ABSTRACT

17,21-Dimethyl-19-nor-preg-4,9-diene-3,20-dione (promegestone) was used to characterize the mechanism of inhibition of nicotinic acetylcholine (ACh) receptors (AChR) by progestin steroids. Promegestone reversibly inhibited ACh-induced currents of *Torpedo* AChRs expressed in *Xenopus* oocytes. Between 1–30 μM promegestone produced a concentration-dependent enhancement of the equilibrium binding affinity of [3H]ACh to *Torpedo* AChR-rich membranes. For AChRs in the presence of agonist (desensitized state) promegestone was a more potent inhibitor of the binding of the noncompetitive antagonist [3H]phencyclidine (IC50 = 9 μM) than of [3H]histidionicotinocin (IC50 ~100 μM). To identify AChR domains in contact with the steroid, AChR-rich membranes equilibrated with [3H]promegestone were irradiated at 312 nm, and 3H-labeled amino acids were identified by amino-terminal sequencing of fragments isolated from subunit proteolytic digests. Within AChR α-subunit, 70% of 3H was covalently incorporated in a 10-kDa fragment beginning at Asn-339 and containing the M4 membrane spanning segment, and 30% was in a 20-kDa fragment beginning at Ser-173 and containing the M1–M3 segments. Fragments containing the M2 channel domains as well as the M4 segments were isolated from proteolytic digests of AChR subunits and subjected to amino-terminal sequence analysis. No evidence of [3H]promegestone incorporation was detected in any of the M2 segments. The amino acids in the M4 segments labeled by [3H]promegestone were among those previously shown to be in contact with the lipid bilayer (Blanton and Cohen, 1994). These results indicate that the steroid promegestone is an AChR noncompetitive antagonist that may alter AChR function by interactions at the lipid-protein interface.

Steroid hormones, including endogenously occurring metabolites of progesterone, testosterone, and deoxycorticosterone, as well as synthetic derivatives, act as allosteric modulators of the nicotinic acetylcholine (ACh) receptor (AChR) family of ligand-gated ion channels (reviewed in Franks and Lieb, 1994; MacDonald and Olsen, 1994; Lambert et al., 1995). Progesterone is a weak allosteric potentiator of type A γ-aminobutyric acid (GABA_A) receptors (Wu et al., 1990), whereas endogenous and synthetic 3α-hydroxy derivatives act at submicromolar concentrations (Harrison et al., 1987; Gee et al., 1995). In contrast, at micromolar concentrations progesterone and its derivatives inhibit ACh-activated responses of both neuronal and muscle-type AChRs (Gillo and Lass, 1984; Valera et al., 1992; Ke and Lukas, 1996; Bullock et al., 1997) as well as glycine receptor-activated currents in spinal cord neurons (Wu et al., 1990). For GABA_A receptors electrophysiological studies show that potentiation by steroids is not associated with changes in channel conductance but with an increase in open channel probability at low agonist concentrations and an alteration of the kinetics of desensitization at high agonist concentrations (Twyman and MacDonald, 1992; Lambert et al., 1996; Zhu and Vicini, 1997). For muscle AChR, single-channel analyses of the acute effects of hydrocortisone and corticosterone indicate a dose-dependent decrease in the mean channel open time.

