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Research paper

Animal experiments show impact of vaccination on reduction of SARS-CoV-2 virus circulation: A model for vaccine development?

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ABSTRACT

Background: In the pre-clinical phase, SARS-CoV-2 vaccines were tested in animal models, including exposure trials, to investigate protection against SARS-CoV-2. These studies paved the way for clinical development. The objective of our review was to provide an overview of published animal exposure results, focussing on the capacity of vaccines to reduce/prevent viral shedding.

Method: Using Medline, we retrieved eighteen papers on eight different vaccine platforms in four animal models. Data were extracted on presence/absence of viral RNA in nose, throat, or lungs, and neutralizing antibody levels in the blood.

Results: All vaccines showed a tendency of reduced viral load after exposure. Particularly nasal swab results are likely to give an indication about the impact on virus excretion in the environment. Similarly, the reduction or prevention of viral replication in the bronchoalveolar environment might be related with disease prevention, explaining the high efficacy in clinical trials.

Discussion: Although it remains difficult to compare the results directly, the potential for a strong reduction of transmission was shown, indicating that the animal models predicted what is observed in the field after large scale human vaccination. This merits further attention for standardization of exposure experiments, with the intention to speed up future vaccine development.

1. Introduction

SARS-CoV-2 has overwhelmed the globe in less than one year with more than 150 million known infections globally and a death toll due to COVID-19 exceeding 3.2 million deaths.¹ The SARS-CoV-2 viral genome was published on January 11, 2020 (GenBank accession number MN908947) [1]. The use of new platform technologies, particularly mRNA and recombinant vector technology [2], the result of decades of fundamental research and development investments, greatly facilitated rapid vaccine development. To assure complete coverage of the almost 8 billion people of this planet, many vaccines and vaccine production sites will be needed. The standardization effort developed by WHO, CEPI and GAVI, the Vaccine Alliance, merits strong support [3].

A number of vaccines has reached conditional market authorization

[4] or emergency use authorization [5], while many others are in pre-clinical or in clinical development phase. Phase III studies revealed high efficacy against disease and hospitalization and good safety profiles. Real-world data with authorized vaccines [6,7] revealed that vaccination markedly reduced viral load in vaccinated individuals which may thus likely impact transmission. This was further substantiated in recent studies looking at transmissibility from vaccinated healthcare workers to their family members in Scotland (14 days after dose 1, 30% reduction) [8] and in England (14–21 days after dose 1, 38–49% reduction) [9].

A non-human primate model based on rhesus macaques [10,11] and cynomolgus macaques [11,12], and a small animal model using ferrets [13] or Syrian golden hamsters [14] were developed by many groups for SARS-CoV-2 infection and countermeasure development. A number of

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¹ Johns Hopkins; <https://gisanddata.maps.arcgis.com/apps/opsdashboard/index.html#/bda7594740fd40299423467b48e9ecf6>.

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vaccines, including mRNA vaccines (Pfizer BioNTech, Moderna and Curevac), Adeno vector recombinant vaccines (AstraZeneca and J&J), Yellow fever vector recombinant vaccines (University of Leuven, Belgium, Regavax), Measles recombinant vaccines, nanoparticle vaccines, subunit vaccines, and purified inactivated vaccines were used in these animal models. Here we provide a concise overview of published results, in which we focus particularly on the capacity of the vaccines to reduce or prevent viral shedding following exposure.

2. Methods

A review was performed for SARS-CoV-2 exposure studies in animal models, after vaccination with COVID-19 vaccine candidates. We searched MEDLINE (PubMed, which includes bioRxiv) for relevant articles. Mammal models were included, based on susceptibility to SARS-CoV-2 infection [15–19]. Search terms used were: (cat OR dog OR ferret OR cynomolgus macaque OR rhesus macaque OR African green monkey OR Syrian hamster) AND SARS-CoV-2 AND infection AND vaccine. Citations from eligible articles were also searched to identify other relevant studies.

