

1 **SARS-CoV-2 infection negatively affects ovarian function in ART patients**

2

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25 **Highlights**

26 ✓ COVID-19 impairs ovarian function in ART patients.

27 ✓ Patients with higher levels of SARS-CoV-2 IgG show a decrease in the number of
28 retrieved oocytes.

29 ✓ VEGF and IL-1 β were lower in post COVID-19 follicular fluids.

30 ✓ Post COVID-19 follicular fluids affect DNA integrity in both granulosa and
31 endothelial cells.

32

33 **ABSTRACT**

34 Several organs, such as the heart, breasts, intestine, testes, and ovaries, have been reported
35 to be target tissues of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)
36 infection. To date, no studies have demonstrated SARS-CoV-2 infection in the female
37 reproductive system. In the present study, we investigated the effects of SARS-CoV-2
38 infection on ovarian function by comparing follicular fluid (FF) from control and recovered
39 coronavirus disease 2019 (COVID-19) patients and by evaluating the influence of these FF
40 on human endothelial and non-luteinized granulosa cell cultures. Our results showed that
41 most FFs (91.3 %) from screened post COVID-19 patients were positive for IgG antibodies
42 against SARS-CoV-2. Additionally, patients with higher levels of IgG against SARS-CoV-2
43 had lower numbers of retrieved oocytes. While VEGF and IL-1 β were significantly lower in
44 post COVID-19 FF, IL-10 did not differ from that in control FF. Moreover, in COV434 cells
45 stimulated with FF from post COVID-19 patients, steroidogenic acute regulatory protein
46 (StAR), estrogen-receptor β (Er β), and vascular endothelial growth factor (VEGF) expression
47 were significantly decreased, whereas estrogen-receptor α (ER α) and 3 β -hydroxysteroid
48 dehydrogenase (3 β -HSD) did not change. In endothelial cells stimulated with post COVID-
49 19 FF, we observed a decrease in cell migration without changes in protein expression of
50 certain angiogenic factors. Both cell types showed a significantly higher γ H2AX expression
51 when exposed to post COVID-19 FF. In conclusion, our results describe for the first time
52 that the SARS-CoV-2 infection adversely affects the follicular microenvironment, thus
53 dysregulating ovarian function.

54

55 **Keywords:** COVID-19, SARS-CoV-2 IgG antibodies, follicular fluid, retrieved oocytes,
56 angiogenesis

57

58 **1 INTRODUCTION**

59 Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has spread throughout the
60 world. As of June 14, 2021, more than 175 million cases and 3.7 million deaths are attributed
61 to this virus worldwide. In Argentina, around 3.48 million cases were confirmed with 73,391
62 reported deaths (1, 2).

63 SARS-CoV-2 invades the target cell by binding to angiotensin-converting enzyme 2 (ACE-
64 2). The viral entry is further processed by the transmembrane serine protease 2 (TMPRSS2),
65 thus allowing the fusion of the cell membranes of virus and host cell (3). It is public
66 knowledge that SARS-CoV-2 can cause severe damage, particularly in the respiratory system
67 (4). The most frequently observed symptoms in COVID-19 patients include fever, cough,
68 and pneumonia. However, other symptoms such as thrombosis, pulmonary embolism, and
69 high blood pressure have been reported as well, suggesting that the virus targets the
70 endothelium (5, 6). It is well known that ACE-2 is also expressed in endothelial cells (7, 8).
71 Additionally, dysregulated immune responses, as those observed in COVID-19, are a major
72 culprit in endothelial dysfunction, since they alter microvascular permeability and induce
73 vascular inflammation (6). Nonetheless, other organs such as the heart, breasts, intestine,
74 testes, and ovaries have also been reported to be target tissues of this viral infection (9, 10).
75 To date, no studies have presented evidence of SARS-CoV-2 infecting the female
76 reproductive system.

77 ACE-2 is expressed in the uterus, vagina, placenta, and ovary (11, 12). In particular, ACE-2
78 mRNA transcripts have been detected in ovaries from reproductive-age and postmenopausal
79 women. Both stromal and granulosa cells have been found to be positive for ACE-2 in the
80 human ovary (13). Furthermore, ACE-2 expression in rat and bovine granulosa cells is

81 regulated by gonadotropic hormones (14, 15). Whether this virus binds to ACE-2 receptors
82 in the ovary and which effects, if any, this infection would have on ovarian function and
83 oocyte quality remains unclear. Nevertheless, to the best of our knowledge, no reports have
84 addressed the consequences of COVID-19 on ovarian function.

85 During the final stages of folliculogenesis, the oocyte is localized in an antral follicle in the
86 ovary. The female gamete is exposed to a microenvironment that includes follicular fluid
87 (FF) and somatic cells (namely granulosa and theca cells) within the follicle. The
88 composition of FF differs from that of serum—it is a complex mixture of hormones,
89 cytokines, metabolites, and other proteins secreted mainly by granulosa cells (16, 17). FF
90 composition reflects the stage of oocyte development and oocyte quality (18, 19). Therefore,
91 an altered FF composition is associated with a reduced reproductive function.

92 Based on these considerations, we hypothesized that the SARS-CoV-2 infection can
93 potentially affect ovarian function, disturbing the follicular microenvironment and thus
94 affecting oocyte quality in recovered women. Hence, we evaluated the presence of SARS-
95 CoV-2 IgG antibodies and antigens, interleukin-1 β (IL-1 β), interleukin-10 (IL-10), and
96 vascular endothelial growth factor (VEGF) levels in FF from healthy and recovered SARS-
97 CoV-2 women undergoing assisted reproductive technology (ART) procedures. We also
98 examined the effect of FFs obtained from the above-mentioned patients on: a) the
99 proliferation, migration, angiopoietins 1 and 2 (ANGPT-1/2), and VEGF expression of a
100 human endothelial cell culture; and b) the proliferation and protein expression of estrogen-
101 receptor α (ER α) and β (ER β), steroidogenic acute regulatory protein (StAR), 3 β -
102 hydroxysteroid dehydrogenase (3 β -HSD), and VEGF in human non-luteinized granulosa
103 cells. Additionally, we analyzed the effect of FFs on nuclear DNA damage in both cell types.

104

105 **2 MATERIALS AND METHODS**

106

107 **2.1 Ethical approval**

108 This study was approved by the ethics committee of the Instituto de Biología y Medicina
109 Experimental (IBYME-CONICET; Study No. 2850). Written informed consent was given
110 by all patients before recruitment.