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ABBREVIATIONS: ACh, acetylcholine; AChR, nicotinic acetylcholine receptor; Promegestone, 17,21-dimethyl-19-nor-preg-4,9-diene-3,20-dione; 1-AP, 1-azidopyrene; PAGE, polyacrylamide gel electrophoresis; HPLC, high-performance liquid chromatography; NCA, noncompetitive antagonist; HTX, d,3-hydroxydicocotinocin; [125I]TID, 3-(trifluoromethyl)-3-[125I]iodophenyl)diazirine; EKC, endoproteinase Lys-C; PCP, phenycyclidine; PTH, phenylthiohydantoin; TPS, *Torpedo* physiological saline (250 mM NaCl, 3 mM CaCl2, 2 mM MgCl2, 5 mM sodium phosphate, pH 7.0); T, total acrylamide concentration; C, bis-acrylamide cross-linker concentration relative to total acrylamide concentration; GABA AChR, γ-aminobutyric acid; αV8–20, 20-kDa V8 protease fragment of the AChR α-subunit; αV8–10, 10-kDa V8 protease fragment of the α-subunit.
Materials. \([^{3}H]\)Promegestone (86.7 Ci/mmol; Fig. 1), nonradioactive progesterone, and \([^{3}H]\)phenacyclidine (\([^{3}H]\)PCP; 52 Ci/mmol) were obtained from New England Nuclear (Boston, MA). \([^{3}H]\)Tetra- 
cine (36 Ci/mmol) and \([^{3}H]\)histrionicotin (\([^{3}H]\)HTX; 60 Ci/mmol) were prepared at New England Nuclear by the tritium gas catalytic 
reduction of 3,5 dibromotetracaine and \(dl\)-ethyl ketone allowing a covalent bond to be formed 
between the steroid and an adjacent polypeptide (Benisek, 1977). Photoincorporation of \([^{3}H]\)promegestone has been 
used to identify several different progesterone receptors (Sadler and Maller, 1982; Stromstedt et al., 1990). The Torpedo 
electric organ is an extremely rich source of muscle-type 
AChR containing upwards of 100 mg of receptor protein/kg 
electroplaque tissue, thus facilitating the use of protein 
chemistry techniques to identify sites of photoincorporation 
of competitive and noncompetitive antagonists (reviewed 
in Hucho et al., 1996).

We report here that promegestone reversibly inhibits ACh-
evoked currents of Torpedo AChR expressed in Xenopus oo-
cytes and that it interacts with both the resting and desen-
sitized states of the AChR, inhibiting the specific binding of 
radiolabeled noncompetitive antagonists to Torpedo AChR-
rich membranes in the absence and in the presence of car-
bamylycholine, respectively. \([^{3}H]\)Promegestone photoincorpo-
rates into each of the AChR subunits with the extent of incorporation insensitive to AChR conformational state. No 
evidence of \([^{3}H]\)promegestone incorporation was detected in 
any of the channel lining M2 segments, but labeled residues 
were identified in the M4 hydrophobic segments at positions 
shown previously to be at the AChR-lipid interface. These 
results support the hypothesis that inhibition of AChRs by 
progesterone steroids results from direct interactions at the 
AChR-lipid interface.
sites) were equilibrated with radioligand and appropriate concentrations of modulatory drug for 2–3 h at room temperature ([3H]HTX, 10 nM) or at 4°C ([3H]PCP, 6 nM; [3H]tetracaine, 2 nM) before centrifugation. Nonspecific binding of [3H]ACh was measured in the presence of 0.1 mM carbamylcholine, that of [3H]HTX and [3H]PCP in the presence of 0.2 mM meprobamid, and that of [3H]tetracaine in the presence of 0.2 mM tetracaine.

Photolabeling AChR-Rich Membranes with [3H]Promegestone. Membranes in TPS (2 mg of protein/ml) were incubated with [3H]promegestone at a final concentration 80–110 nM in the absence or presence of 0.2 mM carbamylcholine. After a 1-h incubation, suspensions were irradiated for 7 min at a distance of <1 cm with a 312-nm lamp (EB-Spectroline, Spectronics, Westbury, NY). Each sample was then pelleted (15,000 g) and, for analytical labeling, the pellets were then solubilized in sample loading buffer (Laemmli, 1970) and submitted to SDS-polyacrylamide gel electrophoresis (PAGE). For preparative scale labelings (12–15 mg of AChR-rich membranes), the pellets were then resuspended in TPS at 2 mg/ml of protein and 1-AP was added to a final concentration of 350 μM. After a 30-min incubation, membranes were once again irradiated (365 nm for 5 min, at <1 cm; EN-Spectroline) and each sample was pelleted. Samples were then solubilized in electrophoresis sample loading buffer and submitted to preparative scale SDS-PAGE. Labeling with the fluorescent hydrophobic probe 1-AP was used to assist in the initial identification and isolation of AChR subunits and in the subsequent isolation of hydrophobic segments of these subunits (Blanton et al., 1994).

