# Molecular Evolution of the Nicotinic Acetylcholine Receptor: An Example of Multigene Family in Excitable Cells 

Nicolas Le Novère, Jean-Pierre Changeux<br>Laboratoire de Neurobiologie Moléculaire, 25, rue du Dr Roux, 75015 Paris, France

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#### Abstract

An extensive phylogenetic analysis of the nicotinic-acetylcholine-receptor subunit gene family has been performed by cladistic and phenetic methods. The conserved parts of amino acid sequences have been analyzed by CLUSTAL V and PHYLIP software. The structure of the genes was also taken in consideration. The results show that a first gene duplication may have occurred before the appearance of Bilateria. Three subfamilies then appeared: I-the neuronal $\alpha$-bungarotoxin binding-site subunits ( $\alpha 7, \alpha 8$ ); III-the neuronal nicotinic subunits ( $\alpha 2-\alpha 6, \beta 2-\beta 4$ ), which also contain the muscle acetylcholine-binding subunit ( $\alpha 1$ ); and IV-the muscle non- $\alpha$ subunits ( $\beta 1, \gamma, \delta, \epsilon$ ). The Insecta subunits (subfamily II) could be orthologous to family III and IV. Several tissular switches of expression from neuron to muscle and the converse can be inferred from the extant expression of subunits and the reconstructed trees. The diversification of the neuronal nicotinic subfamily begins in the stem lineage of chordates, the last duplications occurring shortly before the onset of the mammalian lineage. Such evolution parallels the increase in complexity of the cholinergic systems.


Key words: Nicotinic receptor - Ligand-gated channel - Multigene family - Gene phylogeny

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## Introduction

Acetylcholine ( ACh ) has long been recognized as a neurotransmitter active in Bilateria nervous system and muscle. Two distinct categories of receptors are engaged in the biological effects of ACh : the muscarinic and nicotinic receptors. Muscarinic receptors belong to the superfamily of G-protein-coupled receptors; they consist of single integral proteins with seven transmembrane segments and interact, on their cytoplasmic face, with heterotrimeric G-proteins. Nicotinic receptors ( nAChR ) belong to the superfamily of ligand-gated ion channels; they are hetero-oligomers composed of five subunits, each with four transmembrane domains (DevillersThiéry et al. 1993; Galzi and Changeux 1994). ACh binding causes an ionic channel, most often cationic, to open, resulting in a rapid change in the electrical, and secondarily metabolic, state of the target cell (Greenberg et al. 1986; Bertrand et al. 1993).

The nAChR of striated muscle is the best-characterized member of the ligand gated-ion-channel superfamily (Changeux 1990; Karlin 1993): it is a heteropentamer (with the stoichiometry $\alpha_{2} \beta \gamma \delta$ ). According to current models (Bertrand et al. 1993), the ion channel forms along the axis of pseudosymmetry perpendicular to the cell membrane. The subunits share a similar hydropathic profile with four short hydrophobic domains (MI-MIV) and two long hydrophilic domains. The largest, relatively conserved, hydrophilic domain is located at the amino-terminal side of the subunit polypeptide, and the other, highly variable, joins hydrophobic do-
mains MIII and MIV. The amino-terminal hydrophilic domain carries the ACh binding site (Devillers-Thiéry et al. 1993) and faces the synaptic cleft, whereas the other hydrophilic domain is exposed to the cytoplasm.

Molecular cloning and sequencing studies have revealed the existence of a family of genes, expressed in neurons, which code for nAChR subunits homologous (see Appendix 1 for definitions of boldface terms) to those of muscle nAChR (Sargent 1993). In the jawed vertebrate nervous systems, several subunits (named $\alpha 2$ $\alpha 8$ ) have been identified which share with the muscletype receptor $\alpha 1$ subunit the pair of cysteines shown to contribute to the ACh binding site (Wada et al. 1988; Shoepfer et al. 1990; Cockcroft et al. 1992; Karlin 1993). Other homologous chains, lacking the cysteine pair, have been characterized and named non- $\alpha$ or $\beta 2-\beta 4$. As for muscle $n A C h R$, the functional neuronal $n A C h R$ is an heteropentamer made up by the assembly of $\alpha$ and $\beta$ subunits, with a putative stoichiometry in vitro of $\alpha_{2} \beta_{3}$ (Anand et al. 1991; Cooper et al. 1991). The recent evidence that $\alpha 5$ is coprecipitated with another $\alpha$ and $\beta$ subunit in some neuronal nAChRs indicates that more than two different subunits may assemble together to form a receptor molecule (Conroy et al. 1992; Vernallis et al. 1993). In contrast, in reconstituted systems, the $\alpha 7$ or $\alpha 8$ subunits can form functional homo-oligomers (Couturier et al. 1990; Revah et al. 1991; Anand et al. 1993). The autoradiographic studies in the brain revealed that ${ }^{3} \mathrm{H}$-nicotine labels receptors formed by subunits $\alpha 2$ $\alpha 6$ and $\beta 2-\beta 4$ but not receptors formed by subunits $\alpha 7$ and $\alpha 8$ (Clarke et al. 1985), which are labeled by $\alpha$-bungarotoxin ( $\alpha$-Bgt).

The combinatorial diversity resulting from the assembly of the multiple neuronal subunits results in a wide spectrum of structurally and functionally distinct nAChRs with different pharmacological specificities and ion-channel properties (Role 1992). Such differences have been directly demonstrated in Xenopus oocytes and mouse fibroblasts after heterologous expression (Luetje and Patrick 1991; Whiting et al. 1991). Furthermore, multiple functionally distinct types of nAChRs have been detected in different brain areas and subcellular compartments (Mulle et al. 1991).

The nAChR is present in the whole phylum of Bilateria, from nematodes to humans (Gerschenfeld 1973; Darlison et al. 1993; Fleming et al. 1993; Leech and Sattelle 1993). Several nAChR neuronal subunits have been cloned in Drosophila, locust, and nematode (Gundelfinger 1992; Fleming et al. 1993). In the insect nervous system, ACh is the major excitatory neurotransmitter, in contrast to vertebrates, where glutamate predominates. At the neuromuscular junction, glutamate is the excitatory transmitter in arthropods, whereas it is ACh in vertebrates. Since some lines of evidence suggest that nAChR is also responsible for neuromuscular transmission in nematodes, molluscs, and annelids (Gerschenfeld 1973; Segerberg and Stretton 1993), it is of interest
to assess whether the original form of nAChR appeared in muscle or in neurons.

The neuronal nAChRs provide a good example of a multigene family differentially expressed in the nervous system. Its evolution deserves comparison with the increase in complexity of the vertebrate nervous system and, in particular, cholinergic systems. Some partial trees have already been constructed, but without comparative methods and without statistical support (Brehm et al. 1991; Cockcroft et al. 1992). Here we provide a molecular phylogenetic study of the whole family of $n A C h R$ genes.

## Materials and Methods

The programs used in this work were run on a Sun computer in a UNIX environment. The sequences were loaded from Genbank and EMBL databases (Table 1) with Sequence Analysis Software Package 7.1 from the Genetic Computer Group.

Alignments of the Sequences. Alignments were performed using CLUSTAL V software (Higgins and Sharp 1988). This program compares the sequences in pairs according to Wilbur and Lipman (1983) (gap penalty $=3$ ) and builds a preliminary tree by an unweighted pair-group method of arithmetic averages (UPGMA) (Sneath and Sokal 1973). Then the program aligns all sequences in order of decreased similarity according to Feng and Doolittle (1987) (fixed and floated gap penalty $=10$ ). The use of different values of gap cost changed neither topology nor the ratio of branch lengths but did result in a homothetic transformation of the trees. The similarities have been determined by the Dayhoff PAM 250 matrix. The protein sequences were aligned after the following modifications:

Deletions of the signal peptide (corresponding to t $\alpha 1$ aa 1-27), the small nonconserved part in amino-terminal part (corresponding to tal R188), the highly variable cytoplasmic region (corresponding to t $\alpha 1$ aa 356-393), and the carboxy-terminal part (corresponding to tox1 aa 452461). The alignment obtained with 48 sequences shows 394 sites with 357 informative sites (Appendix 2).

To determine the branching of the nematode sequence onachr (Fig. 4) which amino-terminal part is not known, a further deletion (corresponding to the 38 amino-terminal aa of co from the Appendix 2 alignment) was performed on 12 sequences. The alignment of the 13 sequences shows 351 sites with 263 informative sites (Appendix 3).

