Viral neuroinvasion and neurotropism without neuronal damage in the hACE2 mouse model of COVID-19

Running title: CNS involvement in SARS-CoV-2 infection of hACE2 mice

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Abstract

Coronavirus disease 2019 (COVID-19) is a primarily respiratory disease with variable

clinical courses for which animal models are needed to gather insights into the

pathogenesis of its causative virus, Severe Acute Respiratory Syndrome Coronavirus

2 (SARS-CoV-2), in human patients. SARS-CoV-2 not only affects the respiratory

tract but also the central nervous system (CNS), leading to neurological symptoms

such as loss of smell and taste, headache, fatigue or severe complications like

cerebrovascular diseases. Transgenic mice expressing human angiotensin-

converting enzyme 2 (hACE2) under the cytokeratin 18 promoter (K18-hACE2)

represent a well-known model of SARS-CoV-2 infection. In the present study, it

served to investigate the spatiotemporal distribution and pathomorphological features

in the CNS following intranasal infection with relatively low SARS-CoV-2 doses and

after prior influenza A virus infection.

In K18-hACE2 mice, SARS-CoV-2 was found to frequently spread to and within the

CNS during the later phase (day 7) of infection. Infection was restricted to neurons

and appeared to first affect the olfactory bulb and spread from there mainly in basally

orientated regions in the brain and into the spinal cord, in a dose dependent manner

and independent of ACE2 expression. Neuronal infection was not associated with

cell death, axonal damage or demyelination. However, microglial activation,

microgliosis and a mild macrophage and T cell dominated inflammatory response

was consistently observed. This was accompanied by apoptotic death of endothelial,

microglial and immune cells, without evidence of viral infection of glial cells,

endothelial cells and leukocytes.

Taken together, microgliosis and immune cell apoptosis indicate a potential important

role of microglial cells for the pathogenesis and viral effect in COVID-19 and possible

impairment of neurological functions, especially in long COVID. These data may also

be informative for the selection of therapeutic candidates, and broadly support

investigation of agents with adequate penetration into relevant regions of the CNS.

Keywords: Severe Acute Respiratory Syndrome Coronavirus 2, mouse model,

COVID-19, encephalitis, microgliosis, influenza A virus coinfection

Introduction

As of April 2021, the newly emerged betacoronavirus, Severe Acute Respiratory

Syndrome Coronavirus-2 (SARS-CoV-2) has infected over 135 million people

globally, with over 2.9 million deaths due to the associated disease, COVID-19

(WHO, COVID-19 Weekly Epidemiological Update, 13th April 2021). The majority of

COVID-19 patients display respiratory symptoms. However, a proportion of patients

develop mostly transient unspecific neurological signs like loss of smell and taste

(anosmia, ageusia), headache, or dizziness. Fatal cases can also be associated with

ischemic stroke, hemorrhagic encephalopathy and epileptic seizures as well as

meningoencephalitis (Bernard-Valnet et al., 2020; Helms et al., 2020a; Huang et al.,

2020; Mao et al., 2020; Moriguchi et al., 2020; Oxley et al., 2020; Poyiadji et al.,

2020).

There is evidence of viral entry into the brain through the olfactory or vagal nerve

and/or the oral and ophthalmic routes, with trans-synaptic neuronal spread to other

brain regions (Cantuti-Castelvetri et al., 2020; Matschke et al., 2020; Meinhardt et al.,

2021); this could provide a link to the frequently reported (initial) anosmia and

ageusia. In addition, hematogenous spread to the brain via infection of endothelial

cells and/or immune cells is suspected (Paniz-Mondolfi et al., 2020; Al-Sarraj et al.,

2021).

Pathomorphological findings reported in the brain of fatal human COVID-19 cases

are variable and present as vascular/hemodynamic/ischemic lesions like ischemic

infarcts and/or mild inflammatory changes; neuronal or axonal damage and acute

disseminated encephalomyelitis have been reported in rare cases (Deigendesch et

al., 2020; Fabbri et al., 2021; Jaunmuktane et al., 2020; Kantonen et al., 2020;

Matschke et al, 2020; Schurink et al., 2020; Solomon et al., 2020; Reichard et al.,

2020; von Weyhern et al., 2020). Focal or diffuse microglial activation or microglial

nodules have also been observed (Al-Dalahmah et al., 2020; Bussani et al., 2020;

Deigendesch et al., 2020; Jaunmuktane et al., 2020; Matschke et al., 2020; Schurink

et al., 2020; Fabbri et al., 2021). COVID-19 patients can harbor SARS-CoV-2 RNA

and protein in the brain (Matschke et al., 2020; Puelles et al., 2020; Meinhardt et al.,

2021), and a recent study using human brain organoids provided strong evidence

that SARS-CoV-2 replicates in neurons (Song et al., 2021). However, presence of the

virus was not found to be associated with the severity of neuropathological changes

(Matschke et al., 2020), and in a recent study, immunohistochemical staining for

SARS-CoV-2 failed to detect viral antigen in all 18 investigated patients, while low

levels of viral RNA were detected by RT-PCR in five patients (Solomon et al., 2020).

Encephalopathy, as a severe complication in COVID-19, is often associated with

systemic hyperinflammation mainly provoked by an aberrantly excessive innate

immune response (Najjar et al. 2020). It is suspected that not only a direct virus

induced endotheliitis, but also a maladaptive innate immune response may impair

neurovascular endothelial function and cause disruption of the blood-brain barrier

(BBB), activation of innate immune signalling pathways and a parainfectious

autoimmunity (Najjar et al., 2020).