SDS-PAGE. SDS-PAGE was performed as described (Laemmli, 1970) with either 1.0-mm (analytical) or 1.5-mm thick (preparative scale) 8% T (total acrylamide concentration), 4% bis-acrylamide cross-linker concentration relative to total acrylamide concentration (C). For analytical gels, polypeptides were visualized by staining with Coomassie blue R-250 (0.25% w/v in 45% methanol and 10% acetic acid) and destaining in 25% methanol and 10% acetic acid. The gels were then impregnated with fluid (Amplify; Amersham, Arlington Heights, IL) for 20 min with rapid shaking, dried, and exposed at −80°C to X-OMAT LS film (Eastman Kodak Co., Rochester, NY) for various times (4–16 weeks). For preparative scale gels, polypeptides incorporating 1-AP were visualized from their associated fluorescence when the gels were illuminated at 365 nm on a UV-light box. Bands corresponding to AChR subunits were excised either for polypeptide isolation or in the case of the AChR α-subunit for proteolytic digestion once the gel piece was transferred to the well of a 15% mapping gel (Cleveland et al., 1977; Pedersen et al., 1986). Merging maps were composed of a 4.5% T, 2.6% C stacking gel and a 15% T, 2.6% C separating gel. The α-subunit gel piece was overlaid with 350 μl of buffer (5% sucrose, 125 mM Tris-HCl, 0.1% SDS, pH 6.8) containing 250 μg of Staphylococcus aureus V8 protease. Electrophoresis was carried out overnight at 15 mA constant current. 1-AP/[3H]promegestone-labeled proteolytic fragments were isolated from the excised gel pieces by a passive elution protocol as described (Blanton et al., 1998) with a Brownlee Aquapore C4 column (100 × 2.1 mm). Solvent A was 0.08% trifluoroacetic acid in water, and solvent B was 0.05% trifluoroacetic acid in 60% acetonitrile/40% 2-propanol. The elution of [3H]promegestone was monitored by scintillation counting of an aliquot (25 μl) of each 0.5-ml fraction.

Sequence Analysis. Amino-terminal sequence analysis was performed on a ABI model 477A (Applied Biosystems, Foster City, CA) protein sequencer with gas phase cycles. Pooled HPLC samples were dried by vacuum centrifugation, resuspended in a small volume of 0.05% SDS (−20 μl), and immobilized on chemically modified glass fiber disks (Beckman Instruments). Approximately 30% of the released phenylthiohydantoin (PTH)-amino acids were separated by an on-line model 120A PTH-amino acid analyzer, and −60% was collected for determination of released [3H] by scintillation counting of each sample for three 5-min intervals. Initial yield (Io) and repetitive yield (R) were calculated by nonlinear least-squares regression of the observed release (M) for each cycle (n): M = Io R^n (PTH-derivatives of Ser, Thr, Cys, and His were omitted from the fit).

Results

To determine whether promegestone was an antagonist of Torpedo AChRs, we tested it as an inhibitor of AChRs expressed in Xenopus oocytes. When coapplied for 5 s with ACh, promegestone produced a dose-dependent and reversible inhibition of the ACh-induced currents (Fig. 2A). In the absence of promegestone, the ACh concentration-response relation was characterized by K_{eq} = 20 μM and a Hill coefficient of 1.5 (data not shown). When applied in the presence of 3 μM ACh, 30 μM promegestone produced ~50% reduction of the peak current response, whereas that same concentration resulted in a 90% reduction of the current seen after 5 s exposure. After a 1-min wash after exposure to 30 μM promegestone, there was a 50% recovery of the ACh peak current and a full recovery within 5 min. The potency of promegestone as well as its kinetics of inhibition were similar to that of progesterone (Fig. 2B). Although the time-dependent decrease of the ACh-response could indicate that both steroids increase the rate of agonist-dependent desensitization, it was also possible that neither steroid equilibrated with its binding site during the 5 s exposure. To determine whether kinetic factors were important determinants of the extent of inhibition seen for these drugs, ACh responses were determined after preincubation with progesterone. When oocytes were perfused with 1 μM progesterone for 5 min, there was a dramatic, time-dependent increase in progesterone potency, with 50% inhibition of the peak current seen after a 60-s preincubation (Fig. 2C). After 5 min, the peak current was reduced by 65%, and after a 2.5-min wash, there was a 40% recovery of the peak response (not shown). Although further experimentation is required to analyze the time and concentration dependence of the observed
inhibition, these first experiments established that promegestone was in fact an AChR antagonist similar in potency and action to progesterone.

