

THEMATIC REVIEW

Impact of ACE2 on the susceptibility and vulnerability to COVID-19

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Abstract

Angiotensin-converting enzyme 2 (ACE2) is not only the viral receptor for the novel coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) but is also classically known as a key carboxypeptidase, which through multiple interacting partners plays vital physiological roles in the heart, kidney, lung, and gastrointestinal tract. An accumulating body of evidence has implicated the dysregulation of ACE2 abundance and activity in the pathophysiology of multiple disease states. ACE2 has recently regained attention due to its evolving role in driving the susceptibility and disease severity of coronavirus disease 2019 (COVID-19). This narrative review outlines the current knowledge of the structure and tissue distribution of ACE2, its role in mediating SARS-CoV-2 cellular entry, its interacting partners, and functions. It also highlights how SARS-CoV-2-mediated dysregulation of membrane-bound and circulating soluble ACE2 during infection plays an important role in the pathogenesis of COVID-19. We explore contemporary evidence for the dysregulation of ACE2 in populations that have emerged as most vulnerable to COVID-19 morbidity and mortality, including the elderly, men, and pregnant women, and draw attention to ACE2 dynamics and discrepancies across the mRNA, protein (membrane-bound and circulating), and activity levels. This review highlights the need for improved understanding of the basic biology of ACE2 in populations vulnerable to COVID-19 to best ensure their clinical management and the appropriate prescription of targeted therapeutics.

Key Words

- ▶ angiotensin-converting enzyme 2 (ACE2)
- ▶ COVID-19
- ▶ age
- ▶ sex
- ▶ pregnancy

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Introduction

Angiotensin-converting enzyme 2 (ACE2) is a critical regulator of cardiovascular, respiratory, renal, and gastrointestinal physiology and pathology, through its actions as part of the renin-angiotensin system (RAS) and kallikrein-kinin system, among others. The enzymatic activity of ACE2 is protective against cardiovascular and kidney diseases as well as acute respiratory distress

syndrome (Oudit *et al.* 2003, Kuba *et al.* 2010, 2013). ACE2 is also the receptor for several coronaviruses, including human coronavirus NL63 (HCoV-NL63), severe acute respiratory syndrome coronavirus (SARS-CoV), and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Li *et al.* 2003, Hoffmann *et al.* 2005, 2020b, Zhou *et al.* 2020a).

ACE2 can be found in most tissues and organs of the body, including the lung, cardiovascular system, gastrointestinal tract, renal system, brain and nervous system, liver, pancreas, gallbladder, as well as the male and female reproductive tracts (Donoghue *et al.* 2000, Tipnis *et al.* 2000, Komatsu *et al.* 2002, Hamming *et al.* 2004, Beyerstedt *et al.* 2021), thereby allowing coronaviruses to access a wide variety of tissues and organ systems. A novel short isoform of ACE2, delta ACE2 (dACE2), that is enriched in lung airway and bile duct epithelia in the liver has recently been identified; however, dACE2 lacks SARS-CoV-2 binding sites and is unlikely to directly contribute to host susceptibility to SARS-CoV-2 infection (Onabajo *et al.* 2020, Williams *et al.* 2021). A soluble form of ACE2, sACE2, can also be found in extracellular compartments and may serve as a biomarker of certain disease states, including hypertension and heart failure (Uri *et al.* 2014).

Importantly, binding of the SARS-CoV-2 spike protein to membrane-bound ACE2 reduces surface ACE2 expression, resulting in loss of the protective actions of ACE2. Thus, ACE2 is not only the SARS-CoV-2 receptor but might also play an important role in multiple aspects of coronavirus disease 2019 (COVID-19) pathogenesis and possibly post-COVID-19 syndromes. Furthermore, the relative levels of tissue ACE2 and sACE2 may be a factor in determining the susceptibility to certain COVID-19 pathologies.

In this narrative review we outline the current knowledge surrounding ACE2 as the receptor for SARS-CoV-2, its interacting partners, hormonal regulation, and functions, highlighting the importance of ACE2 dysregulation in the pathogenesis of COVID-19. We also discuss the plethora of evidence demonstrating that ACE2 drives COVID-19 age, sex, and pregnancy-associated vulnerabilities and the culminating need for greater understanding of ACE2 and its pathophysiological role. The objective of this narrative review was to explore changes in the expression and regulation of ACE2 that may drive vulnerability to COVID-19 morbidity. As such, we undertook a comprehensive broad-sweeping literature search through PubMed using key words including ACE2, hormones, sex (or gender), age, pregnancy, COVID-19, and SARS-CoV-2, which were distilled into the following narrative.

ACE2 as the entry receptor for coronaviruses

ACE2 serves as a viral receptor for the SARS-CoV (Li *et al.* 2003), HCoV-NL63 (Hofmann *et al.* 2005), and

SARS-CoV-2 (Hoffmann *et al.* 2020b, Zhou *et al.* 2020a). Both SARS-CoV and SARS-CoV-2 are structurally and genetically highly similar; both are enveloped single-stranded RNA viruses that carry a transmembrane spike protein on their surface. The binding of the spike protein to ACE2 on the host cell surface leads to viral entry into cells, a process that is required to establish infection (Hoffmann *et al.* 2020b). The spike protein (S) consists of an S1 region containing the receptor-binding domain (RBD), which binds ACE2, and an S2 region that promotes fusion of the viral membrane with the host cell (Walls *et al.* 2020). Membrane fusion between host cells and the infectious virus particles requires spike protein priming, which involves cleavage at the S1/S2 and the S2' site by proteases such as furin (Hoffmann *et al.* 2020a), transmembrane protease serine 2 (TMPRSS2), and cathepsin (Simmons *et al.* 2005, Matsuyama *et al.* 2010, Shulla *et al.* 2011, Glowacka *et al.* 2011, Hoffmann *et al.* 2020b, Shang *et al.* 2020, Peacock *et al.* 2021, Zhao *et al.* 2021, Jackson *et al.* 2022). Spike protein priming allows fusion of viral and cellular membranes, a process driven by the S2 subunit. Although the SARS-CoV-2 RBD binds to ACE2 with a greater affinity than the SARS-CoV RBD, the spike protein itself has an affinity similar to or less than SARS-CoV (Shang *et al.* 2020). The prefusion spike protein trimer fluctuates between the three RBD down (closed) conformations, which enhances its ability to evade immune defence mechanisms, and the one RBD up (open) conformation, which is required to bind to ACE2 (Fan *et al.* 2020, Walls *et al.* 2020). The importance of ACE2 and TMPRSS2 to viral entry has been demonstrated through gene knockout studies. Exposure of *Ace2* null mice to SARS-CoV infection results in lower infectivity and viral copy number in the lungs, and reduced pathological lung injury, compared to wild-type mice (Kuba *et al.* 2005). Similarly, mice lacking *TMPRSS2* show lower viral titre in the lungs, a weaker proinflammatory response, and less severe lung pathology following SARS-CoV infection, compared to wild-type animals (Iwata-Yoshikawa *et al.* 2019).

ACE2 is not only critical to initial viral infection through surface receptor binding but also to COVID-19 progression following changes in membrane-bound and sACE2 action and their interactome. SARS-CoV and SARS-CoV-2 affect ACE2 levels in two ways. SARS-CoV-2 binding to ACE2 causes endocytosis of ACE2 alongside viral particles into endosomes and induces shedding of the ACE2 ectodomain (Haga *et al.* 2008, Wang *et al.* 2008). ACE2 shedding of the catalytically active ectodomain is mediated by A disintegrin and metalloprotease 17

(ADAM17; also known as TACE (tumour necrosis factor alpha-converting enzyme)) both *in vitro* and *in vivo* (Lambert *et al.* 2005, Jia *et al.* 2009).

