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Wonhyo Seo, Christophe Prehaud, Zakir Khan, Claude Sabeta, Monique Lafon. Investigation of rabies virus glycoprotein carboxyl terminus as an in vitro predictive tool of neurovirulence. A 3R approach.. Microbes and Infection, 2017, 19 (9-10), pp.476 - 484. 10.1016/j.micinf.2017.05.006 . pasteur-01783671

HAL Id: pasteur-01783671 https://pasteur.hal.science/pasteur-01783671

Submitted on 2 May 2018 $\,$

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1	Investigation of rabies virus glycoprotein carboxyl terminus as an in vitro predictive tool of
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25	Abstract

In the field of live viral vaccines production, there is an unmet need for *in vitro* tests complying 26 a 3R approach (Refine, Replace and Reduce the use of animal experimentation) to replace the 27 post-licensing safety tests currently assayed in animals. Here, we performed a pilot study 28 evaluating whether virulence of rabies virus, RABV, can be forecast by an in vitro test of neurite 29 outgrowth. The rationale to use neurite outgrowth as a read-out for this test is based on the 30 salient property of the cytoplasmic domain of the G-protein (Cyto-G) of virulent RABV strains 31 - not of attenuated RABV strains - to stimulate neurite outgrowth in vitro. We observed that 32 neurite elongation triggered by the Cyto-Gs encoded by different RABV field isolates correlate 33 with the distinct virulence scores obtained in a mouse model of experimental rabies. Our results 34 cast the idea that it could be feasible to predict RABV virulence by testing the *in vitro* property 35 of a RABV strain to promote neurite outgrowth without the use of animal experimentation. 36

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Key words: 3R; post-licensing safety test; live viral vaccine; rabies virus; neurite outgrowth;
PDZ

41

42 **1. Introduction**

Vaccines are invaluable tools to prevent diseases and to increase the live expectancy of humans. 43 Some vaccines are prepared with live non-virulent microbes. Their safe use requires that they 44 are devoid of mutants which have acquired virulent features back. Before release for human 45 immunization, batches of live viral vaccines such as those of Yellow Fever, Measles or 46 Polioviruses, have to be tested for the absence of neurovirulence. At the moment, this post-lic 47 ensing safety testing is performed in animals. Ethical considerations questioning the use of 48 animals, monkeys in particular, in research strongly advocate for alternative methods. The 3R 49 approach (Reduce, Refine, Replace the use of animals) is now clearly a priority for the world 50 health authorities and a real challenge for scientists to stimulate their ingenuity on alternative 51 in vitro tests that do not require animal experimentation [1]. A cellular test, which could 52 amplify and make detectable phenotypic trait linked to neurovirulence is highly desirable. 53 Nevertheless, because neurovirulence is a polygenic trait often not completely elucidated, the 54 design of relevant in vitro test may not be an easy task. 55

Here, we performed a pilot study to bring a proof of concept to validate the relevance of such 56 an approach. To this purpose, the neurotropic rabies virus (RABV) was chosen as a model since 57 some mechanisms controlling RABV pathogenicity start to be unravelled. The virulent RABV 58 59 strain CVS, referred as CVS-NIV, which invades the nervous system of the mouse and on being injected in the hind limb causes a fatal encephalitis [2], whereas the non-neurotropic strain 60 ERA-NIV does not [3, 4] and triggers striking distinct features (attenuation, apoptosis and a 61 robust antibody induction). Surprisingly enough for such a lethal neurotropic virus, CVS-NIV 62 promotes neuron survival and triggers neurite elongation (neurite outgrowth), whereas ERA-63 NIV does not share these properties and instead induces the death of the infected neurons. 64

Amongst the five RABV proteins, the glycoprotein (G-protein), an integral trans-membrane protein, has been identified as playing a critical role in the fate of viral properties [3, 5-12].