**Effects of Promegestone on \[^3\text{H}\]ACh and \[^3\text{H}\]-Noncompetitive Antagonist Binding to Torpedo Membranes.** Equilibrium binding of \[^3\text{H}\]ACh was assayed at a concentration sufficient to occupy ~20% of sites. At this subsaturating concentration, the assay is sensitive to drugs that either increase or decrease ACh binding affinity (Boyd and Cohen, 1984). Promegestone at concentrations up to 100 \(\mu\)M did not inhibit the equilibrium binding of \[^3\text{H}\]ACh, and, in fact, at concentrations between 1 and 30 \(\mu\)M it increased binding by 50% (Fig. 3A). In comparison, proadifen, an aromatic amine noncompetitive antagonist known to stabilize the desensitized state of the AChR (Boyd and Cohen, 1984), increased \[^3\text{H}\]ACh binding by 300%.

Promegestone was also tested as an inhibitor of the equilibrium binding of radiolabeled, positively charged AChR noncompetitive antagonists (NCAs) (Fig. 3B). \[^3\text{H}\]HTX is bound at equilibrium with high affinity to a single site in the AChR in the absence (resting state, \(K_{eq} = 1 \mu\)M) or presence of agonist (desensitized state, \(K_{eq} = 0.3 \mu\)M) (Heidmann et al., 1983). \[^3\text{H}\]Phencyclidine (\[^3\text{H}\]PCP) binds with high affinity (\(K_{eq} = 1 \mu\)M) to a single site per AChR in the desensitized state (Heidmann et al., 1983). \[^3\text{H}\]Tetracaine binds with high affinity (\(K_{eq} = 0.3 \mu\)M) in the absence of agonist to...
a single site per AChR and it is bound only weakly ($K_a = 30 \mu M$) in the desensitized state (Cohen et al., 1985). Based on photoaffinity labeling, the [3H]tetracaine binding site has been localized within M2 ion channel domain (Gallagher and Cohen, 1994; Gallagher, 1996). In the presence of agonist, promegestone was a potent inhibitor of [3H]PCP binding. High concentrations inhibited specific binding by $>95\%$, and the concentration dependence of inhibition could be modeled as competitive with IC$_{50} = 9 \mu M$ (Fig. 3B). In contrast, 100 $\mu M$ promegestone did not inhibit [3H]HTX binding in the absence of agonist and produced only partial inhibition in the presence of agonist. For [3H]tetracaine in the absence of agonist, high concentrations of promegestone inhibited binding by at least 80% with an IC$_{50}$ of 75 $\mu M$.

**Photoincorporation of [3H]Promegestone in the AChR.** Experiments were first designed to characterize the general pattern of [3H]promegestone photoincorporation into Torpedo AChR-rich membranes, as well as to test the sensitivity of the photoincorporation to cholinergic ligands. Membranes (2 mg/ml) were equilibrated with 80 nM [3H]promegestone in the absence and in the presence of 200 $\mu M$ carbamylcholine. This promegestone concentration provided a sufficient level of radioactivity to detect AChR subunit labeling even though only a small amount of the total [3H] ($\sim 2\%$) was incorporated. After irradiation, membrane suspensions were pelleted and resuspended in electrophoresis sample buffer, and the pattern of incorporation was monitored by SDS-PAGE followed by fluorography. As is evident in the fluorograph of an 8% polyacrylamide gel (Fig. 4), there was incorporation of [3H]promegestone into each of the AChR subunits. Neither the pattern of incorporation into individual AChR subunits nor the overall labeling pattern was affected by the inclusion of 200 $\mu M$ carbamylcholine (Fig. 4, lane 2). The additional presence of nonradioactive progesterone (1.2 $\mu M$, 12 $\mu M$, and 100 $\mu M$) had no observable effect on the extent of incorporation into any of the AChR subunits either in the presence or absence of agonist (data not shown). Based upon quantification of [3H]incorporation in excised gel slices, $\sim 0.1\%$ of $\alpha$-subunits were labeled with the relative incorporation within subunits: $\alpha/\beta/\gamma/\delta/\epsilon/1.6/1.1/2.1/2.1$ in the absence of agonist. Similar ratios were seen for photolabeling in the presence of agonist as well as from the amount of [3H] present in subunits isolated from preparative scale labelings.