In mice, SARS-CoV infection reduces ACE2 protein in the lungs, following spike protein binding and subsequent downregulation of transmembrane ACE2, exposing them to severe lung injury through the pathological impacts of RAS deregulation (Kuba *et al.* 2005). Through gene knockout and recombinant protein rescue studies, downregulation of lung ACE2 following severe acute lung injury has been shown to drive lung disease pathogenesis, promoting oedema and impaired lung function (Imai *et al.* 2005). In turn, ACE2 cleavage from the cell surface by interacting enzymes (e.g. TMPRSS2) and shedding results in increased sACE2 in the plasma (Heurich *et al.* 2014, Kragstrup *et al.* 2021, Daniell *et al.* 2022) and saliva (Daniell *et al.* 2022) of patients with COVID-19. A recent study has shown that sACE2 activity in plasma remains elevated for at least 2–3 months after SARS-CoV-2 infection and is associated with disease severity (Patel *et al.* 2021), suggesting that there is prolonged shedding of ACE2 and potentially prolonged dysregulation of tissue RASs. There is a major gap in the literature surrounding ACE2 changes with long COVID (long COVID/long-hauler COVID/post-acute sequelae of SARS-CoV-2); inevitably, this will be a key research question in time, as more follow-up datasets of patients in recovery and post-recovery from COVID-19 become available to the scientific community. Given the multifaceted downregulation of ACE2 triggered by SARS-CoV-2 infection, ACE2 dysregulation has been proposed to play a central role in the pathogenesis of COVID-19 and in driving vulnerability to severe COVID-19 illness in at-risk populations, likely contributed to by knock-on effects for the ACE2 interactome.

ACE2 and the renin-angiotensin system

ACE2 was first discovered as an enzyme involved in the RAS. Two independent genomic screens led to the discovery, expression, and characterisation of human ACE2 just over 20 years ago (Donoghue *et al.* 2000, Tipnis *et al.* 2000). The predicted ACE2 protein sequence revealed characteristic features of a plasma membrane-bound zinc metallopeptidase with 41.8% similarity to the N-terminal catalytic domain of angiotensin-converting enzyme (ACE) (Donoghue *et al.* 2000, Tipnis *et al.* 2000, Turner & Hooper 2002). Like ACE, ACE2 is a single-span transmembrane protein with an extracellular facing N-terminal catalytic site available to hydrolyse circulating

vasoactive and other regulatory peptides. However, in contrast to ACE, ACE2 functions exclusively as a carboxypeptidase, removing a single C-terminal amino acid from angiotensin (Ang) II generating Ang-(1–7) or, much less efficiently, from Ang I forming Ang-(1–9) (Turner 2015) (Fig. 1).

Ang II is the major peptide of the Ang II type 1 receptor (AT₁R) axis of the RAS cascade. Ang II acting via the AT₁R is important in cardiovascular homeostasis but when unbalanced it can cause vasoconstriction, inflammation, oxidative stress, cell proliferation, hypertrophy, fibrosis, and tissue remodelling (Dasgupta & Zhang 2011). ACE2 metabolises and thus limits the abundance of Ang II. It converts Ang II into Ang-(1–7), which counterbalances the actions of Ang II via the Mas receptor (Fig. 1). Therefore, ACE2 protects against organ damage via two processes: (i) by metabolising Ang I and Ang II, so limiting substrate availability to the AT₁R axis, and (ii) by generating Ang-(1–7), which increases the activity of the Mas receptor axis and has protective roles that stimulate vasodilatation and antioxidant pathways and inhibit inflammation, fibrosis, and hypertrophy (Simões e Silva *et al.* 2013). Thus, dysregulation of ACE2, as seen in COVID-19 patients, results in loss of the protective actions of ACE2 in the RAS.

ACE2 and its other regulatory peptides

ACE2 has a diverse substrate specificity and hydrolyses several other regulatory peptides (Fig. 1). These include apelin peptides, des-Arg⁹-BK (but not bradykinin (BK) itself), neurotensin metabolites, dynorphin A (1–13), and ghrelin (Donoghue *et al.* 2000, Vickers *et al.* 2002). Whether the cleavage of neurotensin metabolites, dynorphin A (1–13), and ghrelin occurs *in vivo* remains unexplored; thus, the functions of these peptides will not be discussed.

Apelin is an inotropic and cardioprotective peptide. It acts on the apelin receptor (APJ) to regulate vascular homeostasis, angiogenesis, myocardial adaptation to stress, and fluid balance, thereby playing a key role in vascular diseases, such as systemic and pulmonary arterial hypertension, myocardial infarction, and heart failure (Pitkin *et al.* 2010, Wang *et al.* 2016b) (Fig. 1). Apelin is synthesised as a pre-pro-hormone, which is processed into a mature peptide, apelin-36, that is further proteolytically cleaved to apelin-13 and apelin-17 (Tatemoto *et al.* 1998, Lee *et al.* 2000, Lee *et al.* 2006, Pitkin *et al.* 2010). ACE2 hydrolyses apelin-13, apelin-17, and apelin-36 peptides with high catalytic efficiency

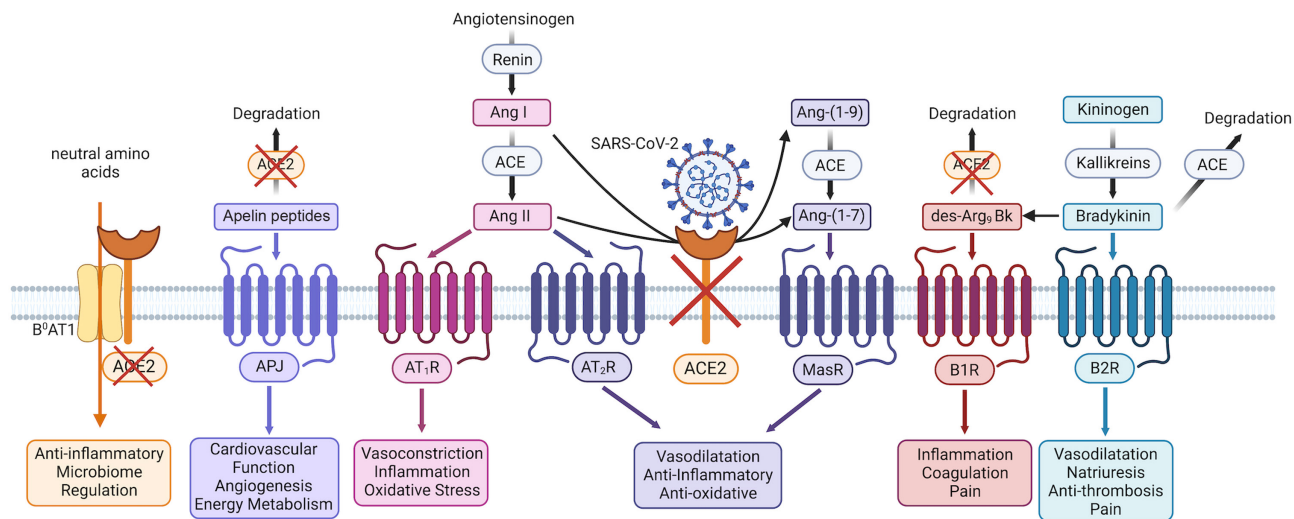


Figure 1

The impact of SARS-CoV-2 on the actions of ACE2 and its interacting partners. Upon entry into cells, SARS-CoV-2 infection causes internalisation and shedding of ACE2 from the cell membrane (indicated by the red crosses). This prevents the conversion of angiotensin (Ang) II to Ang-(1-7) by ACE2 and promotes the actions of Ang II via the angiotensin II type 1 receptor (AT₁R). SARS-CoV-2-mediated downregulation of ACE2 also prevents its degradation of both apelin peptides and des-Arg⁹-bradykinin (des-Arg⁹-BK), which acting via the bradykinin 1 receptor (B1R) causes inflammation, coagulation, and pain. Finally, loss of ACE2's actions in the intestine may cause diarrhoea, nausea, and vomiting, by promoting inflammation and altering the microbiome. Adapted from *American Journal of Pathology*, volume 191, Ramos SG, Cruz Rattis BA de, Ottaviani G, Nunes Celes MR, Dias EP, ACE2 down-regulation may act as a transient molecular disease causing RAAS dysregulation and tissue damage in the microcirculatory environment among COVID-19 patients, pages 1154-1164, 2021, with permission from Elsevier (Ramos *et al.* 2021). Created with BioRender.com. ACE2, angiotensin-converting enzyme 2; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

(Vickers *et al.* 2002, Wang *et al.* 2016b, Yang *et al.* 2017) (Fig. 1). Although an initial investigation suggested that cleavage of apelin-13 and -17 by ACE2 partially inactivates these peptides (Wang *et al.* 2016b), it was subsequently found that apelin-12, the product of apelin-13 cleavage by ACE2, retains biological activity both *in vitro* and *in vivo* (Yang *et al.* 2017). At present, it is unclear of the significance of the cleavage of apelin peptides by ACE2 for the pathogenesis of COVID-19. Apelin could be protective, as it inhibits pulmonary fibrosis in mice by activating ACE2 (Wang *et al.* 2022a). However, like ACE2, apelin is downregulated in SARS-CoV-2-infected cardiomyocytes and COVID-19 patients (Li *et al.* 2021b).