Recent articles have discussed the role of glial cells in COVID-19

encephalopathies (Murta et al., 2020; Vargas et al., 2020). Glial cells might not only

123 represent potential targets for viral infection but are also highly sensitive to systemic

124 proinflammatory cytokines (Perry et al., 2007; Teeling and Perry, 2009; Murta et al.,

125 2015; Murta and Ferrari, 2016). In COVID-19 patients, the massive systemic release

126 of inflammatory cytokines could affect endothelial cells and astrocytes of the BBB,

127 thus facilitating viral entry like in other viral brain diseases such as HIV-1 encephalitis

128 and measles (Swanson and McGavern, 2015). Indeed, a recent study has shown that

129 SARS-CoV-2 spike protein S1 from the blood can pass the BBB and thereby gain

130 access to the brain parenchyma in mice, potentially triggering a parenchymal

131 response without the presence of intact virus (Rhea et al., 2021). Furthermore,

132 astrocytes and microglia may contribute to the local neuroinflammatory response of

133 the CNS (Michael et al., 2020; Murta et al., 2020). Also, microglial cells are

134 hypothesized to be involved in the innate immune response and facilitate viral

135 clearance, recruitment of immune cells as well as activation of antiviral responses

136 and cytokine production in the brain of COVID-19 patients (Vargas et al., 2020).

137 Some authors also propose that a SARS-CoV-2-induced proinflammatory microglial

138 phenotype might contribute to the development of subsequent neurodegenerative

139 disorders (Alam et al., 2020; Mahalaxmi et al., 2020). Furthermore, the

140 proinflammatory priming of microglia, either by direct SARS-CoV-2 infection or a

141 peripheral cytokine storm, could exacerbate disease, as indicated in experimental

142 murine coronavirus (MHV-A59) infection (Lavi and Cong, 2020).

143  The human angiotensin-converting enzyme 2 (hACE2) is considered to be the

144 main host receptor for SARS-CoV-2, binding to the viral spike protein (S) (Hoffmann

145 et al., 2020). The K18-hACE2 transgenic (K18-hACE2) mouse, where hACE2

146 expression is driven by the epithelial cell cytokeratin-18 (K18) promoter, was

147 developed to study the pathogenesis of SARS-CoV infection (McCray et al., 2007); it

148 is now frequently employed to address a broad range of questions regarding SARS-

CoV-2 as expression of human ACE2 (hACE2) appears to convey higher binding

affinity than its murine counterpart. Several recent studies have shown that intranasal

SARS-CoV-2 infection of K18-hACE2 mice reaches the brain where it spreads

widely. Infection of the brain can be associated with non-suppurative

(meningo)encephalitis (Carossino et al., 2021; Clark et al., 2021; Kumari et al, 2021;

Song et al., 2021). With high infectious doses (10^5 PFU), very high viral loads were

found in the brain at a time when lung burdens had already decreased, in association

with upregulation of IFN-α as well as proinflammatory cytokine and chemokine

transcription; the authors posited that lethal outcome of infection in these mice was a

consequence of neuroinvasion (Kumari et al, 2021). Another study using an even

higher viral inoculum (10^6 PFU) elicited CNS signs (tremors, proprioceptive defects,

abnormal gait, imbalance) by day 6/7 after infection (Carossino et al., 2021). Studies

in mice have also confirmed that the virus can get access to the brain via the

olfactory bulb (Rhea et al., 2020; Song et al., 2021).

Detailed information on the effect of SARS-CoV-2 in the brain of COVID-19

patients has so far been collected from fatal cases. However, there is a current

paucity of data relating to what happens in the brain of patients that do not have

severe disease, recover from it or develop long COVID-19. A better understanding of

the viral dynamics within the CNS will provide further insight into the disease

pathology and will be highly informative for therapeutics development by providing

insight into the prerequisites for distribution of new medicines in development. The

present study represents a first attempt to address this question by investigating the

CNS of K18-hACE2 mice after intranasal infection with a low to moderate dose of a

SARS-CoV-2 wildtype strain, also in combination with prior influenza A virus infection

as it seems to foster neuronal spread (Clark et al., 2021).

Material and Methods

Cell culture and virus

A PANGO lineage B strain of strain of SARS-CoV-2 (hCoV-2/human/Liverpool/REMRQ0001/2020) cultured from a nasopharyngeal swab from a patient, was passaged in Vero E6 cells (Patterson et al., 2020). The fourth virus passage (P4) was used for infections after it had been checked for deletions in the mapped reads and the stock confirmed to not contain any deletions that can occur on passage (Clark et al., 2021).

   Influenza virus A/HKx31 (X31, H3N2) was propagated in the allantoic cavity of 9-day-old embryonated chicken eggs at 35 °C. Titres were determined by an influenza plaque assay using MDCK cells (Clark et al., 2021).

Biosafety

All work was performed in accordance with risk assessments and standard operating procedures approved by the University of Liverpool Biohazards Sub-Committee and by the UK Health and Safety Executive. Work with SARS-CoV-2 was performed at containment level 3 by personnel equipped with respirator airstream units with filtered air supply.

Animals and virus infections

Animal work was approved by the local University of Liverpool Animal Welfare and Ethical Review Body and performed under UK Home Office Project Licence PP4715265. Mice carrying the human ACE2 gene under the control of the keratin 18 promoter (K18-hACE2; formally B6.Cg-Tg(K18-ACE2)2Prlmn/J) were purchased

from Jackson Laboratories. Mice were maintained under SPF barrier conditions in

individually ventilated cages.

Animals were randomly assigned into multiple cohorts. For SARS-CoV-2 infection,

mice were anaesthetized lightly with isoflurane and inoculated intra-nasally with 50 µl

containing 10^3 PFU (cohorts 1 and 2) or 10^4 PFU (cohort 3) SARS-CoV-2 in PBS;

control animals received PBS. For double infections (cohort 2), mice were first

infected with IAV; they were anaesthetized lightly with KETASET i.m. and inoculated

intranasally with 10^2 PFU IAV X31 in 50 µl sterile PBS. Three days later, they were

infected with SARS-CoV-2, as described above. Mock-infected mice served as

controls. Mice were monitored for any clinical signs and weighed. Animals were

sacrificed at 3 or 7 days post SARS-CoV-2 infection by an overdose of

pentabarbitone. Tissues were removed immediately for downstream processing; the

lungs were processed for another study (Clark et al., 2021).