The distribution of [3H]promegestone incorporation within the AChR $\alpha$-subunit was examined by determining the amount of labeling in two large proteolytic fragments generated by limited S. aureus V8 protease digestion on a mapping gel: $\alpha$V8–20 (Ser-173–Glu-338), containing the membrane spanning segments M1–M3, and $\alpha$V8–10 (Asn-339–Gly-439), containing the membrane spanning segment M4 (Pedersen et al., 1986; White and Cohen, 1988). In the fluorograph of an analytical mapping gel all the visible labeling was contained within $\alpha$V8–10. However, scintillation counting of the material contained within these two $\alpha$-subunit fragments, isolated from preparative scale labelings, indicated that $\sim 70\%$ of [3H] cpm was incorporated in $\alpha$V8–10 and 30% was in $\alpha$V8–20. The relative incorporation of [3H]promegestone into $\alpha$V8–10 was similar for labelings carried out in the absence (74%) and in the presence (70%) of 200 $\mu M$ carbamylcholine.

**Identification of the Sites of [3H]Promegestone Incorporation in the M4 Segments of the $\alpha$, $\beta$, and $\gamma$ AChR Subunits.** The M4 segments from AChRs labeled with [3H]promegestone in the presence of 200 $\mu M$ carbamylcholine were isolated from tryptic digests of either the intact subunit ($\beta$, $\gamma$, $\sim 250 \mu g$) or $\alpha$V8–10 ($\sim 125 \mu g$). When the tryptic digest of $\alpha$V8–10 was purified by reverse-phase HPLC, [3H] counts eluted in a peak centered at $\sim 82\%$ solvent B (Fig. 5A) along with the peak of 1-AP fluorescence (data not shown). Amino-terminal sequence analysis (Fig. 6A) of the pool of HPLC fractions 31–35 revealed the presence of a primary sequence beginning at $\alpha$Tyr-401 (initial yield, 129 pmol) present at 15-fold higher level than a secondary sequence that began at $\alpha$Ser-388. In the pattern of [3H] release shown in Fig. 6A, there were 620 cpm released in the first cycle, equivalent to 1.5% of loaded cpm and similar in magnitude to the 1.3% of [3H] cpm washed off the filter by acid treatment before the first cycle of Edman degradation (data not shown). The progressively declining [3H] release seen in the first 4 cycles of Edman degradation was likely to result either from release of peptide poorly adsorbed on the glass.  

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**Fig. 4.** Photoincorporation of [3H]promegestone into AChR-rich membranes in the absence and in the presence of carbamylcholine. AChR-rich membranes were equilibrated with 80 nM [3H]promegestone in the absence (lane 1) or presence (lane 2) of 200 $\mu M$ carbamylcholine and irradiated at 312 nm for 7 min. After photolysis, polypeptides were resolved on a 8% polyacrylamide gel and processed for fluorography (5-week exposure). The bulk of the labeled lipid and free photolysis products were electrophoresed from the gel with the tracking dye. AChR subunits and the Na+/K+ ATPase $\alpha$-subunit ($\alpha_{NK}$) are indicated on the left.
support or chemical instability of some incorporated \(^{3}H\). A stable baseline of \(^{3}H\) release was achieved by cycle 5, and, in addition to the prominent \(^{3}H\) release in cycle 12, there was also clear, but lower level, release in cycles 8 and 18. Comparison of the pattern of release with the corresponding amino acids in the primary sequence indicates that the labeled amino acids include His-408 (0.7 cpm/pmol), Cys-412 (9 cpm/pmol), and Cys-418 (2 cpm/pmol). These same three residues were found to have incorporated \([^{3}H]\)promegestone when the M4 region was isolated from membranes labeled in the absence of agonist (data not shown). Cys-412 is the residue in \(\alpha\)M4 at the lipid interface that is labeled most efficiently by the hydrophobic probes 3-(trifluoromethyl)-3-(m-[\(^{125}I\])iodophenyl)diazirine[\(^{125}I\)](TID) and \([^{3}H]\)diazofluorene; Cys-418 is labeled by both probes, and His-408 is labeled only by \([^{3}H]\)diazofluorene (Blanton and Cohen, 1994; Blanton et al., 1998).