111

112 **2.2 Study population and FF collection**

113 For this study, we enrolled a total of 80 women (21–41 years old) undergoing assisted
114 reproductive technology procedures between November 2020 and April 2021 at PREGNA
115 Medicina Reproductiva (Buenos Aires, Argentina), IVI Buenos Aires (Buenos Aires,
116 Argentina), Fertilis (Buenos Aires, Argentina) and InVitro (Buenos Aires, Argentina).
117 Patients with pathologies such as uterine fibroids, endometriosis, pelvic inflammatory
118 disease, premature ovarian failure, and PCOS were excluded from the study. Additionally,
119 we excluded patients with poor ovarian response (less than three antral follicles). The patients
120 were classified into two groups: control patients (n = 34), who had never tested positive for
121 COVID-19 or experienced any COVID-related symptoms, and post COVID-19 patients (n =
122 46), who had at least one positive PCR test for COVID-19 but were given medical clearance
123 before starting the fertility treatment. The patients in this group were asymptomatic or
124 presented mild symptoms such as anosmia, dysgeusia, and flu-like symptoms (fever, sore
125 throat, and cough) (20-22).

126 The time interval between the infection of the patients with SARS-CoV-2 and the retrieval
127 of FF varied between 2 and 9 months, the average being 4.5 months. None of the patients
128 were vaccinated against COVID-19 prior to the study. A protocol for ovarian stimulation was

129 assigned to patients according to their ovarian reserve and following the standard protocol of
130 each clinic. In all cases, it consisted of a gonadotropin protocol (recombinant FSH, highly
131 purified human menopausal gonadotropin, or a combination of both) for an average of
132 10 days (range, 9–12 days). Ovulation was induced by subcutaneous administration of a
133 GnRH agonist or hCG. All patients were included in the statistical analysis, since there were
134 no differences between the parameters studied in either group receiving GnRHa or hCG
135 trigger for ovulation.

136 Oocyte retrieval was conducted under vaginal ultrasound guidance 34-36 hours after
137 ovulation induction. Human FF was extracted from all 16- to 20-mm follicles of each patient.
138 No flush was used after the aspiration of all accessible ovarian follicles. Only
139 macroscopically clear fluids, indicating lack of contamination and blood, were considered in
140 the study. Immediately after oocyte removal, the FF was centrifuged for 10 min at 2000g to
141 remove cellular components and debris. Once transferred to sterile polypropylene tubes, the
142 supernatant was stored at -20°C until assayed. For *in vitro* experiments we selected randomly
143 20 patients per group, and each patient's FF was used individually. The biochemical analyses
144 were performed in the *Laboratory for Studies of the Physiopathology of the Ovary* at
145 IBYME-CONICET ([www.ibyme.org.ar/laboratorios/51/estudios-de-la-fisiopatologia-del-](http://www.ibyme.org.ar/laboratorios/51/estudios-de-la-fisiopatologia-del-ovario)
146 ovario).

147 Serum samples for estradiol determination were obtained on the day of the ovulation trigger.
148 Basal hormone levels prior to ovarian stimulation (estradiol, progesterone, and prolactin)
149 were obtained from the patients' clinic history, when available. Various parameters were
150 used to evaluate the efficacy of ovarian stimulation, including the numbers of retrieved
151 cumulus–oocyte complexes and of mature oocytes that reached metaphase II (MII). In
152 addition, each group of patients (control and post COVID-19) was divided into two subsets

153 according to age as follows: control; ≤ 35 (n=19) and >35 (n=15) and post COVID-19
154 ≤ 35 (n=22) and >35 (n=24), respectively. The analyses of ovarian stimulation outcomes were
155 duplicated for each subset.

156

157 **2.3 Immunoassays**

158 The levels of SARS-COV-2 IgG in FF samples were measured using an enzyme-linked
159 immunosorbent assay (ELISA) designed specifically to measure immunoreactive IgG against
160 SARS-COV-2 in human fluids (COVIDAR IgG, Argentina) (23). This kit, which was
161 generously donated by Dr. Andrea Gamarnik (Fundación Instituto Leloir-CONICET, Buenos
162 Aires, Argentina), uses two viral proteins as antigens—a trimer stabilized spike protein and
163 the receptor binding domain (RBD). The presumed presence or absence of specific IgG
164 antibodies against the SARS-CoV-2 virus was analyzed taking into account the cut-off value,
165 which was defined as the mean optical density (OD) of the negative control + 0.2, according
166 to the manufacturer's instructions. We classified the level of immunoreactivity in each
167 patients' FF based on their absorbance values: low (between 0.22 and 0.5), medium (between
168 0.5 and 1), and high (greater than 1).

169 The presence of SARS-CoV-2 viral antigens in FF was determined using the Panbio™
170 COVID-19 Ag Rapid Test Device (Abbott Diagnostics, Jena, Germany) following
171 manufacturer's instructions.

172 VEGF concentrations in FF were measured with a commercial ELISA kit (Catalog# 900-
173 TM10; Peprotech, NJ, United States), according to the manufacturer's instructions. IL-1 β and
174 IL-10 concentrations in FF were measured using commercial kits (IL-1 β Catalog# 557953;
175 IL-10 Catalog# 555157; BD Biosciences, CA, United States), as previously described by
176 Gori et al. (24).

177

178 **2.4 Granulosa and endothelial cells culture**

179 Human granulosa cell lines are useful, well-known models to study the physiopathological
180 mechanisms that govern follicular development and oocyte maturation *in vitro*. Therefore,
181 we utilized the immortalized human granulosa cell line COV434 (25), which was donated by
182 Dr. M Begoña Ruiz-Larrea (University of the Basque Country UPV/EHU, Leioa, Spain).
183 COV434 cells were maintained in Dulbecco's Medium (DMEM, Invitrogen, NY, USA) with
184 10% fetal bovine serum (FBS) and 200 mM L-glutamine (Gibco, WI, USA), in the presence
185 of 100 U/ml penicillin G and 100 mg/ml streptomycin sulfate at 37°C with 5% CO₂.

186 As for EA.hy926, this is a continuous, cloneable human cell line that displays numerous
187 features of vascular endothelial cells (26) and is a useful *in vitro* model for studying
188 angiogenic processes in the ovary (27-30). EA.hy926 cells were donated by Dr Gareth Owen
189 (Pontifical Catholic University of Chile, Santiago, Chile). EA.hy926 cells were maintained
190 in Iscove's Modified Dulbecco's Medium (IMDM, Invitrogen, NY, USA) with 10% FBS in
191 the presence of 100 U/ml penicillin G and 100 mg/ml streptomycin sulfate at 37°C with 5%
192 CO₂. The number of passages used in both cell lines has not exceeded the 20th.

