The strengths of scanning electron microscopy in deciphering SARS-CoV-2 infectious cycle

- 1 Short title (for the running head): The infectious cycle of SARS-CoV-2 (COVID-19)
- 2 Article type: original research
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19 Abstract

Electron microscopy is a powerful tool in the field of microbiology. It has played a key role in the 20 rapid diagnosis of viruses in patient samples and has contributed significantly to the clarification of 21 virus structure and function, helping to guide the public health response to emerging viral 22 infections. In the present study, we used scanning electron microscopy (SEM) to study the 23 infectious cycle of SARS-CoV-2 (COVID-19) in Vero E6 cells and we controlled some key 24 findings by classical transmission electronic microscopy (TEM). The replication cycle of the virus 25 was followed from 1 to 52 hours post-infection. Our results revealed that SARS-CoV-2infected the 26 cells through membrane fusion. Particles are formed in the peri-nuclear region from a budding of 27 the endoplasmic reticulum - Golgi apparatus complex into morphogenesis matrix vesicae. New 28 SARS-CoV-2 particles were expelled from the cells, through cell lysis or by fusion of virus-29 containing vacuoles with the cell plasma membrane. Overall, this cycle is highly comparable to that 30 31 of SARS-CoV. By providing a detailed and complete SARS-CoV-2 infectious cycle, SEM proves to be a very rapid and efficient tool compared to classical TEM. 32

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34 Key words: SARS CoV-2, infectious cycle, Vero E6 cells, scanning electron microscopy (SEM).

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37 Introduction

The SARS-CoV-2 (COVID-19) outbreak started in late December 2019 in China and has 38 since reached a global pandemic (Zhu et al., 2020), leading to a worldwide battle against COVID-39 19. SARS-CoV-2 is a novel β-coronavirus belonging to the sarbecovirus subgenus of Coronaviridae 40 family (Schoeman and Fielding, 2019; Zhu et al., 2020). Coronaviruses are enveloped viruses with 41 a positive sense, single-stranded RNA genome (Schoeman and Fielding, 2019). One of the first 42 methods used is Electron Microscopy (EM), which has been a reliable tool for the classification of 43 viruses according to their ultra-structure (Curry et al., 2006; Hazelton and Gelderblom, 2003)The 44 characteristic morphology of crown-like structures detected by EM explains the name of 45 Coronaviridae family (Golding et al., 2016) observed as widely spaced club-shaped projections 46 surrounding the virus envelope, thus forming a crown aspect in negative staining protocols 47 (Almeida and Tyrrell, 1967; Oshiro et al., 1971). Coronaviruses have the largest genomes among 48 49 RNA viruses, with genome sizes ranging from 26 to 32 kilobases (kb) in length. These viruses primarily infect birds and mammals, and can also infect humans, causing respiratory and enteric 50 51 diseases, such as upper respiratory tract infections and lower respiratory tract infections (bronchitis, 52 pneumonia, and severe acute respiratory syndrome (SARS). Coronaviruses have caused three worldwide pandemics associated with SARS in the past two decades, including SARS-CoV in 53 2003, Middle East Respiratory Syndrome - Coronavirus (MERS-CoV) in 2012 and the present 54 SARS-CoV-2. 55

Electron microscopy (EM) is a powerful tool in the field of microbiology, because of its resolution power as compared to light microscopy (Koster and Klumperman, 2003). EM contributed significantly to the clarification of viruses structure and function and has played a key role in the rapid diagnosis of viruses in various samples (Goldsmith and Miller, 2009). The ability of EM to detect unknown and unsuspected organisms has made it a suitable tool to guide the public health response during previous outbreaks. Transmission electron microscopy (TEM) was extensively used to describe the morphology or the morphogenesis of SARS-CoV (Ng et al., 2003; Qinfen et al., 2004), MERS-CoV (Alsaad et al., 2018; Kim et al., 2016; Park et al., 2016) or, more recently,
SARS-CoV-2 (Caly et al., 2020; Colson et al., 2020; Kim et al., 2016; Park et al., 2016; Zhu et al., 2020).

66 Scanning electron microscopy (SEM) is another powerful tool for microbiological research 67 and diagnosis of infectious diseases (Golding et al., 2016). We already demonstrated its strengths 68 for ultra-rapid microscope imaging of SARS-CoV-2 when pandemic first reached France (Colson et 69 al., 2020). Here, we used SEM for its capacity to rapidly screen SARS-CoV-2-infected Vero cells in 70 resin ultra-thin sections, allowing the ultrastructural detailed analysis of SARS-CoV-2 throughout 71 the whole infectious cycle.