When the tryptic digest of the intact \[^{3}H\]promegestone-labeled \(\gamma\)-subunit was resolved on a tricine SDS-PAGE gel, a band of fluorescence and \(^{3}H\) migrated with an apparent molecular mass of 5 kDa (\(\gamma\)-T-5K), known to contain the \(\beta\)M4 region (Blanton et al., 1998), which was further purified by HPLC (Fig. 5C). Amino-terminal sequence analysis (Fig. 6C) of the pool of fractions 28–32 revealed the presence of a primary sequence (Fig. 6C) beginning at \(\gamma\)Val-446 and ex-

![Fig. 5. Reverse-phase HPLC purification of proteolytic fragments of \[^{3}H\]promegestone-labeled AChR subunits containing M4 and M2 hydrophobic segments. AChR subunits were isolated from AChR-rich membranes (12 mg protein) labeled with \[^{3}H\]promegestone in the presence of carbamylcholine and in the absence (\(\bullet\)) or presence (\(\bigcirc\)) of 60 \(\mu\)M phencyclidine. Proteolytic digests of subunits were purified by SDS-PAGE and reverse-phase HPLC as described under Materials and Methods. A, trypsin digests of \(\alpha\)V8–10 (Asn-339–Gly-437) were purified directly; B, purification of a 10-kDa band (\(\alpha\)-K-10K) isolated by tricine-SDS-PAGE from Endoprotease-Lys C digests of \(\alpha\)V8–20 (Ser-173–Glu-338). Tryptin digests of \(\beta\), \(\gamma\), and \(\delta\)-subunits were fractionated by tricine-SDS-PAGE to isolate from \(\beta\)-subunit 5 kDa (\(\beta\)-T-5K) and 7-kDa (\(\beta\)-T-7K) bands, from \(\gamma\)-subunit a 5-kDa band (\(\gamma\)-T-5K), and from \(\delta\)-subunit a 5 kDa band (\(\delta\)-T-5K). C and D, reversed-phase HPLC purification of \(\beta\)-T-5K and \(\beta\)-T-7K, respectively. E and F, purification of \(\gamma\)-T-5K and \(\delta\)-T-5K respectively.](molpharm.aspetjournals.org)
tending through γM4 (116 pmol) that was present at 10-fold higher level than secondary sequences that began at γLys-218 (amino terminus of γM1, 10 pmol) and at γVal-273 (amino terminus of γM3, 12 pmol). The ³H released in cycles 6 and 8 indicated that [³H]promegestone was incorporated into γCys-451 (2 cpm/pmol) and γTrp-453 (~0.4 cpm/pmol) within γM4. Incorporation into γCys-451 was also evident in the amino-terminal sequence analysis of γT-5K isolated from membranes labeled in the absence of carbamylcholine (data not shown).

Radiochemical Sequence Analysis of M2 Segments of AChR α-, β-, and δ-subunits. Subunit proteolytic fragments beginning at the amino terminus of the M2 segments of AChR α-, β-, and δ-subunits were isolated from AChRs labeled with [³H]promegestone in the presence of carbamylcholine. For α-subunit, an EKC digest of αV8–20 (~280 µg) was fractionated by tricine SDS-PAGE, and an ~10- kDa fragment (α-K-10K), previously shown to contain the M2-M3 region (Pedersen et al., 1992), was isolated from the gel (see Materials and Methods). When the material eluted from the α-K-10K fragment was further purified by reverse-phase HPLC (Fig. 5B), the majority of ³H counts eluted in a peak centered at 84% solvent B. HPLC fractions 32–35 were pooled and sequenced (Fig. 7A). The primary sequence, which began at αMet-243, the amino terminus of the M2 region (85 pmol), was present at 10-fold higher level than a secondary sequence beginning at the amino terminus of αM3 (αTyr-277, 7 pmol). No significant ³H release above background was observed in any of the 21 sequencing cycles.