ACE2 also plays critical roles in the kinin-kallikrein system, which constitutes the inactive precursor kininogen, the proteolytic kallikrein enzymes, and effector peptides bradykinin and its active metabolite des-Arg⁹-BK (Schmaier 2002, Marceau *et al.* 2020). Bradykinin can be degraded by ACE (Ahmad *et al.* 2006), whereas ACE2 hydrolyses des-Arg⁹-BK, generating biologically inactive breakdown products (Vickers *et al.* 2002, Sodhi *et al.* 2018) (Fig. 1). Bradykinin and des-Arg⁹-BK act on their target organs via two pharmacologically distinct G protein-coupled receptors: the B1 receptor (B1R), whose main agonist is des-Arg⁹-BK; and the B2 receptor (B2R), whose ligand is bradykinin

(Manning & Snyder 1989, Mantione & Rodriguez 1990, Rhaleb *et al.* 2011). Bradykinin is a potent endothelium-dependent vasodilator that possesses vasorelaxant and natriuretic activity (Hornig & Drexler 1997). Bradykinin is also part of the inflammatory response after injury and acts to induce pain (Dray & Perkins 1993), neutrophil recruitment, and vascular permeability (Araujo *et al.* 2001, Stuardo *et al.* 2004, Choi & Hwang 2018). The B2R is constitutively expressed and is involved in the acute phase of inflammatory and pain responses, whereas the B1R is markedly upregulated during inflammation and tissue injury and is involved in the chronic phase of the inflammatory response (Dray 1997). Activation of B1R by des-Arg⁹-BK can stimulate inflammation by modulating leukocyte migration, microglial activation, and cytokine production (Sriramula 2020). Thus, by degrading des-Arg⁹-BK, ACE2 prevents this immune response (Fig. 1). Attenuation of ACE2 activity has been shown to impair des-Arg⁹-BK inactivation and thus to enhance B1R signalling in the lung (Sodhi *et al.* 2018). This could be a possible mechanism by which SARS-CoV-2, via downregulation of ACE2, could promote chronic inflammation in the lung.

ACE2 also regulates aspects of amino acid transport (Fig. 1) as its carboxy-terminal domain shows 48% sequence identity with collectrin (Zhang *et al.*

2001). Collectrin regulates B₀AT1 neutral amino acid transporters in the kidney (Danilczyk *et al.* 2006, Malakauskas *et al.* 2007) and pancreatic insulin secretion (Fukui *et al.* 2005). Conversely, ACE2 binds to the B₀AT1 amino acid transporters in the intestine but not kidney (Kowalczyk *et al.* 2008, Camargo *et al.* 2009) and has been implicated in the pathology of Hartnup's disease, a disorder of amino acid homeostasis. Through this process, ACE2 also appears to regulate intestinal inflammation and diarrhoea, hence modulating the gut microbiome (Hashimoto *et al.* 2012). In patients with COVID-19, dysregulation of ACE2 and thus amino acid transport in the gastrointestinal tract may therefore contribute to the diarrhoea, nausea, and vomiting seen in some cases (Mao *et al.* 2020).

ACE2 and ageing

Changes in ACE2 expression with age

Even prior to the COVID-19 pandemic, age-associated changes in ACE2 expression were described in developing rodents. In CD1 mice, Song *et al.* (2012) reported *Ace2* expression in the lung was lowest in the embryo, increasing into early postnatal life and peaking in adulthood (2 months) (Song *et al.* 2012). Alternatively, Inde *et al.* (2021) showed a biphasic age-driven distribution of *Ace2* in murine lungs and trachea across three different gene expression datasets (Inde *et al.* 2021). First, there was a subtle biphasic distribution in two of the three datasets where lung and tracheal *Ace2* expression was lowest in adolescence (<day (d) 15), with ascending expression in the lung from late adolescence through to middle age (Inde *et al.* 2021). In contrast, there was a distinct biphasic distribution of lung *Ace2* in the third dataset encompassing d0–30, where peak *Ace2* mRNA levels were observed at d1 post-partum compared to lower expression in prenatal and d10 postnatal mice, increasing towards late adolescence (d30). Irrespective of the dataset, *Ace2* expression is low in murine lung homogenates (Inde *et al.* 2021), which likely contributes to the enhanced variability seen across individuals and datasets.

In contrast to mRNA observations, at the protein level ACE2 was lower in lung homogenates of adult CD1 mice compared with postnatal and embryonic tissue (Song *et al.* 2012). Similarly, in Sprague–Dawley rats, ACE2 was lowest in lung homogenates of elderly rats (24 months) compared to middle-aged (12-month-old) and young adult (3-month-old) rats, irrespective of gender

(Xudong *et al.* 2006). However, Inde and colleagues (2021) demonstrated, by immunofluorescent staining of ACE2 protein, that ACE2 abundance slightly increased immediately after birth, dipped at postnatal d7, and rose into adulthood (3 months) (Inde *et al.* 2021). In contrast, Bengs *et al.* (2021) observed no significant change in lung ACE2 immunoreactivity in FVB/N mice with age (4, 12, and 20–22 months), irrespective of gender (Bengs *et al.* 2021), albeit the spread of immunoreactivity was highly variable across samples.

ACE2 activity was also variable across age, markedly peaking at embryonic d14.5 followed by a second peak at d10 post-partum in CD1 mice (Song *et al.* 2012). Circulating sACE2, however, was lowest in adult mice compared to young postnatal CD1 mice (Song *et al.* 2012). These rodent studies are summarised in Fig. 2 and highlight that ACE2 dynamics with ageing heavily depend on the transcriptional, translational, activity, and soluble read-outs of ACE2. Further to this, significant variability exists between studies and may reflect the differences in study design, including ages of tissue collection, species, and strain. Great care should thus be taken in interpreting contrasting literature demonstrating ACE2 abundance in SARS-CoV-2 patients across risk groups.

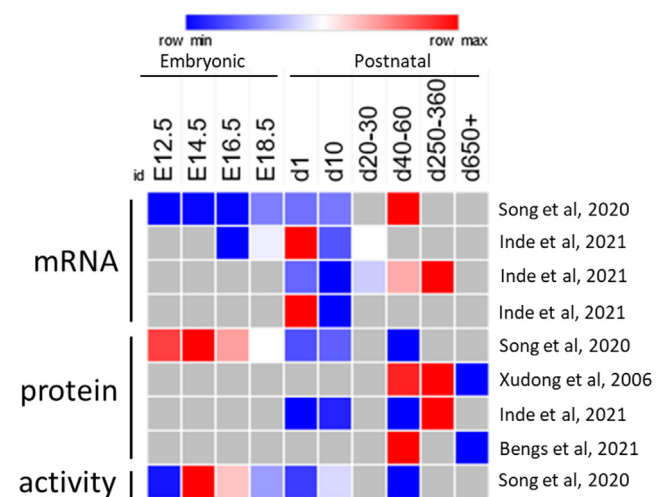


Figure 2

Longitudinal age impact on ACE2 mRNA, protein, and activity in the lungs of rodents. ACE2 mRNA, protein, and activity levels were collated from available rodent studies demonstrating changes with embryonic (embryonic day (E)) and postnatal age (days, d). Morpheus (Broad Institute, <https://software.broadinstitute.org/morpheus>) and approximate mean ACE2 levels in the lungs were used to construct a longitudinal heat map over age, normalised by row. Data were distilled from Song *et al.* (mouse lung), Inde *et al.* (multiple datasets of mouse lung), Xudong *et al.* (rat lung), and Bengs *et al.* (mouse lung) (Xudong *et al.* 2006, Song *et al.* 2020, Bengs *et al.* 2021, Inde *et al.* 2021).