72 Material and methods

73 Cell culture-virus infectious cycle

Vero E6 cells were grown as a monolayer in 25 cm² culture flasks in Dulbecco's Modified 74 Eagle's Medium supplemented with 10% fetal bovine serum for two to three days at 37°C. For the 75 viral infectious cycle, the culture medium was removed and the cells were inoculated with SARS-76 CoV-2. After incubation at 37°C for one hour, the supernatant was then removed and the cultures 77 were gently rinsed three times with culture media to eliminate any excess of viral particles, marking 78 time 0 (H0). For later time points, the infected and rinsed cells were incubated at 37°C in culture 79 medium. Hourly post-infection time points were: H1, H2, H3, H4, H5, H6, H12, H24, H36, H48 80 and H52. For each time point, the infected cells were detached using 500µl of trypsin and pelleted 81 by centrifugation at $500 \times g$ for 10 minutes. 82

83 Scanning and Transmission Electron Microscopy

For electron microscopy infected Vero cells were fixed at least for one hour with 84 glutaraldehyde 2.5% in 0.1M sodium cacodylate buffer. For resin embedding, cells were washed 85 three times with a mixture of 0.2M saccharose/0.1M sodium cacodylate. Cells were post-fixed for 86 one hour with 1% OsO4 diluted in 0.2M Potassium hexa-cyanoferrate (III) / 0.1M sodium 87 cacodylate solution. After three 10-minute washes with distilled water, the cells were gradually 88 dehydrated with ethanol by successive 10-minute baths in 30%, 50%, 70%, 96%, 100% and 100% 89 ethanol. Substitution was achieved by successively placing the cells in 25%, 50% and 75% Epon 90 solutions for 15 minutes. Cells were placed for one hour in 100% Epon solution and in fresh Epon 91 100% over-night under vacuum at room-temperature. Polymerization occured with cells in 100% 92 fresh Epon for 72 hours at 60°C. All solutions used above were 0.2µm filtered. Ultrathin 70 nm 93 sections were cut using a UC7 ultramicrotome (Leica) and placed on HR25 300 Mesh 94 Copper/Rhodium grids (TAAB, UK). Sections were contrasted according to Reynolds (Reynolds, 95 96 1963). For scanning electron microscopy (SEM), sections on grids were platinum-coated with a MC1000 sputter coater (Hitachi) for 40seconds at 10mA. Electron micrographs were obtained on 97 98 either SU5000 SEM (Hitachi High-Tech, HHT, Japan) operated between 7 kV and 10 kV 99 accelerating voltage, in high-vacuum and observation mode (spot size 30), between 4.6 mm and 4.9 mm average working distance with BSE detector, and magnifications ranging from x5,000 to 100 x100,000 or Tecnai G² TEM (Thermo-Fischer/FEI) operated at 200 keV equipped with a 4096 x 101 4096 pixels resolution Eagle camera (FEI). 102

103 **Results**

104 SARS-CoV-2 cell entry

At very early post-infection time-points, from H0 to H5, SARS-CoV-2 virions were not detected in the ultra-thin sections. From H6 further, viral particles could be detected by SEM and TEM at the surface of the cells, mostly at their apical side at the microvilli level (Figure 1). From H6

to H12, most of the viruses attached to cell plasma membranes were seen in cells that were not 108 replicating new virions. In those cells, probably in the process of being infected, no virus-109 proliferation status was observed (see below). However, viruses attached to the plasma membrane 110 were located at the periphery of virus-producing cells starting H12, where viral particles at the 111 surface were located between microvilli, at the level of a smooth plasma membrane or in cellular 112 invaginations. When located on the plasma membrane of non-productive cells, particles were seen 113 i) attached, with their corona spikes located between the particle and the plasma membrane 114 (Figure1.A,B) or ii) less electron-dense, with the capsid fusing with the plasma membrane 115 (Figure1.C-E). The formation of endocytic vesicles with typical clathrin-coated pits was often 116 observed when the particles were attached to the plasma membrane (Figure 2.A-F). In these forming 117 endocytic particles, rod-like amorphous material was present (Figure 2). This kind of material was 118 also observed in clathrin-coated endocytic vesicles located more deeply in the cell cytoplasm 119 120 (Figure 2.G,H). We also observed in the cytoplasm of the non-producing cells electron-dense crescent-shaped intracellular structures (Figure2.A,B) that were also present in control, non-infected 121 122 cells. Inside non-producing cells, a very few virus-like particles were observed inside the cells in endoplasmic reticulum (ER)-derived peripheral canaliculi. From H24 onwards, most of the viruses 123 attached to cell plasma membranes were seen in intact- or lysed- virus producing-cells. 124