Sequence Analyses. Inferences on gene evolution were obtained with the PHYLIP 3.5c software of Felsenstein (1993).

The cladistic method was the maximum of parsimony (MP) (Fitch 1971, program PROTPARS). The mouse $5-\mathrm{HT} 3$ subunit and the rat glycine $\alpha 3$ subunit were used as outgroups. The use of the rat GABA $\alpha 1$ subunit instead of the glycine $\alpha 3$ subunit did not change the results (data not shown). The phenetic method was neighbor-joining (NJ) (Saitou and Nei 1987, program NEIGHBOR). The distance matrix was provided by the Dayhoff PAM matrix (Dayhoff 1979, program PROTDIST). The statistical test used to determine the strength of the trees was bootstrap resampling (Felsenstein 1985) with the SEQBOOT (seed: 5) and CONSENSE programs.

[^1]Table 1. Genes used in this study. Abbreviations are those used in the text and trees. The first letters represent the species, followed by the name of the subunit ${ }^{3}$

| Gene | Species | Acc. no. | Ref. |
| :---: | :---: | :---: | :---: |
| bol 1 | Bos taurus | X02509 | Noda et al. Nature 305:818 (1983) |
| ${ }^{\text {b }} \beta 1$ | Bos taurus | X00962 | Tanabe et al. Eur J Biochem 144:11 (1984) |
| $\mathrm{b} \delta$ | Bos taurus | X02473 | Kubo et al. Eur J Biochem 149:5 (1985) |
| be | Bos taurus | X02597 | Takai et al. Nature 315:761 (1985) |
| b $\gamma$ | Bos taurus | M28307 | Takai et al. Eur J Biochem 143:109 (1984) |
| c $\alpha 2$ | Gallus domesticus | M07339-44 | Nef et al. EMBO J 7:595 (1988) |
| cos | Gallus gallus | M37336 | Couturier et al. $J B C$ 265:17560 (1990) |
| ca4 | Gallus domesticus | X07348-53,99 | Nef et al. EMBO J 7:595 (1988) |
| cas | Gallus gallus | J05642 | Couturier et al. $J B C$ 265:17560 (1990) |
| c $\alpha 7$ | Gallus gallus | X68586 | Couturier et al. Neuron 5:847 (1990) |
| c $\alpha 8$ | Gallus gallus | X52296 | Schoepfer et al. Neuron 5:35 (1990) |
| c $\beta 2$ | Gallus domesticus | X53092 | Schoepfer et al. Neuron 1:241 (1988) |
| $c^{\beta} 4$ | Gallus gallus | J05643 | Couturier et al. JBC 265:17560 (1990) |
| c $\delta$ | Gallus gallus | K02903 | Nef et al. PNAS 81:7975 (1984) |
| cy | Gallus gallus | K02904 | Nef et al. PNAS 81:7975 (1984) |
| d $\alpha$ Li | Drosophila melanogaster | X07194 | Bossy et al. EMBO J 7:611 (1988) |
| d $\alpha 2$ | Drosophila melanogaster | X53583 | Sawruk et al. EMBO J 9:2671 (1990) |
| d $\beta 2$ | Drosophila melanogaster | X55676 | Sawruk et al. FEBS Lett 273:177 (1990) |
| dnachr | Drosophila melanogaster | X04016 | Hermans-Borgmeyer et al. EMBO J 5:1503 (1986) |
| gfo3 | Carassius auratus | X54051 | Hieber et al. NAR 18:5293 (1990) |
| $\mathrm{gf} \beta 2$ | Carassius auratus | X 54052 | Hieber et al. NAR 18:5307 (1990) |
| gfno2 | Carassius auratus | X14786 | Cauley et al. J Cell Biol 108:637 (1989) |
| gfnc3 | Carassius auratus | M29529 | Cauley et al. J Neurosci 10:670 (1990) |
| h $\alpha 1$ | Homo sapiens | Y00762 | Schoepfer et al. FEBS Lett 226:235 (1988) |
| h $\alpha 3$ | Homo sapiens | M37981 | Mihovilovic et al. J Exp Neurol 111:175 (1991) |
| ha5 | Homo sapiens | M83712 | Chini et al. PNAS 89:1572 (1992) |
| h $\alpha 7$ | Homo sapiens | X70297 | Peng et al. Mol Pharmacol 45:546 (1994) |
| h $\beta 1$ | Homo sapiens | X14830 | Beeson et al. NAR 17:4391 (1989) |
| hß2 | Homo sapiens | X53179 | Anand et al. NAR 18:4272 (1990) |
| h $\beta 3$ | Homo sapiens |  | Willoughby et al. Neurosci Lett 155:136 (1993) |
| h 34 | Homo sapiens | X68275 | Tarroni et al. FEBS Lett 312:66 (1992) |
| $\mathrm{h} \delta$ | Homo sapiens | X55019 | Luther et al. J Neurosci 9:1082 (1989) |
| he | Homo sapiens | X66403 | Beeson et al. unpublished |
| mser | Mus musculus | M74425 | Maricq et al. Science 254:432 (1991) |
| $\mathrm{n} \alpha 1$ | Naja naja | M26388 | Neumann et al. PNAS 86:7255 (1989) |
| onachr | Onchocerca volvulus | L20465 | Ajuh and Egwang unpublished (1993) |
| r $\mathrm{\alpha}^{2}$ | Rattus norvegicus | L10077 | Wada et al. Science 240:330 (1988) |
| ra3 | Rattus norvegicus | X03440 | Boulter et al. Nature 319:368 (1986) |
| r $\alpha 4$ | Rattus norvegicus | M15681-82 | Goldman et al. Cell $48: 965$ (1987) |
| ra5 | Rattus norvegicus | J05231 | Boulter et al. J Biol Chem 265:4472 (1990) |
| ra6 | Rattus norvegicus | L08227 | Boulter unpublished (1988) |
| ra7 | Rattus norvegicus | M85273 | Seguele et al. J Neurosci 13:596 (1993) |
| $\mathrm{r} \beta 2$ | Rattus norvegicus | - | Deneris et al. Neuron 1:45 (1988) |
| r $\beta 3$ | Rattus norvegicus | J04636 | Deneris et al. J Biol Chem 264:6268 (1989) |
| r $\beta 4$ | Rattus norvegicus | $\begin{aligned} & \text { J05232, M89971, } \\ & \text { M33951-3, M89989 } \end{aligned}$ | Boulter et al. J Biol Chem 265:4472 (1990) |
| r $\delta$ | Rattus norvegicus | X74835 | Witzemann et al. Eur J Biochem 194:437 (1990) |
| re | Rattus norvegicus | X13252 | Criado et al. NAR 16:10920 (1988) |
| r $\gamma$ | Rattus norvegicus | X74834 | Witzemann et al. Eur J Biochem 194:437 (1990) |
| rglya3 | Rattus norvegicus | M55250 | Kuhse et al. J Biol Chem 265:22317 (1990) |
| $s \alpha \mathrm{~L} 1$ | Schistocerca gregaria | X55439 | Marshall et al. EMBO J 9:4391 (1991) |
| $t \alpha 1$ | Torpedo californica | X00963 | Noda et al. Nature 299:793 (1982) |
| ${ }^{\text {t }} \boldsymbol{\beta} 1$ | Torpedo californica | J00964 | Noda et. al. Nature 301:251 (1983) |
| t $\delta$ | Torpedo californica | J00965 | Noda et al. Nature 301:251 (1983) |
| t $\gamma$ | Torpedo californica | J00966 | Ballivet et al. PNAS 79:4466 (1982) |
| xola | Xenopus laevis | X17244 | Hartman et al. Nature 343:372 (1990) |
| $x \propto 1 b$ | Xenopus laevis | X07067 | Baldwin et al. J Cell Biol 106:469 (1988) |
| xb1 | Xenopus laevis | U04618 | Kullberg et al. Rec Chan (1994) in press |
| $\mathrm{x} \delta$ | Xenopus laevis | X07069 | Baldwin et al. J Cell Biol 106:469 (1988) |
| $\mathrm{x} \gamma$ | Xenopus laevis | X07068 | Baldwin et al. J Cell Biol 106:469 (1988) |

[^2]

12 STEPS


Fig. 1. A Structure of the subunit genes. Only the exons at least partially coding are represented. The gray level grossly reflects the conservation of the exon through the family (i.e., the presence of an exonic frontier at this place in different subunits, but not the sequence similitude between exons). A, B, C: binding site loops. M1, M2, M3, M4: transmembrane segments. The arrowheads mark the informative limits (in a cladistic acception). Adapted from Jonas et al. (1990) with
the help of Alain Bessis. B Cladogram constructed with the exonic structure of the genes from an MP analysis which gave three equivalent trees. The informative limit of each gene is coded at the right of its name ( 0 : absence; 1: presence). Open box: loss of a limit; filled box: gain of a limit. The dendogram is arbitrarily rooted. The branch lengths make no sense.
compatibility method (Le Quesne 1969; Estabrook et al. 1976, program CLIQUE) were used to analyze the genomic structure.

