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## Long distance effect on ligand-gated ion channels extracellular domain may affect interactions with the intracellular machinery

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dulation of receptor traffick-Ling is critical for controlling neurotransmission. A  $\gamma 2(R43Q)$  point mutation on GABA, receptor subunit is linked to epilepsy in human. We recently analyzed the effect of this amino-acid substitution on GABA, receptor trafficking and showed that this mutation as well as agonist application, both affecting GABA receptor extracellular domain, have an effect on receptor endocytosis. By comparing homology models based on ligand gated ion channels in their active and resting states, we reveal that the  $\gamma$ 2R43 domain is located in a loop that is affected by motion resulting from receptor activation. Taken together, these results suggest that endocytosis of GABA, receptors is linked to agonist induced conformational changes. We propose that ligand or modulator binding is followed by a whole chain of interconnections, including the intracellular domain, that may influence ligand-gated channel trafficking.

Fast neurotransmission relies greatly on ligand-gated ion channels (LGICs) that are involved in many physiological functions. Plasticity of neurotransmission in physiological and pathophysiological states depend on LGIC trafficking that is modulated by a number of different mechanisms including surface targeting, mobility, and endocytosis. GABA Rs involved in fast inhibitory neurotransmission are also regulated by the exchange between surface and intracellular compartments via a constitutive clathrinmediated dynamin-dependent endocytosis

pathway.<sup>4</sup> This constitutive internalization is modulated by intracellular mechanisms and is altered in pathological conditions.<sup>5-9</sup> Other LGIC such as AMPA or P2X receptors are also constitutively internalized by a clathrin-dependent endocytosis. In contrast, NMDA receptors are stabilized via an interaction with PDZ domain proteins and are more stable at the postsynaptic membrane.<sup>10</sup> Among P2X subtypes, P2X4-containing receptors are specifically and constitutively internalized.<sup>11</sup>

Genetic evidence has revealed a direct link between epilepsy and GABA, Rs dysfunction, including trafficking alteration.12-14 These mutations also offer an opportunity to obtain new insights into GABA, R structure and function. 15 For example, an R43Q mutation located in the  $\gamma$ 2-subunit N-terminal extracellular domain (Fig. 1A) is linked to childhood absence epilepsy and febrile seizure.<sup>13,14</sup> We recently analyzed  $\gamma$ 2(R43Q) trafficking and showed that the  $\gamma$ 2 subunit containing the R43Q mutation increased a clathrin- and dynamin-dependent endocytosis of GABA Rs, hindering their detection on the cell surface. The  $\gamma 2(R43Q)$ dependent endocytosis was reduced by GABA, Rs antagonists gabazine and picrotoxin, acting at a different site suggesting an allosteric effect i.e., that  $\gamma 2(R43Q)$ containing GABA, Rs are in a conformational state that promotes internalization. Further experiments revealed that agonist exposure triggered an increase of wild-type GABA, R endocytosis, both on native- and recombinant-GABA ARs.16 Application of their respective agonists enhances also

## **Keywords:** trafficking; internalization, receptor model

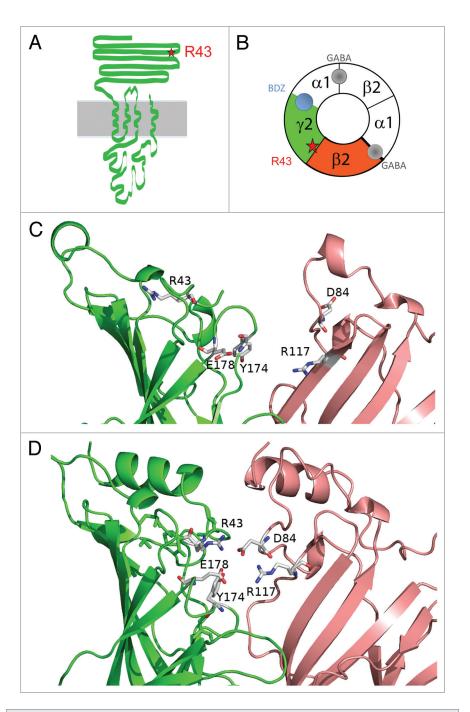
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**Figure 1.** The γ2(R43Q) mutation destabilize the open-channel conformation. (**A**) Schematic representation of GABA, R subunits showing a large N-terminal extracellular domain, 4 transmembrane domains and a large cytoplasmic loop. The location of the γ2(R43Q) point mutation associated with childhood absence epilepsy and febrile seizure is indicated. (**B**) Schematic diagram of a  $\alpha$ 1β2γ2 GABA, R which illustrates the 5 combined subunits that form the complex, the 2 GABA active binding sites at the β2 and  $\alpha$ 1 interfaces (gray circles) and the benzodiazepine (BDZ, blue circle) allosteric binding site at the  $\alpha$ 1 and γ2 interface. In current models, γ2R43 (red star) is at the interface with β2. (**C,D**) Model of a  $\alpha$ 1β2γ2 GABA, R viewed from the outside. Here only the γ2 and β2 subunits are shown for clarity (γ2 in green and β2 in pink, see (**B**). γ2 (R43, Y174, E178) and β2 (D84, R117) residues are represented by sticks. These residues are within loops identified as being involved in the channel-opening motion: (**C**) resting state model, (**D**) active state model.

the rate of AMPA- or P2X4-receptor internalization suggesting that the increase might be caused by an agonist-induced conformational change in the receptor promoting an interaction with components of the endocytotic machinery.<sup>11</sup>

The GABA R extracellular domain contains binding sites for agonists and allosteric modulators (Fig. 1B), while the intracellular domain mediates interactions with trafficking factors. 2,6,8,17 Consequently, our findings<sup>16</sup> suggest that GABA R internalization is driven by a global conformational change. Molecular models show that the  $\gamma 2R43$  residue is at the  $\gamma 2/\beta 2$  interface in the extracellular domain, on a loop positioned above the pocket, which is homologous to the GABA binding sites. Interestingly, many mutations in nicotinic receptors linked to diseases are at the interface between receptor subunits;18 they alter the gating allosterically, i.e., from a distance. 18,19 A model indicates that y2R43 and y2E178 are connected through a bifurcated salt bridge: this model has been used to study the  $\gamma 2(R43Q)$  mutation.<sup>12,20,21</sup> One of these studies has suggested that these positions have a long-range allosteric effect.<sup>20</sup> In our new GABA, R model derived from the Glutamate-gated chloride channel in the active state recently published,22 the R43 residue of the y2-subunit is connected to Y174 and E178 from the loop B and to β2 subunit via polar interactions that should be sensitive to the R43Q substitution and positioned on a loop thought to be involved in the channel-pore opening motion<sup>23</sup> (Fig. 1D). Here we show that these interactions are not present in our novel model of the resting state (Fig. 1C) which was based on the structure of a prokaryotic homolog published very recently.24 These new models (i.e., resting and activated states) point out that the y2R43 domain is affected by the motion resulting from GABA, R activation. This observation is consistent with an allosteric effect of the mutation. Moreover, electrophysiological recordings and kinetic analyses have shown that the long-distance effects of  $\gamma$ 2(R43Q) substitution extend as far as the transmembrane domains.20 Then, the extracellular domain might have an influence on receptor endocytosis in line with the current views on pentameric ligand-gated ion channels, describing a link between extracellular-, transmembrane-, and intracellular-domains. 25-27 This also suggests that allosteric drugs in wide clinical use may have an influence on receptor trafficking.

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## Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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