Roles for N-terminal Extracellular Domains of Nicotinic Acetylcholine Receptor (nAChR) β3 Subunits in Enhanced Functional Expression of Mouse α6β2β3- and α6β4β3-nAChRs*

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Background: Naturally expressed mouse (m) α6*-nAChRs have negligible functional expression in vitro. Functional heterologous expression of naturally expressed mouse α6*-nicotinic acetylcholine receptors (mα6*-nAChRs; where “*” indicates the presence of additional subunits) has been difficult. Here we expressed and characterized wild-type (WT), gain-of-function, chimeric, or gain-of-function chimeric nAChR subunits, sometimes as hybrid nAChRs containing both human (h) and mouse (m) subunits, in Xenopus oocytes. Hybrid mα6mβ4hβ3- (~5–8-fold) or WT mα6mβ4mβ3-nAChRs (~2-fold) yielded higher function than mα6mβ4-nAChRs. Function was not detected when mα6 and mβ2 subunits were expressed together or in the additional presence of hβ3 or mβ3 subunits. However, function emerged upon expression of mα6mβ2mβ3*v9*-nAChRs containing β3 subunits having gain-of-function V9’S (valine to serine at the 9’-position) mutations in transmembrane domain II and was further elevated 9-fold when hβ3*nAChRs subunits were substituted for mβ2*v9*-subunits. Studies involving WT or gain-of-function chimeric mouse/human β3 subunits narrowed the search for domains that influence functional expression of mα6*-nAChRs. Using hβ3 subunits as templates for site-directed mutagenesis studies, substitution with mβ3 subunit residues in extracellular N-terminal domain loops “C” (Glu221 and Phe223), “E” (Ser144 and Ser148), and “B2-B3” (Gln94 and Glu101) increased function of mα6mβ2*- (~2–3-fold) or mα6mβ4*- (~2–4-fold)-nAChRs. EC50 values for nicotine acting at mα6mβ4*-nAChR were unaffected by β3 subunit residue substitutions in loop C or E. Thus, amino acid residues located in primary (loop C) or complementary (loops B2-B3 and E) interfaces of β3 subunits are some of the molecular impediments for functional expression of mα6mβ2β3- or mα6mβ4β3-nAChRs.

Nicotinic acetylcholine receptors (nAChRs)2 are a diverse set of pentameric, transmembrane, signal-transducing proteins found in the nervous system and elsewhere. Vertebrate nAChR subunits α1–α10, β1–β4, γ, δ, and ε are encoded from a family of distinct genes. α1, β1, δ, and either γ or ε subunits form muscle-type nAChRs, and other nAChR subtypes are formed as heteromers or homomers of the remaining subunits (1). Homotrimers α7-nAChRs and heterotrimers α4β2- or α6β4*-nAChRs (* indicates the known or possible presence of additional subunits) are the dominant subtypes in the central nervous system (CNS) (2). α6β4*-nAChRs do not seem to be abundant in the rodent CNS but are found in rat dorsal root ganglion neurons and in human adrenal chromaffin cells (3, 4). α6*-nAChRs seem to participate in the modulation of dopamine release, locomotion, reward, and reinforcement and have been implicated in schizophrenia and Parkinson disease (5–12).

Beyond the known formation of α6β2- or α6β4-nAChRs (3, 4, 13–15), integration of nAChR α4, β3, or α5 subunits can occur (14–17) to yield more complex α6*-nAChR subtypes. nAChR β3 or α5 subunits have been classified as “accessory” subunits because they do not form functional receptors alone or seem to combine with any other single kind of nAChR α or β subunit in a functional way, but they can participate in trinary complexes containing other, selected α and β subunits (15, 18–22). Integration of nAChR β3 subunits in the accessory

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2The abbreviations used are: nAChR, nicotinic acetylcholine receptor; ACh, acetylcholine; I max, peak current response; h, human; m, mouse; AA, amino acid; TM, transmembrane domain; NTD, N-terminal domain; RC, reverse complement.

28338 JOURNAL OF BIOLOGICAL CHEMISTRY VOLUME 289 • NUMBER 41 • OCTOBER 10, 2014

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position is suggested to be a critical, final step in formation, assembly, and stability of mature α6β3*-nAChRs (6, 23) and is important for function of α6*- and other nAChRs (24–31). A positive role of the β3 subunit, rather than a negative role (27), in the function of α6*-nAChRs has been revealed from knock-out animal studies (6). However, structure-function relationships and pharmacological features of α6*-nAChRs are poorly understood because receptors thought to exist naturally have not been easily recreated in heterologous expression systems (13–15, 20).

There have been some successes in expressing functional α6*-nAChRs using Xenopus oocytes (22) or cell lines when a chimeric nAChR (α6/α3) subunit (composed of the α6 subunit extracellular N-terminal domain fused to an otherwise α3 subunit) was used instead of the wild-type (WT) nAChR α6 subunit (32) or when enhanced GFP-tagged α6- and β2-nAChR subunits were coexpressed in Neuro-2a cells (13). Other strategies have been to use gain-of-function variants of β3 or α5 subunits (typically using subunits mutated to express serine instead of valine at the so-called 9'-position in the subunit channel-lining, second transmembrane domain (TM II); V9'S) to express functional α6*-nAChRs in Xenopus oocytes (15, 27).

We also recently succeeded in producing functional, hybrid α6β3*-nAChRs substituting mouse (m) α6 subunits for human (h) α6 subunits to express functional mα6hβ3*- or mο6hβ2hβ3V9'S-nAChRs (15). This kind of study leveraging innate variations in amino acid (AA) residues between subunits from different species produced valuable information regarding structure and function of invertebrate and vertebrate nAChRs (15, 21, 33, 34).

Here we report that an α6ChR β3 or hβ3V9'S (i.e. hβ3(V273S)) subunits coexpressed in oocytes also expressing mα6 subunits in the presence of mβ4 or mβ2 subunits yielded nAChRs with higher levels of function than those of mα6mβ4mβ3- or mο6mβ2mβ3V9'S-nAChRs. Further studies using chimeric or gain-of-function chimeric mouse/human nAChR β3 subunits and site-directed mutagenesis identified AA residues in the extracellular N-terminal domain (NTD; in so-called loops “β2-β3,” C, and E) of mβ3 subunits that when substituted with corresponding residues from hβ3 subunits alone or in some specific combinations increased the function of mα6mβ2*- and mο6mβ4*-nAChRs. These studies elucidate some of the structural bases dictating roles for nAChR β3 subunits in functional expression of mα6mβ2*- and mο6mβ4*-nAChRs.