The following data were extracted from eligible studies: first author, journal name, publication year, animal model, vaccine platform, vaccine name, vaccine route of administration, vaccine dose, vaccine schedule, exposure strain, exposure dose, exposure route of administration, exposure schedule, method to detect neutralizing antibodies, geometric mean titer in control animals, geometric mean titer in vaccinated animals, geometric mean titer in human convalescent sera, neutralizing antibodies ratio vaccinated vs control, neutralizing antibodies ratio vaccinated vs human convalescent serum, method to detect (sub-genomic) RNA, viral load in control animals, number of controls animals positive, viral load in vaccinated animals, number of vaccinated animals positive.

To meet the objectives of the study the focus was on presence or absence of viral RNA in affected organs (nose, throat, lungs) and neutralizing antibody levels in the blood.

3. Results

Our search retrieved 123 studies, of which 18 were eligible for extraction. Distribution by animal model and vaccine type is shown in Table 1. An overview of all data extracted is provided in Supplementary Table S1.

Table 1
Distribution of studies by animal model and vaccine type.

Vaccine \ Model	Syrian hamster	Ferret	Rhesus macaque	Cynomolgus macaque
mRNA	Rauch 2021		Vogel 2020, Corbett 2020, Rauch 2020	
Adenovirus	Tostanoski 2020		Van Doremalen 2020, Van Doremalen 2021, Mercado 2020, Feng 2020	
Yellow fever	Sanchez-Felipe 2021			Sanchez-Felipe 2021
Measles VSV	Horner 2020 Yahalom-Ronen 2020			
Nanoparticle		Kim 2021		Brouwer 2021
Subunit			Liang 2021, Yang 2020	Guebre-Xavier 2020
Inactivated			Gao 2020	

3.1. Syrian hamster model

Syrian hamsters were used to investigate protection against exposure after vaccination with a wide range of vaccine platforms; mRNA vaccine [20], adenovirus [21], measles virus [22], yellow fever virus [23] and VSV [24]. Vaccine was administered to animals via similar routes (intramuscularly, or intraperitoneally), whereas the dose was difficult to compare between different platforms. Three studies used a single dose [21,23,24], while three studies used two doses, one [23], three [22] or four weeks [20] apart. All animals were challenged intranasally, or both intranasally and intratracheally [20], between days 23 and 42 after the last dose of vaccine. However, the dose used for challenge varied markedly, ranging from 10^2 to 5×10^5 median tissue culture infectious dose (TCID₅₀) and from 2×10^5 to 5×10^6 plaque forming units (pfu). All studies checked lungs, and sometimes also nasal turbinates. Limited effects were seen after vaccination with MeVvac2-SARS2-S(H) [22], with only a ten-fold reduction in viral titer in both lungs and nasal turbinates. In contrast, strong reductions, both in number of affected animals and in viral titer in those affected, were seen after vaccination with CVnCoV [20], YF-S0 [23], and rVSV-ΔG-spike [24], with a stronger effect in lungs than in nasal turbinates (see Table 2). In the study using Ad26-S.PP [21] a reduction in mortality was observed, and a strong reduction in the percentage of lung area affected by infection. Although for nasal turbinates, vaccination did not seem to impact the number of animals positive for viral RNA, a 1000-fold reduction in viral load was observed after vaccination with rVSV-ΔG-spike [24].

Neutralizing antibody titers were determined with several techniques and geometric mean titers (GMT) ranged from 20 to 800. Results were not compared to human sera but in one study it was observed that GMTs after vaccination were 2.5–7.5 times higher than in convalescent hamsters [23].

3.2. Ferret model

Only one study was performed in ferrets, to investigate protection against challenge after vaccination with three doses of receptor binding domain (RBD) nanoparticles, at days 0, 14 and 28 [25]. The ferrets were challenged with 10^5 TCID₅₀. Viral loads were determined in the nose and lungs, with a strong effect in the nose from day 6 after challenge, whereas no vaccinated animals were positive in the lungs, either at day 3 or day 6 after challenge (see Table 3). Both intramuscular and combined intramuscular/intranasal immunization were tested and the combination gave slightly better results than intramuscular vaccination only [25]. Neutralizing antibody titers were determined by micro-neutralization assay and a GMT of 64 was observed, with little difference between intramuscular or combined intramuscular/intranasal immunization [25].