193

194 **2.5 Western Blot**

195 For protein analysis, COV434 and EA.hy926 cells were seeded into 24-well cell culture
196 plates at a density of 0.5×10^6 cells/well, allowed to adhere to the surface, and grown to
197 confluence. Then, cells were incubated with FF (25% FF in media) from either control or
198 post COVID-19 patients for 24 h at 37°C. After treatment with FF, EA.hy926 or COV434
199 cells were lysed in lysis buffer (20 mM Tris-HCl pH 8, 137 mM NaCl, 1% Nonidet P-40 and
200 10% glycerol) supplemented with protease inhibitors (0.5 mM PMSF, 0.025 mM N-ethylmaleimide-

201 phenylalanine chloromethyl ketone, 0.025 mM N-p-tosyl-lysine chloromethyl ketone and
202 0.025 mM 1-tosylamide-2-phenylethylchloromethyl ketone). The cell lysates were
203 centrifuged at 10,000 g for 10 min at 4°C. Protein concentration was measured using the
204 Bradford assay. After boiling for 5 min, 20 µg of protein was applied to a SDS-
205 polyacrylamide gel, and electrophoresis was performed at 25 mA for 1.5 h. The resolved
206 proteins were transferred for 2 h onto nitrocellulose membranes. The blot was preincubated
207 in blocking buffer (5% nonfat milk, 0.05% Tween 20 in 20 mM TBS pH 8.0) for 1 h at room
208 temperature and incubated overnight in blocking buffer at 4°C with diluted primary
209 antibodies as follows: β-actin 1:3000 (sc-1616), 3β-HSD 1:1000 (sc-30820), ERα 1:100 (sc-
210 787), ERβ 1:500 (sc-390243), StAR 1:1000 (sc-25806), purchased from Santa Cruz
211 Biotechnology, Inc. (Santa Cruz, USA); VEGF 1:1000 (ab46154), γH2AX 1:1000
212 (ab26350), ANGPT-1 1:1000 (ab133425), ANGPT-2 1:1000 (ab180820) purchased from
213 Abcam (Cambridge, USA); and GAPDH 1/8000 (#2118) from Cell Signaling Technology,
214 Inc. (Danvers, MA, USA). The immunoblots were then incubated with HRP-conjugated
215 secondary antibodies, namely anti-rabbit 1:1000 (A4914) (Sigma Aldrich), anti-mouse
216 1:1000 (HAF007) from R&D Systems (MN, USA) or anti-goat 1:2000 (#1721034), as
217 required. Signal was detected by chemiluminescence. Protein levels were analyzed by
218 densitometry using Scion Image for Windows (Scion Corporation, Worman's Mill, CT,
219 USA). OD data are expressed as arbitrary units ± SEM. All blots shown were representative
220 of at least three independent experiments.

221

222 **2.6 Proliferation assay**

223 EA.hy926 and COV434 cells were exposed for 24 h to control FF and post COVID-19 FF at
224 37°C with 5% CO₂, after which proliferation was determined using WST-1 reagent (4-[3-(4-

225 Iodophenyl)-2-(4-nitro-phenyl)-2H-5-tetrazolio]-1,3-benzene sulfonate; Roche Diagnostics,
226 Mannheim, Germany), following the manufacturer's instructions. Briefly, after stimulation
227 with FF, 10 μ L of WST-1 was added to each well and cells were incubated for an additional
228 2 h. Absorbance was measured using a microplate reader at 450 nm and 620 nm. Experiments
229 were conducted in triplicate.

230

231 **2.7 Endothelial cell migration**

232 A wound healing assay was performed using the EA.hy926 endothelial cell line to study the
233 effect of FF on endothelial cell migration as previously described by Scotti et al. (2013, 2014,
234 2016) (27, 28, 30). Briefly, EA.hy926 cells were detached by trypsinization, resuspended in
235 IMDM, plated at a density of 3×10^5 cells per well in 24-well plates, and grown to confluence.
236 Cell monolayers were wounded by a 1000 μ l micropipette tip in one direction. After the
237 injury, the cells were washed with PBS to remove cellular debris. The wounded cells were
238 then incubated with FF (25%) either from control (n=20) or post COVID-19 patients (n=20).
239 Serum-free DMEM/F12 was used as a negative control (n=16). Cells were then incubated for
240 15 h at 37°C. Cell migration was monitored at initial wounding (t 0 h) and at 12 h (t 12 h)
241 under a phase-contrast microscope and pictures were acquired at the same magnification and
242 location every time. The resulting cell migration was calculated as cell-free area at t 0 h –
243 cell-free area at t 12 h and was expressed as a percentage of the mean migration of negative
244 control wells (without FF). Endothelial cell migration in negative control wells (media
245 without FF) is arbitrarily presented as 100%. We quantified the cell-free wounded areas using
246 ImageJ software (National Institutes of Health, Bethesda, MD). Experiments were conducted
247 in duplicate.

248

249 **2.8 Statistical analysis**

250 Statistical analyses were performed using the statistical software Prism v8.0 (GraphPad
251 Software, San Diego, CA, US). Data are expressed as the mean \pm SEM. Differences between
252 groups were tested for significance using the independent samples Student's t test for
253 parametric variables. For endothelial cell migration, normally distributed data were analyzed
254 using one-way ANOVA followed by Tukey's test for statistical comparison of the groups.
255 Statistical significance was defined as $p < 0.05$.

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259 **RESULTS**

260

261 **3.1 Characteristics of the study population and fertility parameters**

262 The characteristics of the study population are shown in Table 1. No significant differences
263 were found in overall patient age (range, 21–41), which were 33.09 and 33.43 in control and
264 post COVID-19 groups, respectively. Before starting the IVF procedure, patients underwent
265 a general clinical examination. We registered multiple indicators, including BMI, antral
266 follicle count (AFC), basal serum AMH, estradiol, progesterone, and prolactin, as well as
267 estradiol levels on the day of ovulation trigger. There were no significant differences in these
268 parameters when comparing post COVID-19 and control patients. It is worth mentioning that
269 the time interval between the infection of the patients with SARS-CoV-2 and the retrieval of
270 FF varied between 2 and 9 months, being the average 4.5 months. Subsequently, the patients
271 in each group were subdivided into two groups according to their age (≤ 35 years and > 35
272 years) and we evaluated their response to hormonal stimulation. The results showed that a
273 lower number of oocytes was retrieved from post COVID-19 patients over 35 years old than
274 from age-matched control patients, whereas the number of oocytes retrieved in patients ≤ 35
275 years old did not differ between both groups. Oocyte maturation was also evaluated, but no
276 significant differences were observed in the number or percentage of MII oocytes between
277 both groups.

