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Genome Sequences of COVID-19 from Jordanian Patients in Comparison with the Global Pandemic Strains and the Transmission Route

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Abstract

In this research study, we reported a pioneer investigation on the phylogenetic profile of genomic sequences and the prevalence of COVID-19 strains in Jordan; in comparison with global strains, as part of concerted global efforts in combating the COVID-19 pandemic. A total of 28 genome sequences of the hCoV-19/Jordan strain were employed in this study. The phylogenetic analysis of the genome sequences of hCoV-19/Jordan strain, which was conducted on the databases of NCBI and GASAID revealed that the hCoV-19/Jordan strain belongs to the G, V, and S clades with distribution coverage rates of 89%, 7% and 4%, respectively. Comparison of the hCoV-19/Jordan clades with global clades distribution profile showed evidently and conclusively, a unique pandemic profile of multiple geographical sources of COVID-19, imported into Jordan primarily through cryptic means from European countries (UK, Belgium, Sweden, Russia) and Morocco, which are entry points into Jordan. This is due to the reciprocal heavy air traffic route between Jordan and the capitals of these European countries, with Morocco being the primary entry point into Jordan. The results of this study represent a marked addition to investigations on the prevalence rate of the hCovid-19/Jordan strain in comparison to the global strains sequences, and provides a better understanding on comparative diagnosis technique for COVID-19 worldwide. Phylogenetic analysis of the top 100 and top 10 taxonomic trees revealed almost identical homology (99.98% - 100%) between hCoV-19/Jordan strain and the strains that broke out in Wuhan, the MT642226.1. Furthermore, it can be inferred that there was no marked change in the virus mutation that occurred during the period of this study taking into cognizance the fact that there was identical homology (99.98% - 100%) among the 28 sequences of hCoV-19/Jordan strains. Similarly, all sequences of the Jordanian strains of hCoV-19/Jordan

were compared to the England and American strains and showed identical homology of (99.98% - 100%).

1. Introduction

Since the World Health Organization (WHO) officially declared the outbreak of COVID-19 a pandemic on March 11, 2020, there has been a global growing interest in research targeted at combating the virus due to the surge in infection, as well as the prevalence rate. This has made it imperative and expedient for all probable preventative measures to be adopted in combating the global surge in infection pending the discovery of a vaccine for the virus. Currently, there are over 40 million confirmed cases globally as reported by WHO. The COVID-19 strain responsible for the current global pandemic was identified early this year as the β-coronavirus (CoV), which belongs to the *Coronaviridae* family and it has a single positive-strand RNA genome [1] [2] [3]. This strain-type is among several strains of coronaviruses that are pathogenic to humans; most are associated with mild clinical symptoms, with the exception of the Severe Acute Respiratory Syndrome (SARS) coronavirus (SARS-CoV) and it was reported as a novel β-coronavirus two decades ago [4] [5] [6]. In 2012, the same strain-type was detected in Saudi Arabia, and since then, it has been known as the Middle East Respiratory Syndrome (MERS) coronavirus (MERS-CoV) [7] [8]. It was later imported into South Korea, and caused about 2500 confirmed cases of infections [9] [10]. In late December, 2019, after global detection of the COVID-19 strain in many countries, the WHO has declared it as a pandemic on March 11, 2020.

A phylogenetic tree with the geographical mutation transmission of SARS-CoV-2 has previously been reported to have a genome size of about 30 kilobases, and encodes 10 genes of a single positive-stranded RNA (ribonucleic acid) [1] [2] [11]-[17]. Furthermore, a comprehensive study conducted by the World Health Organization [18] (employing 10,022 SARS-CoV-2 genomes from 68 different countries) showed how the SARS-CoV-2 genome has evolved over the years, spreading to different parts of the world. In total, 65,776 variants and 5775 distinct variants, comprised of the most frequent mutations causing the SARS-CoV-2 pandemic were detected by WHO. Additionally, 2969 missense mutations, 1965 synonymous mutations, and 484 mutations in non-coding regions were also discovered by WHO [1]. It was reported by [12] based on data from the public database of the Global Initiative on Sharing All Influenza Data (GISAID) that three major clades of SARS-CoV-2 exists, and have subsequently

been named as clade G (variant of the spike protein S-D614G), clade V (variant of the ORF3a coding protein NS3-G251), and clade S (variant ORF8-L84S).