3.3. Rhesus macaque model

Rhesus macaques were used to investigate protection against exposure after vaccination with a wide range of vaccine platforms; mRNA vaccine [26–28], adenovirus [29–32], subunit vaccine [33,34], and inactivated virus [35]. Vaccine was generally administered to animals intramuscularly, with one study using intranasal administration [32]. The dose ranged from 0.5 to 100 µg for mRNA, 10^{10} to 10^{11} virus particles for adenovirus, and 20–40 µg for subunit vaccines. Two studies used a single dose [29,30], while seven studies used two doses, one [34], three [28,33] or four weeks [20,26,27,31,32] apart. In most studies animals were challenged both intranasally and intratracheally, whereas in one study animals were challenged intranasally [34], and in one study intratracheally [29]. Animals were challenged between days 14 and 56 after the last dose of vaccine. However, the dose used for challenge varied strongly, ranging from 2×10^4 to 2.6×10^6 TCID₅₀ and from 5×10^5 to 5×10^6 pfu.

Samples obtained included brochoalveolar lavage (BAL), nasal,

Table 2
Syrian golden hamster model.

First author	Vaccine name	DPI, RNA*	viral load control	positive controls	viral load vaccinated	positive vaccinated
<i>Lung</i>						
Hörner C.	MeVvac2-SARS2-S(H)	4, RNA	6.3×10^9	6 out of 6	3.2×10^8	6 out of 6
Hörner C.	MeVvac2-SARS2-S(H)	4, ti	3.2×10^5	6 out of 6		1 out of 6
Rauch S.	CvnCoV, low	RNA		5 out of 5		4 out of 5
Rauch S.	CvnCoV, high	RNA		5 out of 5		0 out of 5
Sanchez-Felipe L.	YF-S0, 1 dose, low		5×10^5	12 out of 12	6.3×10^1	4 out of 12
Sanchez-Felipe L.	YF-S0, 1 dose, high		5×10^5	12 out of 12		0 out of 12
Sanchez-Felipe L.	YF-S0, 2 dose		4×10^5	12 out of 12		3 out of 12
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^6	3, RNA	5.6×10^6	4 out of 4	7.3×10^3	2 out of 4
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^4	5, RNA	10^5	7 out of 7		0 out of 3
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^5	5, RNA	10^5	7 out of 7		0 out of 3
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^6	5, RNA	10^5	7 out of 7		0 out of 3
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^7	5, RNA	10^5	7 out of 7		0 out of 3
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^8	5, RNA	10^5	7 out of 7		0 out of 3
<i>Lung, affected tissue</i>						
Rauch S.	CvnCoV, low			5 out of 5		2 out of 5
Rauch S.	CvnCoV, high			5 out of 5		0 out of 5
Tostanoski L.	Ad26-S.PP		14%	5 out of 5	0%	1 out of 6
<i>Nasal turbinates</i>						
Hörner C.	MeVvac2-SARS2-S(H)	4, RNA	2×10^{10}	6 out of 6	2×10^9	6 out of 6
Hörner C.	MeVvac2-SARS2-S(H)	4, ti	3.2×10^5	6 out of 6	10^4	5 out of 6
Rauch S.	CvnCoV, low	RNA		5 out of 5		5 out of 5
Rauch S.	CvnCoV, high	RNA		5 out of 5		4 out of 5
Yahalom-Ronen Y.	rVSV-ΔG-spike, 10^6	3, RNA	1.9×10^5	4 out of 4	2.8×10^2	3 out of 4

DPI – days post infection; * RNA – total RNA; sg – subgenomic RNA; ti – virus titration.

Table 3
Ferret animal model.

