may represent the product of a gene related to GF α -3 (but not GF α -2) or alternative splicing of the GF α -3 gene primary transcript.

GF α -3 identifies a single RNA transcript expressed in retina and brain

To determine the number of RNAs in retina and brain that are identified by the GF α -3 cDNA, S1 nuclease protection experiments were performed with this clone (Fig. 6). The GF α -3 cDNA

Figure 2. Comparison of deduced amino acid sequences for neural nicotinic ACh receptor non-alpha (α) subunits. Shown are α subunit sequences from *Drosophila* ARD α ; (Hermans-Borgmeyer et al., 1986), rat β -2 and β -3 (Deneris et al., 1988, 1989), rat β -4 (clone SCG3, Isenberg and Meyer, 1989) and goldfish (GF α -2 and GF α -3; Cauley et al., 1989). Amino acids conserved in all 6 subunits are indicated by an asterisk. The putative transmembrane and cytoplasmic domains are indicated below the aligned sequences. Diamonds indicate potential glycosylation sites for GF α -3, and daggers indicate conserved cysteine residues. Minus and plus symbols refer to charged amino acid residues appearing on either side of TMD 2 (see Discussion).

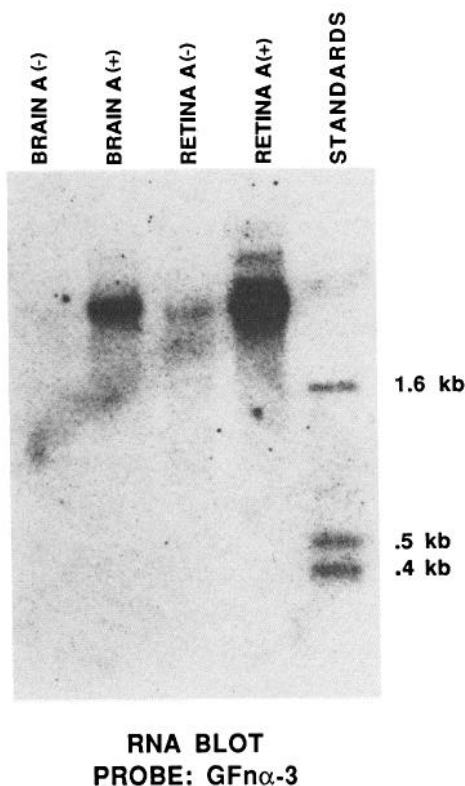


Figure 4. GFn α -3 identifies multiple RNAs in retina and brain. Northern blot analysis of RNAs homologous to the GFn α -3 cDNA. 5 μ g of poly(A)+ RNA from brain (lane 2), 2.5 μ g of poly(A)+ RNA from retina (lane 4) and 10 μ g of poly(A)- RNA from brain (lane 1) and retina (lane 3) was size fractionated on a 2.2 M formaldehyde 1.2% agarose gel and transferred to Gene Screen Plus membrane. The blot was probed with 32 P-labeled GFn α -3 cDNA, and washed at low stringency.

was subcloned into M13mp19 to generate single-stranded DNA. Heteroduplexes were formed between this DNA and poly(A)+ RNA isolated from goldfish brain and retina. Heteroduplexes were then digested with S1 nuclease, and S1-resistant fragments were fractionated on a denaturing agarose gel. This analysis revealed a single protected fragment of \sim 900 bp when either retina or brain RNA was used (Fig. 6). This is the expected size for complete protection of the cDNA by the RNA. In addition, densitometry of the autoradiogram indicates that the relative level of expression of the GF α -3 gene is about 4-fold higher in retina than brain. Since GF α -3 is only a partial cDNA, it was not possible to determine if other RNAs exist that are similar to the GF α -3 gene product but diverge in sequence at their 3' ends. The small amount of signal seen in the control lane in Figure 6 is not reproducible and could represent overflow from neighboring wells or residual undigested M13 DNA.