These features are controlled not only by the ectodomain of the G-protein, but also by the 67 cytoplasmic domain, Cyto-G which was found to control the fate of the infected cell (cellular 68 death or survival) through the interaction with some cellular partners [13, 14]. Commitment of 69 RABV-infected neurons towards cellular survival or death is under the control of the carboxyl 70 terminus (C-terminus) of Cyto-G forming a PDZ Binding Motif (PBM), which interacts with 71 the PDZ domain (Post synaptic density protein, Drosophila disc large tumor suppressor, and 72 Zonula occludens-1 protein domain) of a select group of cellular partners [14-17]. PDZ domains 73 are protein-protein interacting domains and play a central role in cell signaling by favoring 74 spatial contact between enzymes and their substrates, and more generally by assembling and/or 75 76 regulating protein networks [18, 19]. Remarkably, in a model of strictly isogenic recombinant RABVs the introduction of a single point mutation in the C-terminus of Cyto-G (COOH Cyto-77 G) of the CVS-NIV switched neurosurvival to neuronal death. This single change is sufficient 78 to induce the loss of virulence markers (neurite outgrowth, increase in AKT phosphorylation 79 and protection against apoptosis) and the acquisition of markers of attenuation (increase in the 80 number of cellular partners of the Cyto-G, induction of apoptosis). This change also modifies 81 pathogenicity in a mouse model of RABV encephalitis [14]. With this background, it can be 82 expected that the expression of the Cyto-G CVS-NIV or ERA-NIV alone and in the absence of 83 any other RABV components may be sufficient to reproduce the in vitro neurosurvival and 84 attenuation features of RABVs. The delivery of Cyto-Gs could be obtained for example by 85 infecting the cells with recombinant lentiviral vectors. If this was the case, it could be possible 86 to predict virulence of a RABV strain by performing an *in vitro* test of neurite outgrowth. 87

In this study we designed such an *in vitro* test, and challenged this test by assaying whether *in vitro* virulence features of three representative South African RABV isolates (a canid, a mongoose and a spill over corresponding to a dog infected by a mongoose RABV biotype) and whose Cyto-Gs were distinct by a few mutations correlate with the virulence of the strains as

92 previously determined in an experimental mouse model of rabies (Seo, W et al. companion 93 paper). Despite the limited number of strains used for the correlate, this pilot study gave 94 promising results suggesting that virulence, at least in the case of RABV infection, might be 95 forecast by performing *in vitro* tests.

96

97 2. Material and Methods

98 2.1 Cells

Human embryonic kidney cells HEK 293-T were grown at 37 °C with 5% CO₂ in Dulbecco's
Modified Eagle Medium with Glutamax-1 supplemented with 10% fetal calf serum (FCS),
penicillin (10,000 IU/ml) and streptomycin (10 mg/ml). Neuroscreen-1 (Cellomics), derived
from rat pheochromocytoma were grown in RPMI 1640 supplemented with 10% horse serum,
5% FCS, 200 mM glutamine, penicillin (10,000 IU/ml) and streptomycin (10 mg/ml).

104

105 2.2 Construction and Recovery of Recombinant lentivirus

106 Chimeric G-protein constructs were generated by using the plasmid with the deleted 107 ectodomain that resulted in delta EC. The mutant clones were generated by amino acid 108 substitutions using QuikChange Lightning Site-Directed Mutagenesis Kit (Agilent 109 Technologies) with mutagenic primers (Eurogentec Co). The primer sets for site-directed 110 mutagenesis of the 3 constructs are shown below.

Canid	Canid 1	5'TGGGAATCATACAAGAGTGGGGGGGGGAGACCAGACTGTGAGGCCAAG3'
Calliu	Canid 2	3'ACCCTTAGTATGTTCTCACCCCCACTCTGGTCTGACACTCCGGTTC5'
Mangaaga	Mong 1	5'TGGGAATCATACAAGAATGGGGAGGAGACCAGAATGTGAGGCCAAG3'
Mongoose	Mong 2	3'ACCCTTAGTATGTTCTTACCCCTCCTCTGGTCTTACACTCCGGTTC5'
Spill over	Spill over 1	5'TGGGAATCATACAAGAATGGGGGTGAGACCAGAATGTGAGGCCAAG3'
Spin over	Spill over 2	3'ACCCTTAGTATGTTCTTACCCCCACTCTGGTCTTACACTCCGGTTC5'
ERA	ERA 1	5'TGGGAATCACAAGAGTGGGGGGGGGAGACCAGACTGTGAGGCCAAG3'