First author	Vaccine	DPI, RNA*	Positive controls	Positive vaccinated
<i>Nose</i>				
Kim Y. I.	RBD-np	2, RNA	10 out of 10	20 out of 20
Kim Y. I.	RBD-np	4, RNA	7 out of 7	6 out of 14
Kim Y. I.	RBD-np	6, RNA	7 out of 7	0 out of 14
Kim Y. I.	RBD-np	8, RNA	2 out of 4	0 out of 8
Kim Y. I.	RBD-np	10, RNA	0 out of 4	0 out of 8
<i>Lung</i>				
Kim Y. I.	RBD-np	3, RNA	3 out of 3	0 out of 6
Kim Y. I.	RBD-np	6, RNA	3 out of 3	0 out of 6

DPI – days post infection; * RNA – total RNA; sg – subgenomic RNA.

throat and tracheal swabs, and lung tissue. Limited effects on sgRNA in BAL were seen after vaccination with CvnCoV [27], whereas strong reductions in number of sgRNA positive animals were observed after vaccination with mRNA-1273 [26], Ad26-S.PP [30], ChAdOx1 nCoV-19 [31,32], and BNT162b2 [28]. Similarly, strong reductions were seen in lung, nasal swab, throat swab and tracheal swab (Table 4).

Neutralizing antibody titers were determined with several techniques and GMTs ranged from 5 to 27000, with higher doses resulting in higher GMTs [26,27,29], two doses giving higher GMTs than one dose [31], and AS03 adjuvant giving higher GMTs than CpG [33]. Results were compared to human convalescent sera and the GMT ratio ranged from 1 [32,35] to 84 [26].

3.4. Cynomolgus macaque model

Cynomolgus macaques were used to investigate protection against exposure after vaccination with several vaccine platforms; nanoparticle [36], subunit vaccine [37], and yellow fever virus [23]. Vaccine was administrated to animals intramuscularly [36,37], or subcutaneously [23]. Two studies used two doses, one [23], or three weeks [37] apart, while one study used three doses at zero, four and ten weeks [36]. Animals were challenged between days 14 and 21 after the last dose of vaccine. However, the dose used for challenge varied strongly, ranging from 1.04×10^4 to 10^6 pfu, or 100-fold.

Samples obtained included BAL, nasal, throat and tracheal swabs.

Strong reductions in number of sgRNA positive BAL samples were observed after vaccination with SARS-CoV-2 S-I53-50NP [36], and NVX-CoV2373 [37]. Similarly, strong reductions were seen in nasal swabs [36,37], and to a lesser degree in throat swabs [23] and tracheal swabs [36] (see Table 5).

Neutralizing antibody titers ranged from 398 to 26000. Results were compared to human convalescent sera and the GMT ratio ranged from 3 [36] to 10 [37].

4. Discussion

In this study we found 18 papers on eight different vaccine platforms in four animal models. All vaccines show a general tendency of impact on virus reduction after infection. While the list of vaccines is not exhaustive, as results with other vaccines will become available, the published data indicate that vaccine challenge trials in non-human primates, ferrets and hamsters show the potential of COVID-19 vaccines to limit or prevent disease and transmission of the virus. A strong reduction of viral load in lungs would demonstrate impact of the vaccine on disease (presence of clinical signs, need for hospitalization, and ICU). Hence, the reduction or prevention of virus replication in the bronchoalveolar environment, consistently shown in animal models, might be related with disease prevention and might explain the high efficacy in clinical trials [38–40]. On the other hand, a strong reduction in excretion would demonstrate the potential of the vaccine to decrease the spread and transmission of SARS-CoV-2. Particularly nasal swab results are likely to give an indication about the impact of virus excretion in the environment. Interestingly, in the non-human primate models, the impact of the vaccine seems to be larger in the lung than in the nose, whereas in the hamster, a model with more severe clinical signs in non-treated animals, the impact of the vaccine in the lung and in the nose seems to be equal although the data with relation to viral presence in the nasal turbinates of hamsters is limited and needs further exploration. Nevertheless, all data taken together, it means that the hamster is a useful model to study vaccine efficacy and may ethically be more acceptable than the use of non-human primates.

If a correlation between results in animal models and results in human populations could be established, standardized animal models might become a way to advance more quickly to gather efficacy data on

Table 4
Rhesus macaque animal model.

