

Vision Research 38 (1998) 1431-1441

Molecular composition of GABA_C receptors

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Received 9 May 1997

Abstract

In the central nervous system inhibitory neurotransmission is primarily achieved through activation of receptors for γ -aminobutyric acid (GABA). Three types of GABA receptors have been identified on the basis of their pharmacology and electrophysiology. The predominant type, termed GABA_A and a recently identified type, GABA_C, have integral chloride channels, whereas GABA_B receptors couple to separate K⁺ or Ca²⁺ channels via G-proteins. By analogy to nicotinic acetylcholine receptors, native GABA_A receptors are believed to be heterooligomers of five subunits, drawn from five classes (α , β , γ , δ , ϵ/χ). An additional class, called ρ , is often categorized with GABA_A receptor subunits due to a high degree of sequence similarity. However, ρ subunits are capable of forming functional homooligomeric and heterooligomeric receptors, whereas GABA_A receptors only express efficiently as heterooligomers. Intriguingly, the pharmacological properties of receptors formed from ρ subunits are very similar to those exhibited by GABA_C receptors and ρ subunits and GABA_C responses have been colocalized to the same retinal cells, indicating that ρ subunits are the sole components of GABA_C receptors. In contrast, the propensity of GABA_A receptor and ρ subunits to form multimeric structures and their coexistence in retinal cells suggests that GABA_C receptors might be heterooligomers of ρ and GABA_A receptor subunits. This review will summarize our current understanding of the molecular composition of GABA_C receptors based upon studies of ρ subunit assembly. © 1998 Elsevier Science Ltd. All rights reserved.

Keywords: GABA_C receptor; ρ Subunits; Ligand-gated ion channel; Receptor assembly; Retina

1. Introduction

GABA is the most important inhibitory neurotransmitter in the mammalian central nervous system [1]. Traditionally, GABA-gated neurotransmitter receptors were classified in two structurally and pharmacologically distinct subclasses. The GABAA receptor is a ligand-gated ion channel which consists of several subunits: $\alpha 1-6$, $\beta 1-3$, $\gamma 1-3$, ϵ/χ [2] [3]. These subunits containing an extracellular N-terminus and four transmembrane regions (Fig. 1, left side) are thought to assemble into a pentameric Cl⁻ channel [4]. GABA_A receptors contain modulatory binding sites for benzodiazepines, barbiturates, neurosteroides and ethanol [5-7] and are inhibited by the action of bicuculline and picrotoxin [8]. Because different subunits of the GABA_A receptor are expressed in distinct brain regions and each subunit class determines subtle pharmacological differences, a variety of of GABA_A receptors may be composed of the known subunits [9]. In contrast, GABA_B receptors are members of the seven transmembrane family [10] which are coupled to either K^+ or Ca²⁺ channels via G-proteins and are regulated by intracellular second messenger systems (Fig. 1, right side). They are selectively activated by baclofen and do not respond to the known GABA_A receptor modulators [11].

A third type of GABA receptor, termed GABA_C, had been proposed that is distinct from the previously known GABA receptors. GABA_C receptors gate Cl⁻ currents in various parts of the vertebrate brain and were first described in interneurons of the spinal cord [12–17]. Later, GABA_C receptors in the retina were observed by a group led by Miledi expressing mRNA isolated from the bovine retina in *Xenopus* oocytes [18–20]. GABA_C receptors show distinct electrophysiological properties. Compared with GABA_A receptors, GABA_C receptors have a higher sensitivity for GABA, their currents are smaller and do not desensitize. On the

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Fig. 1. Schematic representation of individual subunits of $GABA_A$ and $GABA_C$ receptors (left) and $GABA_B$ receptors (right). (Left) By analogy to the nicotinic acetylcholine receptor, subunits of ligand-gated neurotransmitter receptors consist of four transmembrane regions (TM 1–4), a long extracellular N-terminus, a cytoplasmic loop between TM3 and TM4 and a short extracellular C-terminus. The N-terminus contains domains important for ligand binding. The pore of the ion channel is formed by the TM2. (Right) GABA_B receptors are members of the seven transmembrane protein family (TM 1–7). Binding of the agonist causes activation of a G-protein (G), that in turn can either regulate separate ion channels (permeable for K⁺ or Ca²⁺) directly or use second messenger systems such as phospholipase C (PLC) or adenylcyclase (AC).

single-channel level, these receptors are characterized by longer mean-open times and smaller chloride conductance [21,22].