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284 **Table 1: Clinical information of control patients and post COVID-19 patients**

285 Data are expressed as the mean ± standard error of the mean. Student's T-test was used for
 286 comparisons between groups. Statistical significance was defined as <0.05.

Baseline characteristics of patients	Control patients (n=34)			Recovered COVID-19 patients (n=46)			P value
	Mean	Min-Max	SEM	Mean	Min-Max	SEM	
Age (years)	33.09	23-38	0.60	33.43	21-44	1.02	n.s.
Number of oocytes retrieved in patients ≤35 years	11.84	8-23	0.85	13.80	0-30	2.21	n.s.
Number of oocytes retrieved in patients >35 years	11.11	6-16	0.95	6.95	0-15	0.95	0.0187
MII oocytes (n, %)	9.03 (79.84%)	6-16	0.61	11.98 (82.23%)	0-30	1.41	n.s.
Basal serum estradiol (pg/ml)	33.00	19-46	7.81	42.70	25-56	3.45	n.s.
Serum estradiol on trigger day (pg/ml)	2710	400-5772	576.9	1424	325-3728	1152	n.s.
Basal serum progesterone (ng/ml)	1.09	0.52-1.86	0.18	1.37	0.30-4.38	0.58	n.s.
Basal serum prolactin (ng/ml)	20.37	6.20-48	3.01	15.74	1-36.20	1.83	n.s.
AMH (ng/ml)	2.067	0.5-4.4	0.32	2.917	0.31-5.7	0.48	n.s.
Antral follicles count (AFC)	12.64	7-20	0.77	12.50	4-22	0.99	n.s.
BMI	23.43	18.70-31	0.98	23.01	18-29.36	0.55	n.s.
Time from COVID-19 infection (months)	-	-	-	4.5	2-9	0.37	-

287

288

289 **3.2 Detection of IgG antibodies against SARS-COV-2 in FF from recovered patients**

290 The presence of SARS-CoV-2 IgG antibodies was determined in FF from post COVID-19
291 and control patients (Table 2). The results revealed that 91.3% (42/46) of the FF from post-
292 COVID-19 patients were positive for IgG against SARS-CoV-2, whereas antibodies were
293 not detected in any of the FF from control patients, as expected. Within the post COVID-19
294 group, the ELISA assay yielded different colorimetric intensities, indicating varying levels
295 of SARS-CoV-2 IgG, which we classified as high (38.1%; 16/42 patients), medium (38.1%;
296 16/42 patients) and low (23.8%; 10/42 patients). We found no correlation between SARS-
297 CoV-2 IgG levels and the time from infection. We then evaluated the number of retrieved
298 oocytes in each group and found that this parameter significantly decreased with higher titers
299 of SARS-CoV-2 IgG antibodies (low vs. medium, $p < 0.05$; low vs. high, $p < 0.01$). Similar
300 results were obtained for the number of mature oocytes (those that reached MII stage) from
301 each patient (low vs. medium and high, $p < 0.05$). These findings are shown in Fig. 1 A-B.
302 Additionally, we assessed the presence of SARS-CoV-2 viral antigens in FF from patients,
303 but none of the samples presented positive results (data not shown).

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307

308 **Table 2: Detection of IgG antibodies against SARS-CoV-2 by ELISA in control and**
309 **recovered COVID-19 patients**

310 Of the 46 post COVID-19 patients, 91.30% tested positive for IgG antibodies against
311 SARS-CoV-2 in FF. The titer of SARS-CoV-2 IgG antibodies in FF were classified
312 according to their absorbance values as high (greater than 1), medium (between 0.5 and 1),
313 and low (between 0.22 and 0.5).

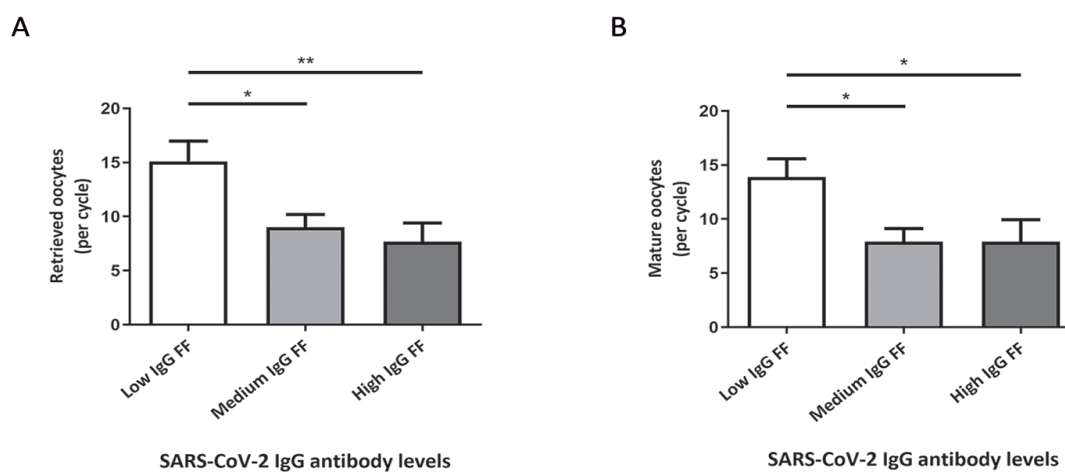
314

Immunoreactivity	Negative (%)	Positive (%)		
		Low-IgG (%)	Medium-IgG (%)	High-IgG (%)
Control FF (n=34)	34/34 (100%)	-	-	-
Post COVID-19 FF (n=46)	4/46 (8.7%)	42/46 (91.3%)		
		10/42 (23.8%)	16/42 (38.1%)	16/42 (38.1%)

315

316

317



318 **FIGURE 1: Retrieved and mature oocytes from patients with low-, medium- and high-**

319 **level SARS-CoV-2 IgG antibodies in FF. (A)** The number of retrieved oocytes was

320 significantly lower in the post COVID-19 subgroups as levels of SARS-CoV-2 IgG were