Jordan and its Mediterranean crossing route, and global tourist attraction centers represent an important route for global spread of COVID-19. The spread of COVID-19 is most likely because of Jordan's heavy air traffic, which is induced by Jordan's route nexus with Europe and many north African countries. It is also attributed to Jordan's close border with Asian countries like China, Pakistan, Nepal, and gulf countries like Saudi, UAE and Bahrain. Up to date of this paper, the COVID-19 pandemic has spread progressively reaching 110,974,862 confirmed cases of COVID-19, including 2,460,792 deaths worldwide and showed a marked increase in infection in Jordan exceeding 364,000 confirmed cases. Therefore, this paper as the first study aimed at investigating the COVID-19 in Jordan as part of the global pandemic and in comparison to global strains, has a vital role for Jordan as well as other parts of the world for better understanding the COVID-19 pandemic across the world which will enhance the global understanding of the transmission routes as well as the mechanism of action to combating the its pandemic.

2. Materials and Methods

2.1. Jordan National SARS-CoV-2 Pandemic Surveillance Committee

After the first confirmed case of SARS-CoV-2 infection in Jordan, a National SARS-CoV-2 Pandemic Surveillance Committee was instituted with the National Order number (17) to oversee the SAR-CoV-2 surveillance and combat program.

2.2. Collection of Clinical Samples and Extraction of RNA Using RT-PCR

A total of 28 nasopharyngeal swab samples (26 from Amman & 2 from Irbid) were collected from symptomatic and high index of suspicion patients at the Biolab Diagnostic Laboratories, Amman, Jordan for SAR-CoV-2 investigation using the RT-PCR and RNA extraction technique (in line with the manufacturer's protocol). Quality control assurance measures for SAR-CoV-2 RNA purity were conducted in line with the extraction protocol. The genome of the 28 samples was later dispatched to the Scripps Research Institute (TSRI), La Jolla, California, USA for genome sequencing.

2.3. Sequencing of the Full Length Genome of Jordanian SAR-CoV-2 Strains

The (28) genome samples from Jordan (26 from Amman and 2 from Irbid) were subjected to complete genome sequencing in the Scripps Research Institute (TSRI), La Jolla, California, USA as previously described [11]. The resultant se-

quences were later deposited by the Scripps Research Institute (TSRI) into the databases of the NCBI GenBank (http://www.ncbi.nlm.nih.gov/) and Global Initiative on Sharing All Influenza Data (GISAID) (http://www.gisaid.org/) employing the tag hCoV-19/Jordan vis-à-vis each respective accession number (see Table 1 for details of the accession numbers and other descriptions).

2.4. Using GISAID (Global Initiative on Sharing All Influenza) Public Domain Databank for Phylogenetic Comparison with COVID-19 Sequences of Global Strains

For comparison of our strains sequences of the COVID-19 with the genomic sequences of the global strains from different countries, we have used with acknowledgments the COVID-19 sequences available on the Public Domain Databank platform of GISAID and EpiFlu™ database, as hosted by the Federal Republic of Germany; which provides us with rapid sharing of COVID-19 sequences enabling us for rapid and conclusive global comparison on the epidemic and pandemic of the COVID-19 (http://www.gisaid.org/).

Sequence alignment was conducted using human coronavirus sequences registered in the Global Initiative on Sharing All Influenza Data (GISAID) and NCBI GenBank. Using the available sequences and the software on the Public Domain of the GISAID (http://www.gisaid.org/) and the NCBI (https://blast.ncbi.nlm.nih.gov); the Phylogenetic trees were constructed employing for Neighbor Joining (NJ); Minimum Evaluation Analysis and the NJ-Taxonomic Distance Tree. The accession numbers of the 28 sequences of hCoV-19/Jordan were used to construct the phylogenetic tree in comparison with the closest sequences of the top 100 and top 10 taxonomic trees, and (99.98% - 100%) semblance to those sequences available on the NCBI (https://blast.ncbi.nlm.nih.gov). In this comparative study, we selected a set of sequences from different parts of the world. Sequences were selected from Europe (3 from United Kingdom, 3 from Belgium, 2 from Sweden, and 3 from Russia), Asia (9 from Pakistan, 1 from Nepal, 9 from Bahrain, and 4 from Lebanon) and Africa (10 from Morocco) because of the geographical limitrophe of Jordan with these countries. Sequences were assembled and mapped to the SARS-CoV-2 that are available on the Public Domain of the GISAID (http://www.gisaid.org/) and the NCBI (https://blast.ncbi.nlm.nih.gov).