 $GABA_C$ receptors also differ in their pharmacological profile compared with $GABA_A$ and $GABA_B$ receptors. They are insensitive to $GABA_A$ receptor modulators, such as barbiturates and benzodiazepines as well as against the typical $GABA_A$ receptor antagonist bicuculline and they are not activated by the $GABA_B$ receptor agonist baclofen (for review see [23]). $GABA_C$ receptors have been characterized most extensively in the retina. In rat, tiger salamander and hybrid bass, $GABA_C$ receptors were found on bipolar cells [21,22,24,91,25,26] and in the white perch on horizontal cells [27,28].

Several lines of evidence indicate that GABA_C receptors are composed of ρ subunits (ρ 1,2 in humans: $[29,30]; \rho 1,2 \text{ in rat: } [31,32]; \rho 2,3 \text{ in rat: } [33,34]; \rho 1,2 \text{ in }$ chicken: [35]). When heterologously expressed, ρ subunits show similar electrophysiological and pharmacological properties compared with GABA_C receptors. Furthermore, RT-PCR and in situ hybridization studies showed the expression of ρ subunits in cells with GABA_C receptors: rod bipolar cells of the rat and H4 horizontal cells of the white perch [36,37]. Finally, antibody staining of retinal sections revealed that ρ subunits are present on dendrites and axonterminal systems of rod as well as cone bipolar cells of different species [38,39]. The molecular characteristics of ρ subunits and their relationship to GABA_C receptors will be the focus of this review.

2. Homooligometric assembly of the $\rho 1$ subunit

A prominent characteristic of ρ subunits is their ability to form functional homooligomeric GABAgated Cl⁻ channels (ρ 1: [29]; ρ 2: [40]). This stands in sharp contrast to GABA_A receptors, where combinations of different subunits are needed for proper function [41]. Therefore ρ subunits provide a useful model system to study the assembly properties of GABA receptor subunits.

Homooligometric assembly of $\rho 1$ subunits from several species into functional GABA receptors has been reported in different heterologous expression systems. Expression of the human and rat $\rho 1$ subunit in *Xenopus* oocytes [29,42,43,40,31] as well as of the human ρ 1 subunit in mammalian HEK 293 cells [44] showed their ability to efficiently form GABA-gated Cl⁻ channels. Whereas Hill coefficients using the Xenopus expression system were around 2, the GABA dose-response curve of the $\rho 1$ subunit expressed in HEK 293 cells is much steeper, with a Hill coefficient between 3 and 4. In contrast, GABA_A receptor subunits expressed in either Xenopus oocytes or 293 cells show Hill coefficients of 1-2 [41,45]. The high Hill coefficient of the expressed ρ 1 subunit supports the idea of homooligometric assembly of five $\rho 1$ subunits into a pentameric GABA_C receptor where each subunit has its own GABA binding pocket. Indeed, mathematical calculations predict the existence of five equivalent and independent GABA binding sites in receptors formed of the human $\rho 1$ subunit. It has been proposed that three GABA

molecules are necessary to open the channel, while two additional binding sites increase ligand sensitivity and stabilize the open state of the receptor [46].

By analogy to subunits of the nicotinic acetylcholine receptor [47] it has been suggested that ρ subunits consist of a long extracellular N-terminus, four membrane-spanning regions (TM1 to TM4) and a short extracellular C-terminus (Fig. 1, left side). Between TM3 and TM4 a long intracellular loop may contain consensus sites for intracellular modulation and for localization of receptors to synaptic sites. The standard model predicts that ρ subunits assemble into a pentameric receptor (Fig. 2) with the second transmembrane domain (TM2) of each subunit facing the ion pore.

The topology of the $\rho 1$ subunit relative to membranes has been studied using human $\rho 1$ subunit protein translated in vitro in the presence of microsomal membrane vesicles [48]. While the N-terminus of the $\rho 1$ subunit was protected from cleavage and thus present in the lumen of the membrane vesicles, the C-terminus was degraded. Since the lumen of the vesicle is equivalent to the lumen of the endoplasmic reticulum, this result suggested an extracellular location of the N-terminus of ρ subunits in mature receptors. This orientation is consistent with the N-terminal localization of two GABA binding domains as well as a histidine (His156), which is important for the inhibitory effect of extracellular Zn²⁺ (see Section 6 and [49,50]).