Consistent with observations in rodents, adult humans have shown significantly greater *ACE2* expression in nasal and respiratory tissue biopsies than children (Saheb Sharif-Askari *et al.* 2020). *ACE2* mRNA levels were reported to be at their lowest in the nasal epithelium of children <10 years of age, and increased into adulthood (Bunyavanich *et al.* 2020). Leveraging single cell (sc) RNAseq, the percentage of cells expressing *ACE2* transcript was greatest in lung alveolar type 2 (AT2) cells, and a higher proportion of positive cells were observed in adult samples, compared to paediatric lungs (Wang *et al.* 2020). Likewise, aggregated scRNAseq and single nucleus (sn) RNAseq of 1,320,896 cells from human nasal, airway, and lung samples from 228 individuals demonstrated increased *ACE2* expression with age in the AT2 and multi-ciliated cells of the airway (Muus *et al.* 2021). Similarly, in human airway epithelium, *ACE2* mRNA expression increased with increasing age; this increase was also observed at both the mRNA and protein levels in endobronchial biopsies (Wark *et al.* 2021). In human samples from autopsies spanning from the fetus (28 weeks' gestation) to early adulthood (28 years), *ACE2* immunostaining increased in the lung with age, plateauing from 5 years of age onwards (Schurink *et al.* 2022). Using lung tissue microarrays immunofluorescently stained for *ACE2*, Inde and colleagues (2021) also demonstrated a rise in the percentage of *ACE2*-positive nucleated cells in adults aged ≥ 40 years, compared to children, adolescents, and young adults (Inde *et al.* 2021). However, in a handful of studies, no age-associated changes in *ACE2* were observed (Barker & Parkkila 2020, Lee *et al.* 2020, Li *et al.* 2020b, Maremanda *et al.* 2020). Furthermore, in one study, children under 10 years of age exhibited greater *ACE2* protein levels than adults (Ortiz *et al.* 2020). The reviewed studies highlight fundamental contradictions across multiple studies, which may be influenced by low sample size and thus power in some studies, but a more profound driver of these conflicting results is the inherent heterogeneity of *ACE2* expression between individuals, and between cell and tissue types within individuals (Inde *et al.* 2021). The diversity of *ACE2* through the human respiratory tract was highlighted by Ortiz *et al.* (2020), whereby *ACE2* was sparse on the surface epithelium of the upper respiratory tract (trachea, bronchi – 12% and 27% of donors, respectively) but more abundant in the distal lung (bronchiolar, alveolar – 36% and 59% of donors) (Ortiz *et al.* 2020). By scRNAseq, alveolar *ACE2* was also heterogeneous across cell types and donors, where 50% of subjects possessed

low *ACE2* transcript in AT2 cells, while the remainder had high *ACE2* (Ortiz *et al.* 2020).

ACE2 abundance in the circulation has also been stratified by age in a handful of studies. A weak curvilinear association of s*ACE2* abundance was observed across age with a positive association in participants below 55 years old and a negative association in those above 55 years (AlGhatrif *et al.* 2021). In healthy human subjects, serum *ACE2* was markedly higher in infants (<1 year of age) compared to levels in children (6–10 years), teens (11–15 years), and adults (Gu *et al.* 2021). In stark contrast, *ACE2* protein was reported to be significantly more abundant in healthy adults than in infants and toddlers (Pavel *et al.* 2021). Similarly, s*ACE2* abundance across five longitudinal youth aging assessment points ranging from age ~9.9 years to ~23.5 years showed low s*ACE2* levels up to age 12 years, with adolescence inducing an increase in s*ACE2* in young men but not women (Sward *et al.* 2020). In a genome-wide association meta-analysis of 28,000 individuals, however, plasma *ACE2* levels were not significantly associated with age (Yang *et al.* 2022b). In contrast to s*ACE2* abundance, even fewer studies have examined s*ACE2* activity with aging. In one study, patients hospitalised for COVID-19 demonstrated that the activity of serum *ACE2* was higher with increasing age, irrespective of disease severity (Fagyas *et al.* 2022). However, when relationships were assessed separately in each disease severity group, no correlation between circulating *ACE2* activity and age was detected (Fagyas *et al.* 2022). Like that observed for membrane-bound *ACE2*, it should be noted that s*ACE2* levels exhibit a high degree of heterogeneity across human subjects.

Influence of age on the susceptibility to COVID-19

Since the pandemic start, age has been considered a major independent risk factor associated with intensive care unit (ICU) admission and mortality, with the aging population exhibiting more severe COVID-19, especially in contrast to children and youths. Children have consistently been reported as most protected from COVID-19 infection and severe illness and mortality (Wu & McGoogan 2020, Milani *et al.* 2021, Martin *et al.* 2022). Early in the pandemic, across Mainland China, increased disease severity resulting in ICU admission, mechanical ventilation, or death was mostly reported in patients >50 years of age, accounting for 81.5% of cases, in comparison to infants and children (0–15 years), in whom there was zero incidence (Guan *et al.* 2020). In Italy,

99.1% of mortality cases were in patients >50 years of age, while the aging population was considered a key contributor to the higher mortality rates observed in Italy at the pandemic onset (Onder *et al.* 2020). Across France, of 16,386 SARS-CoV-2 recorded deaths, 81.6% were in patients >70 years old (Raparelli *et al.* 2020). Individuals >70 years of age also contributed to 50% of a total 95,120 hospitalisations, and mathematical modelling predicted an infection fatality ratio of 0.001% in those <20 years of age, compared to 8.3% in those aged >80 years (Raparelli *et al.* 2020). In the UK, increasing age was a strong predictor of mortality across a hospital cohort of 20,133 COVID-19 patients after adjusting for major comorbidities (reference age <50 years; 50–59, 60–69, 70–79, ≥80 years; hazard ratios 2.63, 4.99, 8.51, 11.09 respectively) (Docherty *et al.* 2020). Furthermore, a comprehensive study of US adults hospitalised with COVID-19 ($n=2491$; 154 acute care hospitals, 74 counties, 13 states) showed that adults with the greatest risk of ICU admission included patients aged 50–64, 65–74, 75–84, and >85 years vs 18–39 years (adjusted risk ratio (aRR) 1.53, 1.65, 1.84, and 1.43 respectively) and those at increased risk of mortality were aged 50–64, 65–74, 75–84, and ≥85 years vs 18–39 years (aRR 3.11, 5.77, 7.67, and 10.98, respectively) (Kim *et al.* 2020). The increased vulnerability of the aged population remains evident in today's latest COVID-19 mortality statistics depicted for the United States (CDC 2022) in Fig. 3. This increased risk in aged populations is stark

COVID-19 Weekly Deaths in the US by Age Group

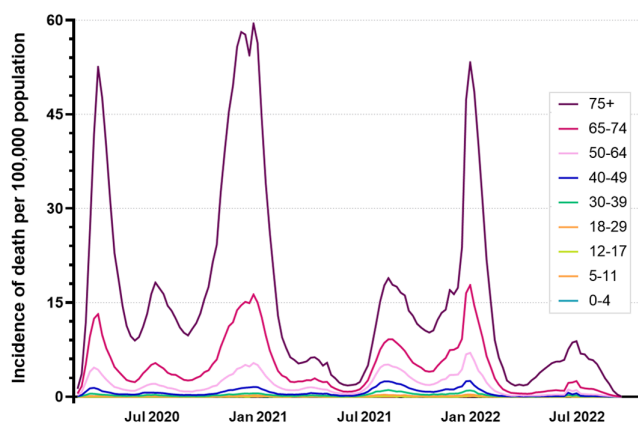


Figure 3

Population statistics for the United States showing the influence of age on SARS-CoV-2 mortality across the COVID-19 pandemic to date. Graph represents COVID-19 incident deaths per 100,000 of the population across the pandemic to date (1 March 2020 to 24 Sept 2022), stratified by age 0–4, 5–11, 12–17, 18–29, 30–39, 40–49, 50–64, 65–74, and 74+ years. Analysed from data obtained from the US Centers for Disease Control and Prevention COVID Data Tracker (CDC 2022).

compared with the low risk in children and infants whom typically contract mild disease (Göttinger *et al.* 2020) and as a population have experienced deaths from COVID-19 at a low 0.48% of the estimated total mortality from all causes in a normal year (Bhopal *et al.* 2021).