125 SARS-CoV-2 morphogenesis

At the nucleus level, round empty particles and round particles with a punctate pattern at their center were observed at nucleus margins (Figure 3.A-F). These nascent particles were seen at locations where the nuclear membrane was not clearly delineated, in contrast to adjacent nuclear regions where the double membrane was properly seen. These nuclear membrane budding sites could be observed in transverse (Figure 3.A-E,G) or in tangential views (Figure 3.F,H), the particles being, in the latter case, located in an electron-dense chromatin-like material, which we called nuclear matrix. The mean diameter of these particles ranged from 80 nm to 112 nm as measured by
SEM and TEM (Figure 3.C-F).

Swollen nuclear membrane, endoplasmic reticulum (ER) and Golgi apparatus (GA) organelles were 134 the most striking features of SARS-CoV-2 infected cells (Figure 4). Thick and distorted ER tubules 135 were observed at peri-nuclear locations between the nucleus and the GA (Figure 4.A,B), and also at 136 peripheral locations below the plasma membrane, where the ER could be seen as zippered (Figure 137 4.G). When intact, the GA was found at peri-nuclear locations, with Golgi stacks lying parallel to 138 the ER and the nuclear membranes (Figure 4.A,B). As infection progressed, the GA was found 139 budding between large ER tubules, resulting in multiple Golgi-derived nascent particles and a loss 140 of intact GA stacks (Figure 4.D-F). The extent of GA budding was variable from a cell to another, 141 being generally proportional to its distance from the nucleus. At early infection stages, myelin-like 142 membranes whorls were observed at proximity of the Golgi apparatus (Figure 4.C). These whorl 143 types are probably not a typical feature of infected cells, as they have also been observed in 144 uninfected cells. We also noticed abundant mitochondria in apical regions of both non-infected and 145 infected cells at all stages, around the ER and Golgi-rich regions. 146

Golgi-derived doughnut-like particles with a pronounced electron-opaque edge were 147 observed at peri-nuclear locations (Figure 5.A,B), dispersed into the cytoplasm, as well as 148 entering vacuoles, which seemed to be derived from the ER (Figure 5.A,B). Such forming 149 virus morphogenesis matrix vesicae (Qinfen et al., 2004), filled with doughnut-like particles, 150 were observed as open sacs, assembling next to the nucleus (Figure 5.A,B), or closed sacs 151 adjacent to or distant from the nucleus, in the cytoplasm or in the vacuoles (Figure 5.C.D). 152 Doughnut-like particles were devoid of corona spikes. Their shape was not perfectly round 153 when observed in the assembling opened sacs, which could present a filopodia-like protrusion 154 (Figure 5.B). 155

As the infection progressed, we observed an extensive network of membrane whorls, with 156 large inter-membranous distances when compared to previous 'small' membrane whorls (Figure 157 6.A). These intermingled membranes were lying at the level of concave nuclear indentations. 158 Nascent virions could be found mixed with such membranes whorls in large bags (Figure 6.B). The 159 appearance of the virus morphogenesis matrix vesicae (VMMV) was variable, with nascent 160 particles located in more or less large vacuoles, containing more or less electron-dense material 161 (Figure.6 C-F). The electron-density of these vacuoles filled with nascent particles was correlated 162 with the heterogeneity of these vacuoles: electron-dense virions-filled vacuoles were homogenous 163 (Figure 6.C,D), while electron-lucent vacuoles contained virions particles as well as heterogeneous 164 materials such as membranes, or distorted compartments (Figure 6.E,F). VMMV located below the 165 plasma membrane were frequently seen translucent, with well-individualized virions particles 166 (Figure 6.F). We also noticed that particles could arrange as circular chains lying on the internal 167 surface of the VMMV (Figure 6.D). 168

169 SARS-CoV-2 cell exit

Mature SARS-CoV-2 particles were observed as spiky round to hexagonal electron-dense particles (Figure7,8). Mature SARS-CoV-2 particles were observed at extra- and intra-cellular locations: in translucent VMMV or vacuoles of early infected intact cells (Figure 6.E, 7), and later found lying between cellular microvilli (Figure 8.A-C), in vacuoles (Figure 8.G), as well as on the surface (Figure 8.F,H) of lysed cells. Intracellular compartments filled with mature virions (Figure 7,8) were observed channeling with the apical side of the Vero cells at the base of the microvilli (Figure 8.C,E).