111

Then, the chimeric transgenes were cloned in the lentivirus vector by using the pLenti6.3/V5-112 TOPO[®] TA Cloning[®] Kits (Invitrogen). A total number of 5×10⁶ HEK 293-T cells were grown 113 overnight to 80% confluence in 10 cm diameter Cell⁺ dishes (Sarstedt). The transfection was 114 conducted using the calcium phosphate method. HIV vectors were prepared as previously 115 described by co-transfecting HEK 293-T cells with a four-plasmid system including the above 116 plasmids carrying the genes of interest, the pMDLg/pRRE, the pRSV-Rev packaging plasmids 117 and the VSV-G envelope protein expression plasmid (pMDG) [20]. HIV Gag protein p24 118 measured in 48 hours supernatants by the enzyme-linked immunosorbent assay (HIV p24 119 ELISA, Perkin Elmer). The infectivity of each stock was monitored on Neuroscreen-1 cells 120 before use. A dose of 33 ng of p24 was needed to infect 5×10^4 Neuroscreen-1 cells. One hundred 121 percent of infection was achieved 48-hour-post infection in these conditions. This dose was 122 determined by using an eGFP (enhanced green fluorescent protein) expressing lentivirus 123 included in each experiment to check the infectivity. Real-time relative qPCR (RT-qPCR) was 124 further conducted and the level of 18S rRNA expression was used to as a house keeping gene. 125

126

127 2.3 Western Blotting and Immunocytochemistry

Lentivirus and non-infected cells were lysed with RIPA buffer (Sigma) supplemented with 128 anti-protease and anti-phosphatase cocktails (Roche Life Science) and stored at -20 °C. Cell 129 130 lysates were electrophoresed on a 4-20% gradient polyacrylamide gel (Pierce Biotechnology) and blotted on PVDF membranes (Hybond-P, GE HealthCare). The membranes were incubated 131 with a customized polyclonal rabbit antibody directed against the Cyto-G (Proteogenix) 132 followed by an incubation with a secondary antibody coupled to horseradish peroxidase 133 (Jackson Immuno Research). Signals were revealed with SuperSignal[®] West Femto Substrate 134 (Pierce Biotechnology), acquired and analyzed with chemiluminescence imaging system 135

136 (G:Box, Syngene).

For immunocytochemistry Neuroscreen-1 cells were infected for 48 hours with recombinant lentiviruses (20 ng of p24/well) on coverslips in a 24-well plate. Fixed cells were incubated with anti Cyto-G polyclonal customized rabbit antibodies (Proteogenix) followed by goat-anti rabbit labeled with Alexa 488 (Molecular Probe). Nuclei were stained with Hoescht 333420 and analyzed with a Leica confocal microscope Zeiss LSM 510.

142

143 2.4 Neurite Outgrowth Assay

A total number of 5×10^4 Neuroscreen-1 cells were seeded in 24 well poly-D-lysine-coated tissue culture dishes (Cell Bind, Corning). After 6-hour-incubation with 200 ng of neuronal growth factor (NGF), recombinant lentiviral stock containing 60 ng of p24 was added and cells were further cultivated for 72 hours. Cells were fixed and stained with crystal violet solution to visualize neurite processes. Cell images were captured (3 field/well, 10 wells/group) with a phase contrast Leica microscope and analyzed with ImageJ 1.44p, Neuron J plug-in.

150

151 2.5 Statistical Analysis

Student's *t-test* (P<0.05 was considered significant) was undertaken using GraphPad Prism
version 6.0 program.

