

## SELECTED ORAL COMMUNICATIONS

## SESSION 46: CURRENT CHALLENGES IN UTERINE DISORDERS

30 June 2021

Stream 1

10:00 - 11:30

**O-141 Mapping of SARS-CoV-2-associated receptors and proteases mRNA in human endometrium during natural and stimulated cycles****D. Haouzi<sup>1</sup>, F. Entezami<sup>2</sup>, S. Brouillet<sup>3</sup>, F. Barry<sup>3</sup>, A. Gala<sup>3</sup>, A. Ferrieres-Hoa<sup>3</sup>, A. Tal<sup>4</sup>, S. Hamamah<sup>3</sup>**<sup>1</sup>INSERM U1203, IRMB- Hôpital St-Eloi- CHRU Montpellier, MONTPELLIER, France ;<sup>2</sup>American Hospital of Paris, ART department, Neuilly-Sur-Seine, France ;<sup>3</sup>IRMB- Inserm U1203, Hôpital St-Eloi- CHRU Montpellier, Montpellier, France ;<sup>4</sup>CHU and University of Montpellier, Department of Reproductive Medicine, Montpellier, France

**Study question:** Covid-19 pandemic has significantly affected the assisted reproductive technology (ART) practice. Understanding whether SARS-CoV-2 could infect endometrial tissues during ART is crucial for risk mitigation

**Summary answer:** Analyses of gene expression profiles of SARS-CoV-2 host entry candidates from microarray data suggest that endometrium should be considered as potential target for SARS-CoV-2 infection.

**What is known already:** Very few studies analyzed the gene expression profiles of SARS-CoV-2-associated receptors and proteases, mainly focusing on ACE2 and TMPRSS2 expression, resulting incomplete knowledge in different specimens from female genital tract. However, no studies have analyzed the

potential impact of controlled ovarian stimulation (COS) protocols during ART procedure on the endometrial gene expression profiles of SARS-CoV-2-associated receptors and proteases

**Study design, size, duration:** To address this question, we retrospectively examined the gene expression profile of SARS-CoV-2-associated receptors and proteases in endometrial biopsies of a cohort of ART candidates using Affymetrix microarray data

**Participants/materials, setting, methods:** Human endometrial tissue under natural (n=62) and COS cycles (n=42) were analyzed. A focus was particularly made on the renin-angiotensin system relates genes with a prominent role in the virus infection, and gene expression levels of receptors and proteases closely related to SARS-CoV-2 infection was also studied.

**Main results and the role of chance:** Using our large cohort of endometrial samples, we reported a high prevalence of genes related to the ACE2 pathway, including *AGT*, *AGTRI*, *ANPEP*, *CTSA*, *ENPEP*, *LNPEP*, *MME*, *NLN*, *THOPI*, *BSG* and *CTSL* during both phases (early- and mid-secretory phase), and mainly during the mid-secretory phase for *ACE2*. The highest signal intensities were found for *CTSA*, *LNPEP*, *MME*, *NLN*, *BSG* and *CTSL*. The most representative of dual co-expression of SARS-CoV-2-associated receptor and protease in endometrium was *BSG-CTSL* and *BSG-CTSA*. It is also important to note high variation of SARS-CoV-2 receptors inter-patients under natural cycle. Globally, the impact of COS on endometrial gene expression profile of SARS-CoV-2-associated receptors and proteases of non Covid-19 patients is low, suggesting no additional potential risks of SARS-CoV-2 infection during stimulated ART procedure compared with natural cycles.

**Limitations, reasons for caution:** Analyses of Affymetrix microarray gene expression data were performed in non-COVID-19 patients. Whether the SARS-CoV-2 infection changes the endometrial gene expression profile of SARS-CoV-2-associated receptors and proteases is under investigation

**Wider implications of the findings:** Specimens from female genital tract may be considered as potential targets for SARS-CoV-2.

**Trial registration number:** not applicable