Tissue collection, preparation and processing

For the present study, the heads and spinal cords (C1-T12) were collected and fixed

in 10% neutral buffered formal saline for 24-48 h. Brains were exenterated and

coronal sections prepared. Heads were sawn longitudinally in the midline for

histological assessment of the nasal cavity, cribriform plate and rostral parts of the

olfactory bulb that had not been removed with the brain. In cases where SARS-CoV-

2 viral antigen was detected in the brain (see below), the spinal cords were sawn into

appr. 1.5 mm thick cross sections, using a diamond saw (Exakt 300; Exakt). Heads

and spinal cord were gently decalcified in RDF (Biosystems) for twice 5 days, at room

temperature (RT) and on a shaker. Brains, heads and spinal cords were routinely

paraffin wax embedded.

Histology, immunohistology

Consecutive sections (3-5 µm) were either stained with hematoxylin and eosin (HE)

or used for immunohistochemistry (IH). IH was performed using the horseradish

peroxidase (HRP) method to detect viral antigens in all examined tissues in all

animals, and to identify macrophages/activated microglial cells (Iba1+), T cells

(CD3+), B cells (CD45R/B220+) and neutrophils (Ly6G+) and to highlight astrocytes

(glial fibrillary acidic protein, GFAP+), apoptotic cells (cleaved caspase 3+),

disturbances of the fast axonal transport indicating acutely damaged neuronal axons

(amyloid precursor protein, APP+) and ACE2 expression in those animals where viral

antigen was detected in the brains. Antibodies and detection systems are listed in

Supplemental Table S1. Briefly, after deparaffination, sections underwent antigen

retrieval in citrate buffer (pH 6.0) or Tris/EDTA buffer (pH 9) for 20 min at 98 °C,

followed by incubation with the primary antibodies (diluted in dilution buffer, Agilent

Dako). This was followed by blocking of endogenous peroxidase (peroxidase block,

Agilent Dako) for 10 min at RT and incubation with the appropriate secondary

antibodies/detection systems, all in an autostainer (Dako Agilent or Ventana).

Sections were subsequently counterstained with hematoxylin.

The brain of a mock-infected control hACE mouse served as normal brain control

for ACE2, GFAP and APP, and a lymph node from a normal mouse for the leukocyte

and apoptosis markers. Sections from the lungs served as internal positive controls

for SARS-CoV-2 and IAV antigen expression, and sections incubated without the

primary antibodies served as negative controls.

RNA in situ hybridization (RNA-ISH)

RNA ISH was performed using the RNAscope® ISH method (Advanced Cell

Diagnostics (ACD Advanced Cell Diagnostics, Newark, California) and the

RNAscope® 2.5 Detection Reagent Kit (Brown) according to the manufacturer's

protocol and as previously described (Salguero et al., 2021; Saura-Martinez et al.,

2021). All cases were first tested for the suitability of the tissue (RNA preservation

and quality) with an oligoprobe for *Mus musculus* peptidylprolyl isomerase B (PPIB)

mRNA (ACD). Those yielding good PPIB signals were then subjected to RNA-ISH for

nCoV2019-S (coding for Wuhan seafood market pneumonia virus isolate Wuhan-Hu-

1 complete genome; Genbank NC_045512.2). Briefly, sections were heated to 60 °C

for 1 h and subsequently deparaffinized. Permeabilization was achieved by

incubating the section in pretreatment solution 1 (RNAscope® Hydrogen Peroxide) for

10 min at RT, followed by boiling in RNAscope® 1X Target Retrieval Reagents

solution at 100 °C for 15 min and washing in distilled water and ethanol. After

digestion with RNAscope® Protease Plus for 30 min at 40 °C, sections were

hybridized with the oligoprobes at 40 °C in a humidity control tray for 2 h (HybEZ™

Oven, ACD). Thereafter a serial amplification with different amplifying solutions

(AMP1, AMP2, AMP3, AMP4: alternating 15 min and 30 min at 40 °C) was

performed. Between each incubation step, slides were washed with washing buffer.

They were subsequently incubated with AMP 5, AMP 6 and DAB at RT for 30 and 15

min respectively. Gill's hematoxylin served to counterstain the sections which were

then dehydrated with graded alcohol and xylene and coverslipped. A lung section

from an infected mouse at 3 dpi served as a positive control. The negative control

was consecutive sections incubated accordingly but without including the

hybridization step.

Results

In K18-hACE2 mice, the later phase of SARS-CoV-2 infection is accompanied by virus spread into the central nervous system

To assess whether SARS-CoV-2 gains access to the CNS after intranasal infection with a low to medium viral dose we examined groups of K18-hACE2 mice that had been infected with a clinical isolate of SARS-CoV-2 (strain hCoV-19/England/Liverpool_REMRQ0001/2020), at 10^3 and 10^4 PFU, respectively. In addition, we examined mice that had been infected with the lower viral inoculum at day 3 post intranasal infection with 10^2 PFU IAV (strain A/X31). SARS-CoV-2 infected mice began to lose weight at 4 dpi and continued to lose weight until the end of the experiment, at 7 dpi. In the sequential IAV then SARS-CoV-2 infected mice, the weight loss was accelerated leading to more rapid and higher mortality, as determined by a humane endpoint of 20% weight loss (Clark et al., 2021).