### Experimental Procedures

**Bioinformatics and Homology Modeling**—Using several Web-available threading methods, the β1 subunit of the muscle nicotinic acetylcholine receptor of the marbled electric ray (Torpedo marmorata) (2BG9.B; Protein Data Bank code 2BG9 Chain B) (35) was identified as a suitable template for three-dimensional modeling of mβ3 subunits (SWISS-MODEL Protein Modeling Server) (36). The overall stereochemical quality of the final model was assessed by the program PROCHECK (37). The homology model for the nAChR mβ3 subunit was rendered using UCSF Chimera, a program for interactive visualization and analysis of molecular structures. Protein sequences for nAChR β3 subunits of several species or mouse nAChR subunits retrieved from the National Center for Biotechnology Information (NCBI) Entrez Web service were aligned with each other using the Web program ClustalW.

**Chemicals**—All chemicals for electrophysiology were obtained from Sigma. Fresh agonist (acetylcholine (ACh) or nicotine) or antagonist (atropine) stock solutions were made daily or diluted from frozen stock in Ringer’s solution (OR2), which consisted of 92.5 mM NaCl, 2.5 mM KCl, 1 mM CaCl2, 1 mM MgCl2, and 5 mM HEPES, pH 7.5.

**Wild-type nAChR Subunits**—nAChR hβ3, mα6, mβ2, mβ3, and mβ4 subunits were subcloned into the oocyte expression vector pGEMHE as described previously (19, 30).

**nAChR β3 Subunit Chimeras**—Guided by an alignment of nAChR hβ3 and mβ3 subunit protein sequences (see Fig. 1A), chimeric mouse/human β3 subunits were designed and created (see Fig. 1B) as described below. We cared to construct chimeras in a manner that isolated domains and/or structural features in β3 subunits.

**Construction of the mβ3(1–187)/hβ3(182–458) Chimeric Subunit (Sall Site-based Construct)**—Mouse nAChR β3 subunits possess an innate Sall restriction site (see Fig. 1) in the NTD around AA residue Val187. A Sall restriction site (Table 1)
Effects of β3 Subunits on Mouse α6*-nAChR Function

was created in the pGEMHE-β3 construct (i.e. pGEMHE-hβ3(Sall)) by site-directed mutagenesis around AA residue Val161 by using primers P1 (forward) and its reverse complement (RC) (Table 1). Both pGEMHE-β3 and pGEMHE-hβ3(Sall) constructs were digested with Sall and XbaI where the XbaI site is located downstream of the sequence encoding the C-terminal end of the β3 or hβ3 cDNA and is in the multiple cloning site. The pGEMHE-β3(XbaI + Sall) (i.e. mβ3(1–187)) and hβ3(Sall + XbaI) (i.e. hβ3(182–458)) cDNA fragments were gel-purified and ligated, producing a chimeric cDNA construct pGEMHE-β3(187)/hβ3(182–458) (i.e. mβ3(Met3–Val187)/hβ3(Asp182–His458)) (see Fig. 1).

Construction of the mβ3(1–329)/hβ3(324–458) Chimera (BglII Site-based Construct)—Both human and mouse β3 subunits possess an innate BglII restriction site right after the third transmembrane domain (TM III). The BglII site allows cutting through human and mouse β3 cDNA at equivalent and homologous residues (see Fig. 1). Both pGEMHE-β3 and pGEMHE-hβ3 plasmids were double digested with BglII and XbaI. pGEMHE-β3(XbaI + BglII) (i.e. mβ3(1–329)) and hβ3(BglII-XbaI) (i.e. hβ3(324–458)) cDNA fragments were gel-purified and ligated to produce the chimeric construct pGEMHE-β3(1–329)/hβ3(324–458) (i.e. mβ3(Met3–Arg324)/hβ3(Ser324–His458)) (see Fig. 1). This chimera could be considered as a combination of the NTD of mβ3 subunit and the rest of the hβ3 subunit because the AA residues between the 239th residue (presumably its N-terminal end) and the BglII site in the mβ3 subunit are identical to those between the 233rd residue (presumably its N-terminal end) and the BglII site in the hβ3 subunit (see Fig. 1).

Construction of the mβ3(1–375)/hβ3(370–458) Chimera (BglII Site-based Construct)—A BglII restriction site around AA residue Arg375 in pGEMHE-mβ3 (using P2 and its RC; Table 1) and another one around AA residue Lys369 in pGEMHE-hβ3 (using P3 and its RC) were created by site-directed mutagenesis (Table 1). Both pGEMHE-β3(BsiWI) and pGEMHE-hβ3(BsiWI) plasmids were double digested with BsiWI and XbaI. pGEMHE-β3(XbaI + BsiWI) (i.e. mβ3(1–375)) and hβ3(BsiWI + XbaI) (i.e. hβ3(370–458)) cDNA fragments were gel-purified and ligated to produce the chimeric pGEMHE-β3(1–375)/hβ3(370–458) (i.e. mβ3(Met3–Arg375)/hβ3(Gly370–His458)) (see Fig. 1).

Gain-of-function Chimeric nAChR β3 Subunits—TM II 9’ valine-to-serine (V9’S) mutations in pGEMHE-β3(1–329)/hβ3(324–458) and pGEMHE-β3(1–375)/hβ3(370–458) constructs were introduced using primer P4 (Table 1) and its RC to produce pGEMHE-β3(1–329)/hβ3(324–458) and pGEMHE-β3(1–375)/hβ3(370–458) constructs, respectively (Fig. 1). Similarly, TM II 9’S mutations in the pGEMHE-β3(1–187)/hβ3(182–458) constructs were introduced using primer P5 (Table 1) and its RC to produce the pGEMHE-β3(1–187)/hβ3(182–458) V273S construct.

Point Mutants—TM II V9’S, I9’S, or V13’S mutations in hβ3 (V9’S = V273S; I9’S = V277S), mβ3 (V9’S = V279S; V13’S = V283S), or mα6 (I9’S = L280S; V13’S = V284S) subunits were introduced into the pGEMHE background using the QuickChange II site-directed mutagenesis kit (Stratagene, La Jolla, CA) as described previously (15, 38).

Single or double mutations in nAChR β3 subunit (i.e. Q94H, E101D, N107H, Q94H/E101D, S144N/S158V, E221D, and E221D/F223V) were introduced using the QuickChange II site-directed mutagenesis kit using their respective forward (P6, P7, P8, P9, P10, P11, and P12; Table 1) and RC primers. The pGEMHE-mβ3(Q94H/N107H) construct was made by site-directed mutagenesis of the pGEMHE-β3(Q94H) construct using primer P8 and its RC.

TM II 9’ valine-to-serine mutations in plasmids encoding mβ3(Q94H), mβ3(E101D), mβ3(N107H), mβ3(Q94H/E101D), mβ3(Q94H/N107H), mβ3(S144N/S158V), mβ3(E221D), or mβ3(E221D/F223V) subunits were introduced using primer P4 (Table 1) and its RC. Construct integrity and accuracy of all subunits were confirmed by DNA sequencing.

