**Abstract: The Cleavage Potential of Cross-Species TMPRSS2 Variants toward SARS-CoV-2 S2’ Subunit**

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a positive-stranded RNA virus, has caused >100,000 infections and >50,000 deaths during the 2020 pandemic. SARS-CoV-2 successful infectivity is in part due to structural motifs and specific cell receptor targeting. SARS-CoV-2 spike (S) glycoprotein mediates cell attachment by recognizing the angiotensin converting enzyme II (ACE2) receptor, which initializes cleavage by host cell proteases to induce cell membrane fusion. In previous studies transmembrane protease/serine subfamily member 2 (TMPRSS2) have increased cleavage efficiency towards the S protein subunits. This study aims to characterize cross-species variants of TMPRSS2 and their potential to cleave S proteins subunits in silico. We hypothesize that TMPRSS2 aids in the spillover of SARS-CoV-2 to alternate host by having a conserved catalytic region. We investigated the conservation of TMPRSS2 sequences amongst several species and assessed their similarity to the human homolog. We utilized protein databanks to form concise amino sequence alignments of six domestic animals for comparisons with the human variant. We characterized differences in catalytically important residues based off the position specific score matrix and changes in amino acid properties. We found that important residues within TMPRSS2 are highly conserved, and found only substitutions likely to have minor effect on catalytic activity. This study has provided insight on possible spillover into alternate host with structurally similar TMPRSS2 variants compared to humans, posing an immense threat for epidemics in domesticated animal populations.

**Introduction**

**Proposed organization:**

1. **Viral entry: introduce ACE2, TMPRSS2, and other important host cell proteins as mediators of viral entry.**
2. **TMPRSS2: describe the salient details of this protein for SARS-CoV-2**
   1. **Receptor binding domain**
   2. **Catalytic triad**
   3. **Role of disulfide bonds**
3. **Viral host range as a property of host entry protein conservation: say a few words here about prior work looking at the conservation of ACE2 across species**
4. **Conclude with a statement on the aim of the research.**

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a novel betacoronavirus, curtailed the world’s health system within a matter of months due to its broad host range. As of July 20th, 2020, 14,348,858 laboratory-confirmed infections and 603,000 SARS-CoV-2 related deaths have been reported globally [12]. This is in part due to the high bonding affinity of the SARS-CoV-2 spike protein (S) for the angiotensin converting enzyme II (ACE2) receptor in airway epithelial cells. The S1 subunit of the S protein binds to ACE2 via its receptor binding domain (RBD), while the S2 subunit is used for virus-cell membrane fusion [1,3,6].

*The Role of TMPRSS2 in SARS-CoV-2 Infection*

Previous studies have shown that SARS-CoV has preference for cells with the transmembrane protease/serine subfamily member 2 (TMPRSS2) endoprotease, which increases the ability for virus-host membrane fusion [6,7,9]. TMPRSS2 is a member of the type II Transmembrane Serine Protease (TTSP), specifically belonging to the Hepsin/TMPRSS subfamily. TTSPs have four defining features: an N-terminal intracellular domain, transmembrane domain, “stem” domain, and a proteolytic domain. TMPRSS2 is synthesized as a zymogen that requires proteolytic processing to activate [2]. This activation results in cleavage of extracellular substrates initialized by a Serine residue at the catalytic site. The TMPRSS2s proteolytic domain has shown increased pathogenesis by cleaving monobasic sites of virus subunits within coronavirus and influenza family [3-7, 21]. The S protein in SARS-Cov-2 has an multibasic S1/S2’ cleavage site containing several arginine residues that are cleave by host cell proteases, which increases the efficacy of cell-cell spread [3]. However, in order for the virus-cell transmembrane fusion to occur, the monobasic S2’ cleavage site must be cleaved by TMPRSS2 [3-4]. TMPRSS2 proteolytic activity results from its catalytic domain, which consist of Ser-His-Asp, but Ser initializes the peptide hydrolysis by attacking the acyl compound of a lys or Arg residue in the S protein [2,4]. During this reaction two tetrahedral intermediates and one acylenzyme but finalizes with the protonation of an amine leaving group, carboxylic acid, water, and reformation of the catalytic triad [2]. Even though TMPRSS2 is a crucial part for virus-host transmembrane fusion, much of its functionality is still unclear. Since there are over 9000 sequences of TMPRSS2, a comparative analysis of its amino acid sequence can help predict its cleaving efficacy of SARS-CoV-2 spike protein.