To identify potential sites of [³H]promegestone photo incorporation in the M2 regions of β- and δ-subunits, trypsin digests of the subunits (~250 µg) were first fractionated by tricine SDS-PAGE. For the β-subunit, a 7-kDa fragment (β-T-7K), known to contain both the M2 and M3 region, was identified as a band of weak fluorescence between two strongly fluorescent bands of 10 and 5.5 kDa when the tricine SDS-PAGE gel was illuminated at 365 nm (data not shown). The material eluted from the β-T-7K band was further purified by reverse-phase HPLC (Fig. 5D), with the majority of ³H counts eluting in a peak centered at 80% solvent B. Sequence analysis of the pool of HPLC fractions 30 to 34 (Fig. 7B) revealed the presence of a peptide beginning at β-Met-249, the amino terminus of the βM2 (86 pmol), along with secondary sequences beginning at the amino termini of βM1 (βLys-216, 15 pmol) and βM4 (βAsp-427, 10 pmol). No ³H release above background was seen in any of the 21 sequencing cycles. Similarly, no [³H]promegestone incorporation was evident in the ³H release profile obtained upon sequencing the β-T-7K fragment labeled in the absence of agonist (data not shown).

When the trypsin digest of [³H]promegestone-labeled δ-subunit was resolved by tricine SDS-PAGE, a 5-kDa fragment (δ-T-5K), known to contain the M2–M3 region, was identified by the use of prestationed molecular weight standards and by the fluorescence associated with 1-azidopyrene incorporation into M3. When the material eluted from the δ-T-5K band was further purified by reverse-phase HPLC (Fig. 5F), the majority of ³H counts eluted in a peak centered at 82% solvent B. When HPLC fractions 30 to 33 were pooled and sequenced (Fig. 7C), a primary sequence was identified beginning at δMet-257, the amino terminus of the δM2 (90 pmol), along with a secondary sequence beginning at the amino terminus of δM4 (δAsn-447, 7 pmol). No clear ³H release above background was detected.
Discussion

We have shown that the synthetic progestin, promegestone, is a NCA of the Torpedo AChR. Promegestone reversibly inhibits ACh-elicited currents for Torpedo AChRs expressed in Xenopus oocytes with the same potency as progesterone. Because promegestone concentrations up to 100 μM increase the [³H]ACh equilibrium binding affinity to AChR-rich membranes, promegestone is a desensitizing NCA. Interestingly, although it is only a weak inhibitor (IC₅₀ = 9 μM) of [³H]HTX binding to AChRs in the desensitized state, it is a potent inhibitor (IC₅₀ = 9 μM) of [³H]PCP binding. Because binding of HTX and PCP appear formally competitive (Heidmann et al., 1983; White et al., 1991), this result appears at first surprising. However, studies with TID, an uncharged, photoactivatable NCA, provide clear evidence that the binding sites for PCP and HTX can be differentiated (White et al., 1991; White and Cohen, 1992): TID is a potent, competitive inhibitor of [³H]PCP binding to AChRs in the desensitized state, whereas it is an allosteric inhibitor of [³H]HTX binding. Although HTX and PCP are presumed to bind within the lumen of the ion channel, their site(s) of high-affinity binding have not been mapped directly. The high-affinity binding site for [³H]tetracaine in the AChR in the resting state has been shown by direct photoaffinity labeling to overlap with the [¹²⁵I]TID site in the M2 ion channel domain (White and Cohen, 1992; Gallagher and Cohen, 1994; Gallagher, 1996). Although promegestone at high concentrations (IC₅₀ = 75 μM) inhibits [³H]tetracaine binding, that inhibition probably occurs because promegestone stabilizes the AChR desensitized state that binds [³H]tetracaine only weakly. Although promegestone clearly can be a potent inhibitor of NCA binding, the results of the radioligand assays provide no clear indication of the nature of the promegestone binding site(s) in the AChR.