At day 3 post intranasal SARS-CoV-2 infection with 10^3 PFU, viral antigen was detected in numerous individual and aggregates of occasionally degenerate epithelial cells in the nasal cavity in all 4 single SARS-CoV-2 infected animals and in 2 of the 4 double infected animals. Viral antigen was also found in the lungs, in both type I and II pneumocytes and, occasionally, capillary endothelial cells, in randomly distributed and variably sized patches of alveoli, with only occasional degenerate cells. This was associated with a mild increase in interstitial cellularity, endothelial cell activation with rolling, emigration and perivascular aggregation of some lymphocytes, and small macrophage aggregates, all as previously reported by this group (Clark et al., 2021). In dual infections, identical SARS-CoV-2 associated lesions were present within areas unaffected by IAV lesions. At this stage, viral antigen was detected in the olfactory epithelium in one animal, but not in brain nerves and brain including

olfactory bulb. In dual infected animals, IAV antigen expression was not detected in

these structures either, and there were no histological changes.

At day 7 post infection, infection of the nasal epithelium was limited; SARS-CoV-2

antigen was detected in only rare nasal epithelial cells in most mice, some were

negative. As reported (Clark et al., 2021), the lungs of both single and dual infected

mice showed multifocal type II pneumocyte activation and syncytial cell formation,

with mild mononuclear infiltration, and mild to moderate lymphocyte-dominated

vasculitis and perivascular infiltration. There were also a few focal areas of mild

desquamative pneumonia with intra-alveolar macrophages/type II pneumocytes,

edema and fibrin. Viral antigen expression was restricted to type I and II

pneumocytes of unaltered appearing alveoli (data not shown). At this stage, viral

antigen was detected in the brain of 2 of the 4 mice that had been infected with the

lower dose of SARS-CoV-2 (10^3 PFU) alone, three of the four double infected mice,

and all mice that had received the single higher dose (10^4 PFU) of SARS-CoV-2. IAV

antigen was not detected in the brain of double infected animals. SARS-CoV-2

antigen expression in the brain was associated with its detection in the main olfactory

epithelium and the olfactory bulb (Fig. 1A) in all but two animals.

In K18-hACE2 mice, SARS-CoV-2 infection in the central nervous system is

restricted to neurons and spreads in the brain and into the spinal cord in a dose

dependent manner

In the present study, all animals that were found to harbor viral antigen in the brain

showed widespread neuronal expression, but in a dose-dependent manner. In the

low dose (10^3 PFU) single infected animals, we only observed individual positive

neurons in the olfactory bulb, but no reaction in cranial nerves or the inner ear. In

contrast, in both the higher dose (10^4 PFU) single infected and the double infected

animals, we found numerous positive neurons in the olfactory bulb (individual

cells/neuronal processes in olfactory nerve layer, glomerular layer, almost all cells in

external plexiform layer, individual cells in mitral cell layer), and sometimes also

aggregates of positive sensory neuronal cells and their dendrites in the olfactory

epithelium layer of the main olfactory epithelium (MOE; Fig. 1A). Again, no reaction

was seen in cranial nerves.

In the brain, viral antigen was detected in a widespread manner across most brain

regions in all animals (Fig. 1B), with less extensive viral antigen expression in the low

dose single infected animals. Positive neurons were found among others in anterior

olfactory nucleus, primary and secondary motor area, primary somatosensory area,

anterior cingulate area, gustatory area, auditory area, infralimbic area, lateral and

medial septal nucleus, caudoputamen, piriform area, visual area, ectorhinal area,

entorhinal area, retrosplenial area, hippocampus and dentate gyrus, subiculum,

nearly all midbrain nuclei, thalamus/hypothalamus, amygdalar nuclei, nucleus

accumbens, several cranial nerve nuclei (trigeminal, vestibular, hypoglossal nuclei),

reticular nucleus, cuneate nucleus, dentate nucleus. These areas are depicted in a

3D reference atlas of the Allen Mouse Brain Common Coordinate Framework (Wang

et al., 2020; open access) in the following link: https://connectivity.brain-map.org/3d-

viewer?v=1&types=PLY&PLY=453%2C1057%2C31%2C44%2C254%2C500%2C92

2%2C895%2C549%2C1097%2C386%2C370%2C1132%2C987%2C669%2C1089%

2C672%2C502%2C909%2C961%2C972%2C507. Viral antigen expression was

most intense in the midbrain. The cerebellum showed only individual or small groups

of SARS-CoV-2 positive neurons in a few individual animals (Fig. 1C).

In the IAV and SARS-CoV-2 double infected animals as well as in the higher dose

single infected animals, the virus had spread to the spinal cord where it was found in

neurons in the grey matter (motor neurons and sensory neurons; Fig. 1D, E),

stretching through the entire cervical and thoracic spinal cord, or decreasing

progressively from the cervical spinal cord.

RNA-ISH yielded similar results as immunohistology (Fig. 1C), confirming

widespread neuronal infection accentuated in the midbrain.

Figure 1. Brain and spinal cord, K18-hACE mice, day 7 post intranasal SARS-CoV-2
infection (10^4 PFU as single infection or 10^3 PFU after initial infection with IAV (10^2
PFU IAV strain A/X31) as double infection). **A)** Double infected animal, main olfactory
epithelium (MOI), cribriform plate and olfactory bulb. Viral antigen is detected in
olfactory neurons and basal cells of the MOI and in granule layer, inner and outer
plexiform layer, mitral layer as well as glomerular layer of the olfactory bulb. Bar = 20
μm. **B)** Double infected animal, examples of viral antigen expression in different
brain regions. Top: frontal cortex with viral antigen expression in almost all neurons

