

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

Amine BERGHICHE

Laboratory of Science and Technique of the Living, University of Mohamed Cherif Messaâdia, Souk Ahras, Algeria

Corresponding author's Email: amine_berghiche@yahoo.com; a.berghiche@univ-soukahras.dz

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.

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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].

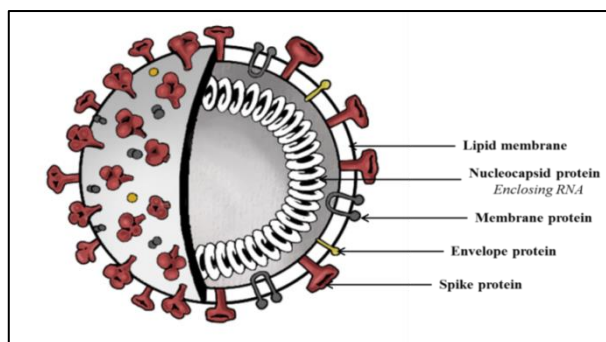


Figure 1. The Typical structure of coronavirus [16-18]

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.

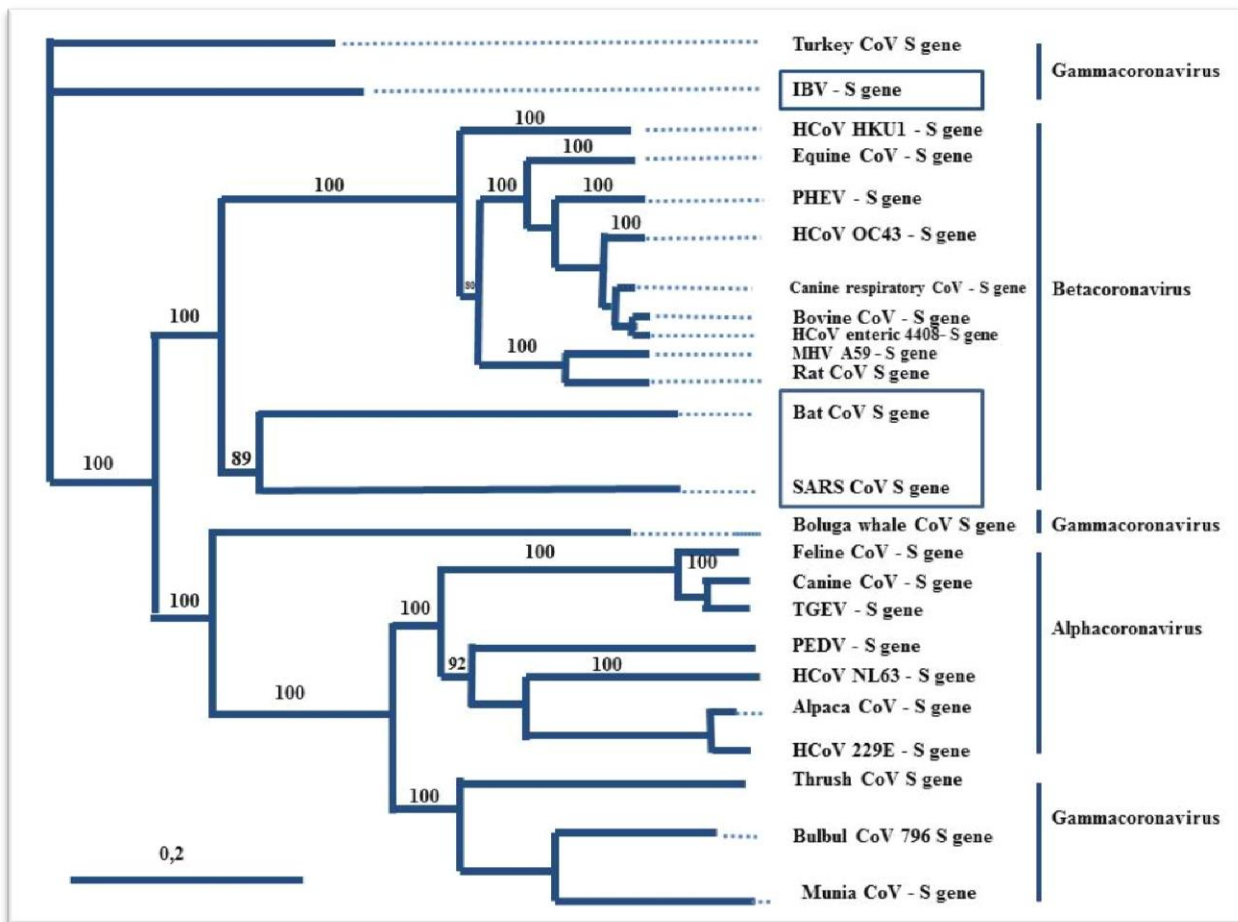


Figure 2. Phylogenetic tree analysis of the nucleocapsid genes from different coronaviruses. The alignments were performed using Clustal W, and the tree was created using a Neighbor Joining method with no outgroup (Past 2.17c).