Inherent differences in ACE2 abundance with age may in part underlie the increased morbidity and mortality observed in older patients with COVID-19. In mice, exposing aged animals to three spike proteins representing different SARS-CoV strains resulted in increased viral titre in the lungs post infection, compared to young mice (Rockx *et al.* 2009). In lung epithelial cells, SARS-CoV infection reduced ACE2 expression 24- and 48-h post infection (Saheb Sharif-Askari *et al.* 2020). Furthermore, in aged mice, ACE2 mRNA was downregulated up to five-fold 48-h post SARS-CoV infection (Rockx *et al.* 2009). In rhesus macaques, SARS-CoV-2 infection reduced the frequency and density of ACE2-positive cells in both young and old lungs by ~30–50% (Zheng *et al.* 2021). However, in aged but not young macaques, this coincided with increased expression of cellular mediators of apoptosis and autophagy, increased inflammatory marker infiltration, and more severe lung lesions (Zheng *et al.* 2021). ACE2 clearly plays a pivotal role in the susceptibility and vulnerability of the aged population to coronavirus infection; however, a greater understanding of its dynamics across infection is needed, especially in considering ACE2 modulation as a therapeutic target.

While age has been determined to be an independent predictor of poor outcome from SARS-CoV-2 infection, the risk of severe COVID-19 outcomes is increased in those with certain underlying health conditions and especially in those over 65 years of age. Across 1100 studies, it was found that having at least one comorbidity, including hypertension, heart disease, obesity, type 2 diabetes mellitus, chronic lung disease, or cancer, resulted in significantly worse outcomes in COVID-19 hospitalised patients (Mason *et al.* 2021). In fact, in one study, the risk of COVID-19-related death associated with at least one age-related comorbidity combined was 1113 times greater compared to that with no comorbidity (Antos *et al.* 2021). The top four comorbidities observed included hypertension, diabetes, cardiovascular disease, and chronic kidney disease (OR 34.73, $P=0.002$; OR 20.16; $P < 0.00001$; OR 18.91, $P=0.002$; OR 12.34, $P < 0.00001$, respectively) (Antos *et al.* 2021). Circulating ACE2 levels have been shown, even prior to the COVID-19 pandemic, to be dysregulated in patients with these disease states (Uri *et al.* 2016, Chirinos *et al.* 2020,

Emilsson *et al.* 2021, Arefin *et al.* 2022). Thus, the age-related risks associated with COVID-19 susceptibility and outcomes are likely to be due, at least in part, to the increased number of underlying health conditions in the ageing population as well as changes in ACE2 levels.

Like the age disparity in COVID-19 severity, the gender disparity has shone the spotlight on ACE2 expression and its underlying contribution to severe disease.

ACE2 and biological sex

Changes in ACE2 expression with sex

Localisation of the *Ace2* gene on the X-chromosome (Komatsu *et al.* 2002) has led to speculation for potential X-driven gene dosing and heterozygosity across *ACE2* copies. This may offer SARS-CoV-2 protection in females, but not males, which, in addition to the X-chromosome featuring many immune function-associated genes, has compounded theories of females having greater immunological advantage than males (Wang *et al.* 2016a, Gemmati *et al.* 2020). While further research into the genomic impacts of gender-based copy number variations and X-inactivation is required to improve our understanding of ACE2 in human COVID-19 pathophysiology, in mice, renal ACE2 activity was shown to be greater in male kidneys than in female kidneys, with no significant link to X-chromosome gene dosage (Liu *et al.* 2010).

Studies assessing the effect of biological sex, referred to herein as sex, in the rodent respiratory tract have shown a degree of sexual dimorphism across studies

(summarised in Table 1). In C57BL6/J mice, females exhibited significantly greater *Ace2* mRNA expression in the lung and oesophagus, and tended to have increased *Ace2* mRNA levels in the trachea, compared to males (Sarver & Wong 2021). Similarly, lung *Ace2* expression was higher in females than males in adult C57BL/6J mice (12 months) but not in young (3-month-old) or aged (18-month-old) mice (Viveiros *et al.* 2022), and in contrast, lung ACE2 protein levels and activity were lower in aged females than males, but again unchanged in young or adult mice. In contrast, *Ace2* mRNA abundance was lower in the mouse airway of females than in males, and concordant results were observed for ACE2 protein (Baratchian *et al.* 2021). While in Sprague-Dawley rats, lung ACE2 protein levels were unchanged by sex in young adult (3-month-old) and middle-aged (12-month-old) rats, in aged females (24 months) the levels were greater than that in males (Xudong *et al.* 2006). ACE2 levels were also unchanged with sex in the lungs and serum (sACE2) of FVB/N mice (Bengs *et al.* 2021), and in the lung (mRNA, protein, and activity) and serum of Wistar rats (Martins *et al.* 2021).

Studies in humans have also reported conflicting findings with regard to sex differences in lung ACE2 levels (Table 1). In humans, *ACE2* transcript expression is increased in lung epithelial cells (Song *et al.* 2020) and lower airway (endobronchial) tissue (Wark *et al.* 2021) of males compared to females; however, other gene expression repositories including the The Genotype-Tissue Expression (Barker & Parkkila 2020, Li *et al.* 2020b) and The Cancer Genome Atlas (Li *et al.* 2020b) showed no difference in lung *ACE2* expression with sex. Likewise, across the nasal cilia, large airway bronchioles,

Table 1 Number of rodent and human studies that report a sex difference in ACE2 mRNA and protein/activity in lung tissue.

	mRNA			Protein/activity		
	1	2	1	3	0	2
Mice	(Viveiros <i>et al.</i> 2022 ^{df}) ^a	(Sarver & Wong 2021, Viveiros <i>et al.</i> 2022 ^e) ^b	(Baratchian <i>et al.</i> 2021) ^c	(Baratchian <i>et al.</i> 2021, Bengs <i>et al.</i> 2021, Viveiros <i>et al.</i> 2022 ^{de}) ^a		(Baratchian <i>et al.</i> 2021, Viveiros <i>et al.</i> 2022 ^f) ^c
Rats	(Martins <i>et al.</i> 2021) ^a	0	0	(Xudong <i>et al.</i> 2006 ^{de} , Martins <i>et al.</i> 2021) ^a	(Xudong <i>et al.</i> 2006 ^f) ^b	0
Humans	(Barker & Parkkila 2020, Camiolo <i>et al.</i> 2020, Lee <i>et al.</i> 2020, Li <i>et al.</i> 2020b, Zhang <i>et al.</i> 2020, Baratchian <i>et al.</i> 2021) ^a	0	(Song <i>et al.</i> 2020, Wark <i>et al.</i> 2021) ^c	(Li <i>et al.</i> 2021a) ^a	0	(Kalidhini <i>et al.</i> 2020, Xie <i>et al.</i> 2023) ^c

^aDepicted are studies that report no sex difference, ^bhigher expression/activity in females, or ^chigher expression/activity in males.

^dYoung (3 months); ^eadult (12 months); ^faged (18–24 months).

and small airway epithelium and lung parenchyma (Camiolo *et al.* 2020, Lee *et al.* 2020, Zhang *et al.* 2020, Baratchian *et al.* 2021), as well as 22 individual human tissues, *ACE2* mRNA abundance remained unchanged with sex (Li *et al.* 2020b). At the protein level, human males have been reported to have an increase in the mean intensity of *ACE2* staining in lung tissue compared to females (Xie *et al.* 2023). Furthermore, baseline *ACE2* protein abundance in airway smooth muscle cells is greater in males (Kalidhindi *et al.* 2020), but similar in the human airway epithelium, than in females (Li *et al.* 2021a).

With regard to levels of soluble *ACE2* in the circulation, studies in rodents and human are conflicting. s*ACE2* levels are reportedly the same in the serum of male and female FVB/N mice (Bengs *et al.* 2021) and Wistar rats (Martins *et al.* 2021). In contrast, human studies consistently report that males have greater plasma levels of *ACE2* than females (Zhou *et al.* 2020b, Kuznetsova & Cauwenberghs 2021, Xie *et al.* 2023).