In situ hybridization identifies cells in retina and tectum expressing nAChR genes

To date we have isolated and characterized 3 different genes expressed in goldfish retina: (1) GFn α -2 (Cauley et al., 1989), (2) GFn α -3, and (3) GF α -3. In order to determine if these genes are expressed in similar cell types, we have compared their pattern of expression in retina and tectum using the high-resolution technique of *in situ* hybridization. In retina, these ex-

periments showed all 3 genes to be expressed in the retinal ganglion cell layer (Fig. 7). In addition, the level of expression of these genes was heterogeneous among individual cells of this layer. Analysis of propidium iodide fluorescently back-labeled retinal sections showed that these cells are ganglion cells (data not shown), and we calculate that greater than 70% of the ganglion cells hybridize positively for each probe. Further study of this heterogeneity in *in situ* hybridization among the ganglion cells is in progress. Besides being expressed by ganglion cells, the GFn α -3 gene is expressed at high levels, relative to GFn α -2 and GF α -3, in the inner nuclear layer of the retina. Sections were examined before staining to verify that emulsion grains resulting from hybridization were not obscured by the histological stains used to visualize individual cells in the ganglion cell layer.

Since nAChRs are synthesized by retinal ganglion cells and transported to the optic tectum (Henley et al., 1986a; Sargent et al., 1987), we were interested in determining if cells in the tectum also express nAChR genes. In the optic tectum *in situ* hybridization identifies cells that express the GFn α -3 and GF α -3 genes; however no detectable expression of the GFn α -2 gene was observed (Fig. 8). Both GFn α -3 and GF α -3 probes hybridize to cells of the deepest, and most cell-dense layer, of the optic tectum. This layer can be identified as layer 3 of the periventricular zone (PVZ; Northcutt, 1983). In addition, positively hybridizing cells are scattered throughout the more superficial tectal layers (Fig. 8C). S1 nuclease protection experiments using single-stranded antisense GFn α -3 cDNA and tectal RNA showed the same multiplicity of protected fragments as observed when retinal RNA was used (data not shown). This result indicates similar processing of the GFn α -3 primary transcripts in tectum as in retina. Additional *in situ* hybridization signal can be seen in lower brain areas, with positive hybridization over the nucleus diffusus (DF), and strong hybridization over cells in the vicinity of the nucleus lateralis thalami (LT; Braford and Northcutt, 1983).

Discussion

We had previously identified a novel structural subunit (GFn α -2) expressed in the goldfish retina (Cauley et al., 1989). Here we report the identification of a second novel goldfish nAChR structural subunit, GFn α -3, and a putative ligand-binding α -subunit, GF α -3. Like GFn α -2, GFn α -3 encodes a protein classified as a non-alpha (α)-like subunit of the nAChR because it lacks the adjacent cysteine residues corresponding to amino acids 192 and 193 of the *Torpedo* nAChR α -subunit (Noda et al., 1982). These residues correspond to a region of the α -subunit that contributes to the ACh binding site (Kao and Karlin, 1986).

GFn α -2 and GFn α -3 are the most homologous nAChR subunits identified to date, possessing 88% amino acid sequence similarity (Table 1). In addition, both of these sequences bear a striking similarity to the rat β 3 sequence (Deneris et al., 1989; 82 and 85% amino acid sequence similarity, respectively; Table 1). Based on this similarity, it is possible that either GFn α -2 or GFn α -3 represents the goldfish homolog of the rat β 3 gene. Unlike GFn α -2 and the rat β -3 sequence, GFn α -3 possesses 2 putative N-glycosylation sites, at positions 113 and 180 (Fig. 2). Posttranslational modifications might contribute to greater differences between the protein products of these genes than amino acid sequence homology would predict. Based on this hypothesis, and in lieu of additional data about the expression of these genes or the properties of their encoded proteins, it is