*SARS-CoV-2 Host Range*

In silico studies have shown that SARS-CoV-2 ability to infect alternate host depends on ACE2 based on the conservation of the enzyme compared to the human strain [8].

With cases of SARS-CoV-2 in domesticated animals such as ferrets and cats, it is imperative to identify transmissible elements between humans and animals.

Additionally, ACE2 variants have been observed in multiple species, which may have lead SARS-CoV2 high infectivity in native and foreign host [1,8]. Exploring TMPRSS2 variants will yield valuable insight into SARS-CoV-2 zoonotic transmission potential to spill over in specie populations.

SARS-CoV-2, a zoonotic pathogen, has evolved to successfully infect a broad host range using common host cell machinery. With its high infectivity and unpredictable nature, SARS-CoV-2 is increasingly difficult to treat and contain. In previous studies, TMPRSS2 was shown to cleave SARS-CoV at a monobasic Arg site, causing cell-cell spread and increased severity of coronaviruses in infected lung cells of mice [20-21]. Additionally, TMPRSS2’s proteolytic activation takes place after SARS-CoV S protein undergoes receptor-induced conformational modifications [21]. However, TMPRSS2 deviations in other species with similar ACE2 receptors (compared to human strains) could lead to unfavorable conditions for SARS-CoV-2 activation. Therefore, we hypothesize that cross-species conservation of TMPRSS2 catalytic residues may play a role in alternate host spillover. By comparing residue alterations of TMPRSS2 multiple sequence alignments between various species and human, we wll be able to score the susceptibility/severity of infection for each species, in silica. Also, we’ll be able to categorize each substitution’s property delta, then visualize the structural context of that change in Pymol. By determining the molecular mechanisms leading to cell entry, we will gain insight on spillover potential of SARS-CoV-2 to alternate host. Which could harbor adaptive advantages for SARS-CoV-2 immune evasion and overall infectivity within a broad host range.

**Methods**

**Data Collection and Curation**

We retrieved 9,757 TMPRSS2 protein sequences from 120 species from EggN0G, as of June 30, 2020 [13]. Using Clustal Omega we generated the full set of each protein sequence alignment independently, which verified the authenticity of each alignment in the EggN0G dataset [14]. We utilized functions in Biopython [citation], a python biological computation package, to parse the lines within the alignment file to convert header and sequence pairs into iterables. We then filtered out target mammalian species (Homo sapiens, Mus musculus, Canis Lupus familiaris, Felis catus, Bos Taurus, Equus caballus, and Gallus gallus) from the multiple sequence alignment of all 120 species. From the target species list we extracted the H. sapien homolog sequence based upon UniProt’s TMPRSS2 homolog [17]. For each non-human species, we selected a sequence for comparison by choosing the sequence record with the greatest percent identity to human TMPRSS2. We used a position specific score matrix (PSSM) to find the percent probability of a particular residue at a specific location.

