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Comparison Diversity Sequences of SARS-CoV-2 Spread in Morocco and Mauritania Insights into Variants and Mutational Impacts

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ABSTRACT— The COVID-19 pandemic, caused by SARS-CoV-2, highlights the need to understand the virus's genomic diversity and evolution. This study analyzes SARS-CoV-2 data from Mauritania and Morocco using molecular diagnostics and bioinformatics tools. In Mauritania, 58 nasopharyngeal samples were analyzed through RNA extraction, RT-PCR detection, and complete genome sequencing using the Illumina COVIDSeq protocol. Moroccan sequences were retrieved from the GISAID database for comparative analysis. Key bioinformatics tools, including MEGA X and Genome Detective, were used to identify variants, mutations, and evolutionary relationships. The results reveal the prevalence of Omicron subvariants (BA.2 and BA.5) in both regions, with notable differences such as the persistence of Delta in Mauritania and the dominance of Omicron in Morocco. These findings emphasize the importance of genomic surveillance and molecular tools to guide public health strategies.

KEYWORDS: Sars-cov2, covid-19, Delta subvariants, Omicron subvariants, Moroccan and Mauritania Population.

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1. Introduction

The COVID-19 pandemic, caused by SARS-CoV-2, has profoundly impacted global public health, triggering an unprecedented scientific mobilization to understand its evolution and genetic diversity. Since its appearance in December 2019, the virus has given rise to multiple lineages and variants of concern (VOCs) that influence its transmissibility, pathogenicity, and immune escape [1], [2]. These evolutionary features are attributable to key mutations, which can be identified and analyzed using powerful bioinformatics tools such as MEGA, Discovery Studio, and NCBI BLAST [3- 5].

The A and B clades, at the origin of the phylogenetic evolution of SARS-CoV-2, have generated significant sub-variants such as Delta (B.1.617.2) and Omicron (BA.1, BA.2, BA.5).

Alpha (B.1.1.7), first detected in the United Kingdom in September 2020, rapidly dominated in Europe and North America due to its increased transmissibility (+50% compared to the original strain). Beta (B.1.351), identified in South Africa, demonstrated significant immune evasion capabilities, posing challenges to vaccination efforts. Gamma (P.1), originating in Brazil, was associated with increased reinfections, underscoring its impact on herd immunity. Delta (B.1.617.2), first identified in India, dominated the pandemic in 2021, exhibiting both higher transmissibility and greater virulence, leading to severe waves of infection globally.

Omicron and its subvariants (BA.1, BA.2, BA.5, XBB) emerged in late 2021, characterized by a high number of mutations in the Spike protein, conferring unprecedented transmissibility and partial immune escape. Subvariants BA.2 and BA.5 replaced previous VOCs in many regions, while XBB, a recombinant lineage, has dominated globally since 2023.

These sub-variants, which currently dominate in several regions of the world, reflect viral adaptability in the face of environmental and immune pressures [6]. In Africa, where genomic surveillance capacities are sometimes limited, bioinformatics analysis plays an essential role in detecting and characterizing variants [7]. To interpret the genetic diversity of SARS-CoV-2, several bioinformatics tools stand out for their efficiency. MEGA (Molecular Evolutionary Genetics Analysis) is widely used to construct phylogenetic trees and analyze evolutionary relationships between genomic sequences [3]. NCBI BLAST (Basic Local Alignment Search Tool) remains essential for sequence alignment and comparison with international databases [4]. Discovery Studio, an advanced molecular modeling platform, explores the structural impact of mutations on viral proteins [5]. Genome Detective automates the detection and annotation of viral genomes, simplifying the analysis of large quantities of sequenced data [8].

In addition, Nextstrain provides interactive visualization of phylogenetic relationships and evolutionary dynamics of SARS-CoV-2, facilitating real-time analysis of global and local data [9]. These combined tools enable in-depth analysis of key mutations, emerging lineages, and local or regional variations in virus evolution, offering essential insights for anticipating future epidemic waves [6], [9].

This study aims to analyze the genomic diversity and evolution of SARS-CoV-2 in Mauritania and Morocco within the global context. By identifying key mutations and dominant lineages, this research contributes to a deeper understanding of evolutionary trajectories and their implications for public health.

2. Materials and Methods

1. Moroccan Samples

The Moroccan sequences were directly retrieved from the GISAID (Global Initiative on Sharing All Influenza Data) database, which holds comprehensive SARS-CoV-2 genomes, thus facilitating a reliable comparison of the variants circulating in Mauritania and Morocco.