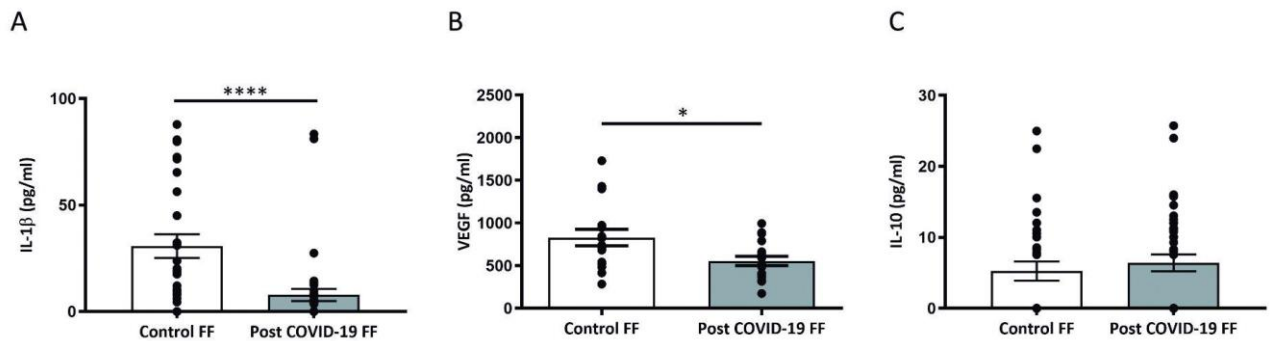
321 higher (low vs. medium, * $p < 0.05$; low vs. high, ** $p < 0.01$). **(B)** Similar results were obtained

322 for the number of mature oocytes (low vs. medium and high, * $p < 0.05$).

323

324 **3.3 VEGF, IL-1 β , and IL-10 concentration in FF from control and post COVID-19**
325 **patients**

326 As shown in Fig. 2 A-B, IL-1 β and VEGF concentrations were significantly lower in FF from
327 post COVID-19 patients than those in FF from control patients (IL-1 β : $p < 0.0001$, VEGF:
328 $p < 0.05$). In contrast, the levels of IL-10 from post COVID-19 FF did not differ significantly
329 from those in control FF (Fig. 2 C). Furthermore, no association was found between the IL-
330 1 β and VEGF levels in FF from post-COVID-19 patients and the time elapsed from the viral
331 infection to the day of oocyte retrieval (data not shown).
332



333 **FIGURE 2: VEGF, IL-1 β and IL-10 concentration in control and post COVID-19 FF**
334 **determined by ELISA.** IL-1 β (A) and VEGF(B) concentrations were decreased in FF from
335 post COVID-19 compared with that in FF from control patients (VEGF: $*p < 0.05$, IL-1 β :
336 $****p < 0.0001$). No differences were found between groups in terms of IL-10 levels (C)
337 ($p = 0.4$).

338
339 **3.4 Effects of FF from control and post COVID-19 patients on granulosa cell culture**

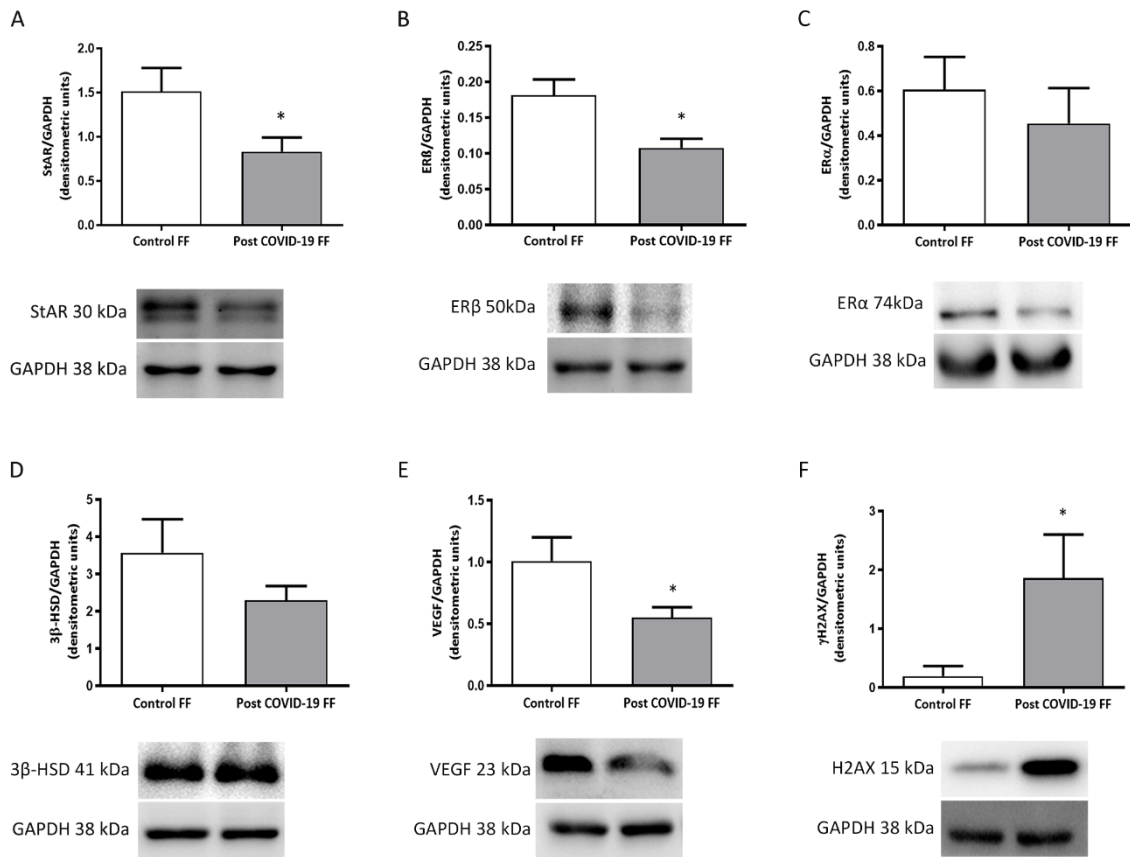
340 To evaluate whether granulosa cells could be affected by FF from recovered COVID-19
341 patients, we stimulated COV434 cells with control or post COVID-19 FF. As illustrated in
342 Fig. 3 A-B, the analysis of endocrine-related proteins showed a significant decrease of StAR
343 and ER β in granulosa cells stimulated with post COVID-19 FF compared with those
344 stimulated with control FF ($p < 0.05$). Protein expression of ER α and 3 β -HSD remained
345 unchanged between both groups (Fig 3 C-D).