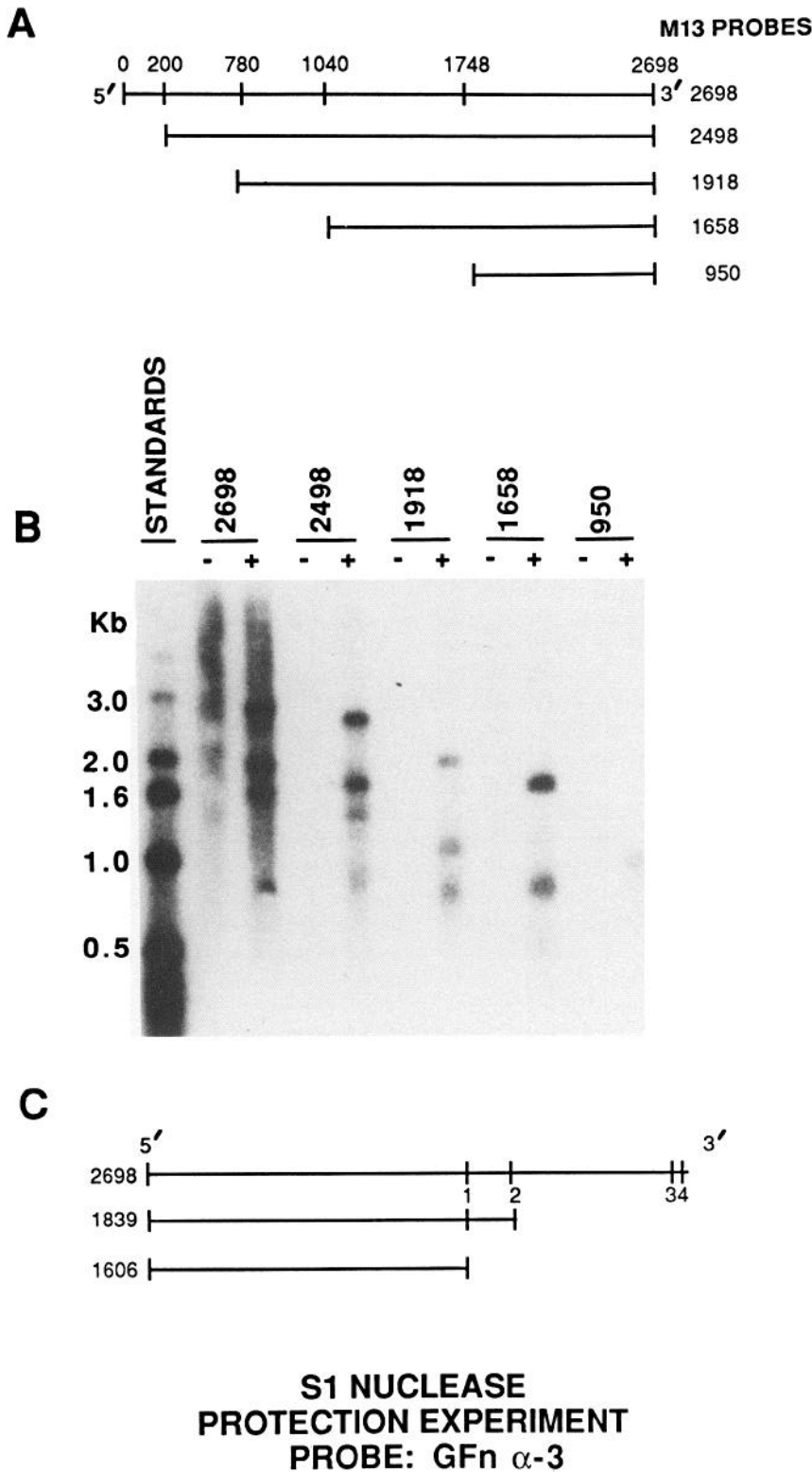


Figure 5. GFn α -3 identifies 3 retinal RNAs differing in their 3' untranslated sequence. S1 nuclease protection experiment with GFn α -3 cDNA and retinal RNA. **A**, Line diagram of GFn α -3 M13 subclones used to hybridize with retinal RNA. The full-length clone is 2698 bases long. Deletions of the 5' end were generated, and these M13 subclones were named according to the number of nucleotides remaining at the 3' end. **B**, Gel profile of S1 nuclease protected fragments generated by S1 nuclease digestion of heteroduplexes formed between 5 μ g poly(A)⁺ RNA isolated from retinal tissue and the M13 probes shown in **A**. (+) lanes contain RNA and (-) lanes are controls lacking RNA. The 4 bands in lane 2698+ are ~2.7, 1.9, 1.7, and 0.8 kb. **C**, Line diagram illustrating putative polyadenylation sites of the GFn α -3, and corresponding length of the mRNA that would be protected by the full-length GFn α -3 cDNA. These potential polyadenylation sites may account for the 3 larger bands generated by the S1 protection experiment (**B**, lane 2698+).

probable that GFn α -2 is more similar to the rat β 3 gene. Assuming that the rat β 3 gene is the rat homolog of either the goldfish GFn α -2 or GFn α -3 gene, and including as well the *Drosophila* ARDn α subunit, the identification of GFn α -3 brings the total number of neural nAChR structural subunits identified to date to 5 (Fig. 2, Table 1).