Construction of Figures. The majority-rule consensus trees were constructed by the program DRAWGRAM. The results of CONSENSE analysis after the bootstrap resamplings are written in ovals on the node considered.

The determination of approximated time divergence between subunits (Fig. 5) is based on the NJ analysis of the Appendix 2 protein alignment. The external branches of the resulting tree showed an approximate molecular clock for each group. We are then able to determine the dates of the last duplications. However, the rates of evolution vary greatly between the subgroups, and the precocious duplications can't be calculated in this way. To determine the date of divergence between two subunits, we averaged the branch lengths and the evolution rate between all the orthologs. The estimated rate of evolution is obtained by dividing the branch length by the duration. The dates used are: Torpedo/osteichthyans 450 MYA , goldfish/Tetrapoda 405 MYA , Xenopus/Amniota 365 MYA , chicken/mammals 310 MYA , mouse/ human 110 MYA (Benton 1990). For instance, each external branch inside the $\delta, \epsilon, \gamma$ group provides an estimated rate of evolution of between $3.2 \times 10^{-10}$ and $7.3 \times 10^{-10}$ substitution per site and per year ( $M=5.3 \sigma=1.2$ ), which is not far from a molecular clock.

## Results

## Evolution of the Gene Structure

The number of exons identified in the gene nAChR subunits varies largely in the family although some common features can be recognized (Fig. 1A). Four subfamilies can be identified on the basis of the genomic structure. These are: I-the neuronal $\alpha$-bungarotoxin-binding-site subunit subfamily; II-the Arthropoda neuronal subunit subfamily; III-the vertebrate neuronal nicotinic subunit subfamily; and IV-the muscle subunit subfamily.

The genes of subfamily IV possess 11 or 12 exons, of which ten are conserved. In subfamily III, the main part of the coding sequence is distributed within a single exon. The structure of $\alpha 1$ and $\alpha 7$ genes differs from the two "holotypes" (III or IV). However, it is difficult to determine if the structure of these two genes is mainly plesiomorph or contains autapomorphies. In order to
extract information from genomic structure, we made a cladistic analysis of the frontiers between introns and exons. Only the ten informative sites were considered (Fig. 1). A parsimony analysis of two-state character (i.e., presence or absence of the frontier) gave three 12step cladograms (summarized in Fig. 1B with an arbitrary root corresponding to sequence analyses; see below). A compatibility analysis gave the same results (although automatically rooted at a different point, i.e., between muscle and neuronal genes). One explanation is that the genic structure of type I subunits is mainly made of autapomorphies, whereas that of $\alpha 1$ is plesiomorphic in subfamily IV. On the basis of gene-structure analysis, this latter subunit would be a sister group of all other subunits of subfamily IV. However, sequence analyses (see below) make $\alpha 1$ a sister group of subfamily III. A translocation (e.g., between exons 4 and 5) could mask the real onset of the $\alpha 1$ subunit. Further studies of sequence homology between exons in paralogs will help to clarify this issue.

## Sequences Analysis

The sequence analysis revealed the existence of the same four subfamilies of nAChR subunits as did analysis of the gene structure (Figs. 2 and 3). We obtained successive divergences of subfamilies I, then II and, at last III and IV. The position of subfamily II as a sister group of subfamily IV is weakly supported by NJ (Fig. 3) analysis and not by MP analysis (Fig. 2). These subunits appeared polyphyletic with MP analysis and monophyletic with NJ analysis. However, their position was supported by very weak bootstrap score. The $\beta 2$ and $\beta 4$ subunits were branched with subfamily IV with a weak bootstrap score. This position may be an artifact resulting from the precocious appearance and the weak divergence of these two subunits.

In subfamily IV, the $\beta 1$ subunit diverged first followed by the $\delta$. A subsequent duplication resulted in the $\gamma$ and $\epsilon$ subunits. This latter duplication seems to have occurred shortly before the divergence of Torpedo subunits (i.e., before the divergence of the elasmobranch lineage).

In subfamily III, several groupings were present in more than $99 \%$ of trials: $(\beta 2, \beta 4),(\beta 3, \alpha 5),(\alpha 2, \alpha 4)$, $(\alpha 3, \alpha 6)$. A first duplication gave $\beta 2$ and $\beta 4$. The position of $\beta 2$ and $\beta 4$ was unstable, jumping between subfamily III and subfamily IV according to the sequences sampled. However, if we consider the gene structure, the neuronal localization, and the pharmacological characteristics of these subunits, $\beta 2$ and $\beta 4$ have to be placed in subfamily III. Then we observe the separation of $\beta 3$ and $\alpha 5$. At last, a monophyletic group formed by the two pairs $(\alpha 4, \alpha 2)$ and $(\alpha 3, \alpha 6)$ is present in MP and NJ analyses. The position of $\alpha 1$ does not match the genestructure analysis. This strange position of $\alpha 1$ inside the


Fig. 2. Bootstrap majority-rule consensus tree obtained from 1000 MP replicates (SEQBOOT, PROTPARS and CONSENSE programs) with the alignment shown in Appendix 2. The nodes indicated by an arrowhead are uncertain.
neuronal subgroup is, however, weakly supported by bootstrap scores. The last clear duplications arose in the lineage of teleosteans which possess two homologs of $\beta 3$ (appeared about 280 MYA ), and in Tetrapoda, which have two homologs of the goldfish $\beta 2, \beta 2$, and $\beta 4$ subunits. Moreover, goldfish $\alpha 3$ is not clearly homolog to tetrapod $\alpha 3$ (NJ Fig. 3) or $\alpha 6$ (MP Fig. 2), which could then appear only after the divergence of teleosteans.

## Evolution of the Stoichiometry

As the nAChR is an oligomer formed by subunits coded by paralogs, it is reasonable to assume that the primitive receptor resulted from the assembly of just one subunit. Thus, the ability for a subunit to form functional homooligomers could reflect a plesiomorphic ("primitive") mode of functioning. $\alpha$-Bgt-sensitive homo-oligomers from Locusta migratoria (Breer et al. 1985) have been purified and reconstituted in vitro (Hanke and Breer 1986). The doLL subunit of Schistocerca gregaria forms


Fig. 3. Bootstrap majority-rule consensus tree obtained from 1000 NJ replicates (SEQBOOT, PROTDIST, NEIGHBOR, and CONSENSE programs) with the alignment shown in Appendix 2. The nodes indicated by an arrowhead are uncertain.
functional homo-oligomeric channels (Marshall et al. 1990 ) blocked by $\alpha$-Bgt in vitro. d $\alpha 2$ (also called SAD for second alpha subunit), the putative Drosophila homolog of locust s $\alpha \mathrm{L} 1$, forms functional receptors alone in Xenopus oocytes (Sawruk et al. 1990) though these receptors display an atypical pharmacology. In the same way, $\alpha 7$ from chicken is able to form homo-oligomers in Xenopus oocytes (Couturier et al. 1990; Revah et al. 1991; Anand et al. 1993). In contrast, vertebrate nAChR subunits from subfamilies III and IV, expressed in Xe nopus oocyte, cannot form functional homo-oligomeric channels.