154

155 **3. Results**

156 *3.1 Construction and expression of Cyto-Gs*

157 The commitment of RABV-infected neurons toward death (i.e. ERA-NIV) or survival (i.e.

158 CVS-NIV) is controlled by the Cyto-G and the PBM located at the COOH terminus of the Cyto-

159 G protein in particular [14]. We wanted here to assay whether Cyto-G expressed alone, in the

absence of any other RABV elements, retains the neurosurvival features. We chose to construct

a Cyto-G of the CVS-NIV (44 amino acids long) and 4 chimeric Cyto-Gs replacing the 12 161 original amino acid residues of CVS-NIV Cyto-G by the 12 amino acids of the COOH terminal 162 of ERA-NIV Cyto-G or those of the three South African RABV (Canid, Mongoose and Spill 163 over) (Fig. 1A). The reason to engraft 12 COOH amino acids and not the 4 COOH amino acids, 164 which is the most common length of a PBM, is motivated by the results of nuclear magnetic 165 resonance (NMR) and X-rays studies indicating that up to 12 amino acids of RABV Cyto-G 166 could be involved in the formation of the PBM/PDZ complexes [15, 16]. The Cyto-G constructs 167 included the transmembrane domain (TM) of the G-protein and G,K amino acids of ectodomain 168 proximal to the TM as well as the entire signal peptide 19 amino acid long (Fig. 1A) to allow 169 sorting and trafficking of the Cyto-Gs from the endoplasmic reticulum. A negative control, 170 consisting in the G-CVS-NIV deleted of the last 4 amino acids, G-CVS-NIVA, was also 171 constructed. Lentiviruses were chosen as a mean to express the Cyto-Gs in Neuroscreen-1 cells. 172 The mRNA transcription levels of lentivirus constructs were evaluated by relative RT-qPCR 173 (Fig. 1B) and ERA-NIV and Spill over constructs exhibited the lowest value, however, the 174 mRNA expression of CVS-NIV showed the highest value. Interestingly, the G-canid and G-175 mongoose constructs displayed similar mRNA transcriptional levels. These data suggested that 176 point mutations in the nucleotide sequence may slightly modify the intrinsic stability of the 177 mRNA transcripts. Nevertheless, when the Cyto-G protein expression was assayed by 178 immunoblotting (Fig. 1C) and immunocytochemistry (Fig. 1D), all chimeric constructs 179 exhibited high levels of protein expression. To note, in contrast to CVS-NIV infected cells, in 180 which the full length G-protein is localized both in the cytoplasm and at the cytoplasmic 181 membrane (data not shown), or in cells infected by a lentiviral vector expressing the entire G-182 protein only [16], the Cyto-Gs were mainly localized in the cytoplasm of the cells. This may 183 suggest that RABV G-protein trafficking was modified by the absence of the ectodomain (but 184 two amino acids) of the RABV G-protein. 185

186

The capacity of Cyto-Gs to trigger neurite outgrowth in a PBM-dependent manner has been previously assayed in human neuroblastoma SH-SY5Y cells infected with isogenic recombinant RABVs [14]. Here, we tested whether the neurite outgrowth triggered by CVS-NIV Cyto-G could also be observed after the Cyto-Gs have been delivered in the cells by a lentiviral vector. For this assay the human neuroblastoma SH-SY5Y cell line was replaced by rat Neuroscreen-1, which compared to human neuroblastoma, are less prone to cellular aggregation, allowing for an easier evaluation of neurite outgrowth in individual cells [21].

Neuroscreen-1 cells were either non-infected or infected with the recombinant lentiviruses G-196 CVS-NIV, G-ERA-NIV, G-CVS-NIV-∆ and the mean neurite length was measured 72-hour-197 post infection (Fig. 2 and table 2). The CVS-NIV construct triggered significantly higher neurite 198 outgrowth compared to non-infected group and to G-CVS-NIV-∆ or ERA-NIV constructs 199 (mean length of 420 µm for CVS-NIV versus 200 µm for the other conditions: non-infected or 200 201 G-CVS-NIV- Δ or ERA-NIV), indicating that the increased neurite outgrowth triggered by CVS-NIV Cyto-G could also be observed after Cyto-Gs has been delivered in rat Neuroscreen-202 1 cells by a lentiviral vector. The lentiviral vector Cyto-G CVS-NIV-∆ triggered a mean neurite 203 outgrowth similar to those observed in non-infected cells (left panel in Fig. 2C and table 2). 204 This observation rules out the possibilities that the lentiviral vector has an effect on neurite 205 outgrowth besides the specific contribution of the Cyto-G-PBM. 206

These data established that Cyto-G of CVS-NIV has an intrinsic property to trigger neurite outgrowth even in the absence of G ectodomain or any other viral components. In this test, the property of Cyto-G of ERA-NIV or of CVS-NIV- Δ (to not stimulate neurite outgrowth) is also maintained. Thus, the *in vitro* test of neurite outgrowth using lentivirus for the ERA or CVS Cyto-G delivery reproduce the *in vitro* neurosurvival and attenuation features triggered by thecomplete viruses.