(left) and mid cortex with proportion of positive neurons (right); bar = 20 μm. Bottom:
patchy virus antigen expression in the hippocampus (CA1 and CA3; left; bar = 50
μm.) and strong expression in the medulla oblongata (right; bar = 20 μm.). **C)** Single
infected animal, medulla oblongata and cerebellum. Viral RNA is abundantly
expressed in neurons in the medulla oblongata (vestibular nuclei). The cerebellar
cortex exhibits a few positive Purkinje cells (see also inset). Bar = 50 μm. **D)** Single
infected animal, thoracic spinal cord. The grey matter exhibits numerous neurons that
express viral antigen (large image and bottom inset) and viral RNA (top inset) in cell
body and processes. Bar = 50 μm. **E, F)** Double infected animal, thoracic spinal cord.
There is extensive viral antigen expression in neurons in the grey matter (E).
Consecutive section showing scattered apoptotic (cleaved caspase 3 positive) glial
cells (F, arrowheads), among intact neurons and in the absence of an inflammatory
reaction. * - central canal. Bars = 20 μm. Immunohistochemistry and RNA-ISH,
hematoxylin counterstain.
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SARS-CoV-2 infection of the brain is associated with diffuse microglial activation and

a mild macrophage and T cell dominated inflammatory response

In all animals where virus was detected in neurons in the brain, this was associated

with a mild nonsuppurative (meningo)encephalitis. The inflammation was only

present in areas with SARS-CoV-2-infected neurons. Therefore, it was most

pronounced in frontal coronary sections of caudoputamen and the

thalamus/hypothalamus region as well as in the hippocampal area and was

represented by infiltration of the wall and the perivascular space of small veins by

predominantly mononuclear cells, accompanied by a mild increase in parenchymal

cellularity (Fig. 2A). The majority of cells in the (peri)vascular infiltrates were Iba1-

positive macrophages (Fig. 2B). These were accompanied by T cells (CD3+) which

comprised up to approximately 30% of the perivascular cells (Fig. 2C). Individual T

cells were also found in the neuroparenchyma, mostly in proximity to perivascular

infiltrates (Fig. 2C). The vascular infiltrates contained rare individual neutrophils

(Ly6G+) and B cells (CD45R/B220+) (Fig. 2D). The inflammatory infiltrates were

accompanied by moderate diffuse microglial activation/microgliosis in areas with

SARS-CoV-2 infected neurons (Figs. 2B, E and 3A, B). Microglial nodules were

detected mainly adjacent to areas with perivascular infiltrates (Fig. 2E).

The double infected animals also showed a mild lympho-histiocytic meningitis

(Clark et al., 2021), more pronounced in caudoputamen, thalamic and hypothalamic

regions compared to single infected animals.

There was no evidence of prominent astrogliosis (Fig. 2F). However, astrocytes

immediately adjacent to perivascular infiltrates showed hypertrophy of the cytoplasm

consistent with activation.

Figure 2. Brain, K18-hACE mouse, day 7 post intranasal SARS-CoV-2 infection (10^4
PFU) after initial infection with IAV (10^2 PFU IAV strain A/X31). **A)** Brain stem with
moderate (peri)vascular leukocyte infiltration and mildly increased cellularity in the
parenchyma. HE stain. **B)** Macrophages (Iba1+) dominate in the (peri)vascular

infiltrate (inset: arrowheads) and the surrounding parenchyma exhibits microglial
activation (Iba1+ stellate shaped cells). **C)** T cells (CD3+) are also abundant in the
(peri)vascular infiltrates and are found infiltrating the adjacent parenchyma. Inset:
vessel with infiltrating T cells; some are degenerate (arrowheads). **D)** Neutrophils
(Ly6G+; top, arrowhead) and B cells (CD45R/B220+; bottom, arrowheads) are very
rare in the infiltrates. **E.** Brain stem with activated microglial cells (Iba1+) and small
microglial nodule (arrow). **F.** Staining of astrocytes (GFAP+) shows hypertrophied
astrocytes around a vessel with a mild perivascular infiltrate. B-F:
immunohistochemistry, hematoxylin counterstain. Bars = 20 µm.
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There is no evidence of viral infection of glial cells, endothelial cells or leukocytes or

of neuronal cell death, axonal damage or demyelination in association with SARS-

CoV-2 infection, but of apoptotic death of endothelial cells and immune cells

Despite widespread infection of neurons, there was no morphological evidence of

neuronal cell death. Staining for cleaved caspase 3 did not mark any neurons. Also,

staining for amyloid precursor protein (APP) to detect disturbances in fast axonal

transport as an indicator of acute axonal damage did not show any evidence of the

latter. Furthermore, there were no changes indicating demyelination of the white

matter. Capillary endothelial cells which are positive for ACE2 throughout the brain

and spinal cord (Fig. 3C) were negative in both SARS-CoV-2 IHC and ISH. However,

in some vessels that exhibited a leukocyte infiltrate, the endothelial layer appeared

focally discontinuous (Fig. 3D), confirming vasculitis. The infiltrate contained

scattered degenerate cells suggesting a leukocytoclastic component. (Fig. 3D, E).

This was confirmed by staining for cleaved caspase 3; both endothelial cells and

leukocytes in the vascular infiltrates were found to be apoptotic. Apoptosis (cleaved

caspase 3+) was also observed in a few leukocytes (morphology consistent with

lymphocytes) in the adjacent parenchyma (likely infiltrating T cells) (Fig. 3E) and in

occasional microglial cells (Fig. 3F). In none of the brains was there any evidence of

SARS-CoV-2 antigen or RNA expression in glial cells.