346 Since VEGF is one of the most important angiogenic factors in the ovary, we measured
347 VEGF protein expression in COV434 by Western blot. The densitometric analysis showed
348 that granulosa cells stimulated with FF from post COVID-19 patients expressed lower levels
349 of VEGF than those stimulated with FF from control patients ($p < 0.05$) (Fig. 3 E).

350 To study the impact of stimulation with FF from recovered COVID-19 patients on granulosa
351 cells, we evaluated the protein expression of γ H2AX, a molecular marker for DNA damage.
352 The results showed that γ H2AX expression in COV434 cells incubated with post COVID-19
353 FF was significantly higher than that in cells incubated with control FF ($p < 0.05$) (Fig 3 F).

354 Finally, in order to determine whether FF from recovered COVID-19 patients altered
355 granulosa cell proliferation, we quantified this parameter using WST-1. No differences were
356 found in COV434 proliferation rates between the groups (data not shown).

357



359 **FIGURE 3: Effect of FF from post COVID-19 patients on protein expression in**
 360 **granulosa cells.** The following proteins were measured by Western Blot: StAR (A); ERβ
 361 (B); ERα (C); 3β-HSD (D); VEGF (E); γH2AX (F). Densitometric quantification showed
 362 decreased levels of StAR (A; $p < 0.05$) and ERβ (B; $p < 0.05$) in cells stimulated with post
 363 COVID-19 FF, whereas protein levels of ERα (C) and 3β-HSD (D) remained unchanged
 364 between both groups. VEGF levels were significantly lower ($p < 0.05$) in COV434 cells
 365 incubated with FF from post COVID-19 patients compared with those incubated with control
 366 FF (E). Ovarian cells stimulated with FF from post COVID-19 patients expressed higher
 367 levels of γH2AX than cells stimulated with control FF (F; $p < 0.05$). In all cases, representative

368 immunoblots are shown in the lower panels. Data are expressed as means \pm SEM normalized
369 to GAPDH. Results were obtained from three independent experiments. * $p < 0.05$.

370

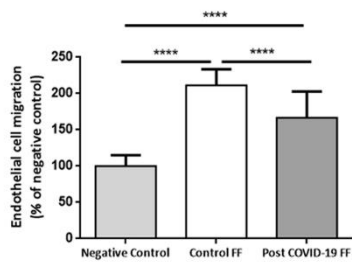
371 **3.5 Effect of FF from control and post COVID-19 patients on endothelial cell culture**

372 To analyze the specific effect of COVID-19 infection on ovarian angiogenesis, migration
373 was quantified in EA.hy926 cells stimulated with FF from control and post COVID-19
374 patients using a wound healing assay. After 12 hours, results showed that FF from post
375 COVID-19 patients significantly decreased endothelial cell migration compared with FF
376 from control patients ($p < 0.0001$) (Fig. 4 A-B). In addition, we analyzed ANGPT-1 and
377 ANGPT-2 protein expression in endothelial cells and no changes were found between groups
378 (Fig. 4 C-E), as well as in VEGF protein levels when cells were stimulated with either control
379 or post COVID-19 FF (Fig. 4 F).

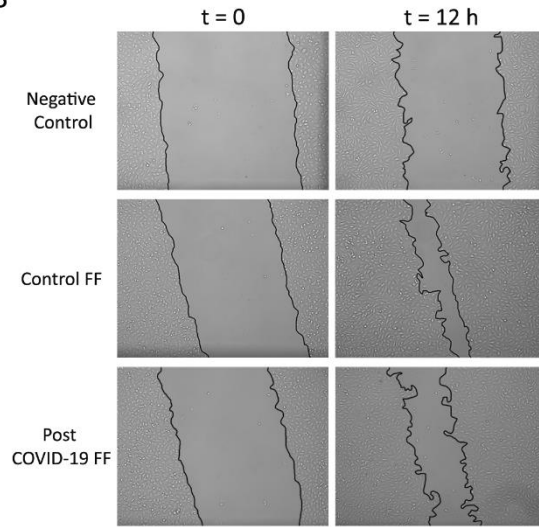
380 Furthermore, we studied the effect of FF from recovered COVID-19 patients on DNA
381 damage, as determined by endothelial cell expression of γ H2AX. Protein levels of γ H2AX
382 in EA.hy926 cells incubated with FF from post COVID-19 patients were significantly higher
383 than in those with FF from control patients ($p < 0.01$) (Fig. 4 G). Lastly, we evaluated whether
384 endothelial cell proliferation was affected by the presence of FF from recovered COVID-19
385 patients, but no differences were found between both groups (data not shown).

386

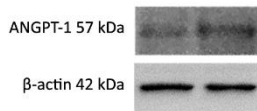
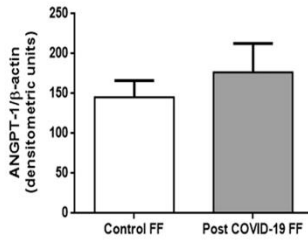
A



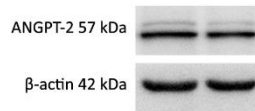
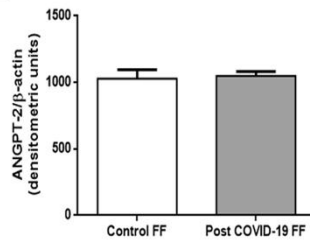
B



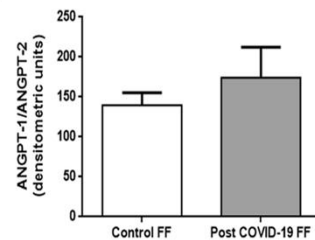
C



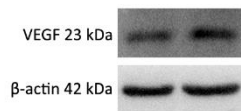
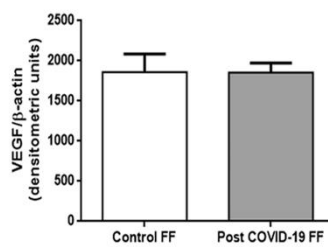
D



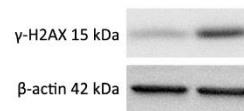
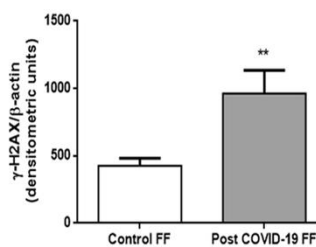
E



F



G



388 **FIGURE 4: Effects of FF from recovered COVID-19 patients on endothelial cells**

389 Endothelial migration of EA.hy926 cells stimulated with control or post COVID-19 FF.

390 (A) Quantification of the wound-healing assay. The columns show the percentage of
391 endothelial cell migration normalized to the negative control, which is presented as 100%.
392 Data are expressed as means \pm SEM. (B) Representative images taken immediately after
393 wound scratching (t 0) and after 12 h (t 12). Black lines represent the migration fronts. Effects
394 of stimulation with control or post COVID-19 FF on the expression of ANGPT-1 (C);
395 ANGPT-2 (D); ANGPT-1/ANGPT-2 (E); VEGF (F) and γ H2AX (G) in EA.hy926 cells.
396 The graphs show the densitometric analysis of protein levels. The density of each band was
397 normalized to the density of the β -actin bands. Lower panels show representative blots for
398 each protein analyzed. * $p < 0.05$.

