**Plasticity, and Cross-Species Transmission of Coronavirus**

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Cross-species, transmission, phylogeny, evolution, virus, human, bat, pig, public health, domestic animals

**Abstract**

**The coronavirus is viral infection that is known to cause numerous health problems in humans and in many animals. According to the Centers for Disease Control, the coronavirus has been linked to human epidemics for the third time in two decades; SARS-2003, MERS-2013, and recently nCoV-2019. Each cross-species transmissions of coronavirus in humans have been traced to the same novel coronavirus found in bats (in forms of betacoronavirus). Known facets of coronavirus attribute to its ability to adapt and evolve into different environments. Thus the reservoirs bats provide give ample opportunity for the coronavirus to generate cross-species transmissible traits. Recent research has delved into gaining a better understanding of what molecular factors influence the cross-species transmission rate of the coronavirus. These findings range from: broad receptor engagements, affirmations of the MERS (Middle East respiratory syndrome) origins, and bat-derived coronavirus strands that gain transmission to pigs. However, an issue that remains is that there is no concrete way to predict/ model cross-species transmission. Meaning global reaction time is still compromised.**

**Introduction**

The coronavirus has been observed in humans, camels, swine, and bats. This virus is known to cause many different forms of infections in multiple animals (The Centers for Disease Control 2019). Bats being the main worldwide reservoir for the coronavirus to spread (camels being a large reservoir in the middle east). Studies have observed that in this reservoir a constant theme seems to be the shared plasticity between bats and a variety of coronavirus strands. A reservoir being an organism or product (like soil) that allows the virus to spread without impediment. A study done in 2006 by Woo et al., implicated that the coronavirus’ ecological plasticity was derived from its high rate of mutation and recombination (2006). There was also a stunning amount of diversity of novel coronavirus found in various species of bats (Woo et al., 2006). A species is labelled as a novel species when it is the “first of its kind”. It has been practice the label the different coronaviruses found in bats into different groups. Some of the more noteworthy bat novel coronaviruses that were mentioned in this study are a group 1 coronavirus: HKU2-CoV and two group 2 coronaviruses HKU4-CoV, and HKU5-CoV. These will be referred back to later in this review.

**Recent Progress**

A recent study done in 2018 by Zhou et al., provided evidence that the previously mentioned HKU2-CoV novel corona virus is related to the swine acute diarrhea syndrome (SADS-CoV). The coronavirus epidemic that was located in China, killed thousands of baby swine across four farms. The pigs in these farms in the province of Guangdong are said to have acquired this virus through cross-species transmission from bats (Zhou et al., 2018). This study was accomplished by capturing bats that were infected with HKU2-CoV and comparing it to the receptors of SADS-CoV. This was accomplished by screening 591 fecal samples collected from bat around the region. The article highlights the importance of studying bat coronavirus reservoirs due to public and domestic animal health issues that may arise from evolving coronavirus strands (Zhou et al., 2018). Much like the health issue we are facing currently today. One could say that if there was enough research on bat reservoirs, and a possible way to quantify coronavirus evolution in said reservoirs. Appropriate community and governmental action can take place. This highlights a necessity for regulating the health of endemic livestock.

A study done by Anthony et al., over the origins Middle East respiratory syndrome (MERS-CoV) suggest that camels are necessary for interspecies transmissions of MERS-CoV but the evolution of the coronavirus originates in infected bats (2017). The camels in the Middle East serve as a endemic species for the coronavirus to spread. Some of the possible phylogenic strands the article mentions that gave rise to MERS-CoV are the same ones that gave rise to the HKU4-CoV and HKU5-CoV. A take away from this, is that between MERS-CoV and the two other group 2 coronaviruses the common ancestor of both gave rise to at least 4 other known strands of coronavirus (Anthony et al. 2017). The study accomplished this by sequencing the genome of multiple strains of coronavirus including MERS-CoV, and comparing them by percentage match. This recording of divergent strains of coronavirus are a tell-tale sign of why we have had a hard time catching the cross-species transmission strains that can affect human life and livestock.

**Discussion**

The unique situation that the bats and strands of the coronavirus share create an issue for scientists. Even though there is a widely agreed upon hypothesis that bats are the primary environment for coronavirus strands to evolve. Its happens at such a pace that phylogenies and common ancestors are becoming hard to quantify (Zhou et al., 2018). A conclusion that can be drawn from these papers is that there is an alarming amount bat reservoirs that can produce new strands of coronavirus that can infect the human species or domesticated animals (Woo et al., 2006). In researching this topic, it is a common conclusion that there is no method or model to which is reliable in predicting coronavirus trends. Much less ones that will give us insight on how it may affect human health or agricultural economies. Extensive monitoring of the bat species in areas such as China and the Middle East will have chances of giving the scientific community better insight on how the viral reservoir of bats effects the evolution of coronaviruses. Thus allowing society to have the equity to plan ahead for future outbreaks of cross-species transmission coronaviruses.

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