213

3.3 Comparison of neurite outgrowth induced by the three South African chimeric constructs in a recombinant lentivirus system

Using these experimental conditions, the capacity of the three South African chimeric Cyto-216 Gs to trigger neurite outgrowth was compared to the positive (CVS-NIV) and negative (ERA-217 NIV) Cyto-G constructs. The G-canid chimeric construct showed the highest level of neurite 218 outgrowth, in the same range as those triggered by the positive control CVS-NIV, whereas G-219 spill over and G-mongoose Cyto-G constructs triggered relatively lower levels of neurite 220 outgrowth, but significantly higher than those induced by chimeric G-ERA-NIV (Fig. 2 and 221 Table 2 for statistical analysis). G-spill over and G-mongoose triggered similar levels of neurite 222 outgrowth. The difference between the efficiency of G-spill over and G-mongoose constructs 223 compared to G-canid construct was not due to a reduced G-protein expression because no 224 significant differences in the level of expression of G constructs were observed after lentiviral 225 vector delivery (Fig. 2D, left plot: 4.99, 5.04 and 5.20 x 10⁷AU for Canid, Mongoose and Spill-226 over G constructs expression respectively). Moreover, as shown in Fig. 2D, when the level of 227 expression of G constructs (G-CVS-NIV, G-CVS-NIVA, G-ERA-NIV and G-canid chimera, G-228 mongoose chimera, G-spill over-chimera) was plotted with the neurite outgrowth scores, it 229 appeared there was no obvious correlation between the expression of G construct an neurite 230 outgrowth values. For example (Fig. 2D, left panel), the neurite outgrowth score of the G-231 mongoose chimera construct was lower compared to those of G-canid chimera, despite a similar 232 G expression, it is the same result for G-CVS-NIV (highest neurite score, lowest level of G 233 expression) and G-CVS-NIV∆ (Lowest neurite score, highest level of G expression) as shown 234 on Fig 2D, right panel. This confirm previous observations establishing that RABV virulence 235

is not correlated to the G-protein expression level, but in fact to the genetic nature of thedelivered G-protein [14, 22].

To conclude, in an attempt to predict relative virulence of the three South African RABVs, the in cellular assay of neurite outgrowth triggered by the C-terminus of the Cyto-Gs allowed us to propose that the G-canid construct exhibited virulent traits of CVS-NIV constructs, whereas both the spill over and the mongoose constructs showed less virulent traits. These *in vitro* findings correlate with the virulence of the three RABV strains as previously established in an experimental mouse model of rabies (Seo W et al, companion paper).

244

245 **4. Discussion**

In the vaccine field, there is an unmet need for a post licensing safety test capable to predict 246 neurovirulence of live viral vaccine samples without the use of in vivo animal models. Safety 247 tests for live vaccine (for example Yellow fever vaccines) require that vaccine samples are 248 injected in monkeys whose brains are collected and checked for the absence of anatomo-249 pathology signs. The rationale of such a test is that neurotoxicity signs will reveal the presence 250 of neurotoxic mutants which have appeared in the process of production and can cause vaccine-251 associated neuropathology. The growth of a pathogenic viral population within the nervous 252 system may result into the acquisition and then fixation of few genomic mutations that confer 253 neurovirulence. 254

Viruses are masters for manipulating the proliferation or death of the infected cells of a host, mainly by interfering with crucial endogenous interactions. RABV pathogenicity relies on its potential to keep the infected neurons alive, thereby allowing efficient viral transmission from one neuron to the next order neuron, from the site of infection up to the brain stem and finally to be secreted by the salivary glands [13]. It has been shown that virulent laboratory RABV strains such as CVS-NIV trigger survival of the infected neurons [3]. In contrast, the attenuated laboratory RABV strain, ERA-NIV, induces neuronal death. The neurosurvival phenotype is characterized by an increase of the neurite length of human neuroblastoma cells and by the activation of the neurosurvival Pi3k-Akt signaling pathway [14]. By using isogenic recombinant RABVs, we previously demonstrated these features are controlled by the cytoplasmic domain of the G protein, and in particular by the C-terminus PBM.