## Pharmacological Argument for Monophyly of Neuronal Nicotinic Subfamily

Although a small number of mutations sometimes suffice to dramatically change the properties of a receptor (e.g., Galzi et al. 1992), the pharmacological properties of the families of ligand-gated ion channels seem to diverge slowly. Ascaris muscle (Walker et al. 1992), Aplysia (Ono and Salvaterra 1981), $\alpha \mathrm{L} 1$ (insect class 2, Marshall
et al. 1990), dnAChR (insect class 1, Schloss et al. 1988), chicken $\alpha 7$ (Couturier et al. 1990; Anand et al. 1993), and vertebrate striated muscle (Lee and Chang 1966; Changeux et al. 1970) receptors are $\alpha-\mathrm{Bgt}$ sensitive. Although $\alpha 1$ belongs to subfamily III, the functional $\alpha$-Bgt sites of the vertebrate muscle receptor are formed partially by the subunits of subfamily IV. Moreover, if $\alpha 1$ is placed as a sister group of all other subunits of subfamily III (as indicated by the gene structure), the loss of $\alpha-\mathrm{Bgt}$ sensitivity in the neuronal nicotinic subfamily is a synapomorphy. In addition, Ascaris muscle receptor (Walker et al. 1992), Aplysia neuronal receptors (Ono and Salvaterra 1981), and the receptor formed by soL1 of Schistocerca (Marshall et al. 1990) are sensitive to strychnine, an antagonist of the glycine receptor, and to bicuculline, an antagonist of the $\mathrm{GABA}_{\mathrm{A}}$ receptor. $\alpha 7$ is also sensitive to strychnine (Anand et al. 1993). The members of a multigene family can then share pharmacological properties, even after a long divergence (probably more than 1,000 MYA here). Receptors of subfamily III do not seem to be blocked by these antagonists (Clément Léna, personal communication). Overall, the evidence from pharmacological studies further supports the notion of the monophyly of the subfamily III.

## Discussion

The analyses presented in this paper lead to the reconstruction of a global history of nAChR evolution. Although several nodes have not been perfectly resolved, the major relationships between subunits were clarified. Except for $\alpha 1$ and $(\beta 2, \beta 4)$ all the analyses performed were congruent.

## Hypothetically Missing Genes

Subfamily I diverged before the split insects/vertebrates, and this subfamily could be present in insects. (The cloned insect subunits are orthologous to the subfamily III and IV.)

Neuromuscular transmission via $n A C h R s$ is known to occur in nematodes (Gerschenfeld 1973; Walker et al. 1992), annelids, molluscs (Gerschenfeld 1973), and vertebrates but not in insects and crustaceans. The chemical excitation of muscle in the Bilateria nonvertebrates/ nonarthropods has to be mediated by subunits which do not belong to the subfamily IV (Fig. 2). Thus, neuromuscular transmission in vertebrates is not homologous to that occurring in other phyla.

The $\epsilon$ subunit seems to be present in the whole Gnathostomata phylum. This is consistent with the reported presence of an $\epsilon$ subunit in Xenopus, yet this subunit has not been cloned in chicken.

The bootstrap confirms that $\alpha 7$ and $\alpha 8$ diverged prior
to the separation of Sauropsida and Theropsida. Thus, an $\alpha 8$ subunit may be present in mammals.

## Reconstructed History of the nAChR-Subunit Gene Family

Based on present and previous results, the history of the nAChR-subunit gene family can be reconstructed as follows (Fig. 5):

We can plausibly assume (still without proof) that in the primitive metazoans (e.g., coelenterates) nAChR was made of a single subunit able to form homo-oligomers. The coelenterates have no true muscle cells but already have multipolar neurons, of ectodermal origin. This first nAChR presumably had a neuronal localization. With the appearance of a third embryonic sheet, the nAChR acquired a novel role in neuromuscular transmission. However, if the nematodes and the molluscs have a muscle nAChR, it is not homologous to the vertebrate subfamily IV. Indeed, this latter plausibly appeared after the differentiation of Deuterostomata. The subunit cloned in Onchocerca does not possess the third loop of the ACh binding site (Devillers-Thiéry et al. 1993) and might be a non- $\alpha$ subunit. The NJ analysis of the alignment shown in appendix 3 (Fig. 4) determined this subunit to be an extra group of three Drosophila subunits containing two $\alpha$ and one non- $\alpha$ subunits. The idea of a precocious emergence of the insect subunits is supported by the ability of these subunits to form homo-oligomers in vitro. Assuming that alphaL1 of Schistocerca and alpha 2 of Drosophila are orthologs, the duplication between them and d $\alpha \mathrm{Li}$ is older than the divergence of Orthoptera and Diptera-i.e., older than 300 MYA (Labandeira and Sepkoski 1993). In Deuterostomata, several duplications occurred to give extant subfamily IV, which was complete in vertebrate phylum before the appearance of chondrichthyes ( 450 MYA ) and extant subfamily III, one of the paralogs being expressed in muscle.

Several tissular switches of expression from neuron to muscle or from muscle to neuron can be hypothetized (Fig. 5). Between the divergence of subfamily II and the split subfamily III/subfamily IV (in the chordate lineage), one switch of expression might have given a muscle receptor, possibly homopentameric. After the first duplication between the ancestor of subfamily IV and $\alpha 1$ (a duplication which is responsible of the heteromeric muscle receptor), a further duplication from $\alpha 1$ provided a new gene, which expression became neuronal. The evolution of the promoters (and of the transcription regulators) may thus have played a role as important as gene duplication in the diversification of the nAChR family.

The neuronal non- $\alpha$ subunit group is likely to be polyphyletic, whereas the neuronal $\alpha$ subunits (the "binding subunits'") would form a monophyletic group. $\alpha 5$, which lacks some important aromatic amino acids in the third


Fig. 4. Bootstrap majority-rule consensus tree obtained from 1,000 NJ replicates with the alignment shown in Appendix 3, presenting the possible emergence of the nematode subunit. The nodes indicated by an arrowhead are uncertain.
loop of the ACh binding site, cannot form functional receptors in vitro with any $\beta$ subunit (Boulter et al. 1990) but is coprecipitated from endogeneous material with other $\alpha$ subunits (Conroy et al. 1992; Vernallis et al. 1993); it thus may represent a new type of "structural" subunit and should therefore be given another name. $\alpha 5$ and $\beta 3$ could be called $\gamma 2$ and $\gamma 3$. Then the three types of subfamily III subunits could form monophyletic groups-the tribes $\alpha, \beta$, and $\gamma$.

## Growth of the Neuronal Nicotinic Subfamily and Increase in Complexity of the Cholinergic System

The multiple duplications in subfamily III parallel the progressive increased complexity of the chordate nervous system-in particular, of the cholinergic system. At the beginning of the evolution of this phylum, one subunit was plausibly present in the nervous system, resulting from the duplication of $\alpha 1$ (in addition to the ancestor of $\alpha 7$ and $\alpha 8$ ). The diversity of the group increased during the first 400 MY , until the appearance of Tetrapoda. The whole evolution of the subfamily occurred in


Fig. 5. Summary tree, integrating the results of the whole study. The dates of the last divergences have been calculated from the protein alignment of Appendix 2 (cf. Materials and Methods). $\alpha 7 / \alpha 8$ : 380 MYA; $\epsilon / \gamma: 508$ MYA; $\epsilon, \gamma / \delta: 711 \mathrm{MYA} ; \epsilon, \gamma, \delta / \beta 1: 926 \mathrm{MYA} ; \alpha 3 / \alpha 6:$ 529 MYA; $\alpha 2 / \alpha 4: 669 \mathrm{MYA} ; \alpha 5 / \beta 3: 770 \mathrm{MYA}$. The ages of the precocious divergences have been approximately inferred from the divergence of nematodes (1,000 MYA: Vanfleteren et al. 1994). M: muscle subunit; $N$ : neuronal subunit. The gray branches represent subunits putatively expressed in neurons. The black branches represent subunits possibly expressed in muscle.
the first half of Deuterostomata history (from 600-800 MYA to about 300 MYA ). In the first prechordate fossils, we find only two ganglia, the peripheral and the cerebroid ganglia. Branchiostoma has only one pseudovesicle in the head. Spinal chord and cholinergic peripheral nervous system were present early in the vertebrate lineage (although the complete autonomous system was reached only in mammals). Lamprey already has five vesicles but the main development of the brain and particularly of the forebrain occurred in Gnathostomata.