MATERIAL AND METHODS

Etiology

The *Coronaviridae* belong to the order *Nirovirales* which includes two other viral families, the *Arteriviridae* and the *Ronoviridae*; the *Coronaviridae* include the genera *Coronaviridae* and *Toroviridae* [19], with the following characteristics (Table 1). Infections of humans and animals with coronaviruses appear to be ubiquitous, as evidence of infection has been obtained in all countries where serological and virological studies have been carried out [20, 21]. According to the Baltimore classification [22, 23], coronaviruses are single-stranded viruses (unsegmented RNA+) of the 4th multiplication class (Figure 3).

Table 1. Characteristics of *Coronaviridae* [24-27].

Specifications	Description
Enveloped	+
Positive single-stranded RNA with polyA tail	+
5'Polymerase gene - 3' structural protein genes	+
The incipient 3'co-terminal carries at least 4 subgenomic mRNAs.	+
Only the 5' region of the mRNA is translationally active.	+
Ribosomal reading frame shift in the polymerase gene	+
An M protein with at least 3 membrane-crossing sequences	+
Intracellular sprouting	+
Genome size in kB	27-31,5
Sequence 5' Leader	+
Core	+
Nucleocapsid	Helicoidale
Prominent spicules (spike)	+
Spicules helix/propeller structure	+

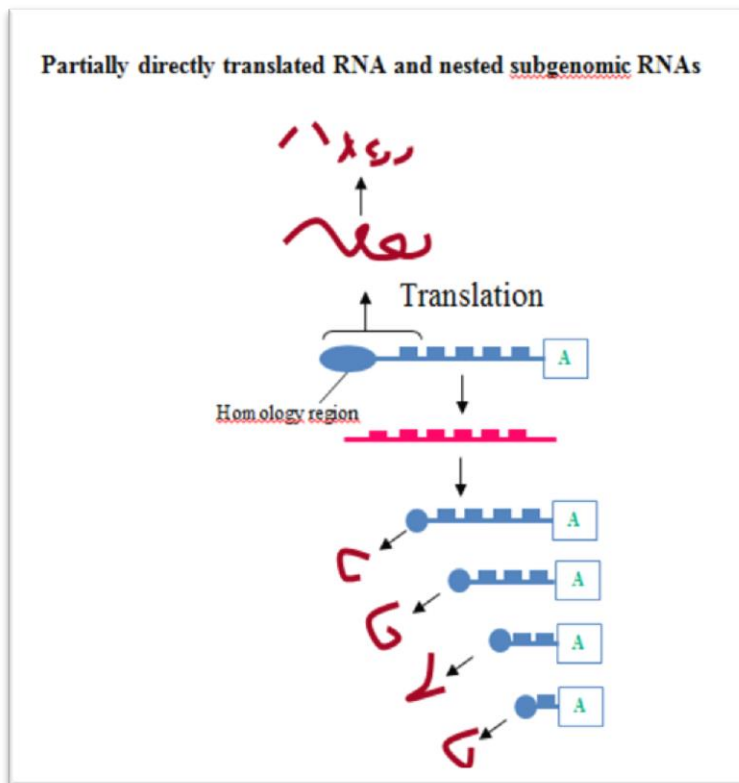


Figure 3. Multiplication of Coronavirus [28].

Epidemiological comparison

In table 2, we have summarized the difference between COVID-19 and avian corona viruses through the different epidemiological points.

Table 2. Epidemiological comparison between human and avian coronaviruses

Comparative aspects	Avian corona virus	COVID-19
Epidemiology	Epidemic [29]	Pandemic [30]
Transmission Routes	The respiratory tract, through aerosols and faeces [31]	The respiratory tract [30]
Mode of Transmission	Horizontal Direct and indirect; Vertical direct [32]	Horizontal Direct [33]
Incubation	18-36 hours [32]	2 day to 14 day 5.2 days (95% confidence interval [CI], 4.1 to 7.0), with the 95 th percentile of the distribution at 12.5 days. [34, 35]
Morbidity	100 % [31]	WHO ^s estimated (on Jan. 23, 2020) Ro^1 to be between 1.4 and 2.5. Other studies have estimated a Ro between 3.6 and 4.0, and between 2.24 to 3.58. [36]
Mortality	20% to 30% (except for the renal tropism strain) [31]	2% (the elderly, Chronic diseases and immunodeficiency) [36]
Symptoms	Signes respiratoires Signes reproducteurs Signes rénaux [37]	Fever Cough Shortness of breath [38]
Diagnostic	Indirect ELISA (easy to use, but expensive), Hemagglutination inhibition (applicable and less expensive) and Viral neutralization (more specific when it comes to serotyping). [32]	RT-PCR [39]

¹ Transmissibility or the attack rate of virus is indicated by its reproductive number (Ro , pronounced R-nought or r-zero), which represents the average number of people to which a single infected person will transmit the virus.