2. Mauritanian Samples

58 Nasopharyngeal samples, collected between September and November 2021, were randomly selected from samples stored at the National Institute of Public Health Research (INRSP)[12]. Clinical and socio-demographic information of the patients was extracted from their medical records, following data anonymization. This study was approved by the Ethics Committee of the University of Nouakchott under reference number 2020-010. [13].

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Extraction of viral RNA

Viral RNA was isolated using the MagMax Viral RNA Isolation Kit (Thermo Fisher Scientific, Waltham, MA, USA), following the manufacturer's recommendations. The quality and concentration of extracted RNA were measured using a NanoDrop spectrophotometer (Thermo Fisher Scientific). The extracted RNAs were immediately used for viral detection.

Real-time RT-PCR

Detection of SARS-CoV-2 was performed by real-time RT-PCR using the commercial kit BGI Health (HK) Co. Ltd (Shenzhen, China). This kit detects SARS-CoV-2 in a single step using the ORF1ab probe. RT-PCR was performed on a LightCycler® 480 Instrument II thermal cycler (Roche, Basel, Switzerland) [19]. The PCR amplification was performed using the following program: initial denaturation at 50°C for 20 minutes, followed by denaturation at 94°C for 10 minutes. Amplification was carried out for 40 cycles, consisting of denaturation at 95°C for 15 seconds, and annealing at 60°C for 30 seconds. Only samples with a cycle threshold (Ct) value less than or equal to 30 were considered positive and used for sequencing.

Sequencing of the complete SARS-CoV-2 genome

Full genome sequencing was performed for the 18 SARS-CoV-2-positive patients according to the Illumina COVIDSeq protocol (Illumina Inc., San Diego, CA, USA). First, extracted RNA from each patient sample was converted to complementary DNA (cDNA) through reverse transcription using a random hexamer primer. The resulting cDNA was then amplified to cover the target regions of the SARS-CoV-2 genome. Following amplification, the sequencing library was prepared following the Illumina protocol. Sequencing was performed on an Illumina platform, following the manufacturer's standard specifications.

3. Bioinformatic Analysis

Several bioinformatics tools were used to analyze SARS-CoV-2 sequences. NCBI BLAST compared the obtained sequences with public databases to identify similarities and detect rare mutations. Discovery was employed for detailed mutation analysis, focusing on key viral proteins like the Spike protein, to assess potential impacts on vaccine efficacy. Genome Detective identified SARS-CoV-2 variants by comparing sequences to known variants, providing insights into variant dynamics in Mauritania and Morocco. SNPeff annotated genetic mutations and evaluated their functional effects, particularly on the Spike protein and viral virulence. MEGA X was used for phylogenetic analyses, generating evolutionary trees to study the relationships and diversity of variants, with statistical tests to assess result robustness. Finally, IQTree was used to perform additional phylogenetic analyses, offering reliable insights into genetic diversity and the presence of mutations within variants.

3. Results

The distribution of clinicopathological parameters across a cohort of 58 patients. (Table 1) In terms of age, the majority of the participants were aged between 40 and 60 years, accounting for 44.8% of the sample, while 50% were under 40 years of age, and only 5.2% were over 60 years. Regarding gender, a higher proportion of male participants (62.1%) was observed compared to females, who represented 37.9% of the sample. As for COVID-19 status, a significant majority of participants were negative for the virus (70.7%), with only 29.3% testing positive. Notably, the patients who tested positive for COVID-19 underwent sequencing for SARS-CoV-2.

Table 1: Distribution of Clinicopathological Parameters in the Mauritanian Population

Clinicopathological Parameters	N (%)

Age	
< 40	29 (50.0%)
40-60	26 (44.8%)
> 60	3 (5.2%)
Gender	
Female	22 (37.9%)
Male	36 (62.1%)
Covid19	
Positive	17 (29.3%)
Negative	41 (70.7%)

The distribution of SARS-CoV-2 sequences within the Mauritanian population (Table 2) according to dominant genetic variants. The Omicron subvariant (BA.5 22B) is the most prevalent, accounting for 27.8% of the sequences analyzed, followed by the Delta variant (B.1.617.2), which makes up 22.2% of the total. Other subvariants, such as Omicron (BA.2 21L) and Alpha (B.1.1.7 I20), are also present, though in smaller proportions, each representing 5.56% of the sequences. In total, the 18 sequences analyzed reveal the genetic diversity circulating within the Mauritanian population, with a predominance of the Omicron and Delta subvariants, reflecting the current dynamics of variant transmission in the country.