**Protein Sequence Analysis**

We identified 24 TMPRSS2 amino acid residues that were previously reported to be important for proteolytic cleavage and conformation [2,4,15,16,17]. These residues include the assumed monobasic recognition site (K223 and K224), disulfide bonds (C113, C120, C126, C133, C139, C148, C172, C185, C231, C241, C281, C297 C365, C410, C426, C437, and C465), catalytic triad (D345, H296, and S441), and the binding site (D435). We compared the residues of each mammalian species to the human TMPRSS2 sequence in search of differences in particular residues of interest. Each substitution at a residue of interest was categorized as a mutation, which was then analyzed for its property difference based on data from previous studies (tryna get the reference from a prof). We retrieved the predicted structure of TMPRSS2 from SWISS-MODEL [18]. We modified the structure of TMPRSS2 in Pymol to visualize sequence comparisons [19].

Work in progress

**Results**

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Notes.

Partial cleavage can be accomplished by using enzymes, such as trypsin and chymotrypsin, that break bonds between specific amino acids.

* Trypsin: Cleaves the chain at the carboxyl groups of the basic amino acids lysine and arginine. The cleavage takes place in such a way that the amino acid with the charged side chain ends up at the C-terminal end of one of the peptides produced by the reaction. A peptide can be automatically identified as the C-terminal end of the original chain if its C-terminal amino acid is not a site of cleavage.
* Chymotryspin: Cleaves the chain at the carboxyl groups of the aromatic amino acids phenylalanine, tyrosine, and tryptophan.
* Protein domain- a conserved part of a given protein sequence and tertiary structure that can evolve, function, and exist independently of the rest of the protein chain.
* Quaternary structure is the final level of protein structure which is formed by two or more polypeptide chains. Each chain is termed a subunit of the structure.
  + Dimers, trimers, tetramers, consist of two, three, and four polypeptide chains, respectively.
  + Oligomer- an aggregate of several smaller units (monomers); bonding may be covalent or noncovalent.
    - Chains with noncovalent bond result in subtle changes that can alter the structure at one site of the protein molecule. This is known as allosteric hindess, which can cause conformational change in one subunit that induces a change in another subunit.
* Consensus Sequences- DNA sequences to which RNA polymerase binds; they are identical in many organisms
* Protein kinases- a class of enzymes that modify a protein by attaching a phosphate group to it
* I hypothesis that variation in the serine domain of TMPRSS2 will have an adverse effect on cross-species transmission of COVID-19. Specifically focusing on domesticated animal’s TMPRSS2 amino acid sequence. Protein folding and bonding affinity play a critical role in determining the cleavage potential for the proteolytic domain of TMPRSS2.

Interpreting Data

Hypothesis- This study aims to characterize cross-species variants of TMPRSS2 and its potential to cleave deviates of S proteins in silico. We hypothesize that TMPRSS2-like endoprotease aids in the spillover of SARS-CoV-2 to alternate host by cleaving S protein subunits.

* Compare the similarity of each animal sequence to the human strain
  + If the similarity of each sequence is high that means that TMPRSS2 has a highly conserved sequence meaning that cells supporting TMPRSS2 are susceptible to SARS-CoV-19
* Look at the residues of interest and count the frequency of each
  + Will give an assumption of the cleavage efficiency for TMPRSS2
* See the mutation rate among the species of interest
  + Will track the evolution of TMPRSS2 which will give an estimate for its ability to alter cleavage potential
* If there is a change in amino acid, what kind of change is it (volume, hydrophobicity, percent buried

Code

* I want to compare two alignment sequences to return both similarities and differences with their positions labeled
* I want to pull a particular *species*  from the main list of species and place it as a variable
* Run a multisequence alignment on the species to find the consensus sequence in the Desired species list (DS)
* Take the position of the DS that matches with the positions of the trimmed Human sequence
* Convert the DS consensus sequence to a SeqRecord to compare to the human sequence
* Run a multiple sequence alignment of both DS and human
* Find the frequency of changes at specific sequence locations compare to the human sequence
  + Find out if these changes result in changes in amino acid properties (specifically hydrophobic to hydrophilic or basic to acid)
  + Also find other differences in the amino sequence such as changes in disulfide bonding
* Find the similarities in the two sequences and record the position of those similarities