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Galileu Barbosa Costa, Anne Lavergne, Edith Darcissac, Vincent Lacoste, Betania Paiva Drumond, et al.. Absence of vaccinia virus detection in a remote region of the Northern Amazon forests, 2005-2015: Absence of vaccinia virus detection in French Guiana. Archives of Virology, 2017, 162 (8), pp.2369 - 2373. 10.1007/s00705-017-3353-x. pasteur-01585618

HAL Id: pasteur-01585618 https://riip.hal.science/pasteur-01585618

Submitted on 18 Sep 2017

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Title: Absence of Vaccinia virus detection in a remote region from Northern Amazon forests, 2005-2015

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17 Abstract

Vaccinia virus (VACV) circulates in Brazil and other South America countries, being responsible 18 for a zoonotic disease that usually affects dairy cattle and humans, causing economic losses and 19 impacting animal and human health. Furthermore, VACV was already detected in wild areas from 20 Brazilian Amazon. To better understand the natural history of VACV, we investigated its 21 circulation in wildlife from French Guiana, a remote region in Northern Amazon forests. ELISA 22 and plaque reduction neutralization test were performed to detect anti-Orthopoxvirus antibodies. 23 Real-time and standard PCR targeting C11R, A56R and A26L were applied to detect VACV DNA 24 in serum, saliva and tissue samples. VACV was not evidenced in any samples tested. These 25

26 findings provide additional information on the VACV epidemiological puzzle. The virus could
27 nevertheless be circulating at low levels that were not detected in areas with no human or cattle
28 presence.

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Vaccinia virus (VACV) is the prototype of the *Orthopoxvirus* (OPV) genus, *Poxviridae* family, and was used as a live vaccine around the world to eradicate smallpox. VACV circulates in zoonotic cycles involving bovine herd and dairy workers in rural areas from Brazil, causing a disease named Bovine Vaccinia (BV) which accounts for several economical losses and increasing the public health concerns [1].

In the last seventeen years, VACV spread throughout all Brazilian territory [1], though its occurrence varies among different regions. Furthermore, VACV has been detected in countries bordering Brazil, such as Argentina [2], Uruguay [3], and Colombia [4]. Although since 1999, several BV outbreaks affecting mainly dairy cattle and humans have been reported [1], natural VACV circulation had already been described in a rodent of *Oryzomys* genus captured in the 60's in the Amazon region [5].

During these last years in which reports of BV outbreaks have been observed, VACV 42 circulation has been described in the Amazon region, in mammal species such as bovines, primates, 43 coatis, and also humans [6-12]. Nevertheless, there is little information on a possible VACV 44 sylvatic cycle and on its natural reservoirs since the origin of VACV is still unknown and its natural 45 reservoir is still unidentified [13-16]. Given that VACV has a broad host range and that wild 46 animals might be implicated in its transmission chain, we decided to search for VACV circulation 47 48 in wildlife animals (rodents, marsupials, and bats) captured in pristine forest areas with the absence or limited anthropogenic impacts of Northern Amazon forests. 49

We analyzed a total of 2,365 wild mammals from French Guiana, captured between 2005 50 and 2015 in tropical upland rain forest, Amazon region [17, 18]. Captured sites were located in 51 remote forests, slightly disturbed forests (facing selective logging, hunting pressure, and low 52 53 fragmentation level), secondary forests and edge between forest and open habitats (Figure 1). Wild mammals included rodents (n = 420), marsupials (n = 606) and Chiroptera (n = 1.339) (Table 1). 54 All samples underwent molecular testing for VACV. To detect VACV DNA we used real-time PCR 55 56 targeting the C11R and A56R genes, and semi-nested PCR targeting C11R and A26L genes [19]. A molecular approach was performed in serum and tissue samples from rodents and marsupials, and 57 in DNA extracted from saliva and blood clots of bats. The positive controls used on molecular assays 58 59 were DNA extracted from serum and liver of experimental infected Balb/c mice with Vaccinia virus Western 60 Reserve (VACV-WR) strain and Brazilian Vaccinia (Br-VACV) group 1 and 2 viruses [20]. For those for which we were not able to have an experimental infected animal (marsupials and bats), we provided 61 an experimentally contamination of serum and liver samples as in the protocol previously described 62 63 by Dutra and co-authors [21]. Briefly, it was added different concentrations of VACV-WR and Br-VACV strains (with a range from 10^4 pfu/µL to 1 pfu/µL, respectively). The experimentally 64 contaminated samples were tested by PCR, compared to the Balb/c controls, and then used as 65 66 positive controls for marsupials and bats.

In addition, serum samples from the rodents and marsupials were screened for anti-OPV IgG by ELISA and neutralizing antibodies by \geq 50% plaque reduction neutralization test (PRNT₅₀) [19]. Sera were grouped into pools of 2–5 serum samples from animals belonging to the same species that were from the same collection area. No serum samples from bats were available for serological tests. For serological assays, the positive controls were also those provided by experimental infected mouse with VACV-WR and Br-VACV strains [20]. For the ELISA assay particularly, we used purified recombinant A/G protein peroxidase conjugated as secondary antibody. We run rodent and marsupial samples together in the same plate (for ELISA and PRNT), comparing the results with
known positive and negative rodents' serum samples.