177 Discussion

Our results show spiky round to hexagonal 80 to 112 nm in diameter electron-dense mature 178 SARS-CoV-2 particles, similar to the previously described SARS-CoV-2 virions (Colson et al., 179 2020; Kim et al., 2020; Park et al., 2016; Zhu et al., 2020). Previous analysis of ultrathin sections by 180 TEM of SARS-CoV-2 infected- cells showed virus particles in inclusion bodies in human airway 181 cells (Zhu et al., 2020), as well as in a wide range of intracellular organelles, especially in vesicles 182 of Vero cells (Caly et al., 2020; Kim et al., 2020; Park et al., 2016). Here, thanks to our SEM 183 analysis, we were able to show the similarity between SARS-CoV-2 and SARS-CoV infectious 184 cycles, with some exceptions. Our non-observation at very early post-infection time-points of 185 SARS-CoV-2 virions in the ultra-thin sections is probably related to the very brief binding of 186 infectious particles to the cell surface, and the rapid reduction of the particle once attached to the 187 cells. From H6 further, it cannot be ruled out that the particles on the cell surface are neo-188 synthesized virions produced by infected cells. 189

190 Regarding SARS-CoV-2 cell entry process, particles were observed attached at cells plasma membrane similarly to SARS-CoV, located at cells apical sides (Rossen et al., 1994). Full SARS-191 CoV-2 particle endocytosis was not observed, which is consistent with previous studies conducted 192 on SARS-CoV particles infecting cells by membrane fusion (Ng et al., 2003; Oshiro et al., 1971; 193 Qinfen et al., 2004). In fact, we observed a possible fusion of SARS-CoV-2 particles with the cells 194 plasma membranes. Our images suggest that these attached particles were probably caught 195 transferring their content inside the cell cytoplasm. Crescent-shaped intracellular structures, also 196 observed in non-infected cells, might actually correspond either to virions remnants after fusion of 197 the particles with the plasma membrane, or to clathrin-coated vesicle after their uncoating and 198 opening inside the cytoplasm. The role of the clathrin endocytic vesicles containing amorphous 199 material, as intermediate receptacles of SARS-CoV-2 genomic content after fusion of the particles 200 with cells plasma membranes, is likely to be part of the SARS-CoV-2 nucleocapsid cell entry 201 process. 202

Regarding SARS-CoV-2 morphogenesis, previous studies reported nuclear localization of 203 SARS-CoV proteins or particles (Qinfen et al., 2004; Yuan et al., 2005; Zhang et al., 2003). Here, 204 we did not observe intact particles inside the nucleus, but rather nascent particles in a nuclear matrix 205 without a distinctive membranous limit. The abundance of mitochondria next to the ER and GA 206 budding regions, where SARS-CoV-2 morphogenesis occurred, could provide energy for viral 207 multiplication (Castro et al., 2013). It was assumed that doughnut-shaped electron-dense structures 208 (also observed in SARS-CoV infectious cycle studies) probably correspond to assemblies of virus 209 genomes together with helical nucleocapsids (Ng et al., 2003). As in SARS-CoV-2 infected cells, 210 myelin-like membrane whorls have been previously described in SARS-CoV infected cells, closely 211 associated with nascent particles (Ng et al., 2003). We hypothesize that these membrane whorls 212 may be derived from the ER or may be part of an auto-phago-(lyso)somal process, both scenarios 213 providing a support for virions packaging and trafficking until further extracellular release. The 214 215 electron-density and homogeneity difference of the VMMV containing viral particles may be related to the pH of these compartments and/or to the maturation level of the virions. The circular 216 aspect of SARS-CoV-2 assemblies inside some VMMVs may reflect the presence of mature 217 particles, compared to immature and dispersed particles in less organized VMMV. As for SARS-218 CoV infected cells, one of the most obvious ultrastructural changes in SARS-CoV-2 infected cells 219 is the proliferation of the Golgi complexes and related vesicles, accompanied by swelling of some 220 of the Golgi sacs. We also found that VMMVs are most probably derived from the ER. It was 221 shown that SARS-CoV nucleocapsids assemble in the ER and mature by budding into smooth 222 vesicles derived from the GA. In parallel, the GA swells to form smooth vesicles that incorporate 223 the VMMV along with their nucleocapsids (Oshiro et al., 1971; Patterson and Macnaughton, 1982; 224 Qinfen et al., 2004; Siu et al., 2008; Zhang et al., 2003). Rather, our images suggest that nascent 225 particles may bud in the cytoplasm, followed or simultaneous to the filling of the ER-derived 226 VMMV by immature Golgi-derived virions. Nevertheless, the involvement of the Endoplasmic 227