Figure 3. Brain, K18-hACE mice, mock infected and at day 7 post intranasal SARS-CoV-2 infection (10^3 PFU) after initial infection with IAV (10^2 PFU IAV strain A/X31). **A)** Mock infected mouse. Quiescent microglia (Iba1+). **B)** Infected animal. Diffuse microglial activation (Iba1+ stellate cells). **C)** Mock infected mouse. Endothelial cells show cytoplasmic ACE2 expression. **D-F)** Infected animal. **D)** Vessel with moderate leukocyte infiltration with focal destruction of the vessel wall (arrows) and some degenerate leukocytes (leukocytoclastic component). Top: HE stain; bottom: staining for ACE2, showing disruption of the endothelial cells layer. **E)** Vessel with moderate leukocyte infiltration (top: HE stain; bottom: staining for cleaved caspase 3). Individual cells in the infiltrate and in the adjacent parenchyma (top and bottom left: arrowheads) and endothelial cells in an affected vessel (bottom right: arrowhead) undergo apoptosis. **F)** Activated microglia (Iba1+; left). Staining for cleaved caspase 3 (right) shows apoptosis of a microglial cell (arrow) and of small round cells (arrowheads; morphology consistent with lymphocytes). A-E: bars =20 µm; F: bars = 10 µm.

Discussion

COVID-19 is primarily a respiratory disease, with potentially fatal systemic complications that can also involve the CNS. At present, the pathogenetic and clinical role of encephalopathy in COVID-19 patients is controversely discussed. A variety of mild and/or severe clincal signs have been described, and the reported morphological findings in the brain differ between studies; similarly, the presence and distribution of viral RNA or antigen appears to be inconsistent. Many questions are currently still open regarding the infectious route and spatio-temporal distribution of SARS-CoV-2 in the CNS of COVID-19 patients without comorbitidies, showing the need for appropriate animal models.

In this context, the hACE2 transgenic mouse under the control of the human cytokeratin 18 promoter, a commonly used mouse model to study pathogenetic effects of SARS-CoV-2 infection, has been employed not only in the present, but also in several other recent studies using the USA-WA1 strain, predominantly at high doses (10^5 to 1.5×10^6 PFU) (Oladunni et al., 2020; Carossino et al., 2021; Kumari et al., 2021, Song et al., 2021; Yinda et al., 2021; Zheng et al., 2021). All these studies show that intranasal inoculation of K18-hACE2 mice can lead to infection and extensive virus spread in the brain within 6 or 7 days. Infection even stretches into the spinal cord and can basically affect the entire grey matter, including, though only rarely, also the cerebellar cortex (Purkinje cells). This indicates that SARS-CoV-2 has no selective neurotropism.

In the present study, intranasala inoculation of mice with a low viral dose (10^3 PFU of the hCoV-2/human/Liverpool/REMRQ0001/2020) resulted in limited CNS infection; it was most pronounced in basal structures of the brain and did not reach the spinal cord. With the higher infectious dose (10^4 PFU) or with IAV pre-infection, we observed widespread extensive viral antigen expression and involvement of the

485 spinal cord. This suggests some dose dependence of virus spread in the CNS, as it

486 was suspected in another study (Yinda et al., 2021), and an effect of prior damage in

487 the respiratory tract (Clark et al., 2021). At the same time, we and others found virus

488 in the olfactory epithelium and in neurons in the olfactory bulb (Carossino et al., 2021;

489 Kumari et al., 2021). Therefore, a rostral to caudal spread of infection with emphasis

490 on basal structures and consequent infection of cortical areas is most likely. This

491 implies a direct neuronal spread of the virus rather than a disseminated pattern which

492 would be consistent with a hematogenous route of infection. A recent ultrastructural

493 examination on SARS-CoV-2 infected human brain organoids is in agreement with

494 these observations, as it provides evidence of virus cell-to-cell-spread beween

495 neurons in the organoids (Song et al., 2021). Many of the SARS-CoV-2 antigen

496 positive neurons of mice of this study are located in areas which are secondary or

497 tertiary connections of the olfactory bulb. This gives further evidence of virus entry via

498 the olfactory bulb, as confirmed in both mice (Carossino et al., 2021; Zheng et al.,

499 2021) and humans (Meinhard et al., 2020) as a natural route of brain infection by

500 SARS-CoV-2. However, many virus-positive regions that are not directly connected

501 to the olfactory system were also identified, providing further evidence of an

502 additional route of viral dissemination (Zheng et al., 2021).

503  Clinical signs consistent with neurological disease have only been reported in one

504 experimental study to date, where mice had shown hunchbacked posture, ruffled fur,

505 tremors and ataxic gait from day 4 pi, and died after day 6. These mice carried very

506 high levels of infectious virus in the brain and showed an encephalitis with

507 perivascular hemorrhage. Neuronal death via apoptosis was suspected (Kumari et

508 al., 2021). Other studies reported perivascular cuffs or vasculitis, neuronal

509 degeneration and necrosis, satellitosis, parenchymal edema, and occasional

510 microthrombi (Oladunni et al., 2020; Carossino et al., 2021; Yinda et al., 2021; Zheng

et al., 2021), all at day 7 post infection. The present study confirms that SARS-CoV-2 readily infects neurons in the K18-hACE2 mice, with viral protein accumulation in the entire cytoplasm including the cell processes, but does not provide evidence of neuronal cell death in association with infection, indicating that SARS-CoV-2 has no direct cytopathic effect on neurons. This may be due to the lower viral dose, provided that a high viral load would damage neurons directly.

Involvement of the spinal cord, which was a prominent feature in our mouse model, has only been reported in a few human cases (Mondal et al., 2020). It might be a so far under-recognized neurological complication, since neuropathological assessments did not go beyond neuroimaging and evaluation of several CSF parameters.

Similar to Carossino et al. (2021), the present study did not find evidence of demyelination. Furthermore, axonal damage was not present in the investigated murine brain sections. However, while both axonal damage and demyelination can occur in COVID-19 patients, they are apparently not common neuropathological findings (Kantonen et al., 2020; Reichard et al., 2020; Salomon et al., 2020).