Complementary RNA (cRNA) Preparation—All pGEMHE plasmids were linearized immediately downstream of the 3’-polyadenylation sequence. Nhel was used to linearize hβ3, hβ3V9’S, hβ3V13’S, mα6, mα6Q94H, mα6V279S, mβ2, mβ3V9’S, mβ4, mβ3(1–187)/hβ3(182–458), mβ3(1–329)/hβ3(324–458), mβ3(1–375)/hβ3(370–458), mβ3(1–187)/hβ3(182–458) V273S, mβ3(1–329)V279S/hβ3(324–458), mβ3(1–375)V279S/hβ3(370–458), mβ3(Q94H), mβ3(E101D), mβ3(N107H), mβ3(Q94H/E101D), mβ3(Q94H/N107H), mβ3(S144N/S158V), mβ3(E221D), mβ3(E221D/F223V), mβ3(Q94H)V9’S, mβ3(E101D)V9’S, mβ3(N107H)V9’S, mβ3(Q94H/E101D)V9’S, mβ3(Q94H/N107H)V9’S, mβ3(S144N/S158V)V9’S, mβ3(E221D)V9’S, and mβ3(E221D/F223V)V9’S subunit-encoding plasmids. Capped, full-length cRNAs were prepared using individual reaction components as detailed earlier (19) or using the mMESSAGE mMACHINE® T7 kit (Ambion Inc./Invitrogen) following the manufacturer’s instructions. The integrity and quality of the cRNAs were checked by electrophoresis and UV spectroscopy prior to cRNA injection.

Preparation of cRNA Mixtures for Injection—We planned to introduce identical amounts of cRNA, presumably producing equal amounts of each subunit protein, into oocytes largely due to lack of information about the levels of mRNA for each subunit that composes α6*-nAChRs in neurons or cells. We provisionally assumed that α6 subunits or their mutants in association with β2 or β4 subunits would form complexes having 2:3 and/or 3:2 ratios of the indicated subunits and that oocytes also injected with WT, chimeric, or other forms of β3 subunits would express nAChR with 2:2:1 ratios of α6-β3 subunits. For expression of binary nAChRs (i.e. nAChRs containing two subunits; α + β but not β3), cRNA mixtures were prepared by mixing 1 μl of cRNA for each subunit and an additional micro-liter of RNase-free water (i.e. total volume, 3 μl). Similarly, for expression of trinary nAChRs (i.e. nAChRs containing three subunits; (α + β + β) cRNA mixtures were prepared by mixing 1 μl of cRNA for each subunit. Several preparations of each cRNA mixture were prepared and stored at –80 °C until further use.

cRNA concentrations for each nAChR α and β subunit were adjusted to 150 ng/μl for the first set of experiments (data presented in Table 2 and Fig. 2). As noted above, introduction of 69 nl of cRNAs (from a 3-μl cRNA mixture) into each oocyte would deliver ~3.5 ng of cRNA for each α and β subunit whether binary or trinary nAChRs are expressed. For all other
experiments, concentrations of cRNAs prepared for each nAChR \( \alpha \) and \( \beta \) subunit were adjusted to 500 ng \( \mu l^{-1} \). Injection of 138 nl of cRNA of a 3-\( \mu l \) cRNA mixture into each oocyte would deliver \( \sim \)23 ng of cRNAs for each \( \alpha \) and \( \beta \) subunit whether binary or trinary nAChRs are expressed.

**Fig. 1.** **Construction of nAChR \( \beta_3 \) subunit chimeras.** A, alignment of nAChR h3 and m3 subunit protein sequences. Amino acid sequences of nAChR h3 (accession number NP_000740.1) and m3 subunits (accession number AAL75573.1) retrieved from GenBank\textsuperscript{TM} were aligned using protein BLAST. AA numbering begins at the translation start methionine. Identical residues between human and mouse nAChR (3 subunits are indicated by a dash (-). Putative loop regions (A, B, and C in the primary face and D, E, and F in the complementary face), TM domains (I, II, III, and IV), and TM II 9\textsuperscript{\*2} and 13\textsuperscript{\*2} amino acid residues in human and mouse nAChR \( \beta_3 \) subunits are identified. nAChR m3 subunit residues (Gln\textsuperscript{94}, Glu\textsuperscript{101}, Asn\textsuperscript{107}, Ser\textsuperscript{144}, Ser\textsuperscript{148}, Asp\textsuperscript{221}, and Phe\textsuperscript{223}) given prime attention in mutagenesis studies are underlined and in boldface. An upward arrow (↑) indicates junctions for chimeric subunits and the restriction sites used for construction of chimeric mouse/human \( \beta_3 \) subunits. Colors () below sequences indicate conserved residues. B, schematic diagrams of chimeric nAChR \( \beta_3 \) subunits. Chimeric mouse/human nAChR \( \beta_3 \) subunits with or without V9\textsuperscript{\*2}S mutations in their respective TM II were constructed. The 273rd AA in nAChR h3 subunit or the 279th AA in nAChR m3 subunit is a valine and is noted as the 9\textsuperscript{\*2} AA in TM II. N, N-terminal domain; I, II, III, or IV, respective TM domains; cyto-loop, cytoplasmic loop; C, C terminus. Numbers in brackets are the regions of the indicated subunits that are used for construction of mouse/human \( \beta_3 \) chimeric subunits.
Effects of β3 Subunits on Mouse α6*-nAChR Function

There are limitations in the ability to compare levels of functional nAChR expression even though we injected similar amounts of RNA for all constructs. This is because expression levels assessed as peak current amplitudes are affected by batch-to-batch variation in oocytes, time between cRNA injection and recording, and subunit combination-specific parameters, such as open probability (influenced by gating rate constants and rates and extents of desensitization), single channel conductance, assembly efficiency, and efficiency of receptor trafficking to the cell surface (39). We made no attempt to measure or control for subunit combination-specific effects, but whenever preliminary studies revealed possible differences in peak current amplitudes, findings were further confirmed across different subunit combinations using the same batch of oocytes and the same time between cRNA injection and recording (15, 19, 30, 38). Therefore peak current amplitudes shown for representative traces in some figures, pooled data from limited sets of studies, and mean peak current amplitudes across all studies for a given combination of subunits given in tables or figures sometimes differ. However, when we make statements about results comparing ligand potencies and efficacies across subunit combinations, the observations are clear, significant, and in agreement whether for pooled data or for results from smaller sets of studies (one-way analyses of variance followed by Tukey’s multiple comparison tests).