Reticulum - Golgi Apparatus complex witnessed here, especially the extreme budding of the Golgi apparatus, into the morphogenesis of the SARS-CoV-2, is consistent with the demonstrated efficacy of chloroquine, a pharmacological inhibitor, which interferes with cell trafficking by lowering the pH of intracellular compartments (Devaux et al., 2020).

Regarding SARS-CoV-2 cell exit, mature virions exited the cells at their apical sides, as observed for SARS-CoV (Rossen et al., 1994). The release of mature particles occurred passively in lysed cells or by fusion of the internal compartments with the plasma membrane in intact cells, as previously described (Ng et al., 2003; Oshiro et al., 1971; Qinfen et al., 2004).

Scanning electron microscopy (SEM) has shown several advantages over transmission electron 236 microscopy (TEM) for studying SARS-CoV-2 life cycle. First, it was possible to load multiple 237 ultra-thin sections of resin-embedded infected cells, fixed at different time points post-infection and 238 loaded onto carbon grids that were applied onto one glass slide for simultaneous observation and 239 240 instant comparison after a single vacuum. All conditions were accessible within 10 minutes. Once the beam axis alignment performed, screening of the ultra-thin sections was fast, as only minor 241 adjustments of the focus distance over large regions were needed. The whole SARS-CoV-2 life 242 cycle was thus accessible at once, in a few hours of observation (4.5 hours for 8 time-points, 243 acquiring 320 micrographs), with possibilities to image at the cell population, cellular and sub-244 245 cellular levels. Secondly, the balance between the high-resolution micrographs and the speed and ease of screening large cell numbers, at different scales, in different conditions made it possible to 246 rapidly detect individual SARS-CoV-2 particles and precisely study its morphogenesis and 247 infectious cycle. 248

In conclusion, SEM has proven to be a rapid and effective tool for studying the SARS-CoV-250 2 infectious cycle in Vero cells. Further studies employing the same straightforward methodology 251 may help understand at the cellular level the impact of pharmacological reagents on SARS-CoV-2 252 life cycle to better control this global pandemic.

254 Author Contributions

D-BB, J-PB, GH, MB, AF and JBK did the experiments and analyzed the data. D-BB, J-PB, GH
wrote the manuscript. J-PB , JBK, DR and BL conceived the project, supervised the experiments,
and wrote the manuscript.

258 Funding

This work was supported by the French Government under the "Investments for the Future" programme managed by the National Agency for Research (ANR), Méditerranée-Infection 10-IAHU-03 and was also supported by Région Provence-Alpes-Côte d'Azur and European funding FEDER PRIMMI (Fonds Européen de Développement Régional - Plateformes de Recherche et d'Innovation Mutualisées Méditerranée Infection). In addition, collaborative study conducted by IHU Méditerranée Infection and the Hitachi High-Tech Corporation is funded by the Hitachi High-Tech Corporation.

266 **Conflict of Interest**

Authors would like to declare that Didier Raoult is a consultant for the Hitachi High-Tech Corporation. Funding sources had no role in the design and conduct of the study, the collection, management, analysis and interpretation of the data, nor in the preparation, review or approval of the manuscript.

271 Acknowledgments

We sincerely thank Rita Jaafar, Isabelle Duflot and Julien Andreani for their technical help. We also thank Takashi Irie, Kyoko Imai, Shigeki Matsubara, Taku Sakazume, Toshihide Agemura, Yusuke Ominami and the Hitachi team in Japan from Hitachi High-Tech Corporation and Hitachi Ltd. for the collaborative study conducted together with IHU Méditerranée Infection, and for the installation of a SU5000 microscope at the IHU Méditerranée Infection facility.