In situ hybridization (Deneris et al. 1989; Wada et al. 1989, 1990; Zoli et al. 1995) as well as immunohistochemical (Britto et al. 1992; Hill et al. 1993) studies have shown that, in rat and chicken brain, $\alpha 4$ and $\beta 2$ mRNA distribution is diffuse, whereas $\alpha 2, \alpha 3, \alpha 5, \alpha 6, \beta 3$, and $\beta 4$ are mainly restricted to a few major cholinergic or cholinoceptive pathways, which, however, also express $\alpha 4$ and $\beta 2$. $\beta 2$ has diverged early in the neuronal subfamily history (Figs. 2, 3, and Results). $\alpha 4$ and $\beta 2$ could represent a "fossil" expression, which was present in most areas of the ancestral brain. When a duplication occurred, one of the paralogs kept the specific role of the "father gene," whereas the other paralog had to acquire a new role. This role can be defined by a new domain of expression (like the switches muscle/neuron developed before) or by a modified function. The hypothesis that $\alpha 4$ maintained its previous role while another paralog ac-
quired a new role is supported by some evidence on the $\alpha 2$ subunit. In chick brain, the $\alpha 2$ subunit is restricted to the lateral spiriform nucleus (Daubas et al. 1990) but, in rat brain it is restricted to the interpeduncular nucleus (Wada et al. 1989)-a nonhomolog structure. (The interpeduncular nucleus also exists in the chick brain.) Moreover, there is no homolog of the lateral spiriform nucleus in rat brain, a fact that points to the genesis of this structure after the divergence of the bird lineage. It is attractive to suppose that a gene duplication occurred a short time before the branching of Theropsida and Sauropsida (i.e., before 310 MYA, Benton 1990). This time would have been too short to define the specificity of $\alpha 2$ (in contrast to $\alpha 4$, which maintained its ancient role). Then two independent specificities of expression took place in the two phyla. Accordingly, a transgene with the avian $\alpha 2$ gene (including the promoter) is expressed throughout the rat brain, mostly in cholinergic structures (motor nuclei and basal telencephalon) (Daubas et al. 1993). (Nevertheless, this distribution corresponds neither to the distribution of endogenous $\alpha 2$ nor to that of $\alpha 4$.)

In the same way, the duplications $\alpha 3 / \alpha 6$ and $\beta 2 / \beta 4$ occurred a little before, or a little after, the split between the teleost and the tetrapod lineages. In the rat brain, $\alpha 3$ and $\beta 4$ are mainly expressed in the medial habenula, a cholinergic and cholinoceptive structure. However, in a teleost fish (Phoxinus phoxinus), an immunocytochemical study did not find any cholinergic cell and found only a small number of cholinergic fibers in the habenula (Ekström 1987). If these characteristics are plesiomorph, there could be again a correlation between gene duplications and a further change of function. $\alpha 4$ and $\beta 2$ could thus have kept the ancestor role of the neuronal nAChR , whereas other paralogs could have found new functional specificities in the evolving cholinergic systems.

We have shown, on the basis of cladograms and phenograms, that the first duplications in the nAChR occurred before the divergence of nematodes. Several nAChR subfamilies were identified. There is congruence between sequence and gene-structure analyses, and the three subfamilies present in vertebrates correspond closely to the functional subgroups (described from anatomical, pharmacological, and structural considerations). Two phenomena seem to have generated the wealth of the family. First, several switches of expression seem to have occurred from neuron to muscle and the opposite. Second, multiple gene duplications gave the extant number of paralogs. The neuronal nicotinicsubunit subfamily (type III subunits) appeared at the beginning of the chordate phylum and grew until the separation of Sauropsida and Theropsida lineages. This diversification, both quantitative and functional, paralleled the increase in complexity of the cholinergic systems. A link between an increased combinatorial complexity of subunit combinations and a larger plasticity in the functioning of these pathways is plausible.

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## Appendix 1: Glossary of the Cladistic Terms Present in the Text

Homology: Two similar characters are homologous when they come from a common ancestor. There is homology between two genes if they arose by duplication. Characters are homologous if (1) they look like each other, (2) they do not coexist in the same organism (the arms and the wings of angels), and (3) if they provide the same phylogenies as other homologous characters.
Ortholog: Two orthologs are homologs that have arisen by speciation (the "same" gene in two different species).
Paralog: Two paralogs are homologs that have arisen by duplication in the same organism.
Monophyly: A monophyletic group is formed by one ancestor and all its descendants.
Polyphyly: A polyphyletic group is formed by different subgroups, which do not share any common ancestor belonging to the group.
A plesiomorphy is an ancestor character. It is not useful in reconstructing phylogenies.
An autapomorphy is a derived character, present in one descendant only. It is not useful in reconstructing phylogenies
A synapomorphy is a derived character, shared by a monophyletic group of several descendants. The synapomorphies are the only useful characters with which to infer phylogenies
Informative site: A character is informative if it exists under at least two states present twice. A character presenting everytime the same state as well as a character different in every compared object are not informative

|  |  |  |  | TVGLQLIQLI | NVDEVNQIVT |
| :---: | :---: | :---: | :---: | :---: | :---: |
| . | EGRLREKLFS | --GYDSTVRP | AREVGDRVWV | SIGLTLAQLI | SLNEKDEEMS |
| b $\delta$ | EERLIRHLEE | EKAYNKELRP | AAHKESV-EI | SLALTLSNLI | SLKEVEETLT |
| be | ELRLYHYLFD | --TYDPGRRP | VQEPEDTVTI | SLKVTLTNLI | SLNEKEETLT |
| by | EERLLGDLMQ | --GYNPHLRP | AEHDSDVVNV | SLKLTLTNLI | SLNEREEALT |
| c $\alpha 2$ | EDRLFKHLFT | G--YNRWSRP | VPNTSDVVIV | KFGLSIAQLI | DVDEKNQMMT |
| ca3 | EHRLYAALFK | N--YNQFVRP | VKNASDPVII | QF'EVSMSQLV | KVDEVNQIME |
| ca4 | EERLLKKLES | G--YNKWSRP | VANISDVVLV | RFGLSIAQLI | DVDEKNQMMT |
| cas | EDRLFKHLFE | D--YQRWVRP | VEHLNDTIKI | KFGLAISQLV | DVDEKNQLMT |
|  | QRKLYKELIK | N--YNPLERP | VANDSQPLTV | YFTLSLMQIM | DVDEKNQVLT |
| ca8 | QRRLYRDLLR | N--YNRLERP | VMNDSQPIV | ELQLSLLQII | DVDEKNQVLI |
| c $\beta 2$ | EERLVEYLID | PTRYNKLIRP | ATNGSQLVTV | QLMVSLAQLI | SVFEREQIMT |
| c $\beta 4$ | EEKLMNHLLS | PDRYNKLIRP | AVNSSQLVSI | ELQVSLAQLI | SVINEREQIMT |
| $c \gamma$ | EEKLLQDLMT | -NYNRHLRP | ALRGDQVIDV | TLKLTLTNLI | SLNEREETLT |
| d $\alpha^{2}$ | AKRLYDDLLS | N--YNRLIRP | VSNNTDTVLV | KLGLRLSQLI | DLNTLKDQILT |
| d $\alpha$ Li | AKRLYDDLLS | N--YNRLIRP | VGNNSDRLTV | KMGLRLSQLI | DVNLKNQIMT |
| d $\beta 2$ | TKRLYDDLLS | N--YNRLIRP | VVNNTETLTV | WLGLKLSQLI | EVNLKNQVMT |
| dnach | EERLVRDLFR | G--YNKLIRP | VQNMTRQKVGV | RFGLAFVQLI | NVNEKNQVMK |
| gfa $\times 3$ | EDRLFRRLFR | R--YNQFIRP | VENVSDPVTV | EFEVSISQLV | KVDEVNQIME |
| gfß2 | LRS--DFLLG | PERYNKLIRP | AVNKSQQVTI | GIKVSLAQLI | SVINEREQIMT |
| $\mathrm{gfn} \alpha$ | EDALLRELFQ | G--YQRWVRP | VQHANHSVKV | RFGLKISQLV | DVDEKNQLMT |
| gfno | EDTLLRNLFR | G--YQKWVRP | ILHANDTITV | RFGLKISQLV | DVDEKNHLMT |
|  | ETRLVAKLFK | D--YSSVVRP | VEDHRQVVEV | TVGLQLIQLI | NVDEVNQIVT |
| ha3 | EHRLFERLFE | D--YNEIIRP | VANVSDPVII | HFEVSMSQLV | KVDEVNQIME |
|  | EDSLLKDLFQ | D--YERWVRP | VEHLNDKIKI | KFGLAISQLV | DVDEKNQLMT |
| ha7 | QRKLYKELVK | N--YNPLERP | VANDSQPLTV | YFSLSLEQTM | DVDEKNQVIT |
| $\mathrm{h} \beta 1$ | EGRLREKLFS | --GYDSSVRP | AREVGDRVRV | SVGLILAQLI | SLNEKDEEMS |
| $\mathrm{h} \beta 2$ | EERLVEHLILD | PSRYNKLIRP | ATNGSELVTV | QLMVSLAQLI | SVHEREQIMT |
| 研 | LLRLSDHLLA | --NYKKGVRP | VRDWRKPTTV | SIDVIMYAIL | NVDEKNQVIT |
| ra2 | EDRIFKHLFG | G--YNRWARP | VPNTSDVVIV | RFGLSIAQLI | DVDEKNQMMT |
| ra3 | EHRLFQYLFE | D--YNEIIRP | VANVSHPVII | QFEVSMSQLV | KVDEVNQIME |
| ra4 | EERLIKRLFS | G--YNKWSRP | VGNISDVVLV | RFGLSIAQLI | DVDEKNQMMT |
| ras | EDSLFRDLFE | D--YERWVRP | VEHLSDKIKI | KFGLAISQLV | DVDEKNQLIMT |
| r 26 | EEQLFHTLFA | H--YNREIRP | VENVSDPVTV | HFELAITQLA | NVDEVNQIME |
| r $\alpha 7$ | QRRLYKELVK | N--YNPIERP | VANDSQPLTV | YFSLSLLQIM | DVDEKNQVLT |
| ז $\beta 2$ | EERLVEHLID | PSRYNKLIRP | ATNGSELVTV | QLMVSLAQLI | SVHEREQIMT |
| r $\beta 3$ | EDALIRHLFQ | G--YQKWVRP | VLNSSDIIKV | YFGLKISQLV | DVDEKNQLMT |
| r $\beta 4$ | EEKLMDDLLN | KTRYNNLIRP | ATSSSQLISI | RLELSLSQLI | SVNEREQIMT |
| r $\delta$ | EQRLIQHLFE | EKGYNKELRP | VARKEDIVDV | ALSLTLSNLI | SLKEVEETIT |
| ז¢ | ELSLYHHLFD | --NYDPECRP | VRRPEDTVTI | TLKVTLJTNLI | SLNEKEETLT |
| r $\gamma$ | EERLIADLMR | --NYDPHLRP | AERDSDVVNV | SLKLTLTNLI | SLNEREEALT |
| rgly 03 | SDFLDKLMGR | TSGYDARIRP | -NFKGPPVNV | TCNIFINSFG | SIAETTMDYR |
| sall | AKRLYDDLLS | N--YNRLIRP | VSNNTDTVLV | KLGLRLSQLI | DLNLKDQILT |
| tal | ETRLVANLLE | N--YNKVIRP | VEHHTHFVDI | TVGLQLIQLI | SVDEVNQIVE |
|  | EGRLIEKLIG | --DYDKRIIP | AKTLDHIIDV | TLRLTLTNLI | SLNEKEEALT |
| xala | ESRLINDLFK | S--YNKVVRP | VKAFKDKVVV | TVGLQLIQLI | NVNEVNQIVT |
| $x \propto 1 b$ | ETRLIGDLFA | N--YNKVVRP | VETYKDQVVV | TVGLQLIQLI | NVDEVNQIVS |
| $x \gamma$ | EERLINDLMK | --NYNKNLRP | VERDGDIISV | SIKLTLTNLI | SLNEKEEALT |