399

400 **4 DISCUSSION**

401

402 The data presented in this study demonstrate for the first time the presence of IgG antibodies
403 against SARS-CoV-2 in FF from recovered COVID-19 patients undergoing ART treatments.
404 Additionally, we demonstrated that VEGF and IL-1 β levels in FF from post COVID-19
405 patients were decreased compared with those in the control group (patients that were never
406 infected with SARS-CoV-2). FF contributes to maintaining the controlled microenvironment
407 required to support female gamete development and is composed of a complex mixture of
408 proteins, metabolites, and cytokines. Based on these considerations, several biochemical
409 characteristics of the FF may determine oocyte quality and thus influence the potential
410 reproductive performance.

411 In our study, in addition to detecting antibodies against SARS-CoV-2, we found that the
412 numbers of retrieved oocytes as well as the mature oocytes were lower in the subgroups with

413 higher SARS-CoV-2 IgG levels. Recently, Peghin et al. (2021) have indicated that the
414 persistent high titers of the serological response against SARS-CoV-2 might play a crucial
415 role as an independent risk factor for severe post COVID-19 symptoms, in addition to gender
416 and the number of symptoms at onset and ICU admission (31).

417 A number of studies have reported that the presence of certain pathogens can affect the
418 success of IVF treatments. Cortiñas et al. (2004) and Pacchiarotti et al. (2009) have
419 demonstrated that high levels of anti-*Chlamydia trachomatis* IgG and IgA, both in serum and
420 FF, harm implantation rate in women undergoing IVF (32, 33). Therefore, it is reasonable to
421 think that the high titers of SARS-COV-2 IgG antibodies could alter oocyte number and/or
422 quality. Nonetheless, further research is necessary to elucidate whether the presence of
423 immunoglobulins for SARS-CoV-2 adversely affects the reproductive outcome of women.
424 In particular, the impact of these antibodies in FF on oocyte quality should be further explored
425 and its assessment is beyond the objective of the present work.

426 Several of the growth factors and interleukins in FF are known to be associated with ovarian
427 response and fertilization rates (17, 34, 35). The follicles and corpora lutea are able to
428 produce many of these, including numerous angiogenic factors. This is especially relevant
429 since a functional ovarian microvasculature is crucial to guarantee the supply of cytokines,
430 hormones, and oxygen that make follicular growth and corpus luteum formation possible.

431 VEGF, one of the central angiogenic factors, plays a key role in the regulation of normal and
432 abnormal angiogenesis in the ovary (36). Inhibition of VEGF expression results in reduced
433 follicle angiogenesis and lack of antral follicle development. In addition, it is well known
434 that VEGF is involved in the ovulatory process. Accordingly, increased expression of VEGF
435 after administration of an ovulatory dose of gonadotropins is correlated with prostaglandin
436 concentration (37). In our study, VEGF levels in FF from recovered COVID-19 patients

437 undergoing *in vitro* fertility treatments were lower than those in the control group. Decreased
438 VEGF levels could lead to an abnormal development of the ovarian vasculature and,
439 consequently, fail to provide nutrients and hormones to the growing follicles, affecting the
440 oocyte quality.

441 In the ovary, cytokines and macrophages are intimately involved in follicular development,
442 ovulation, and luteal function. Our study evidenced that IL-1 β levels were decreased in FF
443 from recovered COVID-19 patients compared with those in control FF. In particular, it has
444 been reported that IL-1 β promotes several processes associated with ovulation, as well as
445 regulates folliculogenesis and atresia (38, 39). Intra-ovarian macrophages, which represent
446 from 5 to 15% of the total cellular population in FF (40), are responsible for the production
447 of IL-1 β (41), a cytokine that is also secreted by oocytes, granulosa, theca, and cumulus cells
448 in human ovaries (42-44). Additionally, IL-1 β is hormonally regulated and its levels increase
449 during the peri-ovulatory period (45, 46). IL-1 β , IL-6, and TNF α have been detected in FF
450 of women undergoing *in vitro* fertilization (47, 48), and serum levels of IL-1 β positively
451 correlate with estradiol levels on the day of hCG injection (49). Furthermore, Mendoza *et al.*
452 (2019) demonstrated that increased levels of IL-1 β in FF were associated with enhanced
453 fertilization rates (35). Although we did not find any correlation between IL-1 β levels and
454 the reproductive outcome in terms of retrieved or mature oocyte numbers, this IL-1 β
455 deficiency observed in FF from post COVID-19 patients could have implications for oocyte
456 quality and for prospective reproductive outcomes.

457 Given that follicles developing healthy oocytes produce high levels of IL-1 β and TNF α (35),
458 it is therefore likely that both cytokines are involved in oocyte quality. IL-1 β also induces the
459 secretion of TNF α and directly increases vascular permeability (50) and, in turn, TNF α
460 enhances new blood vessel growth during inflammatory processes (51). Based on these data

461 from the literature, it could conceivably be hypothesized that lower IL-1 β levels in post
462 COVID-19 patients decrease TNF α production, which can lead to impaired blood vessel
463 formation in the ovary. This explanation would be consistent with the decrease in VEGF
464 levels observed in post COVID-19 FF. More studies are needed to elucidate the effect of
465 these cytokines on ovarian angiogenesis in recovered COVID-19 patients.

466 To study the potentially detrimental consequences of altered FF composition in post COVID-
467 19 women, we evaluated the effects of these FF on two pivotal cell types in the ovary—
468 granulosa and endothelial cells. To this purpose, we stimulated a granulosa cell line
469 (COV434) and an endothelial cell line (EA.hy926) with FF from either control or post
470 COVID-19 patients and analyzed endocrine-related proteins, angiogenic markers, and
471 nuclear DNA damage in these cells.