Most of the rodents captured belong to the species *Proechimys guyannensis* (46,4%), followed by *Proechimys cuvieri* (11,2%) and *Zygodontomys brevicauda* (9,5%). The main marsupials studied were *Didelphis marsupialis* (34,1%) and *Marmosa murina* (26,2%). For bat species, most of them were *Desmodus rotundus* (32,3%), *Carollia perspicillata* (17,2%) and *Pteronotus* spp. (14,0%). All animals tested by both serological and molecular techniques were negative for VACV.

In this study, we assessed numerous forest mammal species and found no serological or 82 molecular evidence for VACV circulation among them. Increasing efforts have been done regarding 83 VACV ecology in South America, and some studies have highlighted the importance of wild 84 85 animals and peridomestic rodents as VACV carriers [7, 22, 23, Miranda JB, personal communication/in peer review]. Our negative results contrast with the above-mentioned ones and 86 some hypotheses can be considered in explaining the lack of evidence for VACV circulation in wild 87 88 animals in French Guiana during the 2005-2015 period. One hypothesis is that wildlife was investigated in a highly preserved Northern Amazon region, where natural geographic barriers of 89 unfavorable forest habitats exist, preventing VACV dissemination from Brazil to French Guiana. 90 91 This could also be emphasized by the "dilution effect" hypothesis, taking into account that in a 92 highly preserved environment, the maintenance of a highly diverse mammal community may 93 prevent infection of putative more sensitive species. A great diversity of mammal species was studied, but with only a small sampling of species from which VACV has been detected in Brazil, 94 such as Mus musculus [20], Oryzomys sp [5], and Caluromys philander [Miranda JB, personal 95 96 communication/in peer review]. Furthermore, the species Didelphis albiventris from which VACV was recently detected in São Paulo State, Southeast region of Brazil [24], is not present in French 97

Guiana. Nevertheless, two closely related species *Didelphis imperfecta* (n = 2) and *D. marsupialis* 99 (n = 207) were tested.

Another explanation for the absence of VACV detection in this study could be the extremely 100 101 low number of bovines in French Guiana. One hypothesis for the broad circulation of VACV in Brazil is that bovines are acting as VACV amplifiers, excreting high loads of viable particles, being 102 a source of infection for themselves and other animals [25]. VACV can be detected in animals 103 104 without clinical disease since it has been detected in blood samples and feces in animals without 105 lesions but presenting neutralizing antibodies [25]. Due to the potential role of cattle as a viral amplifier, the presence of bovines could facilitate VACV persistence and dissemination into the 106 environment. 107

VACV has recently been identified at the borders of Brazil, in countries such as Argentina [2], Uruguay [3], and Colombia [4]. Even though the circumstances of VACV detection in South American countries are still uncertain, the cattle trade and translocation has to be considered, as highlighted in Amazon region (Mato Grosso and Rondônia states) [9]. Furthermore, some authors have hypothesized that the seroprevalence of OPV-antibodies in human populations from the Amazon basin (Acre state) could be linked to agriculture and livestock practices, reinforcing the role of cattle on VACV maintenance [8].

115 Compared to other South American countries where VACV has been detected, a different 116 situation is observed in French Guiana where a lower deforestation rate is observed and where only 117 a few cattle or horses are present [26] (http://www.globalforestwatch.org/) (Figure 1). Nevertheless, 118 our findings do not definitively establish that VACV is not circulating, and also do not exclude the 119 possibility that small mammals can act as its reservoir in nature. However, data presented here 120 strongly suggest the absence of circulation of VACV, or at low levels that were not detected, in 121 remote Amazonian areas with no human impact over a long period of time. The monitoring and surveillance of VACV circulation is important to ensure early warning of zoonotic outbreaks forvulnerable human populations.

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126 Legend for figure:

An overview of French Guiana with the location of the studied regions, where were implemented several trapping sites. The background of the map highlights the human footprint index expected to summarize the anthropic threats on biodiversity. These threats (accessibility, land use, human density) are summed and allowed producing an index with lower pressures strenght in light and higher pressures darker. For each studied region, the dominant habitat is given.

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133 Acknowledgements

We thank colleagues from the Laboratoire des Interactions Virus-Hôtes, Institut Pasteur de la
Guyane for their excellent technical support. We also thank Pró-Reitoria de Pesquisa from
Universidade Federal de Minas Gerais (PRPq/UFMG), CAPES, FAPEMIG and CNPq. JS Abrahão,
EG Kroon, and GS Trindade are researchers from CNPq.

138

139 Funding

140 This study was funded by two European projects, CAROLIA and RESERVOIRS, through ERDF

141 funds and a European Commission "REGPOT-CT-2011-285837-STRonGer" grant within the FP7.

142 This work also benefited from an "Investissements d'Avenir' grant managed by Agence Nationale

143 de la Recherche, France (CEBA, ref. ANR-10-LABX-25-01).

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145 **Conflict of interest**

146 Authors declare no conflict of interest.

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148	Ethical approval
149	Captures of rodents, bats and marsupials do not require ethic committee in French Guiana.
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