bal TNVRLKQQWV DYNLKWNPDD YGGVKKIHIP SEKIWRPDLV LYNNADGDFA
$\mathrm{b} \beta 1$ TKVYLDLEWT DYRLSWDPEE HEGIDSLRIS AESVWLPDVV LLNNNDGNFD
b $\delta$ TNVWIEQGWT DSRLQWDAED FGNISVLRLP ADMVWLPEIV LENNNDGSFQ
be TSVWIGIDWQ DYRLNYSKGD FGGVETLRVP SELVWLPEIV LENNIDGQFG
b $\gamma$ TNVWIEMQWC DYRLRWDPRD YGGLWVLRVP STMVWRPDIV LENNVDGVFE ca2 TNVWLKQEWS DYKLRWNPED FDNVTSIRVP SEMIWIPDIV LYNNADGEFA
ca3
$c \propto 4$
$c \alpha 5$
$c \alpha 7$
ca8
c 32
c $\beta 4$
CR
da2 TNVWLEHEWQ DHKFKWDPSE YGGVTELYVP TNVWVEQEWN DYK工KWNPDD YGGVDTLHVP SEHTWHPDIV LINNADGEYV
dß2 TNLWVKQRWF DYKLRWDPEE YGGVEQLYVP SEHIWVPDIV LYNNWDGNYE dnachr SNVWLRLVWY DYQLQWDEAD YGGIGVLRLP PDKVWKPDIV LFNNADGNYE
gfa3 TNLWLRHIWN DYKLKWLPAE FDGIEFIRVP SNKIWRPDIV LYNNAVGDFL

Appendix 2: Alignment of 48 nAChR Subunits Made by the CLUSTAL V Software-Total Sites: 394; Informative Sites: 357
gfb2 TNVWLTQEWT DYRLVWDPNE YEGIKKLRIP SQHIWLPDIV LYNNADGVYE gfna2 TNVWLWQEWL DYKLRWNPEN YGGITSIRVP SESIWLPDIV LYENADGRFE gfna3 TNVWLWQEWT DYKLRWNPED YGGITSIRVP SETIWLPDIV LYENADGRFE h $\alpha 1$ TNVRLKQQWV DYNLKWNPDD YGGVKKIHIP SEKIWRPDVV LYNNADGDFA ha3 TNLWLKQIWN DYKLKWNPSD YGGAEFMRVP AQKIWKPDIV LYNNAVGDFQ ha5 TNVWLKQEWI DVKLRWNPDD YGGIKVIRVP SDSSWTPDIV LFDNADGRFE ha7 TNIWLQMSWT DHYLQWNVSE YPGVKTVRFP DGQIWKPDIL LYNSADERFD hß1 TKVYLDLEWT DYRLSWDPAE FEGIDSLRIT AESVWLPDVV LLNNNDGNFD hß2 TNVWLTQEWE DYRLTWKPEE EDNMKKVRLP SKHIWLPDVV LYNNADGMYE mser TYIWYRQYWT DEFLQWTPED FDNVTKLSIP TDSIWVPDIL INEFVDVG-K ra2 TNVWLKQEWN DYNVRWDPAE EGNVTSLRVP SEMIWIPDIV LYNNADGEFA ra3 TNLWLKQIWN DYKLKWKPSD YQGVEFMRVP AEKIWKPDIV LYNNADGDFQ ra4 TNVWVKQEWH DYKLRWDPGD YENVTSIRIP SELIWRPDIV LYNNADGDEA ras TNVWLKQEWI DVKLRWNPDD YGGIKIIRVP SDSLWIPDIV LFDNADGRFE ra6 TNLWLRFVWK DYRLCWDPTE YDGIETLRVP ADNIWKPDIV LYNNAVGDEQ r $\alpha 7$ TNIWLQMSWT DHYLQWNMSE YPGVKNVRFP DGQIWKPDIL LYNSADERFD ז 32 TNVWLTQEWE DYRLTWKPQH FDNMKKVRLP SKHIWLPDVV LYNNADGMYE rß3 TNVWLKQEWT DQKLRWNPEE YGGINSIKVP SESLWLPDIV LFENADGRFE rß4 TSIWLKQEWI DYRLAWNSSC YEGVNILRIP AKRVWIPDIV LYNNADGTYE rס TNVWIDHAWI DSRLQWNANE FGNITVLRLP SDMVWLPEIV LENNNDGSFQ re TSVWIGIEWQ DYRUNFSKDD FAGVEILRVP SEHVWLPEIV LENNIDGQFG
r $\gamma$ TNVWIEMQWC DYRLRWDPKD YEGLWILRVP STMVWQPDIV LGNNVDGVFE
rgly 3 VNIFLRQKWN DPRLAYSEYP DDSLDLDPSM LDSIWKPDLF FANEKGANFH
sall TNVWLEHEWQ DHKFRWDPAE YGGVTELYVP SEHIWLPDIV LYNNADGEYV
tal TNVRLRQQWI DVRIRWNPAD YGGIKKIRLP SDDVWLPDLV LYNNADGDFA
t $\gamma$ TNVWIEIQWN DYRLSWNTSE YEGIDLVRIP SELLWLPDVV IENNVDGQFE
x $\alpha 1 \mathrm{a}$ TNVRLKQQWE DVHLKWDPED YGGIKKVRIP SSDIWRPDIV IYNNADGDFA
$x \alpha 1 b$ TNIRLKQQWR DVNLKWDPAK YGGVKKIRIP SSDVWSPDLV LYNNADGDEA
$x \gamma$ TNVWVEMQWK DYRLSWDPND YHGISMMRIP STSVWLPDVG LENNVDGTFD
bal IVKFTKVLID YTGHITWTPP AIFKSYCEII VTHFPFDEQN CSMKIGTWTY
bß1 VALDINVVVS SDGSMRWQPP GIYRSSCSIQ VTYFPFDWQN CTMVFSSYSY
b $\delta$ ISYSCNVLIY PSGSVYWLPP AIFRSSCPIS VTYFPFDWQN CSLKFSSLKY
be VAYEANVLVS EGGYLSWLPP AIYRSTCAVE VTYFPFDWQN CSLVERSQTY
b $\gamma$ VALYCNVLVS PDGCVYWLPP AIFRSSCPVS VTFFPFDWQN CSLIFQSQTY
ca2 VTHMTKAHLF SNGKVKWVPP AIYKSSCSID VTYFPFDQQN CKMKFGSWTY
co3 VDDKTKALLK YTGDVTWIPP AIFKSSCKID VTYFPFDYQN CTMKFGSWSY
ca4 VTHLTKAHLF YDGRIKWMPP AIYKSSCSID VTFFPFDQQN CKMKFGSWIY
co5 GT-STKTVVK YDGTIAWTPP VNYKSSCTID VTFFPFDLQN CSMKFGSWTY
c $\alpha 7$ ATFHTNVLVN SSGHCQYLPP GIFRSSCYID VRWFPFDVQK CNLKFGSWTY
ca8 ATFHTNVLVN YSGSCQYIPP GILKSTCYID VR
© 32 VSFYSNAVTS
c 34
c $\gamma$
d $\alpha 2$ VTTMTRATTH
daLi VTIMTKAILH
$\mathrm{d} \beta 2$ VTLMTKATLK $Y$
dnachr VRYKSNVLIY P
gfß2 VSFYCNAVVS NTGDTFWTPD ATYKSACAIE
gfna 2 GSLMTKAIVR YNGMITWTPP ASYKSACTMD
gfna3 GSLMTKAIVR FNGTIMWTPP ASYKSSCTMD
hal IVKPTKVLLQ YTGHITWTPP AIFKSYCEII
ho3 VDDKTKALLK YTGEVTWIPP AIFKSSCKID
has GT-STKTVIR YNGTVTWTPP ANYKSSCTID
$h \alpha 7$ ATFHTNVLVN SSGHCQYLPP GIEKSSCYID
hß1 VALDISVVVS SDGSVRWQPP GIYRSSCSIQ
$\mathrm{h} \beta 2$ VSFYSNAVVS YDGSIFWLDP AIYKSACKIE
mser SPNIPYVYVH HRGEVQNYKP LQLVTACSLD
ra2 VTHMTKAHLF FTGTVHWVPP AIYKSSCSID
ra3 VDDKTKALLK YTGEVTWIPP AIFKSSCKID
r $\alpha 4$ VTHLTKAHLF
r $\alpha 5$
ra6
ra7
г $\beta 2$
r 33
r $\delta$ SVI