Recently, site-directed mutagenesis has identified charged res-

idues surrounding transmembrane domain 2 (TMD 2) of each subunit of the *Torpedo* nAChR as influencing ion flow through the channel (Imoto et al., 1988). Analysis of this region in the neural non-alpha subunits indicates 2 general classes. One class, comprising GFn α -3, GFn α -2, and the rat β -3 gene, has 3 negatively charged residues (Asp 235, Glu 236, Glu 238) and 1 positively charged residue (Lys 239) on the putative cytoplasmic

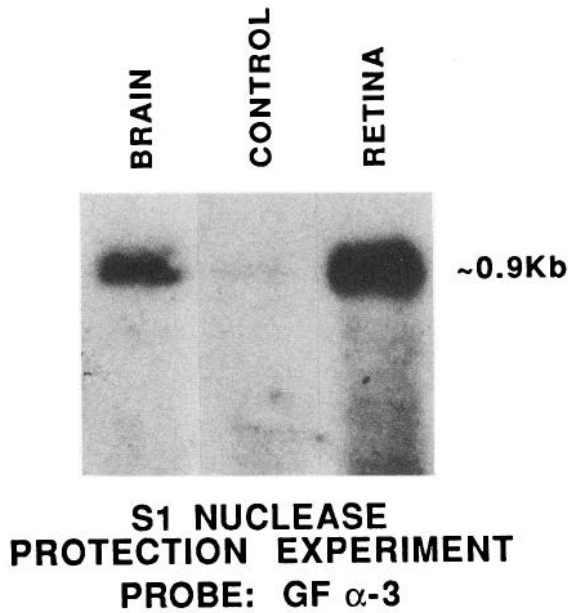


Figure 6. GF α -3 identifies a single RNA in retina and brain. S1 nuclease protection experiment with GF α -3 cDNA and retina or brain RNA. S1 nuclease protected fragments generated from brain (lane 1) and retinal (lane 3) RNA are both \sim 900 bases in length. Control protection (lane 2) was carried out using a sense orientation GF α -3 M13 subclone.

side of TMD 2 (Fig. 2). On the extracellular side of TMD 2, these subunits share 3 negatively charged residues (Glu 258, Glu 259, Glu 273) and 1 positively charged amino acid (Lys 266). The second class, represented by clones rat β 2 (Deneris et al., 1988), ARDn α (Hermans-Borgmeyer et al., 1986), and rat β 4 (clone SCG 3; Isenberg and Meyer, 1989) contain 2 negatively and 1 positively charged residue (Asp or Glu 235, Glu 238, Lys 239) on the cytoplasmic side and 2 positively charged residues (Lys 259, Lys 273) on the extracellular side of TMD 2 (Fig. 2). The neural α - subunits each possess 2 negatively (Asp or Glu) and 1 positively charged (Lys) residue on the cytoplasmic side and 2 negatively charged residues (Glu) on the extracellular side of TMD 2. For the *Torpedo* nAChR subunits, channel conductance is proportional to the net number of negative charges neighboring the hydrophobic segment TMD 2 (Imoto et al., 1988). One can therefore predict that the nAChRs using the GF α -3 class of subunits have a greater conductance than those of the rat β 2 class. Expression and electrophysiological recording studies are necessary to confirm this hypothesis.

Since GF α -2 and GF α -3 represent novel members of the nAChR gene family, it was important to determine whether similar nAChR genes are expressed in fish and higher vertebrates. Clearly the mammalian muscle type of nAChR is expressed in the electric organ of the electric fish (Boulter et al., 1985). In addition, we determined that other known members of the mammalian nAChR gene family were represented in our goldfish retinal cDNA library. From our original library screening we identified a partial cDNA (GF α -3) with 89% amino acid sequence similarity to the rat α -3 sequence (Fig. 3). GF α -3 contains the double cysteine residues corresponding to positions 192 and 193 of the *Torpedo* α -subunit (Noda et al., 1982) consistent with its classification as an α -subunit. An 89% similarity between the GF α -3 and the rat α 3 gene product suggests that

they may be homologous genes. Comparison of the known homologous rat and chick nAChR gene products indicates similarities of 81% for the α -4 polypeptide, 89% for the β -2 polypeptide, and 92% for the α -3 polypeptide (rat α -3 Boulter et al., 1986; rat α -4, Goldman et al., 1987; rat β -2 Deneris et al., 1988; chicken α -3, α -4, β -2, Nef et al., 1988). Therefore, GF α -3 most likely represents the goldfish homolog of the rat and chick α -3 cDNAs and demonstrates that similar members of the nAChR gene family are expressed in these 3 species. Also, as previously mentioned, the rat β -3 gene may represent the rat homolog of either the goldfish GF α -2 or GF α -3 genes.