Here, we showed that the expression of the last 12 C-terminus of G-CVS-NIV in Neuroscreen-1 cells assumes the neurosurvival properties of CVS-NIV, whereas the expression of the last 12 COOH terminus of G-ERA-NIV does not have such an effect. This indicates that the neurosurvival properties of CVS-NIV and ERA-NIV could be described *in vitro* without the need of manipulating RABV isolates, by simply studying the characteristics of the C-terminus of one of the RABV proteins.

Then we challenged the test by assaying the C-terminus properties of three South African 272 RABV strains. We found that the C-terminus of the canid RABV isolate G-protein exhibited a 273 survival phenotype (neurite outgrowth), whereas the C-terminus of mongoose or spill over G-274 protein did not. In this frame, it can be expected that canid strains are more virulent than spill 275 over and mongoose strains. This forecast fits with the in vivo data since virulence of the RABV 276 strains was in this order of magnitude: Canid and CVS virulence superior to those of mongoose 277 and spill over RABV strains (Seo et al., companion paper). These results indicated that the 278 virulence of these three wildlife RABV strains can be predicted by monitoring neurite 279 outgrowth in vitro and again without the need of manipulating RABV isolates and infecting 280 animals. 281

It was previously established by comparing in a recombinant RABV system the role of Gprotein of two laboratory strains CVS-NIV and ERA-NIV that the control of neurosurvival or death relies on the nature of the PBM. In particular, a mutation resulting in a single amino acid change [glutamine (Q) to glutamic acid (E) at -3] in the PBM was sufficient to switch the fate

of the infected cells and the neurite outgrowth suggesting that expression of ETRL_{COOH} in this 286 genetic context (Fig. 1A) was a marker of attenuation [14]. However, ETRL COOH alone might 287 not be a signature of attenuation whatever the genetic context is. Indeed, the virulent canid 288 strain stimulates neurite outgrowth while Cyto-G terminates by ETRL. It is likely that another 289 mutation such as the replacement of the histidine (H) of CVS by Tyrosine (Y) at position -8 290 modifies the pattern. In that case, the combination of Y at -8 with -ETRL_{COOH} should trigger a 291 virulent property. This is strongly supported by the observation that this sequence combination 292 (H at -8 and ETRL COOH) is expressed by the G-protein of several other virulent strains including 293 the CVS-AJ506997 (GenBank Acc. AJ506997.1). The possibility that Y at -8 contributes to the 294 interaction of Cyto-Gs with the PDZ of cellular partners is strongly supported by structural 295 studies resolving the complex formed by the PBM of RABV Cyto-Gs and the PDZ of the 296 cellular partner [16]. 297

A PBM classically corresponds to a stretch of 4 amino acids, allowing the insertion of the peptide into the groove formed by two beta sheets of the PDZ. Nevertheless, in the case of RABV Cyto-G structural studies indicated that more than 4 amino acids of the C-terminus of Cyto-Gs contribute to the formation of the PBM-PDZ complex and that the surface of interaction recruited the 12 amino acids COOH end [16].

The reasons why the replacement of H by Y changes the phenotype driven by the PBM 303 terminated by ETRL are still unclear. A change in the nature of the cellular partners is unlikely 304 because the 12 COOH termini Cyto-Gs of the three South African strains have highly similar 305 patterns of reactivity, when assayed in a PDZ array including 220 distinct human PDZs (Renaud 306 Vincentelli, Nicolas Wolff and Gilles Travé, personal communication). It has been shown in 307 other models, that phosphorylation of residues in the PBM can modulate PBM/PDZ interactions 308 [23, 24]. Thus, we may hypothesize that the swap H/Y at -8 modifies the phosphorylation status 309 of the Cyto-Gs. Such a hypothesis deserves complete studies determining at first whether Cyto-310

Gs terminated by ETRL _{COOH} and expressing Y at -8 instead of H have distinct patterns of phosphorylation and second, whether phosphorylation status of the PBM modulates the pattern of interaction with cellular partners.