Fig. 2. Proposed structure of a GABA_C receptor *in vivo*. Five ρ subunits assemble into a pentameric protein complex forming the Cl⁻ channel as a central pore. The binding sites for agonists (e.g. GABA) as well as competitive antagonists and neuromodulators are located in the extracellular part of the protein complex. Picrotoxinin binds in the channel pore but shows also an use-dependent effect, indicating an allosteric mechanism. The intracellular loop between transmembrane regions 3 and 4 may contain consensus sequences for protein kinases such as PKC.

By dividing the $\rho 1$ subunit into the N-terminal part $(N-\rho 1)$ which contains the protein up to the first transmembrane domain and the C-terminal part $(C-\rho 1)$ which contains all four transmembrane regions and the C-terminus. Hackam and coworkers were able to determine the contribution of each protein fragment in subunit assembly. A mixture of in vitro translated full-length $\rho 1$ (fused to a C-terminal FLAG epitope) was incubated together with N- ρ 1 and subsequently immunoprecipitated with an anti-Flag antibody. $\rho 1$ and N- ρ 1 were detected in the precipitate, indicating that sufficient information for homooligomeric assembly of the $\rho 1$ subunit is located in the extracellular N-terminus. In a complementary experiment, the presence of receptor assembly domains in N- ρ 1 was tested using a heterologous expression system. Xenopus oocytes were injected with different ratios of cRNA encoding for N- ρ 1 and full-length ρ 1. N- ρ 1 contained no transmembrane regions and did not form functional Cl⁻ channels. Moreover, increasing amounts of N- ρ 1 reduced GABA activated $\rho 1$ currents in a dose dependent manner. It was proposed that $N-\rho 1$ contained domains that enabled co-assembly between N- $\rho 1$ and full-length $\rho 1$ proteins, resulting in non-functional receptors (Fig. 3). A 5-fold excess of N- ρ 1 compared with $\rho 1$ was sufficient to eliminate GABA responses. Finally, Hackam and coworkers demonstrated that a 100 amino acid region in the N-terminus of the $\rho 1$ subunit contains signals that are critical for robust homooligomeric expression [51].

Together, these results suggested that the N-terminal region of the $\rho 1$ subunit is extracellular and that it contains sufficient information for the homooligomeric assembly of $\rho 1$ subunits into functional GABA receptors. However, it cannot be excluded that also the second half of the protein, especially the cytoplasmic loop contains assembly sequences which may only be active in combination with the N-terminus.

3. Homooligomeric assembly of $\rho 2$ and $\rho 3$ subunits

In addition to the $\rho 1$ subunit, other members of this subunit class have the ability to form functional homooligomeric GABA receptors. The human $\rho 2$ subunit forms GABA-gated Cl⁻ channels with electrophysiological and pharmacological properties that are very similar to those exhibited by $\rho 1$ [52,40]. However, homooligomeric expressed $\rho 2$ subunits generate considerably lower whole-cell currents compared with $\rho 1$. For example, injection of *Xenopus* oocytes with equal amounts of $\rho 1$ and $\rho 2$ cRNA (5 ng) produces currents ranging from 200 to 1000 pA for the $\rho 1$ subunit and from 10 to 100 pA for $\rho 2$ [40]. This difference appears to be independent of the expression method. Nuclear injection of $\rho 2$ DNA into *Xenopus* oocytes resulted in



Fig. 3. Assembly of ρ subunits in heterologous expression systems. The left side shows magnified views of ρ subunits assembled in intracellular membranes of *Xenopus* oocytes, that are drawn on the right. (Top) Assembly of five ρ subunits in the rough endoplasmic reticulum is followed by trafficking of the assembled receptor via the golgi network to the cell surface (arrows). (Middle) Interaction of full-length ρ subunits with ρ subunit N-termini interferes with assembly into functional receptors. Consequently fewer functional receptors reach the cell surface while non-functional protein complexes are routed to a degradation pathway. Abnormally assembled receptors may also be trafficked to the cell surface, but are non-functional. The net result is a decrease in GABA-gated whole-cell current. (Bottom) Increasing amounts of ρ subunits to the degradation pathway, resulting in a lack of functional GABA receptors at the cell surface.