3. Results

The phylogenetic tree of the hCoV-19/Jordan sequences in comparison with selected global sequences is presented in Figure 1 which shows almost identical homology (99.98% - 100%) with the top 100 and top 10 taxonomic trees. The results showed that the spreading profile in Jordan is composed of (5) geographical clusters vis-à-vis the origin of the pandemic. These include 2 different clusters similar to sequences from the UK, 1 cluster from Morocco and 2 clusters with local transmission designation. The neighbor joining (NJ) of distance-based

Table 1. Sequences description for the Covid-2 of the genus Betacoronavirus and family Coronaviridae; during pandemic period of March 1st. and October 1st. 2020 as compared with selected global strains.

No	GeneBank/Sequence accession number	Submission date	Sequence length	Geographical location
1	MW041156	2020-09-28	29,870	United Kingdom
2	MW031799	2020-09-23	29,903	Pakistan
3	MW031800	2020-09-23	29,903	Pakistan
4	MW031801	2020-09-23	29,903	Pakistan
5	MW031802	2020-09-23	29,903	Pakistan
6	MW031803	2020-09-23	29,903	Pakistan
7	MT890462	2020-08-17	29,903	Russia: Moscow
8	MT879619	2020-08-13	29,897	Pakistan
9	MT873892	2020-08-11	29,821	United Kingdom
10	MT811544	2020-07-29	29,409	Jordan: Amman
11	MT811545	2020-07-29	29,409	Jordan: Amman
12	MT811546	2020-07-29	29,409	Jordan: Amman
13	MT811548	2020-07-29	29,409	Jordan: Amman
14	MT811549	2020-07-29	29,409	Jordan: Amman
15	MT811550	2020-07-29	29,409	Jordan: Amman
16	MT811551	2020-07-29	29,409	Jordan: Amman
17	MT811552	2020-07-29	29,412	Jordan: Amman
18	MT811553	2020-07-29	29,409	Jordan: Amman
19	MT811554	2020-07-29	29,409	Jordan: Amman
20	MT811555	2020-07-29	29,409	Jordan: Amman
21	MT811556	2020-07-29	29,409	Jordan: Amman
22	MT811557	2020-07-29	29,409	Jordan: Amman
23	MT811558	2020-07-29	29,409	Jordan: Amman
24	MT811560	2020-07-29	29,409	Jordan: Irbid
25	MT811561	2020-07-29	29,409	Jordan: Amman
26	MT811562	2020-07-29	29,409	Jordan: Irbid
27	MT811564	2020-07-29	29,409	Jordan: Amman
28	MT811565	2020-07-29	29,409	Jordan: Amman
29	MT811566	2020-07-29	29,406	Jordan: Amman
30	MT811567	2020-07-29	29,409	Jordan: Amman
31	MT811568	2020-07-29	29,409	Jordan: Amman
32	MT811569	2020-07-29	29,409	Jordan: Amman
33	MT801000	2020-07-27	29,854	Lebanon
34	MT801001	2020-07-27	29,829	Lebanon
35	MT801002	2020-07-27	29,865	Lebanon
36	MT801003	2020-07-27	29,779	Lebanon
37	MT789712	2020-07-22	29,856	Bahrain

Continued

38	MT745584	2020-07-13	29,860	Bahrain
39	MT745767	2020-07-13	29,879	Bahrain
40	MT745836	2020-07-13	29,879	Bahrain
41	MT745875	2020-07-13	29,800	Bahrain
42	MT747438	2020-07-13	29,782	Belgium
43	MT742782	2020-07-12	29,885	Bahrain
44	MT742783	2020-07-12	29,856	Bahrain
45	MT742784	2020-07-12	29,766	Bahrain
46	MT731285	2020-07-08	29,903	Morocco
47	MT731292	2020-07-08	29,903	Morocco
48	MT731327	2020-07-08	29,903	Morocco
49	MT731346	2020-07-08	29,867	Bahrain: Capital
50	MT731468	2020-07-08	29,903	Morocco
51	MT731673	2020-07-08	29,903	Morocco
52	MT731746	2020-07-08	29,903	Morocco
53	MT731764	2020-07-08	29,903	Morocco
54	MT733120	2020-07-08	29,903	Morocco
55	MT635445	2020-06-18	29,727	Russia: Moscow region
56	MT637143	2020-06-18	29,883	Russia: Moscow region
57	MT568645	2020-06-05	29,838	Morocco: Casablanca
58	MT513758	2020-06-03	29,875	Morocco
59	MT500122	2020-05-21	29,819	Pakistan: Karachi
60	MT262993	2020-03-31	29,836	Pakistan: KPK
61	MT240479	2020-03-25	29,836	Pakistan: Gilgit
62	MT093571	2020-02-21	29,886	Sweden
63	MT072688	2020-02-18	29,811	Nepal
64	MW031799	2020-09-23	29,903	Pakistan

