A novel mutation in the transmembrane 6 domain of GABBR2 leads to a Rett-like phenotype
Marie-Laure Vuillaume, Mederic Jeanne, Li Xue, Sophie Blesson, Anne-Sophie Denomme-Pichon, Servane Alirol, Celine Brulard, Estelle Colin, Bertrand Isidor, Brigitte Gilbert-Dussardier, et al.

To cite this version:

HAL Id: hal-01730199
https://hal-univ-rennes1.archives-ouvertes.fr/hal-01730199
Submitted on 13 Dec 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
A novel mutation in the TM6 domain of GABBR2 leads to a Rett-like phenotype


1 Service de Génétique, Centre Hospitalier Universitaire, Tours, France
2 UMR INSERM 930, Faculté de Médecine, Université François-Rabelais, Tours, France
3 Institut de Génomique Fonctionnelle (IGF), CNRS UMR5203 - INSERM U1191- Université de Montpellier, Montpellier, France
4 Service de Génétique, Centre Hospitalier Universitaire, Angers, France
5 UMR INSERM 1083 - CNRS 6015, Faculté de Médecine, Université d’Angers, Angers, France
6 Plateforme Biologie Moléculaire des Cancers, Centre Hospitalier Universitaire, Tours, France
7 Service de Génétique, Centre Hospitalier Universitaire, Nantes, France
8 INSERM, UMR-S 1238, Université de Nantes, Nantes, France
9 Service de Génétique, Centre Hospitalier Universitaire, Poitiers, France
10 EA 3808, Université de Poitiers
11 Service de Génétique Clinique, Centre Hospitalier Universitaire, Rennes, France
12 CNRS UMR 6290 IGDR, Faculté de médecine, Université de Rennes 1, Rennes
13 Génétique médicale, Centre Hospitalier Universitaire, Brest, France
14 INSERM, CNRS, Université de Nantes, Centre Hospitalier Universitaire, l'Institut du thorax, Nantes, France
15 CRCINA, INSERM, Université d'Angers, Université de Nantes, Nantes, France.

Corresponding author: Pr Annick Toutain, Service de Génétique, Centre Hospitalier Universitaire, 2 Boulevard Tonnellé, 37044 Tours cedex 9, France. Tel.: +33247478850; Fax: +33247478653; Email: annick.toutain@univ-tours.fr

Running head: A novel GABBR2 mutation in the TM6 domain
Dear Editor,

We read with great interest the recent article published by Yoo et al.\textsuperscript{1} reporting four additional RETT-like (RTT) patients with the recurring A567T \textit{GABBR2} mutation\textsuperscript{2}. More interestingly, they showed, with \textit{in vitro} and \textit{in vivo} functional studies, that the severity of the phenotype caused by \textit{GABBR2} mutations was directly linked to their impact on GABA signaling activity, this latter being more reduced with the two missense mutations, S695I and I705N associated with epileptic encephalopathy (EE)\textsuperscript{1,3}. They hypothesized that variants position in different transmembrane (TM) domains of \textit{GABBR2}, TM6 for S695I and I705N, and TM3 for A567T, could determine the phenotypic expression. This hypothesis was recently reinforced with the report of a novel \textit{GABBR2} mutation also in TM6 and associated with infantile epileptic spasms\textsuperscript{4}.

We present a novel \textit{de novo} heterozygous \textit{GABBR2} mutation, A707T (Fig 1A), identified by Whole Exome Sequencing also located in TM6 of \textit{GABBR2} (Fig 1B) but associated with a RTT phenotype. The carrier, a 12 year-old girl, had profound intellectual disability, hand stereotypies, sleep and breathing disturbances but no history of seizures. This mutation, predicted pathogenic by \textit{in silico} analyses, lies in a region crucial for GPCR activation and positive allosteric modulation\textsuperscript{5}. To assess its impact on GABA signaling activity, we co-expressed the two GABA\textsubscript{b} subunits with the chimeric G-protein G\textalpha{qi}\textsubscript{9} in HEK-293 cells and measured the accumulation of inositol phosphate (IP-1) induced by the ligand GABA. We showed that the signaling activity of our A707T mutant is weakly induced by the agonist compared to that of the wild-type (Fig 1C), and this without altering \textit{GABBR2} cell surface expression (Fig 1D). The same results were observed with the A567T and I705N mutants (Fig 1C). Moreover, the four mutants tested have a basal activity stronger than that of the wild-type which might explain why the mutated receptor cannot be stimulated efficiently by
GABA (Fig 1C,1E). This basal activity is reversed by the competitive antagonist CGP54626, except for the mutant S695I which is already fully active in the absence of GABA and do not respond to GABA (Fig 1C, E) in accordance with Yoo et al. data\(^1\). To conclude, our results show that GABBR2 mutations located within TM6 can also be associated with a Rett-like phenotype. The novel mutation described here, A707T, also exerts a deleterious effect on GABAB receptor activity. This deleterious effect could result from a constitutive activity of the mutated GABA\(_B\) receptor highlighting a novel putative pathogenic mechanism for GABBR2 variants.