First author	Vaccine	DPI, RNA*	control viral load	controls positive	vaccinated viral load	vaccinated positive
<i>BAL</i>						
Corbett K. S.	mRNA-1273	2, sg		8 out of 8		1 out of 8
Corbett K. S.	mRNA-1273	4, sg		4 out of 8		0 out of 8
Corbett K. S.	mRNA-1273	7, sg		1 out of 8		0 out of 8
Mercado N. B.	Ad26-S.PP	sg	7.9×10^4	20 out of 20	0	0 out of 6
van Doremalen N. ^a	ChAdOx1, 1 dose	5, sg		5 out of 6		0 out of 6
van Doremalen N. ^a	ChAdOx1, 2 dose	5, sg		4 out of 6		0 out of 6
van Doremalen N. ^b	ChAdOx1 nCoV-19	sg		4 out of 4		1 out of 4
Vogel A. B.	BNT162b2	3, RNA	10^6	2 out of 3	0	0 out of 6
Vogel A. B.	BNT162b2	6, RNA	5×10^3	1 out of 3	0	0 out of 6
Rauch S.	CvnCoV, live	sg		1 out of 6		0 out of 6
Rauch S.	CvnCoV, pm	sg		1 out of 6		1 out of 6
<i>Lung</i>						
Feng L.	Ad5-S-nb2	RNA		4 out of 4		0 out of 9
Liang J. G.	S-Trimer + AS03	5, RNA		21 out of 32		0 out of 32
Liang J. G.	S-Trimer + CpG	7, RNA		21 out of 32		0 out of 32
Yang J.	RBD - 20ug	7, sg		11 out of 35		0 out of 3
Yang J.	RBD - 40 ug	7, sg		11 out of 35		0 out of 4
van Doremalen N. ^a	ChAdOx1, 2 dose	sg		17 out of 36		2 out of 36
<i>Nasal swab</i>						
Corbett K. S.	mRNA-1273	1, sg		6 out of 8		3 out of 8
Corbett K. S.	mRNA-1273	2, sg		6 out of 8		0 out of 8
Corbett K. S.	mRNA-1273	4, sg		4 out of 8		1 out of 8
Corbett K. S.	mRNA-1273	7, sg		0 out of 8		0 out of 8
Rauch S.	CvnCoV	sg	3.7×10^4	5 out of 6	4×10^3	3 out of 6
Vogel A. B.	BNT162b2	1, RNA	9×10^3	2 out of 3	10^5	5 out of 6
Vogel A. B.	BNT162b2	3, RNA	1.1×10^4	2 out of 3	0	0 out of 6
Vogel A. B.	BNT162b2	6, RNA	2×10^3	1 out of 3	0	0 out of 6
Liang J. G.	S-Trimer + AS03	1, RNA		6 out of 6		5 out of 6
Liang J. G.	S-Trimer + CpG	1, RNA		6 out of 6		6 out of 6
Liang J. G.	S-Trimer + AS03	3, RNA		4 out of 6		4 out of 6
Liang J. G.	S-Trimer + CpG	3, RNA		4 out of 6		4 out of 6
Liang J. G.	S-Trimer + AS03	5, RNA		2 out of 6		4 out of 6
Liang J. G.	S-Trimer + CpG	5, RNA		2 out of 6		1 out of 6
Liang J. G.	S-Trimer + AS03	7, RNA		1 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	7, RNA		1 out of 6		1 out of 6