RESULTS

Previously (15) we have shown that coexpression of WT nAChR α6 and β2 subunits alone or in combination with β3 or β3V9S subunits in oocytes, all from a single species (human or mouse), did not yield consistent and reproducible current responses to nicotinic agonists. However, under similar experimental conditions, we were able to show that coexpression of m6β2 and h3V9S subunits led to expression of functional hybrid m6h3β2β3V9S-nAChRs (15). Also, hybrid m6h3β4-nAChRs were fully functional, although there was no function for h6h4β3- or m6mβ4β3-nAChRs (15). These studies were carried out by injecting ~1–6 ng of cRNAs for each subunit into oocytes. In continuation of our earlier efforts, in this study, we substituted human β3 subunits for mouse β3 subunits. Initially we injected about ~3.5 ng of cRNAs for each nAChR subunit to express hybrid nAChRs, but later we increased amounts injected to ~23 ng for each subunit to emuluate the approach taken by Kuryatov et al. (14) to express functional human α6β4*-nAChRs.

Incorporation of nAChR hβ3, hβ3V9S, or hβ3V13S Subunits Potentiates m6mβ4β3V9S-nAChR Function—Coexpression with WT hβ3 subunits significantly (p < 0.05) potentiated ACh- or nicotine-induced current responses of m6mβ4β3V9S-nAChRs (Fig. 2 and Table 2). Also, coexpression with nAChR hβ3V9S or hβ3V13S subunits increased (p < 0.05) the current responses further (Fig. 2 and Table 2). The increase in agonist sensitivities and in peak current amplitudes indicate that WT hβ3 subunits incorporate into at least some complexes containing m6β6 and mβ4 subunits and these effects are most likely due to higher levels of functional receptor expression. Moreover, whereas not all oocytes expressing m6β6 and mβ4 subunits yield functional...
responses to nicotinic agonists, almost all oocytes expressing nAChR m6, mβ4, and hβ3 subunits produced functional responses, suggesting that nAChR hβ3 subunits facilitate formation of functional, trinary containing three kinds of subunits nAChRs.

Spontaneously Opening m6mβ4hβ3VYR5 or m6mβ4hβ3VYT55 nAChRs Are Sensitive to Blockade by Atropline—Atropline (1 µM) was always co-applied for ACh-based recordings to eliminate muscarinic acetylcholine receptor responses. Because atropline at higher concentrations also can interact with different nAChR subtypes (15, 40, 41), initially as a simple control, we assessed the effects of atropline at different concentrations alone on all receptor combinations studied. Atropline alone did not produce any effect when assessed using oocytes expressing any combination of WT nAChR subunits (data not shown), but it reversibly produced outward currents when applied to oocytes expressing receptors containing β3VYR5 or β3VYT55 subunits. The concentration-dependent effects of atropline were
Effects of β3 Subunits on Mouse α6*-nAChR Function

**Figure 3.** Effects of agonist exposure on current responses in oocytes expressing **mA6β3(1–375)/hβ3(324–458)**-nAChRs. A, current responses to nicotine (mean ± S.E. error bars; nA) to 100 µM nicotine obtained on the 5th day after injection from oocytes (n = 3 – 6) voltage-clamped at −70 mV and expressing **mA6β3(182–458)**- or **mA6β4hβ3 V95S**-nAChRs. Oocytes were injected with the indicated amount (ng) of cRNA for each subunit. B, concentration-response curve for responses to nicotine (ordinate, mean normalized inward current ± S.E. (error bars); abcissa, ligand concentration in log µM) for oocytes expressing **mA6β2/hβ3 V95S-nAChRs. *, p < 0.05.

defined in terms of IC50 values for half-maximal blockade of spontaneous function, which for **mA6β4hβ3 V95S**- and **mA6β4hβ3 V118S**-nAChRs were 16 and 17 µM, respectively (Fig. 2 and Table 2). It is estimated, based on comparisons of atropine-induced outward current peak amplitudes with the sum of those currents plus inward currents induced by fully efficacious concentrations of nicotine or ACh, that more than 4–16% of these receptors are spontaneously open at any one time.

**Function of mA6β2**-*nAChRs Is Potentiated by Coexpression with nAChR mβ3** Subunits and Is Yet Higher upon Coexpression with hβ3** V95S Instead of mβ3** V95S Subunits—Coexpression of hβ3 or hβ3 V95S subunits in oocytes also expressing mA6 and mβ2 subunits did not lead to reproducible current responses to ACh or nicotine whenever they were expressed using ∼3 ng of cRNA for each subunit (data not shown). We decided to inject higher amounts of cRNA for each subunit (similar to the approach taken by Kuryatov et al. (14) to express hα6hβ4- or hα6hβ4hβ3-nAChRs) to see whether that would influence the functional expression of **mA66β2**-*nAChRs. Current responses to nicotine from oocytes expressing **mA66β2mβ3 V95S**-nAChRs increased with injection of increased amounts of cRNA for each subunit (Fig. 3). However, at the largest amount of cRNA for each subunit injected (∼23 ng), there was no functional expression of **mA66β2mβ3**- or **mA66β2hβ3**-nAChRs. Nonetheless, oocytes expressing **mA66β2hβ3 V95S**-nAChRs yielded higher peak current responses (589 ± 121 vs 167 ± 7 nA; ∼9-fold; p < 0.05) than those expressing **mA66β2mβ3 V95S**-nAChRs (Fig. 3). Oocytes expressing **mA66β2hβ3 V95S-nAChRs**, but not **mA66β2mβ3 V95S-nAChRs**, cultured for prolonged times produced some outward reversible currents in response to atropine (data not shown). The EC50 value for nicotine for activation of **mA66β2hβ3 V95S-nAChRs** is 0.08 µM.

**I**nformation of Chimeric Mouse/Human β3 Subunits into Mouse α6β2**- and α6β4**-nAChRs—We extended our studies to work using chimeric mouse/human nAChR β3 subunits to understand the molecular bases for the differential effect of mβ3 and hβ3 subunits on α6*-nAChR function. We first constructed the BglIII site-based nAChR chimeric subunit mβ3(1–329)/hβ3(324–458). We injected ∼23 ng of cRNA for each subunit as we did for expression of **mA6β2(mβ3 V95S or hβ3 V95S)**-nAChRs to express **mA6β4⁺**, **mA6β4+mβ3⁺**, **mA6β4+hβ3⁺**, or **mA6β4mβ3(1–329)/hβ3(324–458)**-nAChRs. Initial assessments indicated that all these nAChRs were functional, but the current responses from oocytes expressing **mA6β4mβ3(1–329)/hβ3(324–458)**-nAChRs were similar to those from oocytes expressing **mA6β4-nAChRs** and lower than those elicited from oocytes expressing **mA6β4hβ3-nAChRs** (see Fig. 4B). Coexpression of this chimeric subunit with mA6 and mβ2 subunits did not produce any detectable functional nAChR. These results prompted us to construct two additional chimeras that either increased or reduced the length of the hβ3 subunit contribution to mouse/human β3 subunit chimeras. This led to construction of chimeric mβ3(1–187)/hβ3(182–458) (Sall restriction site-based) and mβ3(1–375)/hβ3(370–458) (BsiWI restriction site-based) subunits. All three chimeras were assessed in parallel for their effects on mA6β2⁺- or **mA6β4**-*nAChRs.