Influence of sex hormones on *ACE2* expression

Despite unclear baseline differences in *ACE2* levels between sexes within different species, what is more well defined is that *ACE2* is exquisitely regulated by sex hormones. Exposure of cultured primary differentiated airway smooth muscle cells to female sex hormone 17-beta-oestradiol tended to reduce *ACE2* protein levels in cells of both male and female origin. Similarly 17-beta-oestradiol reduced *ACE2* mRNA abundance in

differentiated primary bronchial epithelial cells (Stelzig *et al.* 2020) (Fig. 4). In contrast, oestrogen has been shown to upregulate *ACE2* in the kidney (Ji *et al.* 2008), adipose tissue (Gupte *et al.* 2012), and heart (Bukowska *et al.* 2017). Treatment of atrial myocardium from elderly men with oestrogen reduced *ACE* mRNA expression and increased the expression of *ACE2* and *MAS* (Bukowska *et al.* 2017). Treatment with an oestrogen receptor alpha (ER α) antagonist reversed this effect (Bukowska *et al.* 2017). A subsequent report has suggested that oestrogen, primarily through its receptors ER α and G protein-coupled oestrogen receptor, affects cardiac *ACE2* levels and activity by regulating *ACE2* shedding via ADAM-17 and TMPRSS2 (Wang *et al.* 2021). Similarly, exposure of endothelial cells to oestradiol significantly increased *ACE* and *ACE2* mRNA expression, *ACE* protein levels, and both *ACE* and *ACE2* enzyme activities, resulting in increased Ang-(1-7) levels (Mompeon *et al.* 2016). It was concluded that these effects were mediated through ER α activation, since ER antagonists completely abolished the effect of oestradiol.

In contrast, exposure to the male sex steroid, testosterone, elevated *ACE2* protein levels in airway smooth muscle cells, irrespective of sex (Kalidhindi *et al.* 2020). Given that *ACE2* is an established direct transcriptional target of androgen receptor (AR) signalling and is repressed in response to AR knockdown, the highly androgen-responsive nature of *ACE2* could contribute to the sex disparity observed in COVID-19 severity between men and women (Samuel *et al.* 2020) (Fig. 4). The AR antagonist enzalutamide modestly

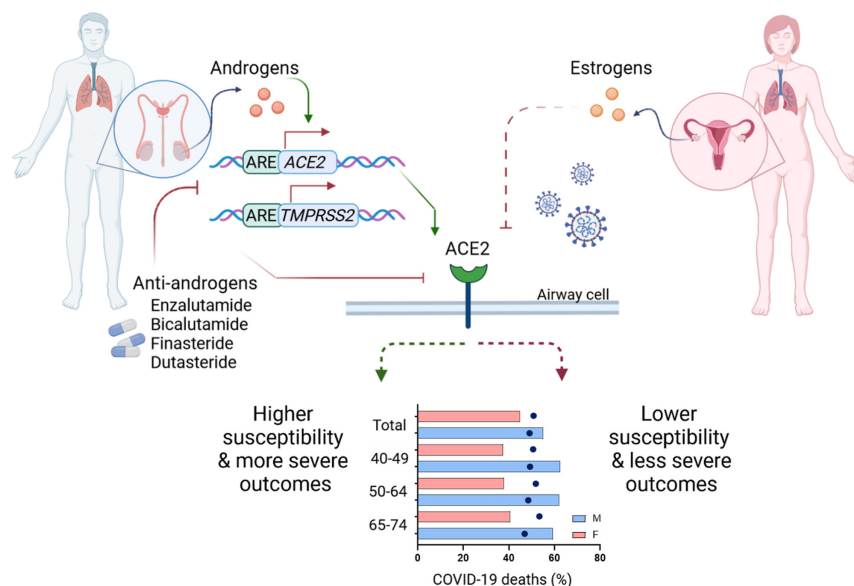


Figure 4

ACE2 – the link between divergent COVID-19 outcomes and sex? Men are more susceptible to SARS-CoV-2 infection, experience more severe disease and are at higher risk of dying from COVID-19. Androgens are described to drive *ACE2* and *TMPRSS2* transcription via an androgen response element in their gene promoter regions, and conversely anti-androgen drugs inhibit *ACE2*. On the other hand, oestrogens have been shown to inhibit *ACE2*. *ACE2* deregulation could be driving the more severe disease observed in men. We highlight the latest US statistics, where more men than women have died from COVID-19, especially when stratified by age, over 40 years old (percentage deaths, compared to '●' the percentage of the US population). Analysed from data obtained from the US Centers for Disease Control and Prevention COVID Data Tracker (CDC 2022). Created with BioRender.com. *ACE2*, angiotensin-converting enzyme 2; COVID-19, coronavirus disease 2019; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

decreased ACE2 levels in males to those similar to that seen in females in the murine lung (Baratchian *et al.* 2021). A study interrogating the role of AR signalling in ACE2 regulation and SARS-CoV-2 infectivity demonstrated that anti-androgens finasteride and dutasteride, which inhibit the conversion of testosterone to potent dihydrotestosterone (DHT), markedly reduced ACE2 immunofluorescence in cardiac cells derived from embryonic stem cells (Samuel *et al.* 2020). On the other hand, dutasteride reduced SARS-CoV-2 virus internalisation in human primary alveolar epithelial cells and anti-androgens reduced ACE2 expression and virus infection of lung epithelial cell-enriched organoids established from differentiated embryonic stem cells (Samuel *et al.* 2020). The interplay between ACE2 and cleavage enzyme TMPRSS2 is also of critical importance in this equation. TMPRSS2, first identified in the prostate, is a long established androgen-regulated protease that is strongly upregulated by androgens and repressed by anti-androgens, exhibiting an androgen response element in its promoter (Lin *et al.* 1999, Afar *et al.* 2001, Wang *et al.* 2007, Leach *et al.* 2021) (Fig. 4). In the lung, TMPRSS2 protein is robustly expressed and by scRNAseq *TMPRSS2* mRNA has been shown to co-localise with the *AR* broadly across lung cell types (Stopsack *et al.* 2020, Leach *et al.* 2021). The androgenicity of TMPRSS2 has prompted suggestion that TMPRSS2 could partly explain the poor outcomes in SARS-CoV-2-infected men. However, baseline *TMPRSS2* mRNA and protein are highly variable between sexes in the human and rodent lung (Stopsack *et al.* 2020). Similarly, in murine lung alveoli and bronchioli, sex did not impact TMPRSS2 protein abundance, while gonadectomy and subsequent hormone replacement had no impact on TMPRSS2 levels in males or females (Bengs *et al.* 2021). These results have been concurred in further studies demonstrating that AR antagonist enzalutamide had no impact on TMPRSS2 in the murine airway (Baratchian *et al.* 2021). In opposition, however, Leach *et al.* (2021) showed significantly higher lung *TMPRSS2* mRNA abundance in human males compared to females, marked *TMPRSS2* upregulation upon DHT exposure, and repression by enzalutamide in human lung A549 and H1944 cells. In contrast, BEAS-2B cells lacked androgen responsiveness (Leach *et al.* 2021). Surgical castration of male mice and enzalutamide treatment also suppressed *TMPRSS2* expression in murine lungs (Leach *et al.* 2021). Like ACE2, TMPRSS2 abundance and its regulation are clearly heterogeneous across studies, and further work is required to elucidate its physiological role across sexes.

Irrespective of the unclear baseline landscape between the sexes, patients with acute respiratory infections exhibit increased ACE2 expression in the (naso)pharynx with SARS-CoV-2, positively correlating with increased viral load (Cai *et al.* 2021). Furthermore, ACE2 protein levels are increased by >two-fold in the lungs of COVID-19 patients compared with non-COVID-19 controls, and positively correlated with inflammatory and coagulation markers CD61 and CD163 (Gheware *et al.* 2022).

Influence of biological sex on the susceptibility to COVID-19

Although several studies report changes in ACE2 abundance across tissues at baseline, with respiratory challenge, and under sex hormone-driven conditions, they also highlight the variability of ACE2 at the mRNA, protein, activity, and circulating levels across studies. Thus, drawing conclusions around the fundamental role of ACE2 in driving health outcomes in vulnerable populations is difficult.

