Introduction

The emergence of new infectious diseases is one of the major threats to human populations and the emergence of new viruses by zoonotic processes is within these threats. Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) is the perfect example to explain how viruses can cross the species barrier from animals to humans and produce an epidemic.

Objectives

- Get to know the phenomenon of Spillover
- Give a brief description of the Coronavirus family and SARS-CoV
- Relate the phenomenon of spillover with SARS-CoV
- Current situation

Spillover Phenomenon

Spillover is the ability of a virus to complete the virus infection cycle in a new secondary host population and is the defining characteristic of a zoonosis.

Coronavirus family

The Coronavirus family, within the order Nidovirales, is formed by 36 coronaviruses. Members of this family are known to cause respiratory or intestinal infections in humans and other mammals and avian species.

SARS-CoV morphology and genome organization

- Non-structural genes are replicase and protease (or TaLo).
- Structural genes are Spike (S), Envelope (E), Membrane (M), and Nucleocapsid (N).
- Spike glycoprotein is involved in the recognition and binding to the host cells receptors. Divided into two domains, S1 and S2.

Contact between species and transmission of the virus

- Serological findings, PCR and genome sequence analysis confirmed the presence of SARS-like coronaviruses in bats of the genus Rhinolophus, suggesting that horseshoe bats are the natural reservoir.
- Palm civets and raccoon dogs, that were in contact with horseshoe bats, in wet markets probably, got infected with SARS-CoV.
- They are the amplifying secondary hosts, because no serological findings were achieved in wild animals and they transmitted the virus into the human population.
- Is still not known if it was possible a direct transmission between bats and humans.
- Transmission between humans was due to droplets and fomite transmission.

Intrinsic and extrinsic biotic factors and molecular changes in the genome

- High replication rates: RNA-dependent polymerase with a mutation rate of 10^-6 per nucleotide and per cycle.
- High mutation rates:
  - Hot spots: non-structural protein 3 (nsp3), a cleavage product from the ORF1a polyprotein. Spike protein, ORF3 and ORF8.
  - Region Binding Domain (RBD) of the Spike Protein. Key region which influence host range expansion. The residues 479 and 487 are the ones that changed in palm civets and increased the binding affinity for human ACE2 receptor (Figure 3).
- Homologous recombination: mammalian ancestry in S domain of the genome (Replication/transcription) and avian ancestry in M domain of the genome (where Spike protein is encoded).
- Persistence:
  - Scanning for homologous receptors: gradual accumulation of mutations that alter the Spike affinity for orthologous receptors in different species.
- Receptor/Coronavirus shift: gene acquisition to recognition of completely different receptors.
- Anthropic influences

Current Situation

- This new virus is not very transmissible between humans but there is a real danger if it spreads to other parts of the world. Member of the 2b coronavirus like SARS-CoV, Bats origin?
- No avirial or immunomodulator is efficacious or approved for clinical use against coronaviruses.
- Intensive care with mechanical ventilation and extracorporal membrane oxygenation support the main modalities of treatment.
- No commercial vaccine is available. Different groups of research are working on it targeting mainly the Spike Protein.
- A rapid response, a united global front and mobilization of resources and expertise are our best tools in preventing or reducing the devastation that some of these viruses can cause.

Conclusions

- SARS-CoV, responsible of SARS disease is a member of the coronavirus family closely related with coronaviruses found in bats and is classified within the 2b of coronaviruses.
- Palm civets and raccoon dogs were only amplifying host that transmitted SARS-CoV into the human population. Bats of the genus Rhinolophus are now believed to be the natural reservoir.
- High mutation rates, high multiplication rates, homologous recombination, and persistence are the main characteristics that favoured the migration of SARS-CoV from animals to humans.
- Amino acid changes in the RBD of the Spike protein changed the receptor binding affinity and drive the host range expansion.
- Anthropic activities influence the emergence of new viruses. A rapid response, a united global front and mobilization of resources and expertise are our best tools in preventing or reducing the devastation that some of these viruses can cause. This is exemplified by the recent events that have led to the recognition for acute respiratory illnesses as SARS-CoV and the recent described MERS-CoV.
- Continued surveillance in mammals, bats and birds, which are believed to be the main source of new coronaviruses, will allow better understanding of the ecology of coronaviruses and may aid in the prevention of animal-to-human transmissions and outbreaks of the future.

References