Coexpression of chimeric mouse/human nAChR subunits (i.e. mβ3(1–187)/hβ3(182–458), mβ3(1–375)/hβ3(370–458), or mβ3(1–375)/hβ3(370–458) with mA6 and mβ2 subunits in oocytes did not result in detectable nAChR function (data not shown). However, these chimeric subunits coexpressed with mA6 and hβ4 subunits yielded minimally functional nAChRs. Results indicated that peak current responses of **mA6β4[mβ3(1–187)/hβ3(182–458)], mA6β4[mβ3(1–329)/hβ3(324–458)], or mA6β4[mβ3(1–375)/hβ3(370–458)]-nAChRs** are similar (p > 0.05) to those of **mA6β4(50 ± 13 nA; 1000 µM nicotine)** or **mA6β4mβ3-nAChRs** (85 ± 15 nA; 100 µM nicotine) but lower (p < 0.05) than those of **mA6β4mβ3-nAChRs** (410 ± 88 nA; 100 µM nicotine) (Fig. 4B).

**I**ncorporation of Gain-of-function Chimeric Mouse/Human nAChR β3 Subunits into Mouse α6β2**- and α6β4**-nAChRs—To evaluate whether the chimeric nAChR mβ3/hβ3 subunits are truly participating in α6*-nAChR formation, we assessed the incorporation of gain-of-function mβ3(1–187)/hβ3(182–458) V95S, mβ3(1–329)V95S/hβ3(324–458), or mβ3(1–375)V95S/hβ3(370–458) subunits into **mA6β2**- and **mA6β4**-nAChRs. Coexpression of these gain-of-function chimeric nAChR subunits with mA6 and mβ2 subunits in oocytes resulted in the production of functional nAChRs (Fig. 4A). Current responses from oocytes expressing chimeric mA6β2*-nAChRs progressively decreased when coexpressed with chi-
meric β3 subunits containing shorter N-terminal segments from the mouse β3 subunit. For example, m6βm2β[β3(1–187)/β3(182–458)V9S]-nAChRs were least responsive to nicotine. This suggested that a combination of mβ3 subunit domains and residues contributes to impeded functional expression of m6βm2β*-nAChRs.

Incorporation of mβ3(1–187)/hβ3(1329)V273S, m6βm4β[β3(1–329)V273S] /hβ3(324–458), or mβ3(1–375)V273S/hβ3(370–458) subunits into m6βm4β-nAChRs yielded functional nAChRs (Fig. 4C). Peak current responses from oocytes expressing m6βm4β[β3(1–329)V273S]/hβ3(324–458)-nAChRs (1505 ± 353 nA) were similar (p > 0.05) to those of m6βm4βm3V273S, or m6βm4hβ3V273S-nAChRs. However, oocytes expressing m6βm4β[β3(1–187)/hβ3(182–458)V273S] (148 ± 13 nA) or m6βm4β[mβ3(1–375)V273S]/hβ3(370–458)-nAChRs (122 ± 33 nA) yielded much lower (p < 0.001) peak current responses than those expressing either m6βm4βm3V273S, or m6βm4hβ3V273S-nAChRs. Although the presence of hβ3 subunit residues from TM III through the large, second cytoplasmic domain to the C terminus seems somehow to quell such an effect, this again suggested that a combination of mβ3 subunit domains and residues contributes to reduced functional expression of m6βm4β*-nAChRs. However, strongest implications were that the extracellular N-terminal domain was involved.

N-terminal AA Residues in the nAChR mβ3 Subunit That Influence the Function of Mouse a6β2*- and a6β4*-nAChRs—Because effects on m6βm2β*- and m6βm4β*-nAChR function were most extreme in chimeras containing extracellular N-terminal domains from the mβ3 subunit, we focused on this region and on residues that differ between hβ3 and mβ3 subunits. For all nAChR subunits, there is a “primary” or (+) face and a “complementary” or (−) face where subunit extracellular N-terminal domains interact, forming a subunit interface. Interface interactions are critical for subunits to form dimers and for dimers to join with a single subunit to close the pentamer assembly. Interfaces involving the primary face of specific α subunits and the complementary face of specific β subunits also are known to contain agonist binding pockets, occupancy of which leads to channel opening and where competitive antagonists also bind to affect function (the α subunit was designated as that providing the primary face because it was initially thought that agonist binding sites resided solely within α subunits). nAChR biologists have identified several loops at turns in β-strands that criss-cross subunit extracellular domains as in a woven basket. So-called loop β2-β3 (named so because the loop is formed at the tip of a turn between β strands β2 and β3) and loops D, E, and F are evident from modeling and structural studies to be on the complementary face of a given subunit, whereas loops A, B, and C are on the primary face. Loops A–F appear to be engaged in ligand recognition. For site-directed mutagenesis studies, we focused on some of the very few residues that differ between hβ3 and mβ3 subunits, AAs Gln116, Glu119, and Asn117 in the β2–β3 loop; AAs Ser148 and Ser149 in putative loop E, and AAs Glu221 and Phe222 in putative loop C, to determine roles in functional expression of m6βm2β*- and m6βm4β*-nAChRs (Fig. 1A). Residues in the nAChR mβ3 subunit were mutated to their counterparts in the nAChR hβ3 subunit alone or in specific combinations (i.e. mβ3(Q94H), mβ3(E101D), mβ3(N107H), mβ3(Q49H/E101D), mβ3(Q49H/N107H), mβ3(S144N/S148V), mβ3(E222D), and mβ3(E222D/F223V) (Fig. 5).
Effects of β3 Subunits on Mouse α6*-nAChR Function

![Figure 5](image)

**FIGURE 5. Effects of nAChR mβ3 subunit amino acid substitutions on the current responses of mα6*-nAChRs.** A and B, current responses (mean ± S.E. error bars) from oocytes (n = 3–6) (voltage-clamped at −70 mV) responding to the application of 100 or 1000 μM nicotine (5-s exposure; ordinate) were measured from mα6mβ2*- (A) or m6mβ4*-nAChRs (B) harboring WT, mutant, or gain-of-function mβ3-, m3(Q94H)-, m3(E101D)-, or m3(S144N/S148V)-nAChR subunits (panel i); WT, mutant, or gain-of-function m6- or m6(S144N/S148V)-nAChR subunits (panel ii); or WT, mutant, or gain-of-function m3- or m3(S144N/S148V)-nAChR subunits (panel iii). Current responses were compared using Student’s t test (two-tailed) or one-way analyses of variance (with Tukey’s post hoc comparison). Groups with different letters (a and b) are significantly (p < 0.05) different. *, p < 0.05; **, p < 0.01; ***, p < 0.001.