Table 2: Genomic sequence analysis of SARS-CoV-2 in Mauritania: Variants and clades

Blast/aga assignment	Genotype assignment	Sub-clustering	Sequences count	Percentage
Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 (/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/Olter-SARS-CoV-2)	International A_B Diversity	7	38.9%
	(/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/Olter-SARS-CoV-2)	Omicron (BA.5 22B)	5	27.8%
	(/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/Olter-SARS-CoV-2)	Delta (B.1.617.2 21A,21I,21J)	4	22.2%
	(/app/typingtool/cov/job/32feab6c-050d- 4bb8-8b3d-6a24450f5d48/Olter-SARS- CoV-2)	Omicron (BA.2 21L)	1	5.56%
	(/app/typingtool/cov/job/32feab6c-050d- 4bb8-8b3d-6a24450f5d48/Olter-SARS- CoV-2)	Alpha (B.1.1.7 I20)	1	5.56%
Total			18	100%

The genomic analysis of 18 SARS-CoV-2-positive samples from Mauritanian patients revealed the presence of multiple variants and lineages (Table 3). The sequencing results identified three major clades: Delta (B.1.617.2), Omicron (BA.5.22B and BA.2.11L), and International A and B Diversity. Among these, Omicron was the most prevalent, detected in 10 samples, followed by the Delta variant, found in 2 samples. Three samples were classified under the International A and B Diversity clade. The genome lengths ranged from 29,475 to 29,783 nucleotides, consistent with the SARS-CoV-2 genome size, and all sequences demonstrated complete genomic coverage, ensuring high-quality data. These findings highlight the genetic diversity of

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SARS-CoV-2 circulating in the Mauritanian population at the time of analysis.

Table 3: Genomic Analysis of SARS-CoV-2 Variants in the Mauritanian Population.

Name	Length	Species	Clade, Lineage	Report
hCoV-19MauritaniaIPM-1032022E	29514	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Delta (B.1.617.2, 21A, 21I, 21J)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-0
hCoV-19MauritaniaIPM-1042022E	29757	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A, B Diversity	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-1
hCoV-19MauritaniaIPM-1062022E	29770	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.5.22B)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-2
hCoV-19MauritaniaIPM-1072022E	29763	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2.11L)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-3
hCoV-19MauritaniaIPM-1082022E	29748	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A, B Diversity	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-4
1092022	29756	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.5.22B)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-5
hCoV-19MauritaniaIPM-1102022	29783	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Delta (B.1.617.2, 21A, 21I, 21J)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-6
hCoV-19MauritaniaIPM-1112022	29746	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.5.22B)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-7
hCoV-19MauritaniaIPM-1132022	29669	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A, B Diversity	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-

				6a24450f5d48/sequence-9
hCoV-19MauritaniaIPM-1142022	29475	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.5.22B)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-10
hCoV-19MauritaniaIPM-1152022	29757	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.5.22B)	/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-11
hCoV-19MauritaniaIPM-242020|EP	29823	Severe acute respiratory syndrome- related coronavirus	SARS- CoV-2 InternationalA_B Diversity	Report/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d 6a24450f5d48/sequence-12)
hCoV-19MauritaniaIPM-192020|EP	29806	Severe acute respiratory syndrome- related coronavirus	SARS- CoV-2 InternationalA_B Diversity	Report (/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-12
hCoV-19MauritaniaIPM- 192020|EP	29806	Severe acute respiratory syndrome- related coronavirus	SARS-CoV-2 Delta(B.1.617.2 21A,21I,21J)	Report(/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d 6a24450f5d48/sequence-13)
hCoV-19MauritaniaIPM-412021|EP	29749	Severe acute respiratory syndrome- related coronavirus	SARS- CoV-2 InternationalA_B Diversity	Report(/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d 6a24450f5d48/sequence-14)
hCoV-19MauritaniaIPM-422021|EP	29798	Severe acute respiratory syndrome- related coronavirus	SARS- CoV-2 InternationalA_B Diversity	Report(/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-15)
hCoV-19MauritaniaIPM-502021|EP	29786	Severe acute respiratory syndrome- related coronavirus	SARS- CoV-2 InternationalA_B Diversity	Report (/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-6a24450f5d48/sequence-16)
hCoV-19MauritaniaIPM-382021|EP	29803	Severe acute respiratory syndrome- related coronavirus	SARS-CoV-2 Alpha(B.1.1.7 I20	Report (/app/typingtool/cov/job/32feab6c-050d-4bb8-8b3d-