RESULTS AND DISCUSSION

Genetic approach; descriptive data

The genome analysis of the complete avian infectious bronchitis virus and SARS-CoV-2 virus shows a length of 27608 and 29903 amino acids respectively. Genomic composition analysis of the two viruses show the results summarized in Table 3. The comparison of the composition of the two viruses shows that there is a remarkable difference in the numbers of adenine for the avian virus (Figure 4).

Table 3. Genomic composition of avian infectious bronchitis virus and SARS-CoV-2

Genomic composition	SARS Cov-2	Avian Cov	Difference
Total count	29903	27608	2295
Adenine	8954	7967	987
Thymine	9594	9169	425
Guanine	5863	5993	-130
Cytosine	5493	4479	1014

Genetic sequences are collected from the NCBI GenBank and the analysis is performed using the bio edit software [40].

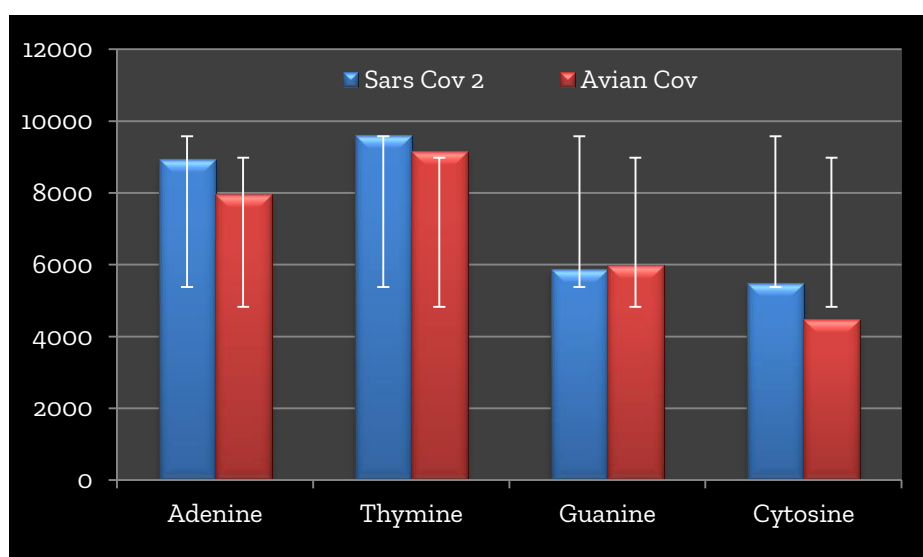


Figure 4. Comparison between the amino acid composition of Avian Infectious Bronchitis Virus and SARS-CoV-2

Genetic approach: Statistical analysis

On the basis of the results using the software *Past*, of the composition of the two viruses, the *F* and *t* test (non-parametric test) was carried out, in order to estimate the existence of a significant difference between the different components of the same virus family, and whether the amino acid level shows a variety of pathogenesis of the virus species [41]. The analysis show a signification with *F* test which means that little difference in virus composition don't change the pathogenicity characters according to [42].

Table 4. *F* and *t* test Statistical table of composition

Items	SARS CoV-2	Avian Cov
N	4	4
Mean	7476	6902
95%	4137.7 10814	3593.3 10211
Variance	4.4015E06	4.3236E06
95% Confidence for difference between means	-3039.9	4187.9
Bootstrapped	-1936	3057.3
<i>F</i> : 1.018	p: 0.98863**	
<i>t</i> : 0.38865	p: 0.71095	
Welch test: unequal variance <i>t</i> =0.38865	p: 0.71095	
Permutation <i>t</i> test (N=9999):	p: 0.6524	