The level of GF α -3 and GF α -3 gene expression in goldfish retina and brain was investigated by Northern blot analysis and S1 nuclease protection experiments. Both genes are expressed in retina and in brain (Figs. 4–6). This is in contrast to the GF α -2 gene, whose expression was not detected in 5 μ g of poly(A)+ brain RNA (Cauley et al., 1989). In addition, GF α -3 gene expression results in synthesis of multiple RNAs most likely generated by alternative use of polyadenylation signal sequences (Fig. 5).

In situ hybridization was used to determine which cells in the goldfish retina express the GF α -3 and GF α -3 genes and to compare this expression to that seen for the GF α -2 gene. All 3 genes are expressed in the ganglion cell and inner nuclear layer of the goldfish retina (Fig. 7). However, unlike GF α -2 and GF α -3, GF α -3 is expressed at a significantly higher level in the inner nuclear layer than in the ganglion cell layer (Fig. 7). Hybridization of these probes to cells of the inner nuclear layer is not due to displaced ganglion cells, as only a few percent of ganglion cells are displaced in the goldfish retina (Hitchcock and Easter, 1986; Tumosa and Stell, 1986). Consistent with these results, Keyser et al. (1988) and Sargent et al. (1989) report nAChR-like immunoreactivity in the inner nuclear layer and ganglion cell layer of chick and frog retina, respectively.

For each probe, hybridization in the retinal ganglion cell layer is heterogeneous. Some ganglion cells (established by fluorescent backfilling) express the nAChR genes at relatively high levels, while others express these genes at low or undetectable levels. Whether this reflects a functional difference between ganglion cells is not clear. Our observations are consistent with previous reports that nonganglion cell neuronal somata in the ganglion cell layer are infrequent occurrences in the goldfish retina (Hitchcock and Easter, 1986; Tumosa and Stell, 1986).

The retina's inner nuclear layer is comprised primarily of amacrine, horizontal and bipolar neurons (Dowling, 1987). α -BTX binding sites are reported to be expressed by bipolar cells in the turtle retina (James and Klein, 1985) and by amacrine, bipolar, and ganglion cells in the goldfish retina (Schwartz et al., 1980; Zucker and Yazulla, 1982; Henley et al., 1986a). Most of these sites appear to be extrasynaptic (Zucker and Yazulla, 1982). The cholinergic amacrine cell appears to be the only cholinergic neuron in the retina (Masland and Mills, 1979; Tumosa and Stell, 1986). Though electron microscopy studies suggest that cholinergic amacrine cells synapse only upon ganglion cells (Famiglietti, 1983), a more recent study reports synapses between cholinergic amacrine cells (Millar and Morgan, 1987). Therefore, the expression of nAChRs genes by cells of the inner nuclear layer may reflect the synthesis of (1) extrasynaptic receptors on amacrine, horizontal, and/or bipolar cells; (2) presynaptic receptors; or (3) receptors synthesized by cells of the inner nuclear layer that are postsynaptic to cholinergic amacrine cell input. GF α -2 shows preferential hybridization