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				6a24450f5d48/sequence-17)

The phylogenetic tree generated by the Coronavirus Typing Tool illustrates the genetic relationships among SARS-CoV-2 isolates from Mauritania and other coronaviruses (Figure 1). The analysis clusters the Mauritanian SARS-CoV-2 samples (hCoV-19Mauritania_11 to hCoV-19Mauritania_16) with other SARS-CoV-2 sequences, confirming their classification within the SARS-CoV-2 clade. The SARS-CoV-2 group is distinct from related coronaviruses, including Bat SARS-CoV HKU3, Bat SARS-CoV ZXC21/ZC45, SARS-CoV-1, and SARS-related coronaviruses, which are grouped in separate clades. A similar phylogenetic tree highlights samples collected in Mauritania (in blue). These samples stand out for their clustering, indicating specific genetic relationships with other bat and human coronaviruses. This clustering supports the genetic homogeneity of SARS-CoV-2 within the sampled population and its divergence from other coronaviruses.

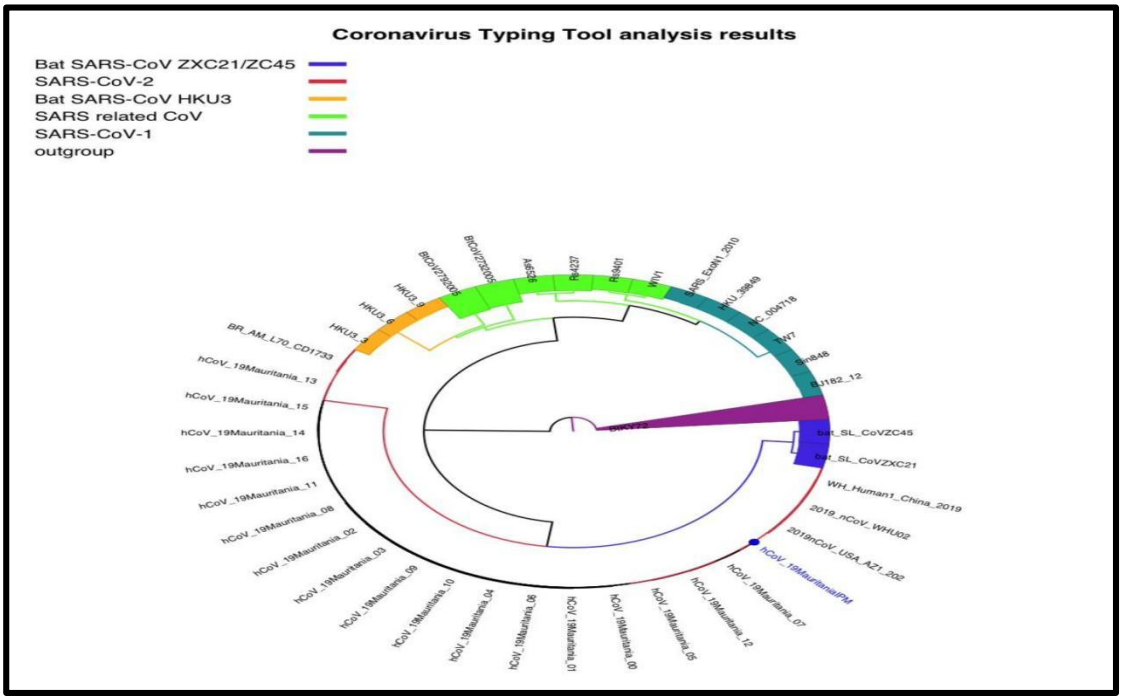

Figure 1: Phylogenetic exploration of Mauritanian samples: overview of links with global coronaviruses.

The genomic analysis of SARS-CoV-2 sequences in Morocco, as summarized in Table 4, highlights the distribution of variants and clades among the sampled population. A total of 20 sequences were analyzed, revealing the dominance of the Omicron variant, which accounted for 65% of the sequences. Specifically, the Omicron (BA.2 21L) sub-clustering represented the largest proportion, with 8 sequences (40.0%), followed by the Omicron (BA.1 21K) sub-clustering, which comprised 5 sequences (25.0%).