Although country-specific nuances in pandemic response, COVID-19 reporting, and the capture of COVID-19-related deaths have resulted in inherent differences in disease statistics across countries, it quickly became apparent that being male is associated with increased risk of death from COVID-19 (Williamson *et al.* 2020). Through multiple independent studies across the globe, concurred by today's latest disease statistics (Fig. 4) (CDC 2022), men have consistently been identified as most vulnerable to increased disease severity and mortality from COVID-19. An analysis of the characteristics of 1096 SARS-CoV-2 patients hospitalised across 552 sites in Mainland China demonstrated that men were more likely to die from COVID-19 (67.2%), be admitted to hospital (58.1%), and experience more severe disease (57.8%) (Guan *et al.* 2020). Likewise, a retrospective analysis of mortality in Italy in 3517 SARS-CoV-2-positive patients captured a robust sex disparity, with men representing 66.7% of deaths (Raparelli *et al.* 2020). In the UK, a prospective observational study of 20,133 hospital in-patients with COVID-19 revealed that men often entered acute hospital care for COVID-19 (60%), while being female was associated with significantly lower risk of death (Docherty *et al.* 2020). In Australia, despite a starkly different strategic response to pandemic management (Rang *et al.* 2020), longitudinal data have demonstrated an increased incidence of COVID-19-related death in men (56.3%) and a particular prominence of male deaths in the 60–69-year-of-age and

70–79-year-of-age groups (65.1% and 65.1%, respectively), despite no increased incidence of infection (49% and 52.1%, respectively) (CADHAC 2022). The increased vulnerability of men to more severe COVID-19, resulting in higher ICU admissions and death, has been echoed in many other studies internationally (Chen *et al.* 2020b, Grasselli *et al.* 2020, Li *et al.* 2020a, Nikpouraghdam *et al.* 2020, Salje *et al.* 2020, Yanez *et al.* 2020, Dalal *et al.* 2021, Lewnard *et al.* 2022).

While sociodemographic research has demonstrated a clear gender disparity in social attributes surrounding risk perception and behaviour, which could act as potential drivers of COVID-19 severity (Alsan *et al.* 2020, Galasso *et al.* 2020), the biological sex differences and underlying hormonal, immunological, and genetic mechanisms driving disparities in disease severity have been a hot topic of research enquiry. Naturally, the sex-linked differences in the expression and hormonal regulation of SARS-CoV-2 viral entry factors have been highlighted. This has not only stemmed from the greater mortality in males but the reported partial protection from SARS-CoV-2 infection of men with prostate cancer receiving androgen deprivation therapy (ADT) (Montopoli *et al.* 2020). In a population-based study of 68 hospitals in Veneto, Italy ($n=4532$ males), men undergoing ADT for prostate cancer had >four-fold decreased risk of SARS-CoV-2 infection than patients not receiving ADT (OR: 4.05), and compared with patients suffering from other cancers (OR: 4.86) (Montopoli *et al.* 2020). This was supported *in vitro* whereby targeting androgen signalling in SARS-CoV-2-infected human lung cells dampened SARS-CoV-2 cellular entry and subsequent infection, using two drugs that block the androgen axis, bicalutamide, an gonadotropin-releasing hormone agonist, and enzalutamide (Leach *et al.* 2021). The exact factors driving this putative sex hormone-mediated response (be it androgens or oestrogen) remain controversial, while a further physiological state with altered sex hormone milieu that also shows changes with COVID-19 susceptibility and severity is pregnancy.

ACE2 and pregnant women

Changes in ACE2 levels during pregnancy

In the maternal circulation of healthy pregnant women, sACE2 levels and activity are increased compared with non-pregnant women and remain high throughout gestation (Tamanna *et al.* 2020). This may be driven by the high levels of oestrogen and progesterone from early

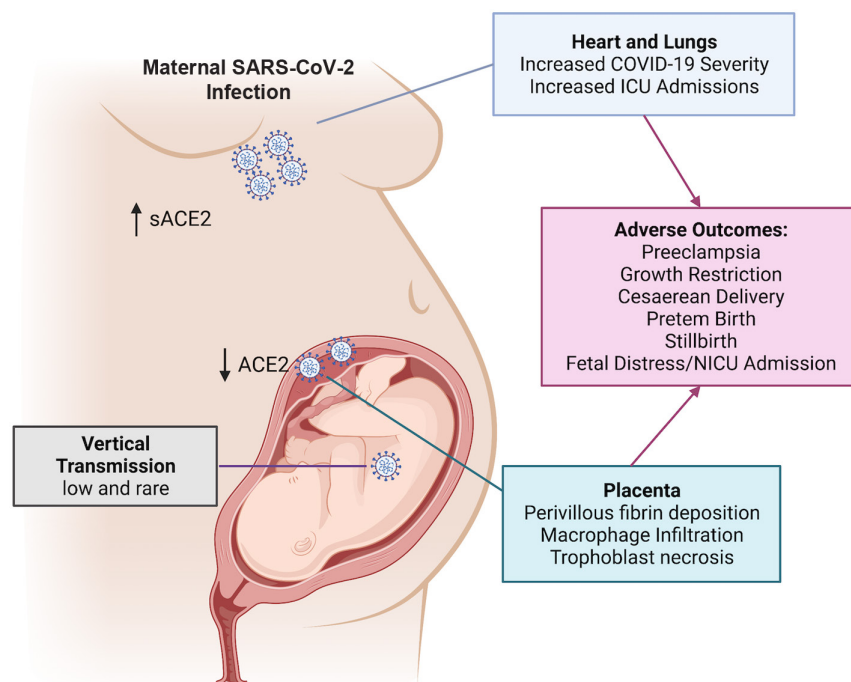
in gestation (Schock *et al.* 2016), which could regulate ACE2 levels. Ang-(1–7) levels are also increased in pregnant compared with non-pregnant women (Merrill *et al.* 2002, Tamanna *et al.* 2020) and could counterbalance the high levels of Ang II (Merrill *et al.* 2002) and its vascular actions. Furthermore, Ang-(1–7) levels are positively correlated with sACE2 levels and activity (Tamanna *et al.* 2020), suggesting that the amount and activity of sACE2 in the circulation are rate-limiting in terms of the production of Ang-(1–7).

Locally in intrauterine tissues, the human endometrium (both non-pregnant and pregnant) and placenta express ACE2 (Marques *et al.* 2011, Pringle *et al.* 2011, Wang *et al.* 2015, Delforce *et al.* 2017), and in mice, uterine ACE2 expression has been shown to be stimulated by progesterone (Chadchan *et al.* 2021). In the human placenta, immunohistochemical analysis has shown that ACE2 and Ang-(1–7) are expressed in cytotrophoblasts, syncytiotrophoblasts, and invading and intravascular trophoblasts (Valdes *et al.* 2006, Marques *et al.* 2011). The expression of ACE2 in the syncytiotrophoblast, which is in direct contact with maternal blood, means that placental ACE2 can be accessed by SARS-CoV-2 and affect the balance between Ang II and Ang-(1–7) both locally and in the maternal circulation. In this way, placental ACE2 could play a role in regulating maternal inflammation and vascular tone as well as protecting the placenta through the anti-oxidant and anti-inflammatory properties of the Ang-(1–7)Mas axis (Tamanna *et al.* 2020).

Importantly, placental ACE2 expression is highest in the first trimester and decreases with gestation (Marques *et al.* 2011, Bloise *et al.* 2021, Colson *et al.* 2021). Similarly, expression of TMPRSS2 in the placenta is also reduced with gestation (Colson *et al.* 2021). Therefore, the placenta may be less susceptible to infection by SARS-CoV-2 in the third trimester.