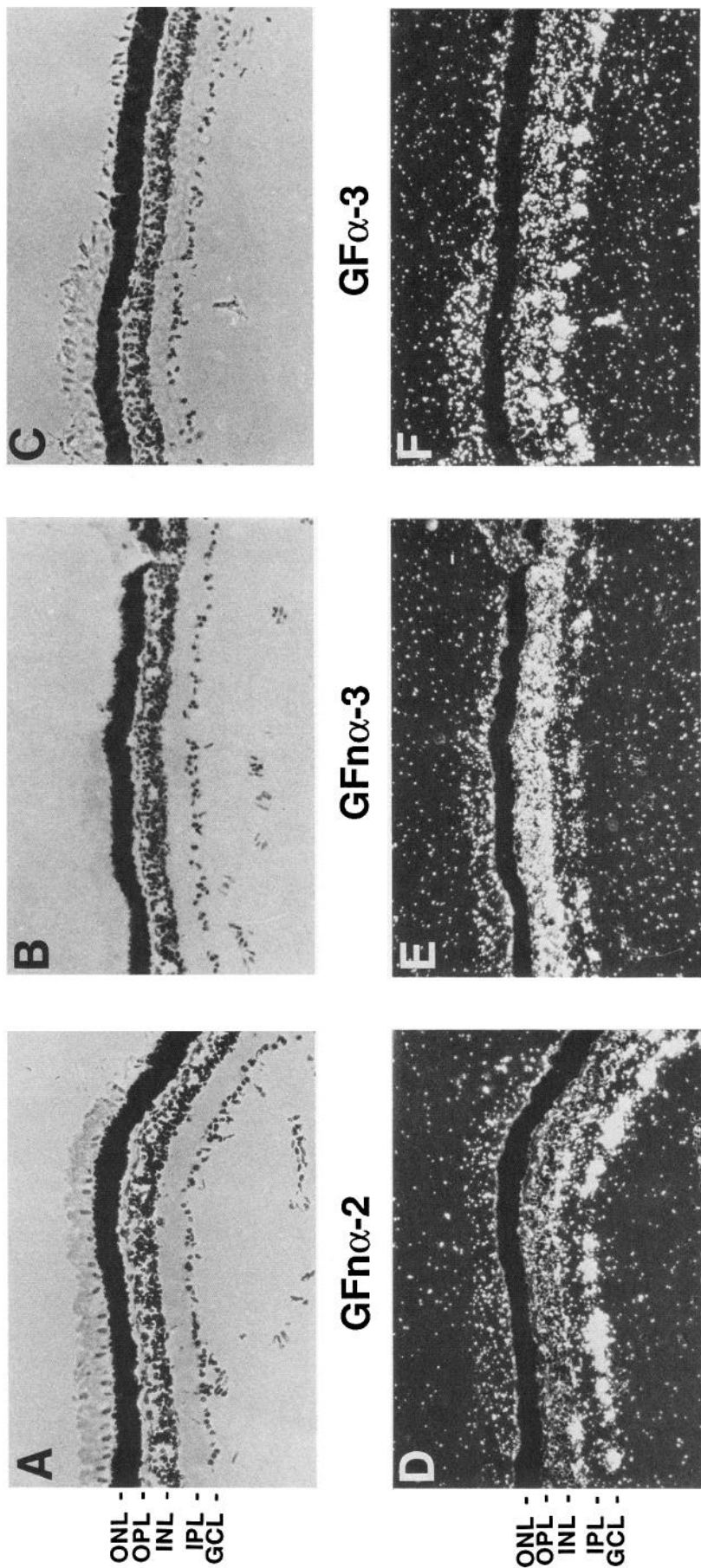
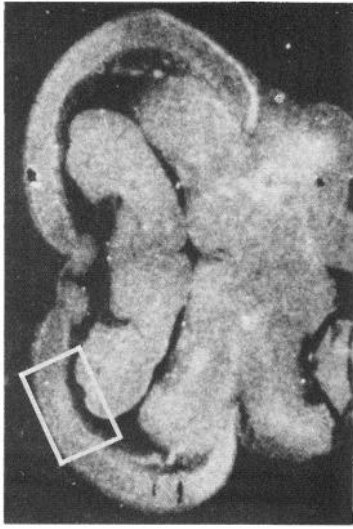
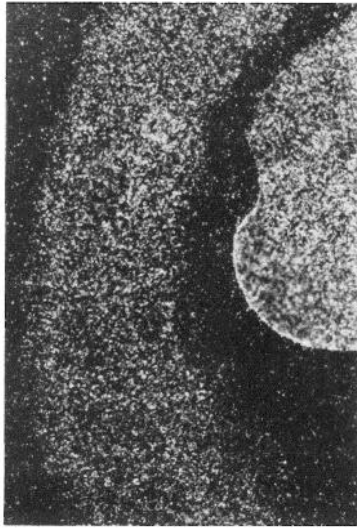