phylogenetic analysis of the top 100 (Figure 2) and top 10 (Figure 3) taxonomic trees revealed almost identical homology between hCoV-19/Jordan strain and the strains that broke out in Wuhan, the MT642226.1.

The sequence description of the hCoV-19/Jordan strain in comparison with global sequences homology (99.98% - 100%) based on NCBI database filter results is presented in Table 1. All sequences of the hCoV-19/Jordan strain were complete, exceeding (29,400 bp), and example of the complete sequence of the hCoV-19/Jordan is given in Figure 3, which were therefore compared with similar complete global sequences. The clades and sub-clades descriptions of the genealogical lineage of the hCoV-19/Jordan strain are presented in Table 2; which shows that the hCoV-19/Jordan strain belongs to the G, V, and S clades with spreading frequencies of 89%, 7% and 4%, respectively.
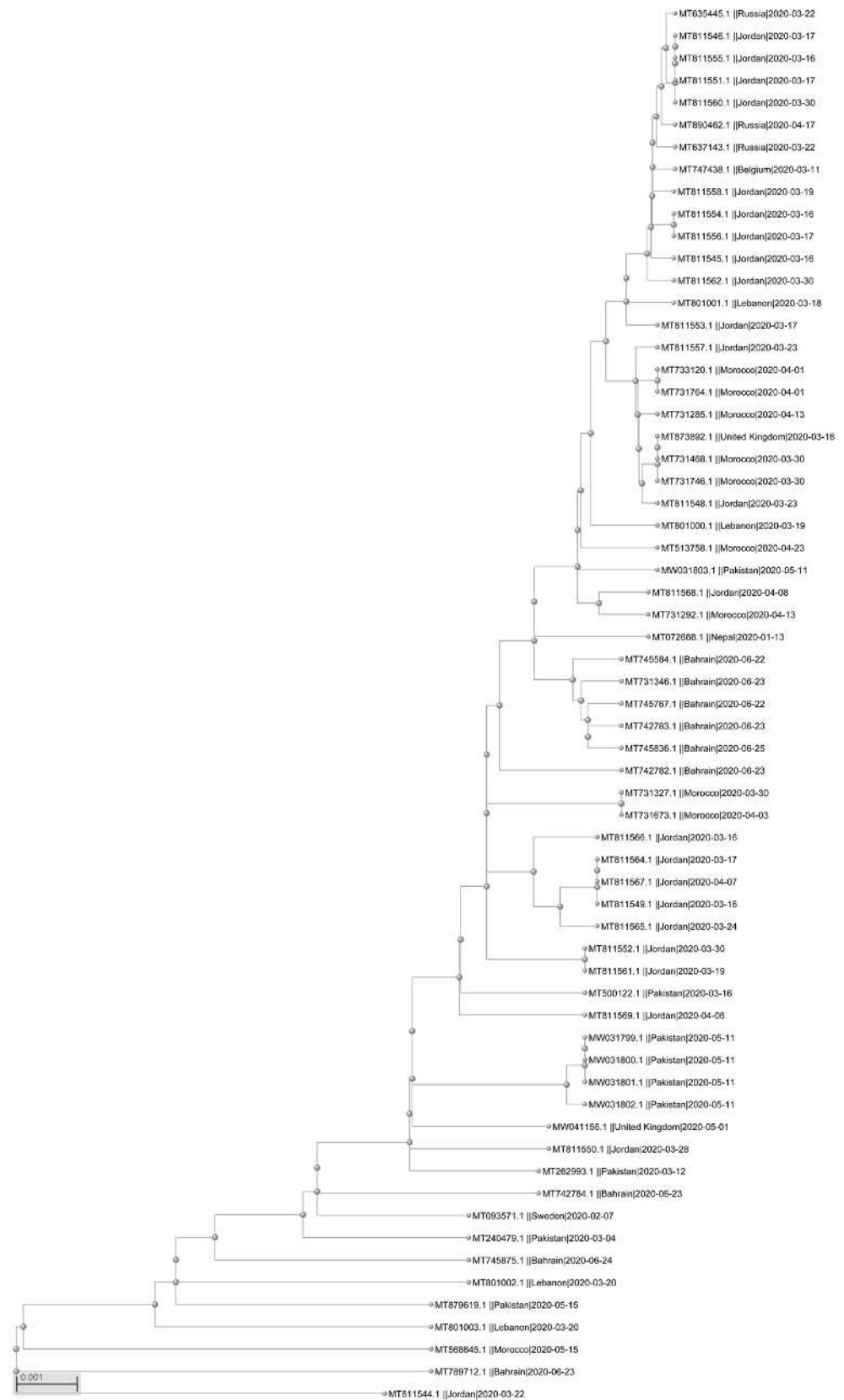
Figure 1. NJ-distance phylogenetic of the hCoV-19/Jordan sequences as compared to the global sequences.
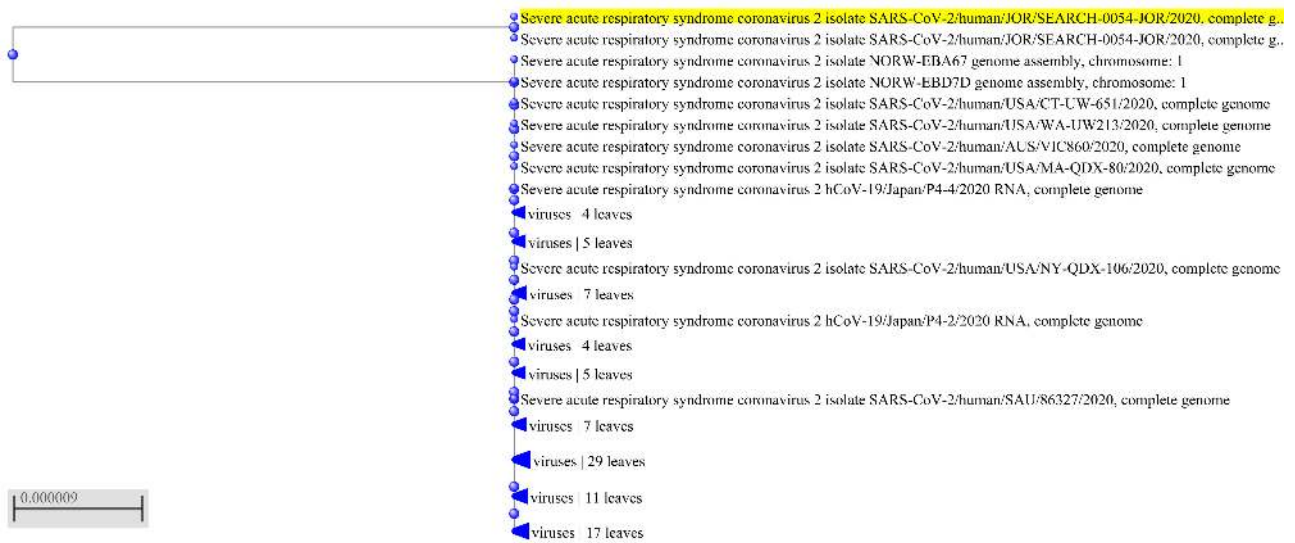
Figure 2. NJ-distance phylogenetic of the hCoV-19/Jordan sequences as compared to the top-100 hits of global sequences.
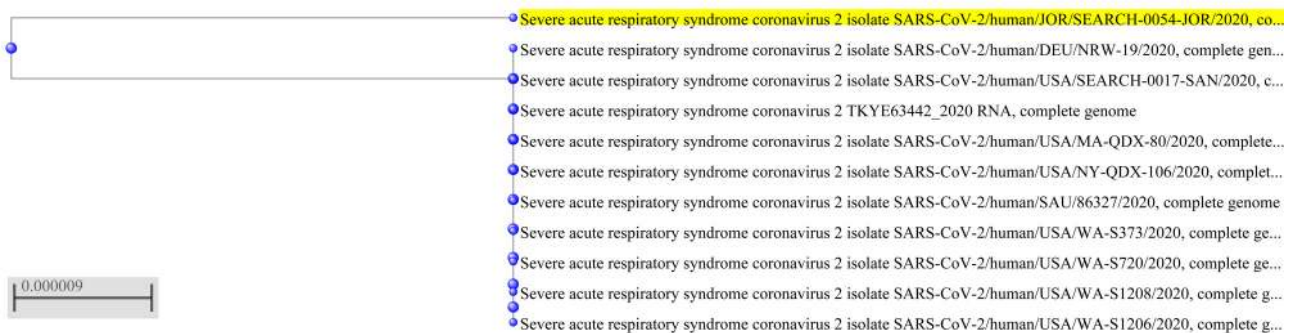
Figure 3. NJ-distance phylogenetic of the hCoV-19/Jordan sequences as compared to the top-10 hits of global sequences.

