A channelopathy mutation in the voltage-sensor discloses contributions of a conserved phenylalanine to gating properties of Kv1.1 channels and ataxia

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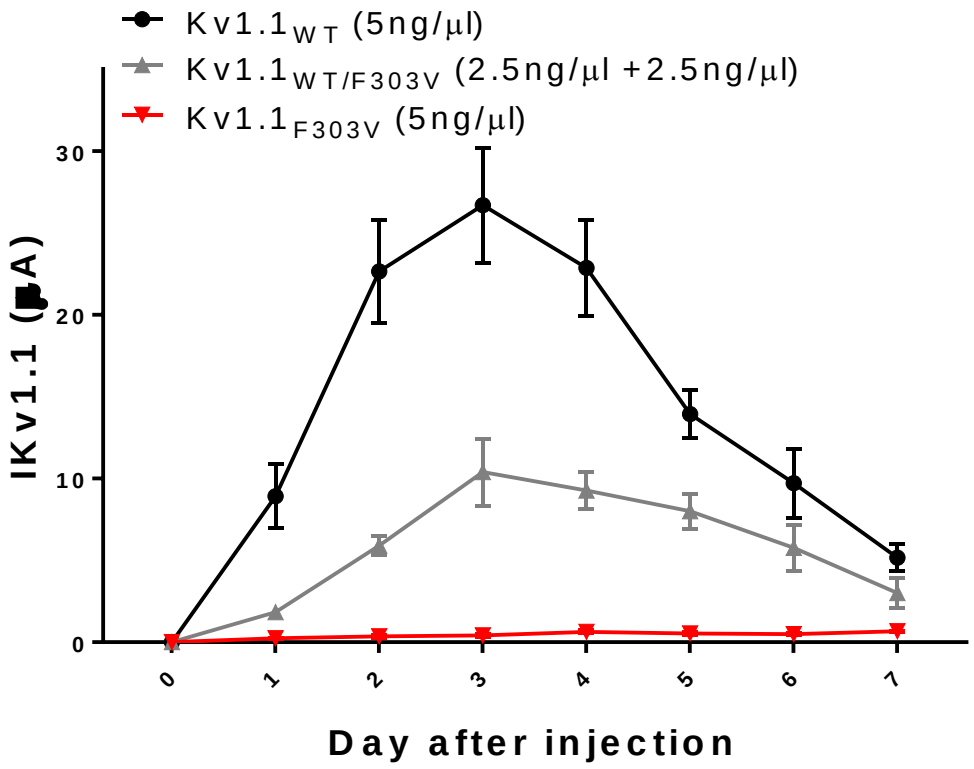

Figure S1: Time course of Kv1.1 expression. Oocytes were depolarized from a holding potential of -80mV to a voltage of +60mV for 500ms. Current amplitudes were plotted as a function of days after oocytes were injected. The data points are mean ± SE of 10 cells.

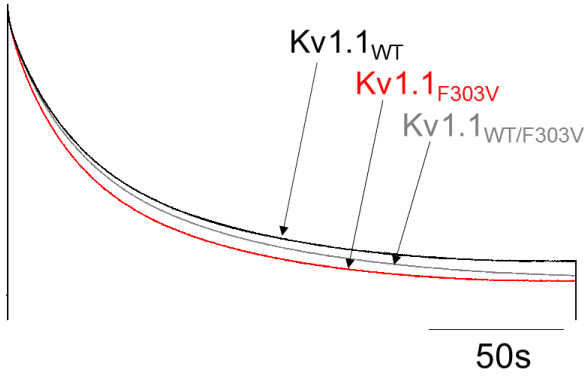

Figure S2: Effect of mutation on slow inactivation. Normalized and overlaid current traces showing the slow inactivation time course for the indicated channels. The membrane potential of oocytes were held at -80 mV and current traces were evoked by depolarizations at +60 mV for 3.5min. I_{peak} is the instantaneous current whereas I_{final} is the current amplitude measured at the end of the depolarizing step. The traces were fitted with two exponential functions and no statistical differences were found in either τ_{fast} or τ_{slow} of all channel types (data not shown).

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Kv1.1          1 mtvmsgenvdeasaapghpqdgsyprqadhddheccervvinisglrfet     50
Kv1.2          1 mtvatgdpvdeaaalpghpqd-tydpea---dheccervvinisglrfet     46

Kv1.1         51 qlktlaqfpntllgnpkkrmryfdplrneyffdrnrpsfdailyyyqsgg    100
Kv1.2         47 qlktlaqfpetllgdpkkrmryfdplrneyffdrnrpsfdailyyyqsgg     96

Kv1.1        101 rlrrpvnvpldmfseeikfyelgeeamekfredegfikeeerplpekeyq    150
Kv1.2         97 rlrrpvnvpldifseeirfyelgeeamemfredegyikeeerplpenefq    146

Kv1.1        151 rqvwllfeypessgparviaivsvmvilisivifcletlpelkdd-kdft    199
Kv1.2        147 rqvwllfeypessgpariiaivsvmvilisivsfcletlpifrdenedmh    196

Kv1.1        200 g---tvhridnttviy-nsniftdpffivetlciiwfsfelvvrffacps    245
Kv1.2        197 gggvtfhtysnstigyqqstsftdpffivetlciiwfsfeflvrffacps    246

Kv1.1        246 ktdffknimnfidivaiipyfitlgteiaeq-egnqkgeqatslailrvi    294
Kv1.2        247 kagfftnimniidivaiipyfitlgtelaekpedaqqgqqamslailrvi    296

Kv1.1        295 rlvrvfrifklsrhskglqilgqtlkasmrelgllifflfigvillfssav    344
Kv1.2        297 rlvrvfrifklsrhskglqilgqtlkasmrelgllifflfigvillfssav    346

Kv1.1        345 yfaeaeeaeshfssipdafwwavvsmttvgygdmypvtiggkivgslcai    394
Kv1.2        347 yfaeaderdsqfpsipdafwwavvsmttvgygdmvpttiggkivgslcai    396

Kv1.1        395 agvltialpvpvivsnfnyfyhretegeeqaqllhvss-pnlasdsdlsr    443
Kv1.2        397 agvltialpvpvivsnfnyfyhretegeeqaqylqvtscpkipsspdlkk    446

Kv1.1        444 -rssstmskseymeieedmnnsiahyrqvnirtancttanqncvnkskll    492
Kv1.2        447 srsastisksdymeiqegvnnsnedfreenlktanctlantnyvnitkml    496

Kv1.1        493 tdv    495
Kv1.2        497 tdv    499
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Figure S3: Human Kv1.1 protein sequence aligned with rat Kv1.2. Alignment was performed using EMBOSS[1] Needle alignment program. Kv1.1 F303 and its corresponding Kv1.2 are highlighted in yellow. The L339 and I335 residues and the corresponding Kv1.2 L341 and I337 are highlighted in blue.

Reference

1. Rice, P., Longden, I. & Bleasby, A. EMBOSS: The European Molecular Biology Open Software Suite. *Trends Genet* **16**, 276-277 (2000).