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COVID-19 and ACE2 in the liver and gastrointestinal tract: Putative biological explanations of sexual dimorphism

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The presence of SARS-CoV-2 gastrointestinal infection has recently been reported by two independent groups from China ^{1,2}. Also, liver injury -in part presumably explained by viral infection of liver cells may be present in about 60% of the infected patients ³. Therefore, patients with chronic liver disease may be vulnerable to the serious clinical consequences of COVID-19 infection. Likewise, emerging clinical data suggest that males with comorbidities, including obesity, are more likely to present severe disease ^{4,5}. While the biological mechanisms behind this observation are unclear, it has been speculated that sex-based immunological and or/ hormonal differences may account in part for that.

There is evidence highlighting angiotensin-converting enzyme 2 (ACE2) as one of the host receptors for cell entry of members of the SARS-CoV group, including SARS-CoV-2 ⁶.

Structural analysis showed several binding motifs between the SARS-CoV spike protein receptor-binding domain and human ACE2 ⁶. Besides its role in catalyzing the cleavage of angiotensin I into angiotensin 1-9, and angiotensin II into the vasodilator angiotensin 1-7, ACE2 is involved in cellular pathways associated with other viral entry into host cells.

Gene expression levels of *ACE2* differ across human body . The highest expression levels are in the small intestine and terminal ileum, and *ACE2* expression levels in the liver and lung are much lower than that of the gastrointestinal tract. One remarkable aspect of the *ACE2* is that the gene maps on the non-pseudoautosomal, that is, the X-specific, region of the chromosome X (Xp22.2). It is largely known that in order to balance the dosage effect of X-linked genes, one of the two X chromosomes is randomly inactivated in females during development; this process is called X inactivation. Nevertheless, while most genes are silenced, about 15% of X-linked human genes escape from inactivation ⁷. More importantly, X-escape is not uniform across different tissues. In fact, it was shown that ~10% of gene escape occurs selectively in specific tissues ⁷. These molecular aspects are of medical importance because they could explain sex differences in the natural course of human diseases, including COVID-19.

A recent systematic survey of the landscape of human X-linked genes inactivation using RNA sequencing-based approaches showed that *ACE2* presents remarkable differences in male–female expression levels⁸. Tukiainen et al. suggested that tissue differences in X-escape can directly translate into tissue-specific sex biases in gene expression⁸. Specifically, the study showed not only that *ACE2* is among the 82 X-escaping genes but also highlighted that there might be differences in the liver and lung *ACE2* expression levels between males and females⁸. Paradoxically, escape of *ACE2* from X-inactivation resulted in low levels of expression in the liver, lung, and visceral adipose tissue of women⁸. Conversely, *ACE2* expression levels in colon transverse and subcutaneous adipose tissue were significantly higher in females than males⁸.

Collectively, these novel observations may have important clinical implications for COVID-19 infected patients. First, differences between men and women in liver *ACE2* expression levels may help to explain potential clinical differences in the course of COVID-19 infection in patients with underlying chronic liver disease. Second, differences between men and women in *ACE2* expression levels in gastrointestinal tissues due to escaping from X-inactivation, including colon, could result in different transmission patterns, including fecal-oral transmission. Third, gender-linked differential expression levels in adipose tissue and/or visceral fat, might also shed light into potential differences in the odds of presenting severe complications and in-hospital death associated with comorbidities, including severe obesity.

Declaration of interests: None

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