4. Discussion

The phylogenetic analysis of the hCoV-19/Jordan strain constructed from selected global genomes deposited into GISAID for comparison purposes revealed that the 28 genome sequences from Jordan employed in this study were compatible with the evolutionary tree of SARS-CoV-2, and had a complete genome length of 29,400 bp and homology of (99.98% - 100%) (Figure 1). This provides a conclusive evidence that the hCoV-19/Jordan is part of the global pandemic strains of SARS-CoV-2. The results of our study showed that the genome length and homology of the hCoV-19/Jordan strain are in consonance with those reported for the SARS-CoV-2 strains globally [1] [3] [11]. The neighbor joining phylogenetic analysis of the top 100 (Figure 2) and top 10 taxonomic trees (Figure 3) showed conclusively that the hCoV-19/Jordan strain had almost identical homology (99.98% - 100%) with the strains that broke out in Wuhan, the MT642226.1. This suggests that it is the most recent strain, and has a common ancestry with the strains transmitted and detected in Jordan. Similarly, all sequences of the Jordanian strains of hCoV-19/Jordan were compared to the England and American strains and showed identical homology of (99.98% -

Table 2. Characterization of the clades & genealogical-lineages of the COVID-19 strains clusters during pandemic in Jordan.

No	Clade/ Lineage	Virus name	Accession ID	Collection date	Submission date	Length	Geographical region
1	G/B.1.1	hCoV-19/Jordan/SR-055/2020	EPI_ISL_430013	2020-04-02	2020-04-24	29,409	Asia/Jordan/Amman
2		hCoV-19/Jordan/SR-049/2020	EPI_ISL_430007	2020-03-19	2020-04-24	29,409	Asia/Jordan/Amman
3		hCoV-19/Jordan/SR-048/2020	EPI_ISL_430006	2020-03-23	2020-04-24	29,409	Asia/Jordan/Amman
4		hCoV-19/Jordan/SR-047/2020	EPI_ISL_430005	2020-03-26	2020-04-24	29,397	Asia/Jordan/Amman
5		hCoV-19/Jordan/SR-046/2020	EPI_ISL_430004	2020-03-17	2020-04-24	29,409	Asia/Jordan/Amman
6		hCoV-19/Jordan/SR-045/2020	EPI_ISL_430003	2020-03-16	2020-04-24	29,409	Asia/Jordan/Amman
7		hCoV-19/Jordan/SR-044/2020	EPI_ISL_430002	2020-03-16	2020-04-24	29,409	Asia/Jordan/Amman
8		hCoV-19/Jordan/SR-043/2020	EPI_ISL_430001	2020-03-17	2020-04-24	29,409	Asia/Jordan/Amman
9		hCoV-19/Jordan/SR-041/2020	EPI_ISL_429999	2020-03-17	2020-04-24	29,409	Asia/Jordan/Amman
10		hCoV-19/Jordan/SR-036/2020	EPI_ISL_429996	2020-03-23	2020-04-24	29,409	Asia/Jordan/Amman
11		hCoV-19/Jordan/SR-034/2020	EPI_ISL_429994	2020-03-17	2020-04-24	29,409	Asia/Jordan/Amman
12		hCoV-19/Jordan/SR-033/2020	EPI_ISL_429993	2020-03-16	2020-04-24	29,409	Asia/Jordan/Amman
13		hCoV-19/Jordan/SR-032/2020	EPI_ISL_429992	2020-03-22	2020-04-24	29,409	Asia/Jordan/Amman
14	G/B.1.1	hCoV-19/Jordan/SR-054/2020	EPI_ISL_430012	2020-03-30	2020-04-24	29,409	Asia/Jordan/Irbid
15	G/B.1.1	hCoV-19/Jordan/SR-052/2020	EPI_ISL_430009	2020-03-30	2020-04-24	29,409	Asia/Jordan/Irbid
16	GH/B.1.36	hCoV-19/Jordan/SR-0335/2020	EPI_ISL_450187	2020-04-08	2020-05-20	29,864	Asia/Jordan/Amman
17	B.2.1(O)	hCoV-19/Jordan/SR-084/2020	EPI_ISL_434516	2020-03-16	2020-04-29	29,406	Asia/Jordan/Amman
18		hCoV-19/Jordan/SR-057/2020	EPI_ISL_430015	2020-03-24	2020-04-24	29,409	Asia/Jordan/Amman
19		hCoV-19/Jordan/SR-056/2020	EPI_ISL_430014	2020-03-17	2020-04-24	29,409	Asia/Jordan/Amman
20		hCoV-19/Jordan/SR-053/2020	EPI_ISL_430011	2020-03-19	2020-04-24	29,409	Asia/Jordan/Amman
21		hCoV-19/Jordan/SR-051/2020	EPI_ISL_430008	2020-04-04	2020-04-24	29,409	Asia/Jordan/Amman
22		hCoV-19/Jordan/SR-042/2020	EPI_ISL_430000	2020-03-30	2020-04-24	29,412	Asia/Jordan/Amman
23		hCoV-19/Jordan/SR-039/2020	EPI_ISL_429998	2020-03-28	2020-04-24	29,409	Asia/Jordan/Amman
24		hCoV-19/Jordan/SR-037/2020	EPI_ISL_429997	2020-03-16	2020-04-24	29,409	Asia/Jordan/Amman
25		hCoV-19/Jordan/SR-035/2020	EPI_ISL_429995	2020-03-30	2020-04-24	29,412	Asia/Jordan/Amman
26	S/A	hCoV-19/Jordan/SR-0336/2020	EPI_ISL_450188	2020-04-06	2020-05-20	29,864	Asia/Jordan/Amman
27	V/B.2	hCoV-19/Jordan/SR-0338/2020	EPI_ISL_450189	2020-04-06	2020-05-20	29,883	Asia/Jordan/Amman
28	V/B.2	hCoV-19/Jordan/SR-0333/2020	EPI_ISL_450186	2020-04-07	2020-05-20	29,864	Asia/Jordan/Amman