Neuronal SARS-CoV-2 infection without obvious neuronal degeneration is reminiscent of other neurotropic and persistent viral infections, like herpes simplex virus (HSV). HSV-1 establishes latency in the mouse model within the earliest stages of acute infection, with the viral genome reaching the neuronal ganglia within the first 24 hours of infection (Steiner et al., 1990). Further studies would now be required to determine whether SARS-CoV-2 also establishes latency or whether there is subsequent neuronal damage.

Viral infection of neurons is evidently associated with an antiviral response in the mice, as indicated by a reported increase in IFN-α mRNA in the brain from day 5 pi onwards, with a peak of both mRNA and protein on day 6 (Kumari et al., 2021). This

is accompanied by an inflammatory response in the brain parenchyma. Similar to a

previous study (Oladunni et al., 2020), we observed a mild non-suppurative,

macrophage and T cell driven encephalitis (perivascular infiltrates and occasional

vasculitis) in all mice that harbored viral antigen in the brains at 7 dpi. This appeared

to be slightly more intense with more extensive neuronal virus antigen expression in

animals that had received the higher viral dose (10^4 PFU) or had been preinfected

with IAV, suggesting some dependence on the infectious dose or easier access to

the brain with pre-existing damage due to IAV infection (Clark et al., 2021; Yinda et

al., 2021). Transcriptional investigations also confirmed the inflammatory state of the

brain, demonstrating an increase in infammatory cytokines and chemokines (IL-6,

TNF-α, IFN-γ, IL-1β, MIP-1α.MIP-2, IP-10) in the brain of infected mice (Oladunni et

al., 2020; Kumari et al., 2021). This might also explain the activation/hypertrophy of

astrocytes in areas with perivascular infiltrates and the diffuse microglial activation

and multifocal microgliosis that we and others observed (Winkler et al., 2020;

Carossino et al., 2021; Yinda et al., 2021). Both glial cell populations are responsive

to proinflammatory signals from endothelial cells, macrophages and/or neurons

(Murta et al., 2020). The proinflammatory gene expression program initiated after

viral infection would expand neuroinflammation (Murta et al., 2020). Activated

microglia may itself undergo a phenotypic shift and display exaggerated release of

pro-inflammatory mediators and aberrant phagocytic activity, inducing

neurodegeneration (Tremblay et al., 2020). This could explain the diffuse astrogliosis

reported from other mouse and human studies (Carossino et al., 2021; Matschke et

al., 2020) as well as neuronophagia by microglial cells which was seen in some

human COVID-19 patients (Al-Dalahmah et al., 2020) and one mouse study

(Carossino et al., 2021).

In previous studies we and others have shown that IAV pre-infection of hACE2

mice results in more severe SARS-CoV-2 associated pulmonary changes and higher

amounts of infectious virus at 6 or 7 days post SARS-CoV-2 infection (Bai et al.,

2021; Clark et al., 2021). Interestingly though, viral loads in the brain were not found

to be increased (Bai et al., 2021), although we observed higher frequency and more

widespread brain infection after the lower SARS-CoV-2 dose in animals that were

infected with IAV. Also, the inflammatory response was slightly more intense in these

animals. It is currently unclear which direct impact IAV infection has for the

subsequent SARS-CoV-2 challenge, but more efficient virus entry could be an option,

since IAV infection was shown to upregulate ACE2 expression *in vitro* (Bai et al.,

2021).

While we did not find evidence of neuronal death, we observed apoptosis of

infiltrating lymphocytes, capillary endothelial cells and macrophages/microglial cells

in proximity to perivascular infiltrates. As in a previous study (Carossino et al., 2021),

none of these cells were found to be SARS-CoV-2 infected. This result is in line with

recent findings in SARS-CoV-2 infected human brain organoids which provided

evidence that infected neurons do not die but can promote the death of adjacent

uninfected cells (Song et al., 2021). Using single cell RNA sequencing, the study

showed that SARS-CoV-2 infected cells in the organoids were in a hypermetabolic

state, whereas uninfected cells nearby were in a catabolic state and a hypoxic

environment, as shown by HIF1α expression (Song et al., 2021). The same may be

true for the brain of K18-hACE2 mice with widespread neuronal SARS-CoV-2

infection. Also, coupled proliferation and apoptosis are assumed to maintain the quite

rapid turnover of microglia in the adult brain (Askew et al., 2017). We did not

determine the proliferation rate in this study, but such "physiological" turnover should

be considered when interpreting microglial apoptosis in SARS-CoV-2 infected mice.

Several morphological changes in the mice used in the present study recapitulate

findings reported in brains of human COVID-19 patients, like mild perivascular

inflammatory infiltrates (Solomon et al., 2020) and microgliosis (Schuhrink et al.,

2020). In the mice, the inflammatory processes were only mild and more pronounced

in frontal regions like caudoputamen and the thalamus/hypothalamus region as well

as the hippocampal area. Further vascular lesions apart from vasculitis/endotheliitis,

like ischemic infarcts (Kantonen et al., 2020; Song et al., 2021) or microthrombi

(Fabbri et al., 2020) that seem to be frequent in fatal human COVID-19 cases, are

obviously not a regular feature in this mouse model, since only two studies reported

occasional microthrombi in the brain (Yinda et al., 2021; Zheng et al., 2021). This

could be due to the lack of endothelial cell infection in the brain of the mice, whereas

it was seen in association with fresh ischemic infarcts in the brain of a COVID-19

patient (Meinhardt et al., 2021; Song et al., 2021). Interestingly, the presence of virus

in the brain of the human patients is apparently not consistently associated with

leukocyte infiltration, indicating that SARS-CoV-2 does not necessarily induce an

immune response like other neurotropic viruses (Song et al., 2021).

