

SUPPLEMENTARY MATERIAL

Effect of the general anaesthetic ketamine on electrical and Ca^{2+} signal propagation in the *Arabidopsis thaliana*.

Andrej Pavlovič^{1*}, Lucie Ševčíková¹, Martin Hřivňacký¹, Marek Rác¹

¹Department of Biophysics, Faculty of Science, Palacký University, Šlechtitelů 27, CZ-783 71, Olomouc, Czech Republic.

Figure S1 The plants of *Arabidopsis thaliana* 24 h (A) and 15 days (B) after experiments with ketamin application.

Figure S2 Aminoacid alignment of human glutamate receptor NMDA 2A isoform 1 (NP_000824.1) and *Arabidopsis thaliana* GLR3.3 (NP_001322169.1) and GLR 3.6 (NP_001326369.1).

Movie S1 The $[\text{Ca}^{2+}]_{\text{cyt}}$ signals in transgenic *Arabidopsis thaliana* expressing APOAEQUORIN in response to heat wounding in control plants

Movie S2 The $[\text{Ca}^{2+}]_{\text{cyt}}$ signals in transgenic *Arabidopsis thaliana* expressing APOAEQUORIN in response to heat wounding in ketamine-treated plants.

Table S1 Primers sequences used in qPCR.

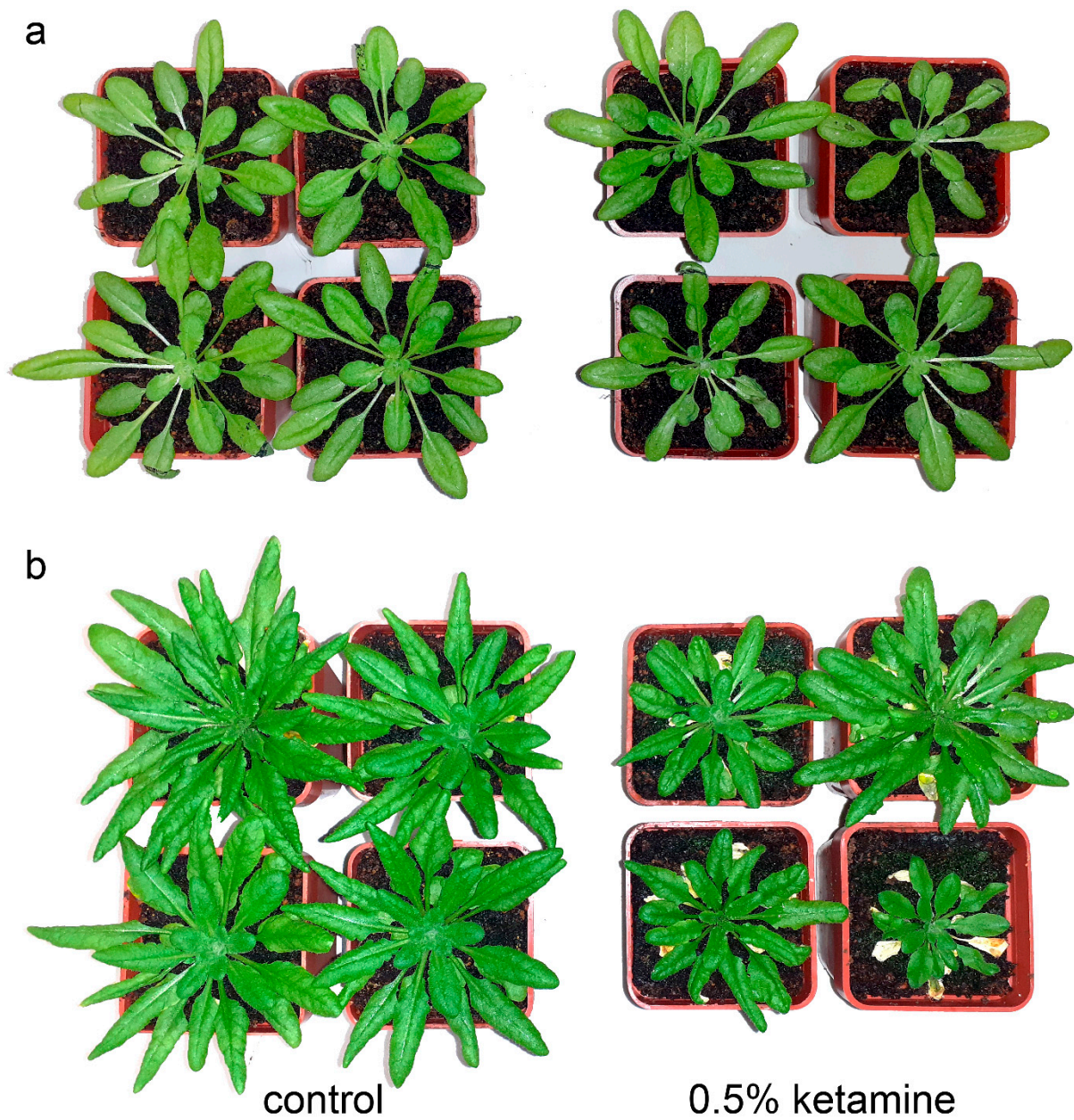


Figure S1 The plants of *Arabidopsis thaliana* 24 h (A) and 15 days (B) after experiments with ketamin application.

glutamate receptor 3.3 [*Arabidopsis thaliana*]