GABA-gated whole-cell currents that were consistently in the 100–200 pA range, compared with ρ 1-generated currents (more than 1000 pA) under the same conditions (Wang and Cutting, unpublished observation). The human ρ 2 subunit also forms homooligomeric GABA receptors following transient transfection of HEK 293 cells (Enz and Cutting, unpublished observation). In contrast to the human ρ 2 subunit, the rat counterpart does not seem to form functional GABA receptors when ρ 2 cRNA was injected into *Xenopus* oocytes [31]. However, the authors did not use nuclear injection to increase the expression level.

It has also been reported that the rat ρ 3 subunit as well as a white perch ρ subunit can form functional homooligomeric GABA receptors after cRNA injection in *Xenopus* oocytes [90,37]. In both cases, GABA-gated Cl⁻ currents were similar to the typical GABA_C receptor characteristics described above. Interestingly, the white perch ρ subunit shares the highest similarity with the human ρ 2 subunit (90%). Therefore, the authors suggest that this subunit may be the ρ 2 counterpart of the white perch. Indeed, amplitudes of GABA-gated Cl⁻ currents recorded of the expressed fish subunit are comparable with those obtained from the homooligomeric expressed human ρ 2 subunit. These data provide further evidence that functional homooligomeric GABA receptors can not only be formed of the homooligomeric expressed ρ 1 subunit but also of other subunits of the ρ family.

4. Heterooligometric assembly of ρ subunits

At this time, only a few studies have explored the possibility that ρ subunits may heterooligomerize. Coinjection of the rat $\rho 1$ and $\rho 2$ subunits in *Xenopus* oocytes generated functional GABA receptors with distinct pharmacology compared with the $\rho 1$ subunit injected alone [31]. Immunoprecipitation studies using a specific antibody showed that the N-terminal part of human $\rho 1$ is able to interact with the human $\rho 2$ subunit in vitro [48]. Together, these studies suggest that ρ subunits are able to form heterooligomeric GABA receptors. The latter study indicates that information for assembly is located in the N-terminal part of the protein, similar to what was found for homooligomeric assembly of the $\rho 1$ subunit [48].

This result is consistent with studies on GABA_A, glycine and nicotinic acetylcholine receptors, where domains important for heterooligomeric subunit assembly have been localized in the N-terminal region [53-56]. However, it it is not known whether different regions of the N-terminus facilitate homooligomeric and heterooligomeric subunit assembly. This information could be important in understanding how the stoichiometry of ρ subunits in a pentameric receptor is controlled. If homooligomeric and heterooligomeric assembly signals are identical, the subunit composition may be determined by the relative abundance of each subunit at the location where assembly occurs. Indeed, different groups have reported transport of mRNA in neurons into dendrites that enable protein biosynthesis and receptor assembly near the synapse (for review see [57,58]). Thus, the presence and number of different ρ subunits in an oligomeric GABA receptor might be controlled by targeting different mRNA types to specific locations within a neuron. In addition, the number of neurotransmitter receptors at specific neuronal sites could be determined by synaptic activity that influences mRNA translation at local areas. For example, it has been shown that the expression of Homer, important for clustering metabotropic glutamate receptors at

synaptic sites, is regulated by neuronal activity [59]. If, in contrast, homo- and heterooligomeric assembly signals are different, then GABA receptors would be formed independent of the local concentrations of each ρ subunit. This was found to be the case for glycine receptor subunits [55].