The main host receptor for SARS-CoV-2 is the human angiotensin-converting

enzyme 2 (hACE2). While a study in the brain of fatal human COVID-19 cases

showed ACE2 expression in cortical neurons and found evidence that ACE2 is

required for infection of human brain organoids (Song et al., 2021), neuroinvasion

and spread in the K18-hACE2 mice is apparently not directly dependent upon ACE2

expression, because the virus does not infect all ACE2 expressing cells and does

infect cells without apparent ACE2 expression (Carossino et al., 2021). Indeed, in line

with the findings of previous studies we only detected ACE2 protein expression in

capillary endothelial cells, ependymal cells and choroid plexus epithelium in the brain

and spinal cord, in the absence of detectable viral antigen (Carossini et al., 2021;

Clark et al., 2021; Song et al., 2021). In human COVID-19 patients, the endothelium

of capillaries in kidney, liver, heart, lung and small intestine was shown to become

infected, and this was associated with an endotheliitis (Varga et al., 2020).

Furthermore, ultrastructural examination of the brain of one human patient found viral

particles in small vesicles of endothelial cells, suspecting an additional

hematogenous route of brain infection (Paniz-Mondolfi et al., 2020). Indeed, using

intravenously injected radioiodinated SARS-CoV-2 S1 it has been shown that the

viral protein can cross the BBB, and likely by absorptive transcytosis (Rhea et al.,

2020). It may hence be due to the fact that endothelial ACE2 expression in the K18-

hACE2 mice represents only the murine protein (Carassino et al., 2021) that the brain

endothelium of the mice does not become infected by SARS-CoV-2.

Based on current knowledge, it seems likely that in COVID-19 patients the virus can

access the brain in several ways. In severe COVID-19, viremia could allow access to

the brain via the vasculature (Colagrossi et al., 2021). With the platelet hyperactivity

in critically ill patients (Comer et al., 2021) and abnormal blood clotting or unusual

thrombotic presentations (Helms et al., 2020b, Klok et al., 2020) this might lead to the

ischemic changes described in a proportion of fatal cases, without viral infection of

neurons. This might not be mirrored by the murine model as viremia may not occur

(Yinda et al., 2021). In mild COVID-19, i.e. without viremia, infection of the brain via

the olfactory bulb and possible other neurogenic routes could occur. This would then

lead to exclusive neuronal infection and an only mild inflammatory response. It might

be this scenario that explains the loss of taste and smell and severe headaches

reported in patients with mild disease.

The murine model does not fulfil all morphological criteria of acute human

neurological COVID-19. However, brain infection following a lower dose of intranasal

challenge might represent a mouse model for chronic/long COVID-19 studies. The

pathogenesis of this sequel of the acute disease is still unknown, but fatigue, muscle

aches, breathlessness, and headaches are the most frequently reported symptoms

(Dennis et al., 2020; Brodin, 2021). A persistent low-grade smoldering inflammatory

response to newly budding virions might be central to the condition. Also,

degeneration or impaired function of neuronal and glial cells that are cardinal for the

physiological function of the brain might be an option (Baig, 2020). A mild inadequate

immune response with persistent viral load and viral evasion of the immune

surveillance are suspected key factors (Baig, 2020). This is supported by the fact that

COVID-19 patients still exhibit a significant remaining inflammatory response in the

serum at 40-60 days post infection (Doykov et al., 2020). Further investigations of the

inflammatory response at transcriptome and translational level in the murine model

could provide further insights.

These data also have important implications for the development of therapeutic

interventions. Firstly, the endothelium and astrocyte foot processes represent key

components of the BBB, protecting the brain from accumulation of endo- and xeno-

biotics. Future studies should address the consequences of infection for maintenance

of barrier integrity to mitigate potential inadvertent delivery of neurotoxic agents that

wouldn't otherwise permeate the brain. Secondly, several studies have already

sought to understand pulmonary distribution of postulated therapeutic interventions

(Arshad et al., 2020; Hanafin et al., 2021; Rajoli et al., 2021) but robust efficacy of

antivirals and/or immunomodulatory agents may also necessitate adequate exposure

within the CNS. Notably, the repurposed antivirals remdesivir, favipiravir and

molnupiravir exhibit low concentrations in the brain relative to plasma in preclinical

species (Bocan et al., 2019; Painter et al., 2019; EMA, 2020; Jorgensen et al., 2020).

Furthermore, dexamethasone also exhibits low brain penetration in mice with an

intact BBB, but this increases in mice genetically engineered to be absent a critical

drug transporter, P-glycoprotein (Meijer et al., 1998). Further work is required to

define the importance of brain penetration of therapeutics being investigated as

interventions across the spectrum of disease from prevention, mild, moderate, severe

to long COVID-19.

Conclusions

Despite widespread neuronal infection, pathomorphological changes of the course of

disease consisted of mild lymphohistiocytic inflammation and microglial activation.

Solely neuronal cells were infected which supported the infectious route via the

olfactory epithelium, olfacory bulb and transsynaptic spreading. The limited

expression of ACE2 raises the question for ACE2-independent pathogenetic

mechanisms to explain the neurotropism of the virus. Microgliosis and immune cell

apoptosis were main pathological features in our study indicating a potential

important role of microglial cells in the pathogenesis of neuromanifestation in COVID-

19.

Acknowledgements
We are grateful to the technical staff in the Histology Laboratory, Institute of
Veterinary Pathology, Vetsuisse Faculty, University of Zurich (IVPZ), for excellent
technical support. This work was funded in part by the US Food and Drug
Administration (USA) 75F40120C00085, Characterization of severe coronavirus
infection in humans and model systems for medical countermeasure development
and evaluation (JAH). Work in the lab is also supported by MRC grant
MR/W005611/1, G2P-UK; A National Virology Consortium to address phenotypic
consequences of SARSCoV-2 genomic variation (JPS and JAH).

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693   **CONFLICT OF INTEREST**
694   The authors declare that they have no conflict of interest.
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