mβ2 subunits in oocytes and responding to application of 100 μM nicotine produced peak current responses of 110 ± 25, 68 ± 9, 26 ± 7, 78 ± 10, or 99 ± 12 nA, respectively (Fig. 5A, panel i). The peak current responses of mα6mβ2[m3(Q94H)Y9S]-, mα6mβ2[m3(E101D)Y9S]-, mα6mβ2[m3(N107H)Y9S]-, mα6mβ2[m3(Q94H/E101D)Y9S]-, or mα6mβ2[m3(Q94H/N107H)Y9S]-nAChRs did not differ (p > 0.05) from those of mα6mβ2m3Y9S-nAChRs (73 ± 12 nA).

Oocytes expressing mα6 and mβ4 subunits alone or in the additional presence of m3(Q94H), m3(E101D), m3(N107H), or m3(Q94H/E101D), or m3(Q94H/N107H) subunits produced functional nAChRs (Fig. 5B, panel i). Peak current responses of mα6mβ4mβ3-nAChRs (57 ± 13 versus 113 ± 18 nA) were increased (~2-fold; p < 0.05) as a result of Q94H/N107H double substitution in the nAChR mβ3 subunit. Also, the current responses of mα6mβ4mβ3(Q94H/N107H)-nAChRs were higher (~3-fold; p < 0.05) than those of mα6mβ4-nAChRs (39 ± 7 nA).

AA Substitutions in Loop E of the nAChR mβ3 Subunit Influence the Function of mα6mβ2*- or m6mβ4*-nAChRs—Coexpression of gain-of-function nAChR mβ3(S144N/S148V)Y9S subunits, but not nAChR mβ3(S144N/S148V) subunits, in oocytes with mα6 and mβ2 subunits resulted in production of functional nAChRs. Current responses of mα6mβ2[m3(S144N/S148V)Y9S]-nAChRs to 100 μM nicotine (109 ± 31 nA) were not different (p > 0.05) from those of mα6mβ2m3Y9S-nAChRs (73 ± 12 nA) (Fig. 5Aii). Peak current responses of mα6mβ4mβ3-nAChRs were increased (266 ± 27 versus 85 ± 15 nA; ~2.5-fold; p < 0.05) as a result of the S144N/S148V double mutation in the nAChR mβ3 subunit (Fig. 5Bii). EC₅₀ values for nicotine at mα6mβ4Hβ3-, mα6mβ4mβ3-, and
ma6β4m3β(S144V/S148V)-nAChRs (i.e. 4.5, 6.6, and 10 μM, respectively; Fig. 6 and Table 3) were essentially the same (p > 0.05).

AA Substitutions in Loop C of the nAChR m3 Subunit Influence the Function of ma6mβ2* or ma6β4*-nAChRs—Oocytes expressing ma6mβ2[m3β(E221D)VaVa]- (155 ± 38 nA) or ma6mβ2[m3β(E221D/F223V)VaVa] (193 ± 18 nA)—elicited responses higher (~2–3-fold; p < 0.05) peak currents in response to 100 μM nicotine than those expressing ma6mβ2m3VaVa-nAChRs (73 ± 12 nA; Fig. 5Aiii). However, coexpression of nAChR mβ3(E221D) or mβ3(E221D/F223V) subunits in oocytes with ma6 and m2β2 subunits did not result in expression of functional nAChR. Substitution of nAChR mβ3(E221D) (199 ± 34 nA; ~2-fold) or mβ3(E221D/F223V) (307 ± 32 nA; ~6-fold) subunits for mβ3 subunit increased (p < 0.05) the current responses of ma6mβ3m3β2-nAChRs (85 ± 15 nA (Fig. 5Biii)). However, EC50 values for nicotine at ma6mβ4m3β2- (6.6 μM) or ma6mβ4hβ3 (4.5 μM)-nAChRs were not altered (p > 0.05) when mβ3(E221D) (4 μM) or mβ3(E221D/F223V) (6.5 μM) subunits were substituted for mβ3 subunits (Fig. 6 and Table 3).

Effects of β3 Subunits on Mouse α6*-nAChR Function

AA Substitutions in Loop C of the nAChR m3 Subunit Also Influence Function of ma6(V9S or V13S)m2β2*-nAChRs—Previously, we could not detect functional expression of ma6(L9S)m2β2- or ma6(V13S)m2β2-nAChRs or of ma6L9S/m2β3- or ma6V13S/m2β3-nAChRs in oocytes (38). Upon increasing the amount of cRNA injected for each subunit to ~23 ng, there was emergence of functional ma6L9S or V13S)m2β3-nAChRs, but not ma6L9S or V13S)m2β2-nAChRs, in oocytes. However, nicotine-elicted (100 μM) peak current responses from oocytes expressing ma6V13S)m2β2m3β2-nAChRs were higher (70 ± 18 versus 9 ± 1 nA; ~8-fold; p < 0.05) than those expressing ma6L9S)m2β3m3β2-nAChRs (Fig. 7).

We also assessed whether substitutions of AA residues in loop C of the nAChR m3 subunit would increase the peak current responses of ma6L9S)m2β2*- or ma6V13S)m2β2*-nAChRs. Nicotine-elicted (100 μM) peak current responses from oocytes expressing ma6L9S)m2β3m3β3 (9 ± 1 versus 17 ± 2 nA) or ma6V13S)m2β3m3β3 (70 ± 18 versus 170 ± 28 nA)-nAChRs were increased (p < 0.05) as a result of E221D/F223V substitution in the nAChR m3 subunit. Also, oocytes expressing ma6V13S)m2β2m3β3(E221D/F223V) (162 ± 32 nA) yielded higher peak current (p < 0.05) in response to 100 μM nicotine.