When [³H]promegestone was photoincorporated into AChR-rich membranes, its incorporation was readily detected in residues in the M4 segments of the α, β, and γ-subunits that previous work has shown are exposed to lipid (Fig. 8; Blanton and Cohen, 1994; Blanton et al., 1998). In contrast, no incorporation was detected in the sequence analysis of the α, β-, or δ-M2 segments isolated from AChRs labeled in either the absence or presence of agonist. The simplest interpretation of the photolabeling data is that, consistent with its lipophilicity, the steroid promegestone binds to and interacts with the AChR at the lipid-protein interface. The inability of increasing doses of progesterone to affect the photoincorporation of [³H]promegestone, at least at the subunit level, is also consistent with “nonspecific” binding at the lipid-protein interface. Although promegestone interaction at the AChR-lipid protein interface does not meet the classical criteria for a specific drug-receptor binding site, this does not preclude this promegestone-AChR interaction from affecting AChR function. Additional studies are re-
required to determine whether promegestone interactions at the AChR-lipid interface result in the observed inhibition of NCA binding or of ACh-mediated ion currents. Also, additional studies are required to determine whether promegestone is interacting at sites on the AChR surface normally occupied by cholesterol, which is present at 15% (w/w) in the AChR-rich membranes and at an effective concentration of 1 mM. There is strong evidence that cholesterol interacts directly with AChRs and that neutral lipids are required to maintain the AChR in a state responsive to agonist (Rankin et al., 1997 and references therein). Inhibition by promegestone (or progesterone) might occur because it displaces cholesterol from a functionally important site.

Although our studies have found no evidence that \(^{[3H]}\)promegestone binds within the M2 ion channel domain, it remains possible that it binds within the channel but is incapable of photoincorporating into the predominantly aliphatic residues contained within each of the M2 segments. Promegestone photoincorporation proceeds through a "triplet state" biradical, which should readily incorporate into C–H bonds (Benisek, 1977). However, although very limited, the residues that have been shown to react with \(^{[3H]}\)promegestone [Met-759 and Met-909 (human progestin receptor); Met-622 and Cys-754 (rat glucocorticoid receptor) (Stroudmatt et al., 1990); His-408, Cys-412, and Cys-418 (M4); Tyr-441, Cys-447 (βM4); and Cys-451, Trp-453 (M4) AChR, this report] do not include any aliphatic residues. In addition, it is also possible that there is an extracellular binding site for promegestone, but that the efficiency of \(^{[3H]}\)promegestone photoincorporation into this region was too low for us to detect. Finally, it also remains to be determined whether \(^{[3H]}\)promegestone is photoincorporated in the M1 or M3 hydrophobic segments (or in the AChR extracellular domain) because the subunit fragmentation strategies used in this study were chosen specifically to identify possible sites of incorporation in M2 and M4 segments.

By interacting with residues situated at the lipid-protein interface of the AChR, promegestone could allosterically alter the structure of the ion channel, effecting both ion conductance and binding of NCAs. Several recent reports provide support for this conclusion. Mutations at lipid-exposed residues in the M4 segment dramatically affect open channel lifetimes (Bouza et al., 1994, 1998; Lee et al., 1994; Lasalade et al., 1996), and a mutation within the M2 ion channel domain that increases channel lifetime also increases hydrocortisone potency (Bouza and Barrantes, 1996). Finally, progesterone inhibits AChR activity but potentiates GABA\(_{A}\) receptor currents in the same concentration range (EC\(_{50}\) = 26 μM, Wu et al., 1990). Given the emerging evidence of structural homology between these two receptors (reviewed in Sigel and Buhr, 1997), this raises the possibility that steroids may differentially modulate the activities of these two receptors (as well as other members of the AChR family) by interacting with residues at a common site, potentially at the lipid-protein interface. On the other hand the ACh and GABA\(_{A}\) receptors have different steroid structure-activity relationships (Wu et al., 1990). Although these differences may simply reflect the different modulatory affects progesterone and other steroids have on these two receptors, it may also indicate separate steroid binding domains. In this respect, future studies will be aimed at identifying the site(s) of \(^{[3H]}\)promegestone incorporation in GABA\(_{A}\) receptor subunits.

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