472 Endocrine-related proteins, such as steroidogenic enzymes and hormone receptors, are
473 essential for ovarian function since follicular development depends on steroid hormone
474 production. Despite being different, these hormones are all synthesized from a common
475 precursor substrate: cholesterol. Since the rate-limiting step in follicular steroidogenesis is
476 the transport of cholesterol to the site of steroid biosynthesis, this makes steroidogenic acute
477 regulatory protein (StAR) a key player. Indeed, the StAR protein predominantly modulates
478 steroid biosynthesis during the folliculogenesis. Furthermore, estrogens and their receptors,
479 α and β , play a crucial role in the pathogenesis of gynecological disorders and/or cancers,
480 i.e., endometriosis as well as breast, endometrial, and ovarian cancers (52, 53). In the present
481 study, we showed that FF from post COVID-19 patients decreased StAR and ER β expression
482 in human non-luteinized granulosa cells compared with those stimulated with control FF.
483 Dang *et al.* (2017) have previously shown that cytokines such as IL-1 β induce the expression
484 of StAR and stimulate steroid synthesis in human granulosa-lutein cells (54). Taken together,

485 these data suggest that low IL-1 β levels detected in FF from post COVID-19 patients could
486 be partially responsible for the decreased StAR expression and alter the steroid synthesis in
487 granulosa cells, thus affecting oocyte development and maturation.

488 As described above, VEGF is the main angiogenic factor involved in the formation of
489 microvasculature within ovarian follicles (55). Other angiogenic factors, such as
490 angiopoietins, are required for the maturation of newly formed blood vessels. Previously, we
491 showed in a rat model that inhibition of VEGF and ANGPT-1 causes an imbalance in the
492 ratio of antiapoptotic: proapoptotic proteins that leads more follicles to atresia (56, 57). In
493 the present study, stimulation with FF from post COVID-19 patients resulted in a significant
494 decrease in endothelial cell migration compared with that of control FF. This finding is
495 consistent with the decrease in VEGF concentration that we observed in post COVID-19 FF.
496 Indeed, altered endothelial migration could be a direct consequence of low VEGF
497 concentrations since this affects new blood vessel formation.

498 Conversely, several studies, including ours, have demonstrated the cytoprotective effect of
499 VEGF in the bovine and rat ovary (56, 58). Here, we showed that FF from post COVID-19
500 patients significantly decreased the expression of VEGF in non-luteinized human granulosa
501 cells. Even though the presence of post-COVID-19 FF did not seem to influence granulosa
502 cell proliferation compared with that of control FF, our results indicate that decreased VEGF
503 levels might affect follicular cell function and, consequently, damage oocytes.

504 Double-strand breaks (DSBs) affect the stability of the genome and represent one of the most
505 critical lesions for cell survival (59). γ H2AX is a well-known marker for the detection of
506 chromatin modifications linked to DNA damage and is used to assess various cellular
507 processes such as aging, cancer, and inflammation (60-62). In particular, γ H2AX is utilized
508 to predict chronic inflammatory conditions that precede cancer as well as cardiovascular and

509 nervous system disorders. Moreover, the influx of viral antigens can cause an inflammatory
510 response, making γ H2AX a potential marker of viral infection. For instance, Nichols *et al.*
511 (2009) observed that increased γ H2AX levels were induced by replicating viral proteins
512 during adenovirus infection (63). In our study, we demonstrated that FF from recovered
513 COVID-19 patients increased γ H2AX levels compared with FF from control patients in both
514 endothelial and granulosa cells. Therefore, a possible explanation for this is that systemic
515 and/or local infection of SARS-CoV-2 may promote the entry of lymphocytes and
516 macrophages to the ovary. This would affect the synthesis of pro- and anti-inflammatory
517 cytokines that regulate the release of reactive oxygen species, possibly leading to disruption
518 of the DNA integrity of follicular and endothelial cells.

519 In conclusion, the results described for the first time in this study evidence that infection with
520 SARS-CoV-2 could damage ovarian function, alter the follicular microenvironment and
521 potentially affect reproductive outcomes. Our results indicate that this viral infection leads to
522 the presence of IgG antibodies against SARS-CoV-2 in FF, in addition to decreased VEGF
523 and IL-1 β levels in FF. We also found a negative relationship between SARS-CoV-2 IgG
524 levels in FF and the numbers of retrieved and mature oocytes from the same patients, further
525 corroborating that COVID-19 might jeopardize reproductive outcomes. Additionally, post
526 COVID-19 FF alters steroidogenic parameters and VEGF expression in granulosa cells as
527 well as impair migration in endothelial cells. Moreover, these FF severely damage DNA
528 stability and integrity in both granulosa and endothelial cells. Further research on SARS-
529 CoV-2 infection and its impact on ovarian microvasculature and folliculogenesis is of the
530 essence. In particular, elucidating which FF components in the ovarian microenvironment
531 have a negative impact on oocytes should be examined more closely.

532 One of the limitations of our study is that the enrolled patients were analyzed 3 to 9 months
533 after SARS-CoV-2 infection. Therefore, more studies are needed to evaluate whether these
534 ovarian alterations can be reverted after longer periods of time, which would allow physicians
535 to design an optimal fertility protocol for patients recovered from COVID-19 and to prevent
536 potential complications during the ART treatments due to a recent SARS-CoV-2 infection.
537 Studies with a larger population size could provide more definite evidence on the
538 reproductive performance of recovered COVID-19 female patients.

539

540 **5 CONCLUSION**

541 Greater efforts are needed to ensure that COVID-19 is taken into account as a relevant factor
542 influencing female reproduction and to use this information to further improve clinical
543 interventions and public health policies. Finally, our study provides a solid groundwork for
544 future research to continue evaluating the potential effects of SARS-CoV-2 infection on
545 ovarian function and its implications on women's fertility.

546

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552

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557 **Gonzalo Oubiña:** Investigation, Data curation. **Vanesa Hauk:** Investigation, Data curation.
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562 **Abramovich:** Writing – review & editing. **Leopoldina Scotti:** Investigation, Data
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565 original draft, Writing – review & editing, Funding acquisition, Project
566 administration.

567

568 All authors approved the final version of the manuscript.

569

570

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574

575 **CONFLICT OF INTEREST**

576 The authors declare no potential conflicts of interest with respect to the research, authorship,
577 and/or publication of this article.

578

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