5. Assembly of ρ subunits with GABA_A and glycine receptor subunits

GABA and glycine receptors are members of the ligand-gated ion channel family. Their subunits are thought to share the membrane topology shown in Fig. 1 (left side). On the amino acid level the similarity between subunit classes (GABA receptor: α , β , γ , δ , ϵ/χ , ρ ; glycine receptor: α , β) is 20–30%, whereas within one class (for example GABA_A receptor subunits $\alpha 1-6$) the homology is 70-80%. Furthermore, each of these subunits is capable of oligomerization. This raises the possibility that each of these proteins is capable of forming heterooligomeric GABA receptors. Pharmacological and electrical properties of GABA receptors are determined by their subunit composition. For example, it has been shown that the inclusion of the GABA_A receptor γ subunit confers sensitivity for benzodiazepines [41]. Following the same principle, ρ subunits in heterooligomeric GABAA receptors might be predicted to alter its sensitivity for GABA, bicuculline and/or modulatory substances. However, co-expression of the human $\rho 1$ subunit with the GABA_A receptor subunits $\alpha 1$, $\beta 1$ and $\gamma 2$ in *Xenopus* oocytes, as well as with a 10-fold excess of the human glycine receptor β subunit in HEK 293 cells showed no detectable alteration in GABA-gated Cl- currents on the whole-cell level ([42]: Enz and Bormann, unpublished observation). Co-immunoprecipitation of human $\rho 1$, $\rho 2$ subunits or the N-terminus of $\rho 1$ together with the human $\alpha 1$, $\alpha 5$ and $\beta 1$ subunits of the GABA_A receptor showed no physical interaction of $GABA_A$ receptors and ρ subunits in vitro [60]. Furthermore, exchanging the N-terminal domain of the human $\rho 1$ subunit with the corresponding region of the GABA_A receptor $\beta 1$ subunit $(\beta 1 \rho 1)$ produced a chimeric subunit that could be co-precipitated with the $\alpha 1$ subunit of the GABA_A receptor. Co-expressing the opposite construct (N-terminus of $\rho 1$ and C-terminus of $\beta 1$, $\rho 1\beta 1$) with the wildtype $\rho 1$ subunit in *Xenopus* oocytes eliminated Cl⁻ currents, whereas co-expression of wildtype $\beta 1$ and $\rho 1$ produced normal GABA-gated currents [60]. Together, these studies suggest that ρ subunits do not assemble with GABA_A or glycine receptor subunits into functional receptors due to different assembly signals in their N-termini.

In contrast to the assembly properties of ρ subunits described above, a mutant rat $\rho 1$ subunit has been

reported to assemble with the GABA_A receptor subunit $\gamma 2S$ and the glycine receptor subunit $\alpha 1$ [61]. However, because the $\rho 1$ subunit was mutated in the channelforming domain (TM2, T314A) and subsequently showed spontaneous channel opening in the absence of agonists as well as mixed inward and outward currents at different GABA concentrations, these experiments do not represent the in vivo situation. Therefore, it is difficult to draw a conclusion from these results regarding the subunit composition of wildtype GABA_C receptors.

In addition to biochemical and electrophysiological data, there is anatomical evidence that ρ subunits do not interact with GABA_A or glycine receptor subunits. Double immunostaining in the rat retina for ρ subunits and for the α 1,2,3 and β 2,3 subunits of the GABA_A receptor as well as for the α 1,2,3 and β subunits of the glycine receptor associated protein gephyrin showed no colocalization on the light microscopic level [62].

Given evidence that (a) co-expression of a number of GABA_A and glycine receptor subunits with the $\rho 1$ subunit does not alter functional characteristics of the ρ 1 subunit in different expression systems; (b) no physical interaction can be detected in immunoprecipitations of in vitro translated subunits; and (c) ρ subunits are not be colocalized anatomically with GABA_A and glycine receptor subunits, it seems unlikely that "mixed" receptor complexes are present in vivo. Therefore, although ρ subunits as well as a number of subunits of the GABAA and glycine receptor are expressed in bipolar cells of the mammalian retina (ρ subunits: [36,38,63]; GABA_A receptor subunits: [64,65]; glycine receptor subunits: [66,67]), these subunits are likely to assemble in distinct receptor types (Fig. 4). Taken together, these data provide strong evidence that ρ subunits are physically and functionally distinct from subunits of GABA_A and glycine receptors and should therefore be classified as GABA_C receptor subunits.

6. Structure/function studies

Based on the likely composition of GABA_C receptors, identification of functional domains in ρ subunits provides insight into structure/function relationships of GABA_C receptors in vivo. Pharmacological characteristics for ρ subunits that have been investigated include their sensitivity to the Cl⁻ channel blocker picrotoxinin and to divalent cations such as Zn²⁺, as well as the structure of the high affinity GABA binding pocket. As noted above homooligomeric GABA receptors composed of the ρ 1 or ρ 2 subunit differ in the inhibitory effect for picrotoxinin, a drug classically known to block the Cl⁻ channel of glycine and GABA receptors [8,68]. In addition to the non-competitive inhibition of



Fig. 4. Proposed heterogeneity of inhibitory ligand-gated ion channels in a mammalian bipolar cell. Various subunits of the GABA_A and glycine receptor as well as ρ subunits are expressed in this cell type. Although all subunits can form multimeric protein complexes, the most likely situation is that subunits of the same class form distinct pentamers. ρ subunits are thought to form heterooligomeric receptors of differing stoichiometry as well as homooligomeric receptors.