100%) (Figure 2 and Figure 3) and as it can be seen from the example of the complete sequence of the hCoV-19/Jordan strain as given in Figure 4.

Comparison of the clades of hCoV-19/Jordan with that of SARS-CoV-2 showed that the most plausible transmission routes are European countries (UK, Belgium, Sweden, Russia) and Morocco, which are entry points into Jordan. This can be attributed to the fact that both the G and V clades reported in this study for hCoV-19/Jordan strain are similar to those reported earlier in these European countries [12] [19]. This further suggests that the strain was transmitted through the heavy air traffic transmission rout between EU countries-Morocco-Jordan) after the strains were transmitted from China to EU countries. This is

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>MT811562.1:1-13203,13203-21290 Severe acute respiratory syndrome
coronavirus 2 isolate SARS-CoV-2/human/JOR/SEARCH-0054-JOR/2020, complete
genome
ATGGAGAGCCTTGTCCCTGGTTTCAACGAGAAAACACACGTCCAACTCAGTTTGCCTGTTTTACAGGTTC
GCGACGTGCTCGTACGTGGCTTTGGAGACTCCGTGGAGGAGGTCTTATCAGAGGCACGTCAACATCTTAA
AGATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTTC
ATCAAACGTTCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGCAGAACTCGAAG
GCATTCAGTACGGTCGTAGTGGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAATACCAGTGGC
TTACCGCAAGGTTCTTCTTCGTAAGAACGGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTA
AAGTCATTTGACTTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAACTGGAACACTA
AACATAGCAGTGGTGTTACCCGTGAACTCATGCGTGAGCTTAACGGAGGGGCATACACTCGCTATGTCGA
TAACAACTTCTGTGGCCCTGATGGCTACCTCTTGAGTGCATTAAAGACCTTCTAGCACGTGCTGGTAAA
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GTGAAAGGTTTGGATTATAAAGCATTCAAACAAATTGTTGAATCCTGTGGTAATTTTAAAGTTACAAAAG
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CGGTGCACCAACAAAGGTTACTTTTGGTGATGACACTGTGATAGAAGTGCAAGGTTACAAGAGTGTGAAT
ATCACTTTTGAACTTGATGAAAGGATTGATAAAGTACTTAATGAGAAGTGCTCTGCCTATACAGTTGAAC
TCGGTACAGAAGTAAATGAGTTCGCCTGTGTTGTGGCAGATGCTGTCATAAAAACTTTGCAACCAGTATC
TGAATTACTTACACCACTGGGCATTGATTTAGATGAGTGGAGTATGGCTACATACTACTTATTTGATGAG
TCTGGTGAGTTTAAATTGGCTTCACATATGTATTGTTCTTTTACCCTCCAGATGAGGATGAAGAAGAAG
GTGATTGTGAAGAAGAAGAGTTTGAGCCATCAACTCAATATGAGTATGGTACTGAAGATGATTACCAAGG
TAAACCTTTGGAATTTGGTGCCACTTCTGCTGCTCTTCAACCTGAAGAAGAGCAAGAAGAAGATTGGTTA
GATGATGATAGTCAACAAACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACTACTATTCAAA
CAATTGTTGAGGTTCAACCTCAATTAGAGATGGAACTTACACCAGTTGTTCAGACTATTGAAGTGAATAG
TTTTAGTGGTTATTTAAAACTTACTGACAATGTATACATTAAAAATGCAGACATTGTGGAAGAAGCTAAA
