

# COVID-19 and avian corona viruses: epidemiological comparison and genetic approach

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## ABSTRACT

**Aim.** This study aimed to collect and analyse available information on COVID-19 and avian corona viruses in order to conduct a systematic review of the genetic data concerning them. **Methods.** All available research was done according to the strictest data selection criteria, and the databases like NCBI genebank were quantitatively searched in the currently available scientific literature using keywords, analytical statistic and genomic software. All studies on the coronavirus family were dedicated to provide an overview towards an advanced statistical analysis of the collected data. The first step was a descriptive study of COVID-19 and avian corona viruses by an epidemiological comparison between the two cases. **Results.** All corona viruses usually tend to have relatively A-T rich DNAs which is linked to their highly A-T rich codon biases. The results indicate genetic differences between the two viruses, but the results of a percentage analysis showed that the nucleotides A+T are both more abundant and energetically cheaper than nucleotides G+C, this gives viruses a selection advantage. **Conclusion.** These results give us a future positive view of this type of virus with AT-rich genomes which is selectively promoted at the host level. **Recommendation.** A recommendation by our study reveals that thought about the vaccine is very early but prevention has proven to be effective for this virus in chickens.

## Original Article

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## INTRODUCTION

Coronaviruses (so called because they present a crown or corona shape) infect birds and many mammals, including humans [1] (Figure 1). The respiratory tract, gastrointestinal organs, and neurological tissues are the most common targets of coronaviruses, but other organs including the liver, heart, kidneys, and eyes may also be affected [2-4]. Epithelial cells are the primary targets of coronaviruses [5]. Widely distributed cells such as macrophages are also often infected by coronaviruses; mutation by definition late phase of the cycle during which changes in the structure of the viral particle are observed linked to the proteolysis of certain capsid proteins by a viral protease, maturation is essential for the viral particle to be infectious, coronaviruses are relatively restricted in their host spectrum, infecting only their natural host, and relatively close animal species [6, 7].

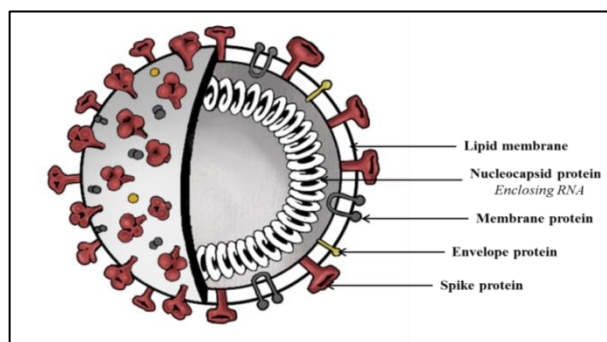


Figure 1. The Typical structure of coronavirus [16-18]

Figure 2 shows that coronavirus infection crosses the species barrier occasionally, as in the case of turkey infection with bovine coronavirus (BCoV), or experimental infection of dogs with TGEV; this may have happened with SARS (Severe Acute Respiratory Syndrome) in 2001, MERS (Middle East respiratory syndrome coronavirus) in 2012 and currently COVID-19 [8-12]. The biological vectors of the virus are poorly known and its transmission by respiratory, faecal and oral routes are common [13]. The coronavirus genome encodes a spike protein (S), an envelope protein, a membrane protein, and a nucleoprotein in this order. Among them, spike protein is the most important surface membrane protein of coronavirus [14, 15].

This study aimed to conduct a systematic review of the genetic data on COVID-19 and avian corona viruses by analyzing available information.