Sequence ID: [NP_001322169.1](#) Length: 933 Number of Matches: 2

[See 7 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 491 to 847 [GenPept](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
84.3 bits(207)	2e-20	Compositional matrix adjust.	84/385(22%)	165/385(42%)	34/385(8%)
Query 457	KGFCIDILKKLSRTVKFTYDLYLVTNGKHGKKVNNVWNGMIGEVVYQRAVMAVGS	LINE	516		
Sbjct 491	KGFCIDVFTAANNLLPYAVPVKFIPIYG-NGKE-NPSYTHMVEITTNFNGVVDVAIVT	548			
Query 517	ERSEVVDVSPFVETGISVMVSRNGTVSPSAFLPFSASVWMMFVMLLIVSAIAVFVF	576			
Sbjct 549	R+++VDF+ P+ +G+ V+ AFL PF+ +W + L V I V++	607			
Query 577	EYFSPVGYNNRLAKGKAPHGPSFTIGKAIWLLWGLVFNNNSVPVQNPKGTTSKIMVSVWAF	636			
Sbjct 608	E+ R + + P P +W + +F +N T ++++++W F	656			
Query 637	FAVIFLASYTANLAAFMIQEEFVDQVTGLSDKKFORPHDYSPPFRFGTVPNGSTERNIRN	696			
Sbjct 657	+I +SYTA+L + + ++ + G+ R D ++ G+ E +RN	709			
Query 697	NYPYMHQYMTKFNQKGVEDALV-SLKTGKLDAFIYDAAVLNKYAGRD---EGCKLVITIG	751			
Sbjct 710	E---LNISESRLVPLGTPEAYAKALDGPSPKGGV-AAIVDERPYVELFLSSNCAYRIVG	764			
Query 752	SGYIFATTGYGIALQKGSPPWKRQIDLALLQFVGDGEMEELETWLWT-GICHNEKNEVMSS	810			
Sbjct 765	F +G+G A + SP + A+L+ +G+++ + WL C E E+ S	822			
Query 811	QLDIDNMAGVFYMLAAAMALSLITF 835				
Sbjct 823	+L + + G+F + A L+L +	847			

glutamate receptor 3.6 [*Arabidopsis thaliana*]