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CCTTAAATAAGGCTACTAACAATGCCATGCAAGTTGAATCTGATGATTACATAGCTACTAATGGACCACT
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TAAGGTTGTCAAAGTGACTATTGACTATACAGAAATTTCATTTATGCTTTGGTGTAAAGATGGCCATGTA
GAAACATTTTACCCAAAATTACAATCTAGTCAAGCGTGGCAACCGGGTGTTGCTATGCCTAATCTTTACA
AAATGCAAAGAATGCTATTAGAAAGTGTGACCTTCAAAATTATGGTGATAGTGCAACATTACCTAAAGG
CATAATGATGAATGTCGCAAAATATACTCAACTGTGTCAATATTTAAACACATTAACATTAGCTGTACCC
TATAATATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGTTGCACCAGGTACAGCTGTTTTAA
GACAGTGGTTGCCTACGGGTACGCTGCTTGTCGATTCAGATCTTAATGACTTTGTCTCTGATGCAGATTC
AACTTTGATTGGTGATTGTGCAACTGTACATACAGCTAATAAATGGGATCTCATTATTAGTGATATGTAC
GACCCTAAGACTAAAAATGTTACAAAAGAAAATGACTCTAAAGAGGGTTTTTTCACTTACATTTGTGGGT
TTATACAACAAAAGCTAGCTCTTGGAGGTTCCGTGGCTATAAAGATAACAGAACATTCTTGGAATGCTGA
TCTTTATAAGCTCATGGGACACTTCGCATGGTGGACAGCCTTTGTTACTAATGTGAATGCGTCATCATCT
GAAGCATTTTTAATTGGATGTAATTATCTTGGCAAACCACGCGAACAAATAGATGGTTATGTCATGCATG
CAAATTACATATTTTGGAGGAATACAAATCCAATTCAGTTGTCTTCCTATTCTTTATTTGACATGAGTAA
ATTTCCCCTTAAATTAAGGGGTACTGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGATTTTA
TCTCTTCTTAGTAAAGGTAGACTTATAATTAGAGAAACAACAGAGTTGTTATTTCTAGTGATGTTCTTG
TTAACAACTAA
```

Figure 4. Example of the complete sequence of the hCoV-19/Jordan.

in consonance with previous reports that stated that clade G apparently originated from Shanghai before it was imported into European countries [17] [20] [21].

5. Conclusion

The results of this study show conclusively a unique pandemic profile of multiple geographical sources of COVID-19 importation into Jordan primarily through UK, Belgium, Sweden, Russia and Morocco, which are entry points into Jordan. This is also due to the reciprocal heavy air traffic route between Jordan and European capitals. It can be inferred based on the identical homology (99.98% - 100%) of the 28 sequences of hCoV-19/Jordan strain that there was no marked change in the virus mutation that occurred during the period of this study.

Acknowledgements

Data Availability

All the 28 sequences of the hCoV-19/Jordan used in this paper have been used as available on the public Domains in both NCBI GeneBank (http://www.ncbi.nlm.nih.gov/) and the Global Initiative on Sharing All Influenza Data (GISAID) (http://www.gisaid.org/) under the name of hCoV-19/Jordan as per each respective accession number. All clinical data of the patients, epidemiological details as well as sampling surveillances were maintained in the National record of the Ministry of Health of Jordan.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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