**Acknowledgement**

This work was supported by grants from the French Ministry of Health and Health Regional Agency from Poitou-Charentes (HUGODIMS, 2013, RC14_0107). The funder has no role in study design, data collection, analysis, interpretation of the data, writing of the report and the decision to submit the paper for publication. We thank Dr. Xavier Rovira (University of Vic, Spain) for the structural model of the human GABAB2 7TM. The inositol-phosphate experiments have been performed using the ARPEGE (Pharmacology Screening-Interactome) platform facility at the Institut de Génomique Fonctionnelle (Montpellier, France).

**Author Contributions**

MLV, MJ, LX, PR, FL and AT contributed to the conception and design of the study. MLV, MJ, LX, SB, ASD, SA, CB, AD, RR, SB, PR, FL and AT contributed to the acquisition and analysis of data. All authors contributed equally to drafting the text and preparing the figures.

**Potential Conflicts of Interest**

Nothing to report.
References


Figure legend

Figure 1: Identification and functional analysis of the A707T mutation

A) Sanger sequencing electrophoregrams showing the GABBR2 heterozygous missense mutation c.2119G>A, p.(Ala707Thr) in the proband and wild-type sequences in her parents and amino-acid alignments showing high conservation of the residue 707 across multiple species. TM: Transmembrane domain.

B-E) Functional analysis of the GABA\textsubscript{B} receptor mutants.  

B) Structural model of the human GABA\textsubscript{B2} heptahelical transmembrane domain (7TM) with the mutated residues in RTT and EE patients indicated in Corey–Pauling–Koltun representation. All the amino acid residues affected by the human mutations are in transmembrane (TM) domains 3 and 6.  

C) Inositol-phosphate accumulation mediated by the wild-type and mutant Flag-tagged GABA\textsubscript{B2} co-expressed with the wild-type GABA\textsubscript{B1a} and the chimeric G protein subunit G\alpha\textsubscript{i9} (a G\alpha\textsubscript{q} protein in which the last nine C-terminal residues have been replaced by those from G\alpha\textsubscript{i2}) which facilitates the coupling of Gi-coupled receptors to the phospholipase C signaling pathway (Monnier et al, 2011). Data are means ± SEM of at least three independent experiments.  

D) Cell surface levels of the Flag-tagged GABA\textsubscript{B2} mutants when co-expressed with the wild-type GABA\textsubscript{B1a}. Amounts of Flag-tagged GABA\textsubscript{B2} mutants at the cell surface were quantified by ELISA in intact (i.e. non-permeabilized) cells using the Flag epitope at the extracellular N-terminus of the GABA\textsubscript{B2} subunit. Data are expressed as means ± SEM of triplicates from a typical experiment repeated at least three times.  

E) Inositol-phosphate accumulation mediated by the wild-type and mutant Flag-tagged GABA\textsubscript{B2} co-expressed with the wild-type GABA\textsubscript{B1a} and G\alpha\textsubscript{i9}, as in panel B. The GABA\textsubscript{B} receptor wild-type and GABA\textsubscript{B} mutants were incubated with 100 µM GABA, 10 µM CGP54626 or both. Data are means ± SEM of at least three independent experiments.
Figure 1: Identification and functional analysis of the A707T mutation

A) Sanger sequencing electrophoregrams showing the GABBR2 heterozygous missense mutation c.2119G>A, p.(Ala707Thr) in the proband and wild-type sequences in her parents and amino-acid alignments showing high conservation of the residue 707 across multiple species. TM: Transmembrane domain.

B-E) Functional analysis of the GABAB receptor mutants. B) Structural model of the human GABAB2 heptahelical transmembrane domain (7TM) with the mutated residues in RTT and EE patients indicated in Corey–Pauling–Koltun representation. All the amino acid residues affected by the human mutations are in transmembrane (TM) domains 3 and 6. C) Inositol-phosphate accumulation mediated by the wild-type and mutant Flag-tagged GABAB2 co-expressed with the wild-type GABAB1a and the chimeric G protein subunit Gαqi9 (a Gαq protein in which the last nine C-terminal residues have been replaced by those from Gαi2) which facilitates the coupling of Gi-coupled receptors to the phospholipase C signaling pathway (Monnier et al, 2011). Data are means ± SEM of at least three independent experiments. D) Cell surface levels of the
Flag-tagged GABAB2 mutants when co-expressed with the wild-type GABAB1a. Amounts of Flag-tagged GABAB2 mutants at the cell surface were quantified by ELISA in intact (i.e. non-permeabilized) cells using the Flag epitope at the extracellular N-terminus of the GABAB2 subunit. Data are expressed as means ± SEM of triplicates from a typical experiment repeated at least three times. E) Inositol-phosphate accumulation mediated by the wild-type and mutant Flag-tagged GABAB2 co-expressed with the wild-type GABAB1a and Gqα9, as in panel B. The GABAB receptor wild-type and GABAB mutants were incubated with 100 µM GABA, 10 µM CGP54626 or both. Data are means ± SEM of at least three independent experiments.