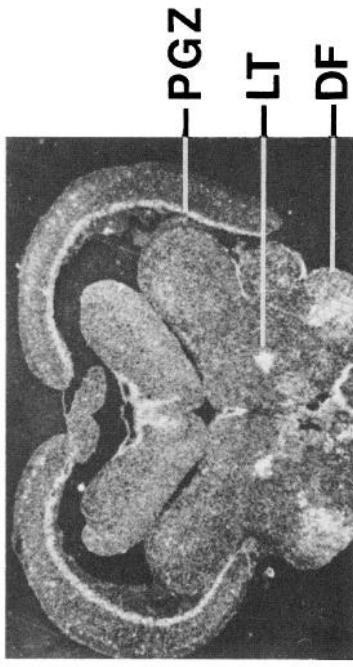
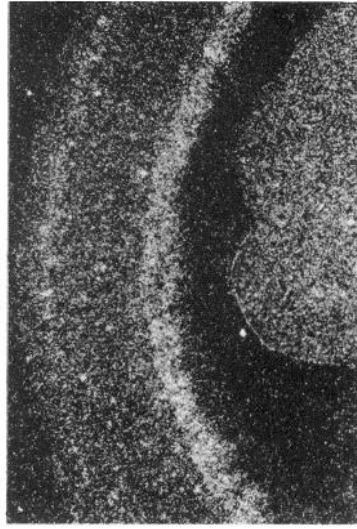
Figure 7. nAChR gene expression in goldfish retina. *In situ* hybridizations of GFn α -2, GFn α -3 and GF α -3 to sections of goldfish retina. Goldfish retinal sections were hybridized with ³⁵S-labeled RNA corresponding to GFn α -2, GFn α -3 or GF α -3 in the antisense orientation. A, B, and C are brightfield photographs of hematoxylin and eosin stained sections, while D, E, and F are the same sections photographed with darkfield illumination, 20X objective. ONL, outer nuclear layer; OPL, outer plexiform layer; INL, inner nuclear layer; IPL, inner plexiform layer; GCL, ganglion cell layer.



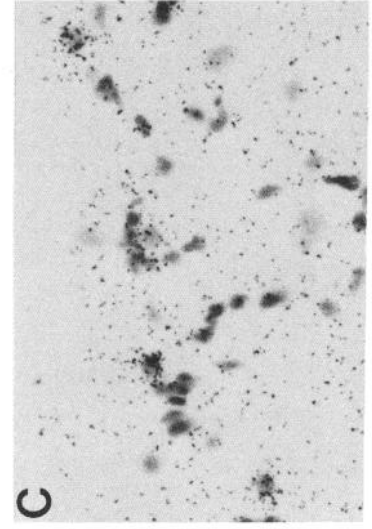
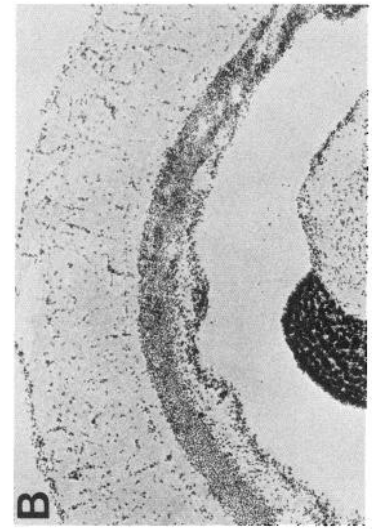
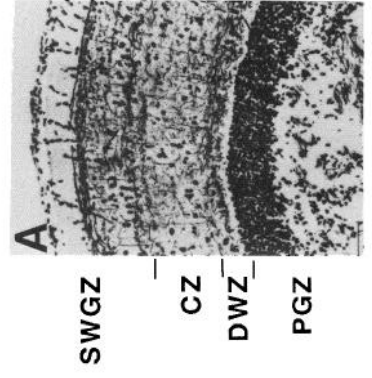
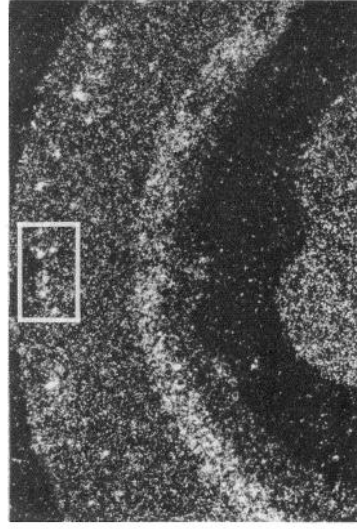
GFn α -2



GFn α -3



GF α -3



along the inner margin of the inner nuclear layer, where amacrine cells reside (Dowling, 1987), and so might be more amacrine cell-specific than GF α -3, which shows hybridization throughout the inner nuclear layer (Fig. 7, D, E). These *in situ* data establish that the goldfish retina expresses multiple members of the nAChR gene family and suggest that the vertebrate retina utilizes more than one type of nicotinic cholinergic synapse.