GABA_C receptors by channel occlusion, picrotoxinin displays also a degree of competitive inhibition [69]. Therefore, the action of this inhibitor has to be interpreted in the light of both components. Interestingly, native GABA_C receptors of various species have different responses to picrotoxinin (for example: [21,27,24]). For an excellent overview of picrotoxinin inhibition of GABA_C-gated currents see refs. Bormann andFeigenspan [23] or Lukasiewicz [70].

Several attempts have been made to determine the molecular domains important for picrotoxinin action in ρ subunits. In the human $\rho 1$ subunit, mutation of a proline in the channel forming transmembrane domain into a serine (P309S) resulted in a ten-fold increase of picrotoxinin sensitivity when expressed in Xenopus oocytes and when saturating GABA concentration were used [69]. In the rat $\rho 1$ subunit, a similar mutation (P310S) produced an increase of picrotoxinin sensitivity when expressed in Xenopus oocytes [31], consistent with the finding in human ρ 1. In contrast, when the human construct was expressed in HEK 293 cells and tested at half-maximal activating GABA concentrations, a fourfold decrease in sensitivity for the blocker was observed compared with the wildtype [44]. Because position 309 in TM2 is also critical for the competitive effect of picrotoxinin [69], the contrary results between Xenopus oocytes and HEK 293 cells might be due to different

GABA concentrations co-applied with the blocker. Interestingly, a similar residue (V257) was identified to be at or near the binding site for picrotoxinin in the TM2 of the $\alpha 1$ subunit of the GABA_A receptor [71]. The authors used the substituted-cystein-accessibility method, where consecutive residues in the critical protein region are one at a time mutated to cysteine. After expressing the constructs in Xenopus oocytes, cysteine residues exposed to the channel lumen can be chemically modified by sulfhydryl-specific reagents applied in the extracellular solution, thus altering the electrical properties of the Cl⁻ channel. If, however, picrotoxinin binds in the Cl⁻ channel, the molecule will protect residues in this region in reacting with the applied chemical reagents, resulting in a footprint of the picrotoxinin binding site. In this way, Xu and coworkers demonstrated that C257 (similar to P309 of the $\rho 1$ subunit) was protected from chemical modification by picrotoxinin.

Additional residues critical for picrotoxinin sensitivity have been identified in rat ρ subunits [31]. Mutation of a threonine of the rat ρ 1 subunit into a methionine (T314M), the amino acid present in the rat ρ 2 subunit at this site, created homooligomeric GABA receptors with only very small Cl⁻ currents. However, co-expression of the mutant with wildtype rat ρ 1 showed a decrease in picrotoxinin sensitivity compared with the homooligomeric expressed $\rho 1$ subunit. The same effect was found after co-expression of the rat $\rho 2$ subunit with $\rho 1$. In both experiments the reduction of picrotoxinin action was proportional to the amount of mutant $\rho 1$ or $\rho 2$ coinjected with wildtype $\rho 1$. Because the GABA_C receptor in the rat appears to be relatively insensitive against picrotoxinin [rat: 100 µM picrotoxinin at saturating GABA concentrations block 19% of the maximal current [21] versus perch: 500 µM picrotoxinin at saturating GABA concentrations block 100% of the maximal current [27]], the authors concluded that the GABA_C receptor in the rat might be a heterooligomeric protein composed of $\rho 1$ and $\rho 2$ subunits.

The homooligomeric expressed $\rho 1$ subunit also demonstrates distinct sensitivity to several substances such as ethanol [72], protons [32], glycine and β -alanine [73] and halogenated fatty acids [74]. However, only for the action of divalent cations, such as Zn^{2+} has a site of interaction been identified [75]. Zinc, present in synaptic terminals of photoreceptors [76] can act as a modulator for GABA_C receptors and heterologous expressed ρ subunits [81,77,25,75,78-80]. GABA-gated currents of the homooligometric expressed human $\rho 1$ subunit in Xenopus oocytes could be reduced after coapplication of ZnCl₂. Change in extracellular pH was found to alter this effect, proposing that histidine residues might play a role in Zn^{2+} binding to ρ subunits. Indeed, mutation of a histidine in the N-terminal extracellular domain of the protein into a tyrosine (H156Y) abolished the Zn^{2+} sensitivity of the expressed construct completely, although other pharmacological and electrical properties did not change. The same residue was also found to be important for the action of other divalent cations such as Ni²⁺, Cu²⁺ and Cd²⁺ [80,69].