Placental infection and fetal transmission of SARS-CoV-2

Placental infection with SARS-CoV-2 has been confirmed in numerous studies (Hosier *et al.* 2020, Schwartz *et al.* 2020, Sanchez *et al.* 2021, Valdespino-Vazquez *et al.* 2021); however, vertical transmission to the fetus is extremely low and rare (Allotey *et al.* 2022, Ezechukwu *et al.* 2022) (Fig. 5). In a recent systematic review of fetoplacental transmission by Ezechukwu *et al.* (2022), out of 45 eligible studies identified, 53.34% showed no evidence of vertical transmission; 33.33%

**Figure 5**

Influence of SARS-CoV-2 infection on pregnant women. Although SARS-CoV-2 infection occurs at similar rates in pregnant and non-pregnant women there is a heightened risk of COVID-19 severity in pregnancy. Placental infection with SARS-CoV-2 is possible, although vertical transmission to the fetus is extremely low and rare. Many placentas, regardless of placental SARS-CoV-2 infection, show signs of chronic histiocytic intervillitis, accompanied by massive infiltration of inflammatory cells, trophoblast necrosis, and fibrin deposition. SARS-CoV-2 infection in pregnant women acutely decreases ACE2 protein levels in the placenta, which likely prevents the protective actions of ACE2 and causes local inflammation and tissue injury. These changes, along with increased severity of COVID-19, are likely to underlie the increased risk of adverse pregnancy outcomes for both the mother and fetus. Created with BioRender.com. ACE2, angiotensin-converting enzyme 2; COVID-19, coronavirus disease 2019; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

supported the hypothesis of very rare, low possibility of vertical transmission; and 13.33% were indecisive and had no comment on vertical transmission. Despite this, a systematic review of histological studies of placentas from SARS-CoV-2 positive pregnant women showed that 6% of placentas have signs of chronic histiocytic intervillitis, accompanied by massive infiltration of inflammatory cells, trophoblast necrosis, and fibrin deposition (Ezechukwu *et al.* 2022). They also have signs of maternal vascular malperfusion including decidual vasculopathy, intervillous thrombosis and infarction, as well as signs of fetal vascular malperfusion, which includes thrombotic vasculopathy and chorangiomas (Ezechukwu *et al.* 2022). Thus, SARS-CoV-2 can cause an inflammatory response in placentas, even in the absence of placental infection, which can adversely affect the developing fetus (Fig. 5).

Verma *et al.* (2021) were the first to examine changes in ACE2 expression in the placenta following SARS-CoV-2 infection. They showed that placental ACE2 mRNA and protein levels are reduced in women with COVID-19 infection and, *in vitro*, culture of a human trophoblast cell line with recombinant SARS-CoV-2 spike protein, or a live modified virus expressing spike protein, reduces ACE2 expression (Verma *et al.* 2021). Furthermore, levels of AT₁R and AT₁R autoantibodies, which act as AT₁R agonists, were increased by SARS-CoV-2 spike protein (Verma *et al.* 2021). Subsequently, several other studies have also investigated ACE2

expression in the placenta. In contrast to Verma *et al.* (2021), Lu-Culligan *et al.* (2021) reported that placental ACE2 levels were elevated in mothers with COVID-19 at term. A more recent study suggests that these differences may be due to a previously unrecognised dynamic expression of ACE2 in the human placenta that can be modulated by the timing of maternal SARS-CoV-2 infection in pregnancy relative to delivery (Taglauer *et al.* 2022). Taglauer *et al.* (2022) showed that although villous placental tissues from remote, second-trimester COVID-19 cases had similar ACE2 expression to those of control placental tissues at term, there is increased placental *Ace2* mRNA and decreased ACE2 protein levels in acute SARS-CoV-2 infection in the third trimester. There is also increased sACE2 in maternal plasma (Taglauer *et al.* 2022), which could suggest increased shedding of ACE2 from the placenta. Overall, these data suggest that SARS-CoV-2 infection in pregnant women is likely to acutely decrease ACE2 protein levels in the placenta, preventing the protective actions of ACE2 and causing local inflammation and tissue injury. These changes are likely to underlie the increased risk of adverse pregnancy outcomes for both the mother and fetus in pregnancies affected by COVID-19 (Fig. 5).

Influence of SARS-CoV-2 on pregnant women

Pregnant women were initially identified as a vulnerable population for COVID-19 (Favre *et al.* 2020,

Schwartz & Graham 2020) as they are at high risk of complications and severe disease from infection with other viruses and coronaviruses (Wong *et al.* 2004, Alfara *et al.* 2019). It appears, however, that SARS-CoV-2 infection occurs at similar rates among pregnant women compared with the general population (Kotlar *et al.* 2021, Overton *et al.* 2022). The most commonly reported symptoms are fever (87.5%) and cough (53.8%), followed by fatigue (22.5%), myalgia (16.3%), dyspnoea (11.3%), diarrhoea (8.8%), and sore throat (7.5%) (Yang *et al.* 2022a). In terms of the severity of infection, although some studies report that clinical characteristics in pregnant patients are similar to those of non-pregnant adults (Chen *et al.* 2020a, Yang *et al.* 2022a), several larger studies suggest that there is a heightened risk of COVID-19 severity in pregnant women (Khan *et al.* 2021, Kotlar *et al.* 2021, Lassi *et al.* 2021, Wang *et al.* 2022b) (Fig. 5). Specifically, Lassi *et al.* (2021), in a systematic review and meta-analysis of 31,016 pregnant women from 62 studies, report that 16.4% of women developed severe COVID-19, although nearly half were asymptomatic (Lassi *et al.* 2021). About 7% were admitted to the ICU, 8% required mechanical ventilation, and 2% died. Importantly, the risk of severe COVID-19 was significantly higher among women who were >35 years old, obese, had smoked, diabetic, or had preeclampsia (Lassi *et al.* 2021).

COVID-19 infection in pregnancy is also associated with a high risk of adverse pregnancy outcomes (Di Mascio *et al.* 2020, Khan *et al.* 2021, Wei *et al.* 2021, Pathirathna *et al.* 2022) (Fig. 5). A systematic review and meta-analysis by Wei *et al.* (2021) including 438,548 pregnant people from 42 studies, found that COVID-19 was associated with an increased risk of pre-eclampsia (OR: 1.33), preterm birth (OR: 1.82), and stillbirth (OR: 2.11). Similarly, Pathirathna *et al.* (2022) in a meta-analysis of 21 studies that included 14,131 COVID-infected and 585,376 non-infected pregnant women found that the odds of maternal death (OR: 7.05), preeclampsia (OR: 1.39), caesarean delivery (OR: 1.67), fetal distress (OR: 1.66), preterm birth (OR: 1.86), low birthweight (OR: 1.69), stillbirth (OR: 1.46), and neonatal ICU admission (OR: 2.12) were higher among COVID-19 infected pregnant women. Compared with mild COVID-19, severe COVID-19 was strongly associated with preeclampsia (OR: 4.16), preterm birth (OR: 4.29), gestational diabetes (OR: 1.99), and low birthweight (OR: 1.9) (Wei *et al.* 2021). Furthermore, symptomatic pregnant women were more likely to have adverse outcomes than asymptomatic pregnant women, with increased

risk of caesarean delivery (OR: 1.40), low birthweight (OR: 1.85), preterm birth (OR: 2.10), and neonatal ICU admissions (OR: 1.96) (Khan *et al.* 2021). These studies highlight the vulnerabilities for women infected with COVID-19 in pregnancy. However, much more needs to be done to better understand the role of ACE2 and alterations to its actions locally within the placenta in mediating some of these adverse outcomes.

Conclusion

This review highlights the fundamental role of ACE2 as the gateway receptor for SARS-CoV-2 infection and subsequent driver of COVID-19 disease pathogenesis. Normally, ACE2 plays a multifaceted physiological role throughout the body given its widespread tissue expression and plentiful interactome. However, the active changes in ACE2 expression and activity following SARS-CoV-2 spike protein binding and the deregulation of ACE2 interacting partners are key to driving one's susceptibility to SARS-CoV-2 infection, severity of COVID-19 symptoms across affected organs, and subsequent clinical outcome. Despite a vast body of evidence supporting this critical role of ACE2, when looking across populations most vulnerable to COVID-19, changes in ACE2 become less clear. This review describes the evidence supporting ACE2 in driving COVID-19 age-, sex-, and pregnancy-associated vulnerabilities. Furthermore, it highlights the disparities in ACE2 expression across studies especially those comparing age- and hormone-mediated states (sex, pregnancy), with large variability in reports of ACE2 mRNA, protein (membrane-bound and circulating), and activity levels and cellular pattern of expression. Fundamentally, improved characterisation of ACE2 is needed to gain a better understanding of the basic biology of ACE2 across groups vulnerable to COVID-19. This improved understanding of ACE2 expression, regulation, and function could reveal potential novel treatments strategies for targeting the deregulation of ACE2 and its interactors in the clinical management of COVID-19 but also other ACE2-mediated disease states.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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