![Figure 6. Effects of nAChR m3β3 subunit amino acid substitutions on nicotine sensitivities of ma6β4*-nAChRs.](image)

### Table 3

Parameters for nicotine action at nAChRs containing ma6 and m3β3 mutant subunits

| nAChR subunit combinations | n | EC50 (95% CI) | nmax ± S.E. | Mean Imax ± S.E. | Imax conc. |
|----------------------------|---|--------------|-------------|-----------------|-----------|
| ma6 + mβ4                  | 6 | 23 (15–37) μM| 0.8 ± 0.13  | 50 ± 13 (1000)| 100       |
| ma6 + mβ4 + mβ3            | 3 | 6.6 (5.1–8.5)μM| 1.1 ± 0.12  | 85 ± 15         | 100       |
| ma6 + mβ4 + mβ3(S144N/S148V)| 5 | 10 (8.2–13)μM| 1.2 ± 0.18  | 266 ± 27 (100)| 100       |
| ma6 + mβ4 + mβ3(E221D)     | 5 | 4 (2.3–7.2)μM| 0.8 ± 0.18  | 199 ± 34 (100)| 100       |
| ma6 + mβ4 + mβ3(E221D/F223V)| 5 | 6.5 (5.1–8.2)μM| 1 ± 0.11    | 307 ± 32 (100)| 100       |

![Figure 7. Effects of nAChR m3β3 subunit loop C amino acid substitutions on functional responsiveness of ma6(V9S or V13S)m2β2*-nAChRs.](image)
Effects of β3 Subunits on Mouse α6*-nAChR Function

than those expressing mα6V13*β2mβ3-nAChRs. These results confirm the previous findings that TM II 13’ valine-to-serine mutations in the mα6 subunit are more capable of attributing gain of function to mα6*-nAChRs than the TM II 9’ leucine-to-serine mutation (38).

DISCUSSION

Functional heterologous expression of human or mouse α6*-nAChRs has been difficult. Various approaches have been undertaken to circumvent this situation for human α6*-nAChRs (14, 15, 19, 22, 31, 38, 42). There is hardly any focus on heterologous expression of functional mouse α6*-nAChRs, although they are known to be physiologically important (3, 8, 10, 12, 43–45). Our initial studies, using ~1–6 ng of cRNA for each subunit, indicated that mouse α6β4-nAChRs expressed in oocytes are minimally functional (15). Although there was no evidence of functional mouse α6β4β3-nAChRs in oocytes, mouse α6β4β3V9*-nAChRs in oocytes were highly functional (15). Functional mα6mβ2-α3V13, mα6mβ2β3-, or mα6mβ2β3V9*-nAChRs or mα6β9*β3mβ2, mα6β9*β3mβ2, mα6β9*β3mβ2, or mα6β9*β3mβ2-nAChRs also were not detected in oocytes (15, 38). In continuation of these studies, here we used various approaches to produce or enhance the functional expression of mouse α6*-nAChRs.

We noticed that upon substitution of nAChR hβ3 subunits for nAChR mβ3 subunits highly functional hybrid mα6mβ4hβ3-nAChRs were produced in oocytes. We also noticed that functional mα6mβ4mβ3-nAChRs were formed in oocytes when they were expressed using an injection of relatively larger amounts of cRNAs (~23 ng) for each subunit. The peak current responses of these mα6mβ4mβ3-nAChRs were nonetheless severalfold lower than those of hybrid mα6mβ4hβ3-nAChRs. Similar to previous observations (15), whether using relatively lower or higher amounts of injected cRNA for each subunit, functional mα6mβ2-, mα6mβ2mβ3-, or mα6mβ2hβ3-nAChRs were not detected in oocytes. However, upon increasing the amount of cRNA injected for each subunit, minimally functional mα6mβ2mβ3V9*- or robustly functional mα6mβ2hβ3V9*-nAChRs emerged on cell surfaces. Additionally, mα6β4*-nAChRs harboring hβ3V9*- or hβ3V13* subunits showed gain of function similar to those of mα6β4mβ3V9*- or mα6mβ4mβ3V13*-nAChRs (15). Therefore, incorporation of hβ3 or mβ3 subunits into mα6mβ4*-nAChRs is evident because it had a potentiation effect. These results also suggest that these WT β3 subunits must be facilitating assembly of functional receptors. Potentiation of agonist sensitivity and levels of functional responses also indicate that there was incorporation of mutant hβ3V9* or mβ3V9* subunits into mα6mβ4*- or mα6mβ2*-nAChRs with further facilitation of functional receptor expression, increased frequency of agonist-gated channel opening, or both. These results also are indicative of efficient incorporation of hβ3 subunits, but not that of mβ3 subunits, into assemblies of mα6 and mβ4 subunits or of mα6 and mβ2 subunits.

Our results confirm that trinary complexes involving mα6 plus mβ2 or mα6 plus mβ4 subunits are formed. The observation that functional mα6mβ4*-nAChRs, but not mα6mβ2*-nAChRs, were formed whenever oocytes were injected with higher amount of cRNAs is consistent with such observations made in studies of expression of human α6*-nAChRs in oocytes (14). We also extended this strategy to ensure expression of functional mα6mβ2mβ3V9*- or mα6mβ2hβ3V9*-nAChRs. The need for elevated subunit abundance in oocytes for formation of cell surface, functional α6*-nAChRs is in contrast to the relative ease of expression of functional WT α2β4-, α3β2-, α3β4-, α4β2-, or α4β4-nAChRs or hybrid mα6hβ4hβ3- or mα6hβ2hβ3V9*-nAChRs in oocytes using ~1–2 ng of cRNAs for each subunit (27, 30). This also suggests that differences in features or AA sequence between mβ3 and hβ3 subunits accounts for increased efficiency of subunit assembly to closure of pentameric and functional mα6*-nAChRs.

Transmembrane II 9’ or 13’ valine-to-serine mutants of hβ3 or mβ3 (hβ3 or mβ3V9* or V13*) subunits whenever coexpressed with mα6mβ4*-nAChRs almost always yielded oocytes giving apparently outward current responses to atropine, indicating integration of β3 subunits into mα6mβ4*-nAChRs. This also indicates that these channels are opening spontaneously, a feature commonly seen for receptors of the ligand-gated ion channel family containing gain-of-function mutations (TM II V9* or V13*) (15, 19, 38, 46). Effects of atropine at high concentrations reflect its open channel blocking ability, which is seen for oocytes expressing mα6mβ2hβ3V9*-nAChRs but not mα6mβ2mβ3V9*-nAChRs (data not shown).

Differences in amino acid composition between hβ3 and mβ3 subunit extracellular N-terminal and second cytoplasmic loop regions (e.g. as opposed to their nearly identical transmembrane domains) that influence effects on α6*-nAChR function were revealed based on studies of chimeric nAChR mouse/human β3 subunits or their gain-of-function variants. The involvement of the NTD of β3 subunits in these effects echoes previous findings that the NTD of h66 subunits influences assembly and function of human α6β3*-nAChRs (15, 19, 38).

The current site-directed mutagenesis studies indicate that substitution of mβ3 subunit AA residues in primary face loop C with hβ3 subunit residues enhanced functional expression of mα6mβ2mβ3V9*-nAChRs. In addition, hβ3 subunit AA substitutions in complementary face β2-β3 and E loops for residues in mβ3 subunits increased functional expression of mα6mβ4mβ3-nAChRs. These results are in agreement with the previous observations that substitutions at extracellular N-terminal loops influence functional expression of h66*-nAChRs and other subtypes of nAChRs (15, 19, 38, 47).