To investigate the molecular basis for the high agonist affinity of GABA_C receptors [23,49] identified five amino acids in the N-terminus of the human ρ 1 subunit between the conserved cysteine loop and TM1 that seem to be important for agonist binding. Mutations in any of these residues (Y198, Y200, Y241, T244, Y247) reduced the GABA affinity. The amino acids are grouped in two domains that have a similar position as the recently proposed agonist binding domain of the GABA_A receptor $\beta 2$ subunit [82]. An additional study mutated several residues in the human $\rho 1$ N-terminus as well as in the extracellular loop between TM2 and TM3, that were identical between $\rho 1$ and $\rho 2$ but distinct from other members of the ligand-gated ion channel family [83]. Whereas several mutations resulted in not functional GABA receptors, others decreased the sensitivity for GABA (Q189H, H141A) or increased cooperativity of GABA binding (R316A). However, it remains difficult to draw a picture of the agonist binding pocket of GABA_C receptors from these data.

7. Possible combinations of ρ subunits in vivo

In the retina of different species, ρ subunits are mainly expressed in bipolar cells (rat, cat, rabbit, monkey: [36,38]; cat, goldfish, chicken: [39]; chicken: [35]) and horizontal cells (perch: [37]; chicken: [35]). The most extensive studies performed so far have been in the rat, where $\rho 1$ and $\rho 2$ transcripts were localized in rod bipolar cells by RT-PCR and in-situ hybridization [36]. The corresponding protein could be detected on dendrites and axon terminals of rod and cone bipolar cells using a ρ subunit specific immunserum [38]. In addition, it has been shown by RT-PCR that $\rho 1$ and ρ^2 proteins were coexpressed in 11 of 17 rod bipolar cells examined [63]. Message for $\rho 2$ has also been found in 5 of 8 examined ganglion cells by RT-PCR, although no GABA_C-like currents could be detected in the same cells, leaving it unclear if $\rho 2$ is expressed at sufficient levels to form functional GABA_C receptors [63].

Outside the retina the $\rho 2$ subunit seems to be more abundant than $\rho 1$ and was detected by RT-PCR in different brain regions [36]. Therefore GABA_C receptors in these regions could be dominantly or perhaps even alone composed of the $\rho 2$ subunit or alternatively of $\rho 2$ and $\rho 3$. For the latter subunit an expression profile has been reported only for the retina [92].

Why might GABA_C receptors be heterooligomers of ρ subunits rather than homooligomers? In GABA_A and glycine receptors, combinations of different subunits into one oligomeric protein complex gives rise to different properties. For example, picrotoxinin sensitivity of the glycine receptor is critically dependent on the presence of the glycine receptor β subunit [68]. Furthermore, targeting of receptors to distinct locations within a neuron can depend on its subunit composition. Whereas GABA_A receptors composed of $\alpha 1\beta 1$ subunits show no special targeting, substitution of $\beta 1$ with $\beta 2$ or β 3 routes the receptor always to the basolateral site of polarized cells [84]. By analogy, the presence of various ρ subunits could result in a heterogeneous population of GABA_C receptors with biophysical and pharmacological properties as well as location determined by its ρ subunit composition. Indeed GABA_C receptors in the rat retina alter their sensitivity for the Cl- channel blocker picrotoxinin depending on the assembled ρ subunits [31].

Regarding the assembly properties discussed above, a typical GABA_C receptor could be composed of a mixture of different ρ subunits. Alternatively, homooligomeric GABA_C receptors formed of different ρ subunits could also be present (Fig. 4, right side). Single-channel patch-clamp experiments or subunit-specific histochemical and pharmacological tools must be developed to help solve these issues. To this end, Miledi and coworkers have designed a new GABA_C specific antagonist [85]. Using this approach it should be possible to design additional subunit specific drugs which help to investigate the molecular composition of $GABA_C$ receptors.