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Figure 1: Early-stage SARS-CoV-2 infection(12 hours post-infection) with virus at the periphery of Vero E6 cells.A,B: SEM (A) and TEM (B) views of the same cellular region with a SARS-CoV-2 particle (arrow) attached to the plasma membrane, the corona spikes of which are located between the particle and the cell plasma membrane. C-E: SEM (C) and TEM (D,E) views of the same cellular region showing SARS-CoV-2 virus particles attached to the cell plasma membrane; one particle (arrow in C-E) is glued to the plasma membrane, fusing with the cell plasma membrane.



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Figure 2: Early-stage SARS-CoV-2 infection (12 hours post-infection) with endocytic vesicles
 in Vero E6 cells.

A-F: SEM (A,C,E,G) and TEM (B,E,F,H) views of the same cellular regions with clathrin-coated vesicles (arrows) containing rod-like amorphous material. Crescent-like electron-dense structures (arrowhead in A) were often depicted in infected cells cytoplasm. Solid arrows (E-H) point to glued SARS-CoV-2 particles on cells plasma membrane.



Figure 3: SARS-CoV-2 infected Vero E6 cells at 18-24 hours post-infection. A-H : SEM (A,G,H) and TEM (B-F) images showing numerous virus-like particles (arrows) at nucleus margins (n.m).A-E,G: Images of nuclear membrane budding sites observed in transverse views. F,H:Images of nuclear membrane budding sites in tangential views. SARS-CoV-2 particles can be seen outside the cells at cell plasma membranes (solid arrows in A and B, which correspond to the same cellular region).



Figure 4: SARS-CoV-2 infected Vero E6 cells at 12-18 hours post-infection. A,B: Thick and 381 distorted endoplasmic reticulum (ER) tubules were observed by SEM at peri-nuclear locations and 382 at the cells periphery. C: SEM view of the extensive enlargement and budding of the ER and Golgi 383 apparatus, as well as a myelin-like membranes whorl (mw) close to the Golgi apparatus and 384 mitochondria (mito.) in the perinuclear region. D,E: SEM (D) and TEM (E) views of the same cell 385 region showing extreme Golgi apparatus budding. F: SEM low-magnification view of Golgi 386 budding between a nucleus and the peripheral plasma membrane. G: SEM image of zippered 387 endoplasmic reticulum (ER) at apical location (arrow). A-F: SEM images. 388





Figure 5: SARS-CoV-2 infected Vero E6 cells at 24-36 hours post-infection. A,B: SEM views of doughnut-like particles (arrow) with a pronounced electron-opaque edge observed at peri-nuclear locations dispersed into the cytoplasm (solid arrowhead), or within vacuoles, which seemed derived from the ER, forming virus morphogenesis matrix vesicae (VMMV). VMMV were observed as opened sacs (asterisk in B), assembling next to the nucleus (A,B). Protrusions of the doughnut-like particles could be observed in the VMMV (arrowhead in B). C,D: VMMV observed as a closed sac (asterisk in D) in a larger vacuole in the cytoplasm. A-D: SEM images.



400

Figure 6: SARS-CoV-2 infected Vero cells at 24-36 hours post-infection A: SEM depiction of an extensive peri-nuclear membrane whorls (mw) network, with larger inner-membranous distances as infection progresses. B: Nascent virions particles (\approx 75 nm) observed by SEM mixed with membranes whorls in large bags. C,F:SARS-CoV-2-morphogenesis matrix vesicae (asterisk) with different appearances, with nascent particles (\approx 75 nm) located in more or less large vacuoles, containing more or less electron-dense materials (asterisk). F: translucent VMMV/vacuoles with well-individualized virions particles (white arrows).



Figure 7: Mature SARS-CoV-2 particles in a Vero E6 cell. A,B: Mature SARS-CoV-2 particles with their corona spikes (arrows) in small cytoplasmic vacuoles between the nucleus and the cell periphery, observed by SEM (A) or TEM (B) in a cell, 12 hours post-infection. Extracellular particles are also present (Solid arrows).



- Figure 8: SEM of SARS-CoV-2 mature particles at 24-48 hours post-infection. observed at
 intra- and extra- cellular locations. A-C:Viral mature particles lying between cellular microvilli.
 D,E :Virus particles within smooth vesicles at the cell periphery and eventually fused with the cell
 membrane (arrowhead) to release the virus (arrow). F-G: Viral particles in translucent vacuoles or
 attached to the plasma membrane of a lysed cell. Small arrow points to a SARS-CoV-2 corona
 spike.