The retinotectal synapse of lower vertebrates is one of the most approachable synapses of the vertebrate CNS (Oswald and Freeman, 1980). nAChRs play a role, albeit yet unclear, in retinotectal synapse function (Schmidt and Freeman, 1980; Langdon and Freeman, 1987). A nAChR-like molecule is synthesized by retinal ganglion cells and transported to the optic tectum in goldfish (Henley et al., 1986a). Pharmacological studies support the notion that the principal neurotransmitter of the retinotectal synapse is an excitatory amino acid (Langdon and Freeman, 1986). The optic neuropil of the tectum, however, receives a cholinergic input from a tegmental visual nucleus, the nucleus isthmi (Ricciuti and Gruberg, 1985). The demonstration of nAChRs on ganglion cell afferents has led to the proposal that ACh release by nucleus isthmi inputs somehow regulates glutamate release from optic axon terminals (Sargent et al., 1989). Such appears to be the role of ACh in the nigrastratial pathway, where dopamine release from striatal terminals can be modulated by presynaptic nAChRs (Giorguieff-Chesselet et al., 1979; Clark and Pert, 1985). To further elucidate the type and localization of nAChRs in the optic tectum, we performed *in situ* hybridization studies in optic tectum with the 3 cDNA clones GF α -2, GF α -3, and GF α -3. These experiments show relatively high levels of expression of the GF α -3 and GF α -3 genes in optic tectum (Fig. 8), while tectal GF α -2 gene expression was not detected. Both GF α -3 and GF α -3 probes show hybridization over cells of layer 3 of the PVZ, and cells scattered throughout the more superficial tectal layers (Fig. 8; Northcutt, 1983).

The identification of cells in the optic tectum expressing nAChR genes shows for the first time that tectal cells have the potential to synthesize nAChRs. Choline acetyltransferase (ChAT) staining in tectum reveals a single population of intrinsic tectal neurons that are cholinergic. These are a subpopulation of the abundant type XIV neurons of the PVZ (Tumosa et al., 1986). These neurons send apical dendrites into the more superficial tectal layers, where optic nerve inputs are found (Ross and Godfrey, 1986; Tumosa et al., 1986). However, the majority of tectal ChAT activity seems to come from tectal inputs originating from the nucleus isthmi (Ricciuti and Gruberg, 1985). It therefore seems likely that nAChRs expressed by cells of the PVZ and more superficial layers (represented by clones GF α -3 and GF α -3) respond to cholinergic inputs from one or both

of these sources. These data indicate that putative nAChRs in the optic tectum result from gene expression of cells both extrinsic (retinal ganglion cell; Henley et al., 1986a) and intrinsic to this area of the visual forebrain.

In conclusion, we have presented the isolation and characterization of 2 members of the nAChR gene family, expressed in goldfish retina and tectum. GF α -3 represents a new gene, encoding a nAChR structural subunit. GF α -3 is highly homologous to the previously identified GF α -2 and rat β -3 genes. In spite of their sequence similarity, the pattern of expression of the GF α -2 and GF α -3 genes in retina and brain is quite different, indicating that they participate in different receptor systems. We have also characterized the expression of a partial cDNA clone, GF α -3, encoding an agonist binding subunit likely to represent the goldfish homolog of the rat and chicken α -3 genes. *In situ* hybridization with these clones evidences the expression of multiple nAChR genes in retina and tectum.

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Figure 8. nAChR gene expression in goldfish brain. *In situ* hybridizations of GF α -2, GF α -3 and GF α -3 to sections of goldfish brain. Coronal sections cut through the optic tectal lobes were hybridized with ³⁵S-labeled RNA corresponding to GF α -2, GF α -3 or GF α -3 in the antisense orientation. Below each coronal section is a 10 \times magnification of optic tectum from a region corresponding to the boxed area of the GF α -2 section. All 6 figures are darkfield illumination. Areas showing positive hybridization for GF α -3 and GF α -3 include the periventricular gray zone (PGZ) and scattered cells of more superficial tectal layers, the vicinity of the nucleus lateralis thalami (LT), and the nucleus diffusus (DF; Braford and Northcutt, 1983). A, lower left, illustrates goldfish tectal anatomy. SWGZ, superficial white and grey zone; CZ, central zone; DWZ, deep white zone; PGZ, periventricular grey zone (Northcutt, 1983). B, lower center, GF α -3 probed tectal section, stained with hematoxylin and eosin, 10 \times magnification and brightfield illumination. C, lower right, GF α -3 hybridizing cells in superficial layer of optic tectum at 40 \times magnification. This region corresponds to the boxed area of the GF α -3 10 \times magnification photograph (directly above) and illustrates GF α -3 gene expression by cells of the tectal superficial white and grey zone.

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