8. Function of GABA_C receptors in the retina

Because the same retinal cells that express GABA_C receptors also express GABA_A receptors, the question arises why one cell should have two GABA-gated receptors that activate intrinsic Cl- channels. The answer probably lies in the different functional properties of each receptor type. For example, in rod bipolar cells of the rat retina, GABA_C receptors are about 8-times more sensitive to GABA than GABA_A receptors. Whereas GABA_A receptors show a fast peak after agonist application and thus are characterized by transient responses, GABA_C receptors mediate smaller but sustained currents with a slower onset. On the single channel level, GABA_C receptors show a mean open time of 150 ms and a conductance of 8 pS in contrast to GABA_A receptors (25 ms, 27 pS; [21]). Thus, GABA_C receptors would activate at lower GABA concentrations with a prolonged response compared with GABA_A receptors.

How could the different response properties of GABA_A and GABA_C receptors to agonists influence neurotransmission in the retina? It has been shown that bipolar cell terminals receive GABAergic input from amacrine cells [86] and that synaptic transmission from bipolar to ganglion cells is modulated by GABA_C and GABA_A receptors [87,88]. Therefore, the low agonist affinity of GABA_C receptors on bipolar cell axon terminals may enable fine control over the excitability of these cells without interfering with the more transient responding GABA_A receptors on bipolar or ganglion cells. In this way amacrine cells could specifically modulate bipolar cell output onto ganglion cells. This may be important for the receptive field properties of ganglion cells, as, for example, their center-surround organization, that contributes to contrast sensitivity of the retina. GABA_C receptors may have the same effect at bipolar cell dendrites since horizontal cells of many species are reported to be GABAergic. Furthermore, the prolonged response of GABA_C receptors compared with GABA_A receptors might enable amacrine or horizontal cells to have a tonic inhibitory influence in addition to the transient Cl- currents generated by GABA_A receptors, thus providing an additional effect upon GABA mediated neurotransmission. Interestingly, the non-spiking retinal neurons, such as horizontal and bipolar cells, express GABA_C receptors, whereas so far GABA_C type currents have not been detected in spiking neurons (ganglion and amacrine cells). Thus, GABA_C receptors may play a role in

regulating the excitability of retinal neurons transmitting graded potentials.

9. Perspectives

Two main questions will be of specific interest for future investigation. First, the mechanisms that govern ρ subunit assembly into GABA_C receptors should be clarified. Since only two or three ρ subunits appear to exist in the mammalian retina, GABA_C receptors may be less complex than GABA_A receptors, providing a workable system to resolve their molecular structure. A second area will be to test the proposed function of GABA_C receptors. Two strategies can be envisioned. First, the generation of knock-out mice would provide a useful model system to study the role of GABA_C receptors in vivo as well as in slice preparations. However, there exist numerous difficulties with this approach. If the situation in mice is the same as in rat, generating a knock-out mouse for GABA_C receptors may require the elimination of the function of three genes ($\rho 1$, $\rho 2$ and $\rho 3$). Furthermore, Northern blots have revealed expression of the $\rho 1$ subunit outside of the retina [29], leaving it unclear if such a mouse will be viable.

A second strategy could be to suppress GABA_C receptor expression in the retina only. This could be done either by RNA antisense methods or by using a "dominant-negative" approach. Specific suppression of neuronal proteins using antisense oligonucleotides against the appropriate mRNA has been achieved (for example, gephyrin: [89]). Alternatively, protein domains that inhibit the assembly of ρ subunits into functional GABA_C receptors could be expressed in retinal cells suppressing GABA_C responses. As described in this review, the N-terminal domains of $\rho 1$ and $\rho 2$ subunits are sufficient for subunit assembly in vitro and are capable of eliminating GABA-gated Cl⁻ currents when coexpressed with full-length ρ subunits in heterologous expression systems. The same assembly domains are likely to be present in the ρ 3 subunit. Therefore, delivery and expression of an N-terminal protein fragment to the appropriate retinal cells should inhibit the formation of GABA_C receptors (Fig. 3) and thus provide a useful model to study the role of GABA_C receptors in vivo.

Acknowledgements

This work was supported by the Deutsche Forschungsgemeinschaft and the NIH grant EY 09531 (GRC).

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