VRWFPFDVQK CDLKFGSWTH VKHFPFDQQN CTMKFRSWTY VKHFPEDQQN CTLKFRSWTY VTYFPFDWQN CTMVFQSQTY VRYFPFDQQT CFMKFGSWTY VEYFPFDEQT CEMKFGSWTY VEYFPYDEQI CFMKFGSWTY VTYFPFDQQT CIMKFGSWTE ITYFPFDYQN CSMKEGSWTY VRNFPFDQQN CTLKFRSWTY VTFFPFDRQN CSMKFGSWTY VTEFPEDRQN CSMKFGSWTY VTHFPFDEQN CSMKLGTWTY VTYFPFDYQN CTMKFGSWSY VTFFPEDLQN CSMKFGSWTY VRWFPFDVQH CKLKFGSWSY VTYFPFDWQN CTMVFSSYSY VKHFPFDQQN CTMKFRSWTY IYNFPEDVQN CSLTETSWLH VTFFPFDQQN CKMKFGSWTY VTYFPFDYQN CTMKEGSWSY VTFEPFDQQN CTMKFGSWTY VTFEPFDLQN CSMKFGSWTY ITFFPFDHQN CSLKFGSWTY VRWEPFDVQQ CKLKFGSWSY VKHFPEDQQN CTMKFRSWTY VTPFPFDRQN CSMKFGSWTY VKHFPFDQQN CTLKFRSWTY VTYFPFDWQN CSLKFSSLKY

Appendix 2: Continued
re VAYDCNVLVY EGGSVSWLPR AIYRSTCAVE VTYFPFDWON CSLIFRSQTY
r $\gamma$ VALYCNVLVS FDGCIYWLPP AIFRSSCSIS VTYFPFDWQN CSLVFQSQTY
rgly 03 EVTTDNKLLR INGNVLYSIR LTLTLSCPMD LKNF PMDVQT CIMQLESFGY
sall VTTMTKAVLH HTGKVVWTPP AIFKSSCEID VRYFPFDQQT CFMKFGSWTY
t $\alpha 1$ IVHMTKLLLD YTGKIMWTPP AIFKSYCEII VTHFPFDQQN CTMRLGIWTY
ty VAYYANVLVY NDGSMYWLPP AIYRSTCPIA VTYFPFDWQN CSLVFRSQTY
x $\alpha$ a

bal DGSVVVINPE SDPDLSNFME SGEWVIKESR GWKHWVFYAC CPST--PYLD
bß1 DSSEVSLQTG LSIHEGTFIE NGQWEIIHKP SRLIQPSVDP RGGGEGREE
b $\delta$ TTKEITLSLK QAIDPEGFTE NGEWEIVHRP ARVNVDPS-V PLDSPNR-QD
be NAEEVEFVFA VDIDTEAYTE NGEWAIDFCP G-VIRRHDGD SAGGPGE-TD
by STNEINLQLS QEIDPEAFTE NGEWAIRHRP AKMLLDEAA- PAEEAGH-QK
ca2 DKAKIDLENM EHVDLKDYWE SGEWAIINAI GRYNSKKYDC CTEI--Y-PD
ca3 DKAKIDLVLI GSMINLKDYWE SGEWAIIKAP GYKHDIKYNC CEEI--Y-TD
ca4 DKAKIDLVSM HSVDQLDYWE SGEWVIINAV GNYNSKKYEC CTEI--Y-PD
caS DGSQVDIILE DYVDKRDFFD NGEWEIVTAT GSKGNRTDGC CW----Y-PF
ca7
ca8
c 32
c 34
$\mathrm{c} \gamma$
da2
d $\alpha$ Li
d ${ }^{2} 2$
dnachr
gfo3
${ }_{\mathrm{g}}^{\mathrm{g} / \mathrm{B}} \mathrm{n} 22$
$\mathrm{gfn} \alpha 3$
hal
h $\alpha 3$
has
ha7
h $\beta 1$
hß2
mser
r $\alpha 2$
r $\alpha 3$
r $\alpha 4$
ros
ra6
r $\mathbf{r} 7$
rß3 DGTMVDI SDASIDD
rß4 DHTEIDMVLK SPAIMDDFTP S
r $\delta$
г
rgly 03 STSEINLQLS QEIDPEAFTE
sall
ty
xala
$x \propto 1 b$
$\mathrm{x} \gamma$

|  | ITYHFVMQRL |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | VTFYLIIRRK | PLFYLVNV | PC |  |  |
|  | VT | PL | PCV | LVF |  |
| b $\varepsilon$ | VIYSLIIRR | PLFYVIN | PCVLISGLV | LAYF |  |
|  | VVFYLIIQRK | PLFYVINIIA | PCVLISSVAI | LIYFLPAKAG |  |
|  | ITFYFVIRRL | PLFYTINLII | PCLLISCLTV | LVFYLPSDCG |  |
|  | ITY | pLF | PCL | LVF |  |
|  | ITYSFIIRRL | PLF | PCL | LVF |  |
|  |  |  | PCI |  |  |
|  |  |  |  |  |  |