Sequence ID: [NP_001326369.1](#) Length: 903 Number of Matches: 1

[See 5 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 458 to 837 [GenPept](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
94.4 bits(233)	2e-23	Compositional matrix adjust.	100/420(24%)	186/420(44%)	54/420(12%)
Query 430	VRNTVPCR-KFVKINNSTNEGMNVKKCKKGFCIDILKKLSRTVKFTYDLYLVTNGK-HGK	487			
Sbjct 458	+R VP R +F ++ + + GM GFC+D+ + + LV G H	512			
Query 488	KVNNVWNGMIGEVVYQRAVMAVGS	547			
Sbjct 513	N+ +I VY VG +TI ER+++ DF+ P+VE+G+ V+ S	569			
Query 548	AFLEPFASVWMMFVMLLIVSAIAVFVFEYFSPVGYNNRLAKGKAPHGPSFTIGKAIWL	607			
Sbjct 570	AFL PF+ +W++ LIV A+ ++ E+ ++ + + P P + W	619			
Query 608	LWGLVFNNNSVPVQNPKGTTT---KIMVSVWAFFAVIFLASYTANLAAFMIQEEFVDQVTG	664			
Sbjct 620	+ +F + + TTS +I++ +W F +I +SYTA+L + + + + G	674			
Query 665	LSDDKKFORPHDYSPPFRFGTVPNGSTERNIRNYPYMHQYMTKFNQ---KGVEDALVSL	720			
Sbjct 675	+ + Q HD P + P GS R+ +H+ ++ + E+ +L	721			
Query 721	KTGKLDAFIYDAAVLNKYAGRD---EGCKLVITIGSGYIFATTGYGIALQKGSPPWKRQID	776			
Sbjct 722	+ G + AAV++ +A + C+ +G F G+G A + SP +	777			
Query 777	LALLQFVGDGEMEELETWLWT-GICHNEKNEVMSSQLDIDNMAGVFYMLAAAMALSLITF	835			
Sbjct 778	A+LQ +G+M+ + WL C + E+ +L++ + G+F + A L+L +	837			

Figure S2 Aminoacid alignment of human glutamate receptor NMDA 2A (GluN2A) isoform 1 (NP_000824.1) and *Arabidopsis thaliana* GLR3.3 (NP_001322169.1) and GLR 3.6 (NP_001326369.1). The critical residues involved in ketamine binding (L642, N614) are highlighted in red rectangles (NCBI Blast).

Table S1 Primer sequences used in qPCR

Gene name	Primer sequences
<i>JAZ8</i>	forward 5'-TGTGTTTTCTTCAGATGTTACCC-3' reverse 5'-TCTCTGCTTGCATCGATATT-3'
<i>JAZ10</i>	forward 5'-ATCCCGATTTCTCCGGTCCA-3' reverse 5'-ACTTTCTCCTTGCATGGGAAGA-3'
<i>OPR3</i>	forward 5'-GCATGGAAGCAAGTTGTGGAAGCA-3' reverse 5'-CATGCGCCCCGTGGATCTCAAT-3'
<i>AOS</i>	forward 5'-GCGACGAGAGATCCGAAGA-3' reverse 5'-CTCGCCACCAAAACAACAAA -3'
<i>UBC21</i>	forward 5'-CAGTCTGTGTGTAGAGCTATCATAGCAT-3' reverse 5'-AGAAGATTCCTGAGTCGCAGTT-3'

Movie S1 The $[Ca^{2+}]_{cyt}$ signals in transgenic *Arabidopsis thaliana* expressing apoaequorine in response to heat wounding in control plants. (a) photograph of plant rosette, (b) $[Ca^{2+}]_{cyt}$ signal, (c) discharge. The site of heat wounding across a midrib of local leaf is marked with red arrow. The leaf was heat wounded between 00:00-00:10 s.

Movie S2 The $[Ca^{2+}]_{cyt}$ signals in transgenic *Arabidopsis thaliana* expressing apoaequorine in response to heat wounding in ketamine-treated plants. (a) photograph of plant rosette, (b) $[Ca^{2+}]_{cyt}$ signal, (c) discharge. The site of heat wounding across a midrib of local leaf is marked with red arrow. The leaf was heat wounded between 00:00-00:10 s.