Expression of SARS-CoV-2 Entry Genes

Subjects: Others

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To address the expression pattern of the SARS-CoV-2 receptor ACE2 and the viral priming protease TMPRSS2 in the respiratory tract, this study investigated RNA sequencing transcriptome profiling of samples of airway and oral mucosa. As shown, ACE2 has medium levels of expression in both small airway epithelium and masticatory mucosa, and high levels of expression in nasal epithelium. TMPRSS2 is highly expressed in small airway epithelium and nasal epithelium and has lower expression in masticatory mucosa. These results provide the molecular basis that the nasal mucosa is the most susceptible locus in the respiratory tract for SARS-CoV-2 infection.

Keywords: SARS-CoV-2 ; angiotensin-I-converting enzyme 2 ; transmembrane serine protease 2 ; COVID-19

1. SARS-CoV-2 Entry Genes in human airway and oral mucosa

The human angiotensin-I-converting enzyme 2 (ACE2) has been suggested to serve as the receptor for the cell entry of SARS-CoV-2 to cause infection [1]. ACE2 is a member of the renin–angiotensin system (RAS), with the function of converting angiotensin II to angiotensin-(1-7) (with seven amino acids), and converting angiotensin I to angiotensin-(1-9) [2], thereby negatively regulating the effects of angiotensin-I-converting enzyme (ACE) and the RAS system. In addition to its critical roles in RAS, ACE2 binds the S1 domain of the SARS-CoV Spike (S) protein as the viral receptor, and accounts for the infection of SARS-CoV and syncytia formation [3]. The genome sequence of SARS-CoV-2 shows significant similarity (79%) to that of SARS-CoV, while its receptor-binding domain shows even higher similarity to that of SARS-CoV [1], further supporting ACE2 as the receptor of SARS-CoV-2. After binding with ACE2, SARS-CoV-2 priming by the serine protease encoded by the transmembrane serine protease 2 gene (*TMPRSS2*) is also required for the viral entry into host cells [4][5]. Knowledge about the expression of *ACE2* and *TMPRSS2* is extremely important to understand the infection of SARS-CoV-2 and to find ways to prevent the infection.

2. RNA sequencing transcriptome profiling of samples of airway and oral mucosa

This study investigated RNA sequencing transcriptome profiling of samples of airway and oral mucosa, including small airway epithelium, alveolar macrophages, nasal epithelium, and masticatory mucosa. As shown by the results, ACE2 has medium levels of expression in both small airway epithelium and masticatory mucosa, and high levels of expression in nasal epithelium. The expression of ACE2 is low in mucosal-associated invariant T (MAIT) cells and cannot be detected in alveolar macrophages. TMPRSS2 is highly expressed in small airway epithelium and nasal epithelium and has lower expression in masticatory mucosa. This study highlights that the nasal mucosa is the most susceptible locus in the respiratory tract for SARS-CoV-2 infection and replication, is responsible for the subsequent high level of droplet transmission. More details seen in https://www.mdpi.com/1999-4915/12/10/1174

Figure 1. The expression of *ACE*, *ACE2*, and *TMPRSS2* in five different types of samples. Y-axis represents FPKM values.

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