The main conclusion of this discrepancy is that it is not sufficient to look at the primary amino acid sequence of Cyto-Gs to forecast virulence of a RABV strain, emphasizing that other tests including *in vitro* tests are mandatory to answer this question.

In an attempt to replace animal use in post-licensing safety tests for live viral vaccines, this 317 pilot study using RABV as a model, proposes that virulence of a RABV strain might be 318 predicted by simply assaying in vitro the capacity of the COOH terminus of its G-protein to 319 trigger neurite outgrowth. We showed that it is feasible to predict virulence of a RABV strain 320 by using appropriate in vitro tests. To note, none of the RABV vaccine for human belongs to 321 the category of live viral vaccines, all of RABV vaccines for human use contain inactivated 322 viral particles. Thus, the test we set up has no ambition to be substituted to safety tests currently 323 in use to check for inactivation or potency of rabies vaccines. We hope such a study may pave 324 the way to propose new tests replacing the injection of animals in the post-licensing safety tests 325 currently requested for several live viral vaccines for human use. 326

327

328 **Conflicts of interest**

All authors confirm that there are no conflicts of interest.

330

331 Acknowledgements

This work was supported by internal grants of Institut Pasteur, Paris.

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405 *Legends*

Fig. 1. Construction and characterization of lentivectors expressing RABV Cyto-G 406 constructs. A) Construction of chimera Cyto-Gs and sequences of the 12 COOH amino acids 407 of the G protein of CVS-NIV, ERA-NIV and the three South Africa RABV strains (Canid, 408 Mongoose or Spill-over, the latter resulting from the infection of a dog by a mongoose RABV 409 strain). Chimera Cyto-Gs (44aa) are formed by the Signal peptide, SP, G and K amino acids 410 from the ectodomain, transmembrane domain, TM, (19 aa), the Constant domain (32aa) from 411 the CVS-NIV Cyto-G and a variable insert (12aa) corresponding to the 12 COOH terminus aa 412 of Cyto-Gs of the different RABV strains distinct by 5 mutations (bold). B) Relative 413 abundance of G mRNA transcription levels in a recombinant lentivirus system obtained by 414 relative RT-qPCR (The left and right panels represent independent experiments). C) 415 Expression of the chimera Cyto-Gs (7.4 kDa) in Neurocreen-1 cells after a 48h-infection with 416 lentivirus expressing either G-ERA-NIV, G-canid chimera, G-mongoose chimera, G-spill-417 over chimera or G-CVS-NIV (N.I. is for non-infected). M= molecular weight marker. **D**) 418 Expression of Cyto-G constructs in 48h transduced (CVS, ERA, DOG, MON = Mongoose or 419 SO =Spill Over) or non-treated (NEG). Neuroscreen- 1 cells was monitored by confocal 420 microscopy using RABV specific Cyto-G polyclonal antibody (green). The nucleus is in blue 421 422 after Hoescht 33342 staining. Scale bars : 10 µm.

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Fig. 2 Neurite outgrowth. Cultures of Neuroscreen cultivated for 72 hours after lentivirus
transduction. Cells were fixed and stained with crystal violet solution to visualize neurite
processes. A) Representative fields of cultures. B) Neurite outgrowth drawing (ImageJ 1.44p,
Neuron J plug-in) of representative N.I (non-infected) or 72h-lentivirus transduced
Neuroscreen-1 cells. C) Comparison of mean neurite outgrowth (µm) triggered in N.I or cells
expressing either: G-CVS NIV and G-CVS NIV∆ (left panel) or N.I., G CVS-NIV, G-canid,

G-mongoose, G-spill-over or G-ERA-NIV chimera (right panel). The data are representative of duplicate independent experiments. Neurites were counted in 55 fields for each condition (with at least one neurite per field). See table 2 for Statistical significance. **D**) Absence of correlation between G constructs and neurite outgrowth experimental values. The level of expression of the G constructs and the mean neurite length obtained are not correlated each other, whatever the nature of the chimera construct (the left and right panels represent independent experiments).