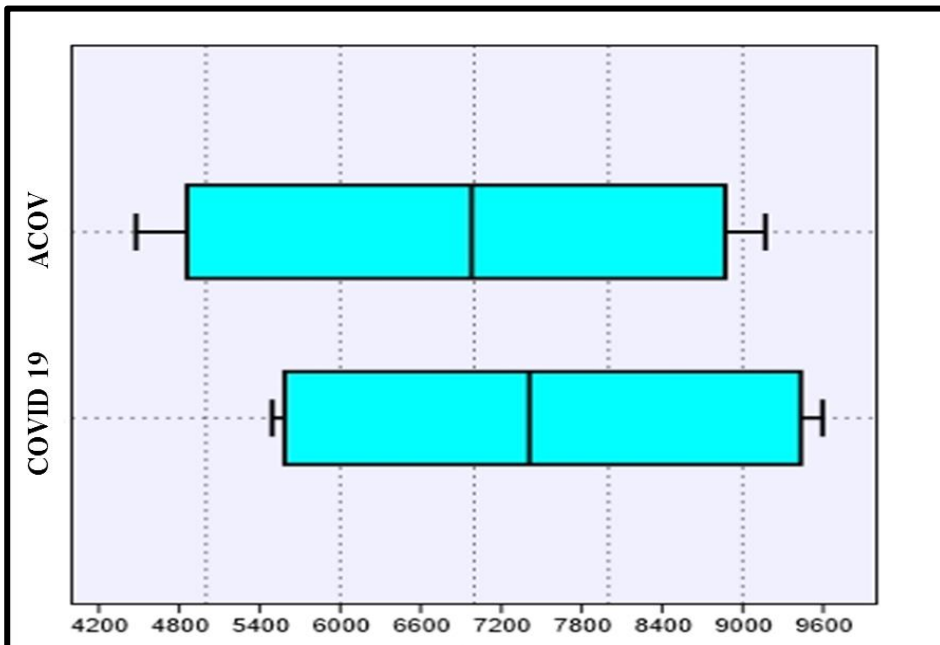


Figure 5. Box plot of Avian Infectious Bronchitis Virus and SARS-CoV-2 composition

Genetic approach: Genomic data analysis

The contents show that both viruses have a low level of G+C with 37.93 and 37.97 and high level of A+T with 62.068 and 62.02 respectively. Meaningfully, intracellular genetic elements that persistently or temporarily exist outside the host chromosome [43, 44], such as viruses, are also generally characterized by a higher AT content than their host genome [45]. The coronavirus genome is filled with A and T [46]. Since nucleotides A + T / U are both more abundant and less energetically expensive than nucleotides G + C, this gives viruses a selection advantage [47, 48]. Intracellular elements, whose genome is richer in A than the host genome, are selectively favoured at the host level [49].

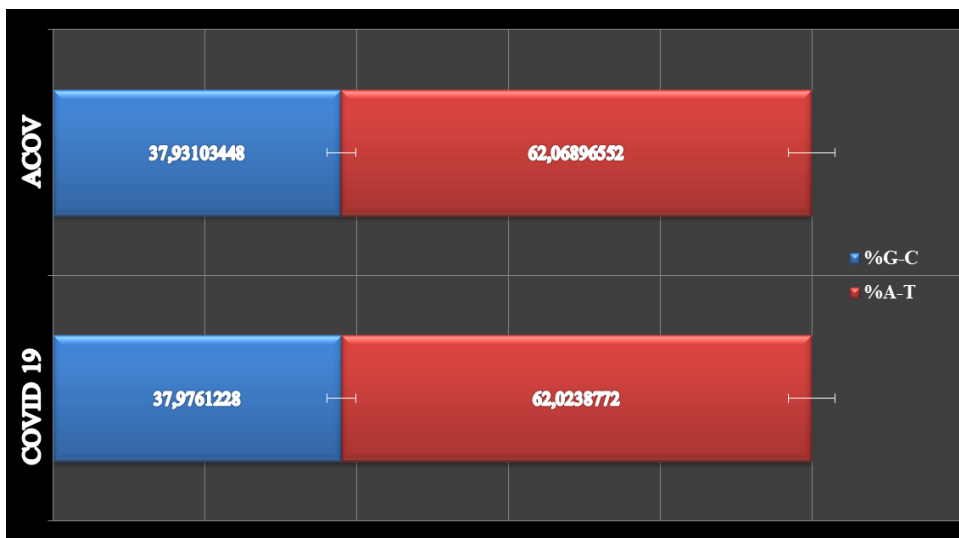


Figure 6. The Guanine+Cytosine and Adenine+Thymine contents of Avian Infectious Bronchitis Virus and SARS-CoV-2

CONCLUSION AND RECOMMENDATIONS

This study gave a complete comparison of the two viruses in an epidemiological context and the exhaustive results of genomic composition contributed strongly to determine the difference between the two viruses and show their selectivity characteristics.

Based on the experience with this virus in poultry, thinking about the vaccine is a bit early because the presence of several serotypes of the virus requires the use of several valences in the same vaccine, but the prediction of the A+T level can help in the preparation of possible vaccine ranges as in the case of the seasonal

influenza vaccine. Also the permanent genetic mutations of this virus may lead to its weakening over time and climatic changes with the probability of increasing its mortality compared to its morbidity, and until the exact virulence profile and existing serotypes become evident. It is recommended to focus on the symptomatic treatment of secondary affections and prevention by confinement, which has proved its effectiveness as previous experience against this virus in chickens has shown its success in intensive farming known by its high population density

DECLARATIONS

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Competing interests

The author declares that he has no conflict of interests.

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