Mercado N. B.	Ad26-S.PP	sg	2.5×10^5	20 out of 20	0	1 out of 6
van Doremalen N. ^a	ChAdOx1, 1 dose	0, sg		1 out of 6		2 out of 6
van Doremalen N. ^a	ChAdOx1, 1 dose	3, sg		4 out of 6		4 out of 6
van Doremalen N. ^a	ChAdOx1, 1 dose	5, sg		0 out of 6		1 out of 6
van Doremalen N. ^a	ChAdOx1, 1 dose	7, sg		0 out of 6		0 out of 6
van Doremalen N. ^a	ChAdOx1, 2 dose	0, sg		1 out of 6		3 out of 6
van Doremalen N. ^a	ChAdOx1, 2 dose	3, sg		4 out of 6		2 out of 6
van Doremalen N. ^a	ChAdOx1, 2 dose	5, sg		0 out of 6		2 out of 6
van Doremalen N. ^a	ChAdOx1, 2 dose	7, sg		0 out of 6		0 out of 6
van Doremalen N. ^b	ChAdOx1 nCoV-19	sg		3 out of 4		1 out of 4
<i>Throat</i>						
Vogel A. B.	BNT162b2	1, RNA	7.5×10^4	3 out of 3	1.2×10^3	3 out of 6
Vogel A. B.	BNT162b2	3, RNA	1.3×10^4	3 out of 3	1.1×10^3	2 out of 6
Vogel A. B.	BNT162b2	10, RNA	10^3	1 out of 3	10^3	1 out of 6
Feng L.	Ad5-S-nb2	AUC	1.3×10^6		5×10^2	
Feng L.	Ad5-S-nb2	7, RNA		5 out of 6		4 out of 9
Liang J. G.	S-Trimer + AS03	1, RNA		5 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	1, RNA		5 out of 6		3 out of 6
Liang J. G.	S-Trimer + AS03	3, RNA		4 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	3, RNA		4 out of 6		0 out of 6
Liang J. G.	S-Trimer + AS03	5, RNA		2 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	5, RNA		2 out of 6		0 out of 6
Liang J. G.	S-Trimer + AS03	7, RNA		1 out of 6		0 out of 6
Liang J. G.	S-Trimer + CpG	7, RNA		1 out of 6		1 out of 6
Yang J.	RBD - 20ug	3, sg		5 out of 5		0 out of 3
Yang J.	RBD - 40 ug	3, sg		5 out of 5		0 out of 4
Yang J.	RBD - 20ug	4, sg		5 out of 5		0 out of 3
Yang J.	RBD - 40 ug	4, sg		5 out of 5		0 out of 4
Yang J.	RBD - 20ug	5, sg		3 out of 5		0 out of 3
Yang J.	RBD - 40 ug	5, sg		3 out of 5		0 out of 4
Yang J.	RBD - 20ug	6, sg		5 out of 5		0 out of 3
Yang J.	RBD - 40 ug	6, sg		5 out of 5		0 out of 4
<i>Tracheal swab</i>						
Liang J. G.	S-Trimer + AS03	1, RNA		6 out of 6		6 out of 6
Liang J. G.	S-Trimer + CpG	1, RNA		6 out of 6		3 out of 6
Liang J. G.	S-Trimer + AS03	3, RNA		5 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	3, RNA		5 out of 6		1 out of 6

