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

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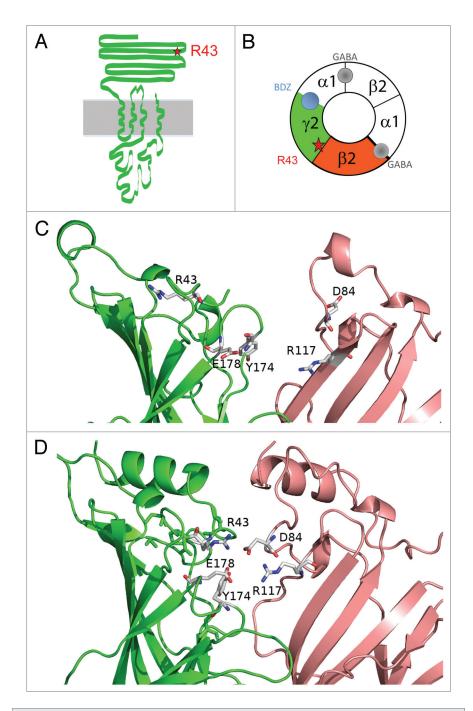
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/ odulation of receptor traffick-Ling is critical for controlling neurotransmission. A  $\gamma 2(R43Q)$  point mutation on GABA, receptor subunit is linked to epilepsy in human. We recently analyzed the effect of this amino-acid substitution on GABA, receptor trafficking and showed that this mutation as well as agonist application, both affecting GABA<sub>A</sub> 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<sub>A</sub> 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.<sup>1-3</sup> GABA<sub>A</sub>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<sub>A</sub>Rs dysfunction, including trafficking alteration.12-14 These mutations also offer an opportunity to obtain new insights into GABA<sub>A</sub>R structure and function.<sup>15</sup> 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.<sup>16</sup> The  $\gamma 2(R43Q)$ dependent endocytosis was reduced by GABA<sub>A</sub>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 <sub>A</sub>Rs.<sup>16</sup> Application of their respective agonists enhances also



**Figure 1.** The  $\gamma 2(R43Q)$  mutation destabilize the open-channel conformation. (**A**) Schematic representation of GABA<sub>A</sub>R subunits showing a large N-terminal extracellular domain, 4 transmembrane domains and a large cytoplasmic loop. The location of the  $\gamma 2(R43Q)$  point mutation associated with childhood absence epilepsy and febrile seizure is indicated. (**B**) Schematic diagram of a  $\alpha 1\beta 2\gamma 2$  GABA<sub>A</sub>R which illustrates the 5 combined subunits that form the complex, the 2 GABA active binding sites at the  $\beta 2$  and  $\alpha 1$  interfaces (gray circles) and the benzodiazepine (BDZ, blue circle) allosteric binding site at the  $\alpha 1$  and  $\gamma 2$  interface. In current models,  $\gamma 2R43$  (red star) is at the interface with  $\beta 2$ . (**C**,**D**) Model of a  $\alpha 1\beta 2\gamma 2$  GABA<sub>A</sub>R viewed from the outside. Here only the  $\gamma 2$  and  $\beta 2$  subunits are shown for clarity ( $\gamma 2$  in green and  $\beta 2$  in pink, see (**B**).  $\gamma 2$  (R43, Y174, E178) and  $\beta 2$  (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<sub>A</sub>R extracellular domain contains binding sites for agonists and allosteric modulators (Fig. 1B), while the intracellular domain mediates interactions with trafficking factors.<sup>2,6,8,17</sup> Consequently, our findings<sup>16</sup> suggest that GABA<sub>A</sub>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;<sup>18</sup> they alter the gating allosterically, i.e., from a distance.<sup>18,19</sup> 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,<sup>22</sup> the R43 residue of the  $\gamma$ 2-subunit is connected to Y174 and E178 from the loop B and to  $\beta 2$  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  $\gamma$ 2R43 domain is affected by the motion resulting from GABA<sub>A</sub>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.<sup>20</sup> 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.<sup>25-27</sup> 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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