The increased functional expression of mα6*-nAChRs seen upon AA substitution in mβ3 subunits must be due to some combination of increases in efficiency of incorporation of subunits into receptor complexes, trafficking to the cell surface, and/or preservation of cell surface receptors. nAChR mβ3 subunit loop E residues Ser114 and Ser118 differ from Asn or Val residues, respectively, in hβ3 subunits in side chain length and possibility of engaging in glycosylation (Ser versus Asn) and hydrophobicity (Ser versus Val) (48). nAChR mβ3 subunit loop C residues Glu221 and Phe223 differ from Asp or Val AAs in hβ3 subunits in side chain length (Glu versus Asp and Phe versus Val) and to some degree in hydrophobicity (Phe versus Val). These differences in AAs could influence interactions with
Effects of β3 Subunits on Mouse α6*-nAChR Function

FIGURE 8. Illustration of nAChR β3 subunit residues and its interfaces that are important in the function of mouse nAChRs. A, sequence alignment of nAChR β3 subunit proteins from several species. nAChR β3 protein sequences extracted from GenBank accession numbers NP_775304.1 (Mouse; Mus musculus), NP_000740.1 (Human; Homo sapiens), NP_990143.1 (Chicken; Gallus gallus), NP_001806562.1 (Frog; X. laevis), NP_598281.1 (Rat; Rattus norvegicus), NP_001329105.1 (Chimpanzee; Pan troglodytes), XP_599970.2 (Cow; Bos taurus), and NP_775394.1 (Zebrafish; Danio rerio) were aligned using ClustalW. B, sequence alignment of mouse nAChR β3 subunit proteins. Mouse nAChR subunits were aligned using ClustalW. For both A and B, numbering begins at the translation start methionine of the mouse nAChR β3 subunit protein and is shown in the N-terminal domain region of interest. Symbols below sequences indicate fully (*), strongly (:), or weakly (.) conserved residues, and underlining in shaded face indicates numbered residues in nAChR β3 subunit targeted for mutagenesis studies. C, a three-dimensional model of the N-terminal domain of mouse nAChR β3 subunit. A three-dimensional model of the mouse nAChR β3 subunit was generated based on the crystal structure of Torpedo muscle nAChR β subunit (Protein Data Bank code 2BG9:B). The N-terminal domain of the nAChR mβ3 subunit possesses β strands that form a β sandwich and conforms to an immunoglobulin fold. AA residues in the β2-β3 loop (Gln194 and Glu191), loop E (Ser144 and Ser146), or loop C (Glu221 and Phe223) that positively influence the current responses of α6*-nAChRs are identified. The figure was drawn using the program Chimera. D, schematic illustration of the composition of mαmβ4*-nAChRs. Adhering to the canonical rule of pentamer formation, mu6m34-nAChRs would be formed of three α6 and two β4 subunits (left) or two α6 and three β4 subunits (middle). In the event β3 subunits are integrated into mu6mβ4*-nAChRs, they would substitute for the third μ6 subunit in the first (left) configuration or the third mβ4 subunit in the second (middle) configuration, occupying what is labeled as the fifth position (yellow). Agonist (ACh or nicotine and others) binding sites at the interfaces between α6 and either β2 or β4 subunits are shown as ovals. Results from the current study (right) support the idea that the β2-β3 loop and loop E residues in the (+) face and/or loop C residues in the (−) face (arrows) of the mβ3 subunit are important in higher functional expression of mu6mβ4*-nAChRs. Mouse α6β2β4*-nAChRs would attain similar configurations, but the β2 subunit would substitute for the β4 subunit.

adjacent (or distant?) B2, B4, or α6 subunits that are important for mu6mβ2*- and mu6mβ4*-nAChR assembly (Fig. 8D).

β2-β3 or E loop residues in the negative (−) or complementary face of the mβ3 subunit would be involved in presumed interactions with residues on the positive (+) or primary faces of the neighboring mβ4 or mβ2 subunit, and loop C residues in the positive (+) or primary face of the β3 subunit would be involved in presumed interactions with residues on the negative (−) or complementary faces of the neighboring mα6 subunit in a complex that has the presumed arrangement of β3 or β3β9VYα_β2 or β4.3 where ligand binding pockets are thought to be located between the primary (+) face of mα6 and complementary (−) face of the mβ2 or mβ4 subunits (i.e. mα6β4 β2 or mβ3 α6 β2) (Fig. 8A). Agonist binding is not expected occur at β6 β2 (or β4) or β3 α6 subunit interfaces. However, recent evidence suggests that interfaces involving subunits in the accessory subunit position where the β3 subunit would be situated can engage in allosteric or co-agonist effects (49–51). Residues in or equivalent to those at mβ3 subunit positions 94, 101, 107, 144, 148, 221, and 223 are...
conserved with those in rats but differ from those that are conserved within primates (human and chimp; Fig. 8A). These mβ3 subunit AAs also are unique across mouse nAChR subunits (Fig. 8B). We have advanced the possibility that these residues could affect efficiency of α6*^-nAChR assembly (not altering agonist potency but affecting peak current responses as for mα6^-nAChRs harboring mβ3(S144N/S148V), mβ3(E221D), or mβ3(E221D/E223V) subunits). Another intriguing possibility is that these unique residues could allow formation of novel classes of ligand binding sites at β2/β4/β3 or β3:α6 subunit interfaces that also could lead to changes in levels of receptor function as for ligand occupancy of the α4:α6 subunit interface in low sensitivity α4β2^-nAChR (51).

Plenty of information is available on the role of primary face loops (A, B, and C) from α subunits and complementary face loops (D, E, and F) from β subunits that participate in ligand binding largely from structural and/or mutagenesis studies of muscle-type, α7^-, or other nAChRs and from lower eukaryotic and prokaryotic proteins structurally homologous to the extra-cellular domain of nAChRs (52–54). Our results presented here, for the first time, show that extracellular N-terminal domain loops of the accessory subunit, β3, regulate the functional expression of mα6^-nAChRs. These results also provide further evidence that nAChR β3 subunits not only form functional receptors in combination with nAChR α6 subunits but also can enhance their function by interacting with adjacent subunits mediated by N-terminal loop residues. Current findings lay a foundation for enhanced functional expression of mα6^-nAChRs that could facilitate the discovery and development of nicotinic ligands that selectively interact with α6^-nAChRs. These results could be useful to fuel and inform emerging interest in α6 and β3 subunits and the receptors they compose with specific reference to possible roles in locomotion, reward and reinforcement behavior, schizophrenia, and Parkinson disease (5, 6, 55).

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