Appendix 2: Continued

|  |  |  |  |
| :---: | :---: | :---: | :---: |
|  |  |  |  |
| c 34 |  |  |  |
| c $\gamma$ | RK | LaV LVYfipakag |  |
|  | IFFNITLRRK TLFYTVNLII |  |  |
| d $\alpha$ L |  |  |  |
| d $\beta$ | K TLFYTVNLIV | CVALTFLTV LVFYLPSDSG |  |
| dnach | K |  |  |
| $\mathrm{gf} \alpha 3$ |  |  | -EKVTLCISV |
|  | ITYDFVIKRK PLFYTINLII | LVFYLPSDCG |  |
| $\mathrm{gfn} \alpha 2$ | ITYSFILKRL |  |  |
| gfno 3 | SFILKRL PLFYTLFLII | EG |  |
|  | L PLYFIVNVII | PCLIFSELTG LVFYLPTDSG |  |
|  | ITYSLYIRRL PLFYTINLII |  | -EKVILLCISV |
|  |  |  |  |
| ha7 | R TLYYGLNLLI |  |  |
|  | VIFYLIIRRK |  |  |
| $\mathrm{h} \beta 2$ | RK PLFYTINLII |  |  |
| mser | MKFYVIIRRR |  |  |
|  |  |  |  |
| ra3 | ITYSLYIRRL PLFYTINLII |  | -EKVTLCISV |
| r $\alpha 4$ | L |  |  |
|  | L |  |  |
| ras | RL PMEYTINLII | PCLFISFLTV LVFYLPSDCG |  |
| r $\times 7$ |  |  |  |
|  | IT |  |  |
| r ${ }^{1} 3$ | VTYSFVLRRL PLFYTIFLII |  |  |
| r 84 |  |  |  |
| - | V |  |  |
| г | VIYTLIIRRK PLEYVINITV | G | V |
|  | VVFYLLIQRK PLFYVINIIV | I | V |
|  | IEVRFHIERQ |  |  |
| sall | IFFNITIRRK TLFYTVNLIV | G |  |
| $t \times 1$ |  |  | V |
| ${ }^{1} \gamma$ |  |  | V |
| x |  |  |  |
| x $\alpha$ |  |  |  |
| $\mathrm{x} \gamma$ |  |  |  |
|  | unsulvinl IVEu-PSiss |  |  |
|  | L | SVPIIIKYLM FTMVVIVTFSV |  |
|  | L | AIPLIGKFLL FGMVLVTMVV | H |
|  | LLAQTVFLFL | SVPLEGRYLI FVMVVATLIV |  |
|  | LLAQTVFLFL VAKKVPETSQ | T |  |
| ca2 | LTVELL | VIPTIGEVIT FTMIFVTI ST | ITVFVLNVH |
|  | LLSLTVFLLV ITETIPSTSI | - |  |
|  | TVFLLL ITEIIPSTSL | IPLIGEYLL |  |
| c | LVSLTVFLLV IEEIIPSSSK | VIPLIGEYLV FTMIFVTLSI |  |
| cos | LLSLTVFMLL VAEI |  |  |
|  | TVFMLL VAEIMPATSD | SVPLIAQYFA STMVIVGISV |  |
| c 32 | TVFLLL |  |  |
| c $\beta 4$ | LLALTVFLIL IS |  |  |
|  | LLAQTVFLFL IAQKVPETSQ | T FTMVVTITVIV |  |
|  | LLSQTMFELL ISEIIPSTSL |  |  |
| d $\alpha$ | LLSLTVFFLL | GKYLI FTMMLVTLSV | AV |
|  | LVSLTVFFLL | GKYLL FTMILVSLSV | - |
| dna | VVFLIL VSK |  |  |
|  |  |  |  |
|  | LLALTVFLLL ISKIVPPTSL | VPLIGKYLM FTMVEVTFSI | - |
|  | LVSLTVFLLV IEEIIPSSSK |  |  |
| gfn $\alpha 3$ |  |  |  |
|  | LISSLTVFLLV IVELIPSTSS | VPIIIGKYML FTMVFVIASI | -1V1010 |
|  | LISLTVFLLV ITETIPSTSL | VIPLIGEYLI FTMIFVTLSI | VITVFVLNVH |
|  | LVSLTVFLLV IEEIIPSSSK | - TGEYIV PTMIFVIST |  |
|  | L VAEIMPATSD |  |  |
|  | LITLTVFLLL LADKVPETSL | SVPIIIKYLM ETMVLVTPSV | -LSVNLNLH |
|  | LLALTVFLLL ISKIVPPTSL | DVPLVGKYLM FTMVLVTFSI |  |
| mse |  |  |  |
| ra2 | LLSLTVFLL ITEIIPSTSL |  |  |

Appendix 2: Continued


Appendix 2: Continued


Appendix 2: Continued


Appendix 3: Alignment of 13 nAChR Subunits Made by the CLUSTAL V Software-Total Sites: 351; Informative Sites: 263
ca8 VVVTVLVLQF HHHDPQAGKM PRWVRVILIN WCAWFLRMKK PTIPVIVKIL
d $\alpha 2$ VVITIIILNI HYRKPSTHKM RPWIRSFFIK RLPKLL-IMR V---ELERAI
d $\alpha \mathrm{Li}$ UTYTTAVTNV NFRSDVTHRM APWTORTFTQ TPKICTER
$\mathrm{d} \beta 2$ VWTTVCVINI HFRSPSTHNM SRIVRKLFLH FMPKLMMMRR T---EVLQAL
dnachr ILVTVIIINW NFRGPRTHRM PMYIRSIFLH YLPAFLFMKR ---PEASKAT
mser LAETIFIVRL VHRQDLQRPV PDWLRHLVLD RIAWILCLPR EASLAVRGLL
onachr VLVTVISLNL HERRPSTHRM PIWVKWLFLR ILPKILFMRR ----HVIKAF
r $\alpha 2$ IVITVFVLNV HHRSPSTHNM PNWVRVALLG RVPRWLMMNR PLSPQIQKAL
$\mathrm{r} \alpha 3$ IVITVFVLNV HYRTPTTHTM PTWVKAVFLN LLPRVMFMTR PLSPEIKEAI
r $\alpha 7$ VVVTVIVLRY HHHDPDGGKM PKWTRIILLN WCAWFLRMKR PGDPDLAKIL
rß2 IVTSVCVLNV HHRSPTTHTM APWVKVVFLE KLPTLLELQQ ---PGLREAV
r $\delta$ VVICVIVLNI HFRTPSTHVL SEGVKKFFLE TLPKLLHMSR PLFNEMKPAV
$r \boldsymbol{\gamma} \quad$ VVNSVVVLNV SLRSPHTHSM ARGVRKVFLR LIPPQLLRMHV HASPAIQACV
ca8 EEVQFIAMRF RKQDEGEEIC SEWKFAAAVI DRLCLVAFTL FAIICTFTIL
d $\alpha 2$ HNVMFIQHHM QRQDEFNAED QDWGFVAMVM DRLFLWLFMI ASLVGT-FVI
daLi EGSRFIAQHV KNKDKFESVE EDWKYVAMVL DRMFLWIFAI ACVVGTALII
dß2 RAVRFIAQHI KDADKDNEIV EDWKFVSMVL DRFFLWLFTL SCVFGTLAII
dnachr EAVEFIAEHL RNEDLYIQTR EDWKYVAMVI DRLQLYIFFI VTTAGTVGIL M
mser QELSSIRHFL EKRDEMREVA RDWLRVGYVL DRLLERIYLL AVLAYSITLV T
onachr ENVCFIAQLL KKKDREAMID EDWKFVARVL DRLFLLLFSI ACFLGTILIL F
ra2 EGVHYIADRL RSEDADSSVK EDWKYVAMVV DRIFLWLFII VCFLGTIGLF L
ra3 QSVKYIAENM KAQNVAKEIQ DDWKYVAMVI DRIFLWVFII VCILGTAGLF L
ra7 EEVRYMPTAY RCQDESEVIC SEWKFAACVV DRLCLMAFSV FTIICTIGIL M
$\mathbf{r} 32$ DGVRFIADHM RSEDDDQSVR EDWKYVAMVI DRLFLWIFVF VCVFGTVGMF L
r $\delta$ DGANFIVNHM RDQNSYNEEK DNWNQVARTV DRLCLFVVITP VMVVGTAWIF L
$\mathbf{r} \gamma$ DACNLMARAR HQQSHFDSGN EEWLLVGRVL DRVCFLAMLS LFICGTAGIF $\rfloor$
Appendix 3: Continued


[^0]:    Correspondence to: N. Le Novère
    Abbreviations: $\alpha$-bungarotoxin ( $\alpha$-Bgt), acetylcholine (ACh), maximum of parsimony (MP), million years ago (MYA), neighbor-joining ( NJ ), nicotinic acetylcholine receptor (nAChR)

[^1]:    Analyses of Gene Structure. The mixed-parsimony algorithm with the Wagner method (Eck and Dayhoff 1966, program MIX) and the

[^2]:    ${ }^{\text {a }}$ The six sign codes are the accession numbers of the Genbank-Embl databases. Rat $\alpha 4$ is the isoform 4-2