(continued on next page)

Table 4 (continued)

First author	Vaccine	DPI, RNA*	control viral load	controls positive	vaccinated viral load	vaccinated positive
Liang J. G.	S-Trimer + AS03	5, RNA		1 out of 6		0 out of 6
Liang J. G.	S-Trimer + CpG	5, RNA		1 out of 6		0 out of 6
Liang J. G.	S-Trimer + AS03	7, RNA		0 out of 6		1 out of 6
Liang J. G.	S-Trimer + CpG	7, RNA		0 out of 6		2 out of 6

AUC – area under the curve; BAL – broncho-alveolar lavage; dpi – days post infection; pm – post mortem; * RNA – total RNA; sg – subgenomic RNA.

Table 5

Cynomolgus macaque.

First author	Vaccine	DPI, RNA*	Control viral load	Controls positive	Vaccinated viral load	Vaccinated positive
<i>BAL</i>						
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	3, RNA	2.3×10^4	4 out of 4	3.2×10^2	0 out of 6
Guebre-Xabier M.	NVX-CoV2373-low	2, sg	7.9×10^3	4 out of 4		1 out of 4
Guebre-Xabier M.	NVX-CoV2373-low	4, sg	4×10^2	3 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-medium	2, sg	8×10^3	4 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-medium	4, sg	4×10^2	3 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-high	2, sg	8×10^3	4 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-high	4, sg	4×10^2	3 out of 4		0 out of 4
<i>Nasal swab</i>						
Guebre-Xabier M.	NVX-CoV2373-low	2, sg		1 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-low	4, sg		2 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-medium	2, sg		1 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-medium	4, sg		2 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-high	2, sg		1 out of 4		0 out of 4
Guebre-Xabier M.	NVX-CoV2373-high	4, sg		2 out of 4		0 out of 4
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	2, RNA	1.6×10^6	4 out of 4	3.2×10^2	0 out of 6
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	5, RNA		3 out of 4		0 out of 6
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	6, RNA		2 out of 4		0 out of 6
<i>Throat</i>						
Sanchez-Felipe L.	YF-S0	1, RNA		2 out of 6		0 out of 6
Sanchez-Felipe L.	YF-S0	2, RNA		3 out of 6		1 out of 6
Sanchez-Felipe L.	YF-S0	3, RNA		1 out of 6		0 out of 6
Sanchez-Felipe L.	YF-S0	4, RNA		1 out of 6		0 out of 6
<i>Trachea</i>						
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	2, RNA	5×10^4	4 out of 4	3.2×10^2	2 out of 6
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	5, RNA		1 out of 4		0 out of 6
Brouwer P. J. M.	SARS-CoV-2 S-I53–50NP	6, RNA		0 out of 4		0 out of 6

BAL – broncho-alveolar lavage; DPI – days post infection; * RNA – total RNA; sg – subgenomic RNA.

SARS-CoV-2 vaccines.

For instance, the study by Mercado et al. [30] shows an inverse correlation between the antibody titer and virus recovery, which is likely the same for all vaccines. Since neutralizing antibodies are relatively easy to determine, if this biomarker proves reliable, it would be an important tool to speed up vaccine development against COVID-19, in association with vaccine challenge results in animal models.

Transmission of SARS-CoV-2 between animals has been observed, both in animal models [41,42] and in farm animals [43]. Vaccine-challenge trials have been performed for a number of infectious agents (mostly viral, occasionally bacterial) in a range of animal species [44–47]. Regrettably, to our knowledge, no vaccine-challenge trials have been performed so far for SARS-CoV-2, which could have shed light on the impact of vaccination on contact and airborne transmission of SARS-CoV-2.

Our review has brought to light several limitations. First, the challenge dose varied strongly between experiments, not only between animal models but also within animal models. Therefore, we limited the comparison to general tendencies, because animal experiments show variability according to challenge administration route and species [48]. Finally, a number of manuscripts covered in this review were published on preprint servers, and have not yet undergone peer review, these studies should therefore be interpreted with caution. Moreover, these studies are often (co-)published by employees of the vaccine manufacturer, who inherently have a conflict of interest, further demanding caution in interpretation of the data.

The findings in animal models have now been confirmed by field

evidence, particularly in countries where the vaccination coverage is already substantial. In Israel, with more than 60% of the population vaccinated with the Pfizer/BioNTech vaccine, vaccination results in a positive effect on the reduction of new infections rates, with a 85% reduction in the symptomatic group and 75% for all SARS-CoV-2 positive cases at 15–28 days after the first dose [7]. A comparable trend has been observed in the UK, where a significant reduction of symptomatic and asymptomatic infections was seen in working age adults [49]. Further observations based on data from 1,14 million vaccinations in Scotland showed that both Pfizer/BioNtech and AstraZeneca vaccines are highly effective and reduce the risk of hospitalization from COVID-19 by up to 85% and 94%, respectively, four weeks after the first dose [50]. In addition, people aged 80 years or more, vaccinated with either vaccine showed an 81% reduction in hospitalization [50]. Recent data also directly showed that transmission is reduced from vaccinated people to their family members [8,9].

In conclusion, all SARS-CoV-2 vaccine candidates in this review, based on various vaccine platforms and different immunogens, reduce – after exposure - viral load in different organs in animal models. It remains difficult to compare the results obtained with vaccines directly, since the animal models and the exposure conditions vary. However, even if the data on viral shedding are scarce or not fully reliable in the animal models, a strong effect on the reduction of transmission is shown. Hence, the animal models predicted what is observed in the field after large scale vaccination of human populations. These interesting results merit further attention for standardization of exposure experiments to estimate more precisely the impact of each vaccine on the circulation of

wild virus in the population, with the intention to speed up future vaccine development.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.biologicals.2021.08.001>.

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