In addition to Omicron, the International A_B Diversity cluster was identified in 6 sequences (30.0%), reflecting the global circulation and genetic variability of SARS-CoV-2. Lastly, the Gamma (P.1 20J) variant was detected in 1 sequence (5.0%), indicating its presence in the analyzed samples, albeit at a low frequency. This distribution underscores the predominance of the Omicron variant in the region during the sampling period and highlights the genetic diversity of circulating SARS-CoV-2 variants.

In comparison, the analysis of sequences from Mauritania shows a slightly different distribution. Among the 18 analyzed sequences, the International A_B Diversity cluster is the most represented (38.9%), followed by

the Omicron variant (27.8%, BA.5 22B).

This comparison highlights regional differences in variant prevalence, with Morocco exhibiting a stronger dominance of Omicron sublineages, while Mauritania shows a more balanced distribution of International A_B Diversity, Omicron, and Delta variants. These findings underline the need for ongoing surveillance to track regional variations in SARS-CoV-2 evolution and spread

Table 4: Genomic Analysis of SARS-CoV-2 Sequences in Morocco - Variants and Clades

Blast/AGA Assignment	Genotype Assignment	Sub-Clustering	Sequences Count	Percentage
Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 (/app/typingtool/cov/job/10784617-be9c- 44bc-98dc-81acdd8baf65/Plter-SARS-CoV- 2)	Omicron (BA.2 21L)	8	40.0%
	(/app/typingtool/cov/job/10784617-be9c- 44bc-98dc-81acdd8baf65/Plter-SARS-CoV- 2)	International A_B Diversity	6	30.0%
	(/app/typingtool/cov/job/10784617-be9c- 44bc-98dc-81acdd8baf65/Plter-SARS-CoV- 2)	Omicron (BA.1 21K)	5	25.0%
	(/app/typingtool/cov/job/10784617-be9c- 44bc-98dc-81acdd8baf65/Plter-SARS-CoV- 2)	Gamma (P.1 20J)	1	5.0%
Total			**20**	**100%**

The genomic analysis of SARS-CoV-2 sequences from Morocco (table 5) reveals a significant prevalence of Omicron variants, specifically the BA.2 21L and BA.1 21K lineages, which dominate the dataset with proportions of 40% and 25%, respectively. Additionally, 30% of the sequences are associated with international A_B diversity, reflecting genetic variation likely linked to cross-border viral transmission. A single sequence belonging to the Gamma (P.1 20J) lineage, representing 5% of the dataset, suggests an isolated introduction of this variant. The genome lengths range from 18,518 to 29,779 nucleotides, consistent with typical SARS-CoV-2 genomic variability. Detailed reports for each sequence, accessible via specific links, provide further insights into the genomic characteristics and analysis. These findings underscore the dominance of Omicron variants in Morocco, aligning with global trends, while also highlighting the importance of genomic surveillance to monitor variant introductions and evolutionary dynamics in a geographically diverse context.

Table 5 : Genomic Analysis of SARS-CoV-2 Variants in Moroccan Population

Name	Length	Species	Clade, Lineage	Report
hCoV-19Morocco672022 EPI_ISL_1	29747	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-0
hCoV-19Morocco682022 EPI_ISL_1	29779	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.1 21K)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-1

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hCoV-19Morocco692022 EPI_ISL_1	29769	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.1 21K)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-2
hCoV-19Morocco702022 EPI_ISL_1	29770	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.1 21K)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-3
hCoV-19Morocco712022 EPI_ISL_1	29747	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-4
hCoV-19Morocco722022 EPI_ISL_1	29747	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-5
hCoV-19Morocco732022 EPI_ISL_1	29755	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.1 21K)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-6
hCoV-19Morocco742022 EPI_ISL_1	29770	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.1 21K)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-7
hCoV-19Morocco752022 EPI_ISL_1	29747	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-8
hCoV-19Morocco762022 EPI_ISL_1	29691	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-9
hCoV-19Morocco772022 EPI_ISL_1	29691	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-10
hCoV-19Morocco782022 EPI_ISL_1	29691	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-11

hCoV-19Morocco792022 EPI_ISL_1	29747	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Omicron (BA.2 21L)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-12
hCoV-19Morocco72020 EPI_ISL_19	25223	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 Gamma (P.1 20J)	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-13
hCoV-19Morocco82020 EPI_ISL_19	25814	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-14
hCoV-19Morocco92020 EPI_ISL_19	18583	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-15
hCoV-19Morocco102020 EPI_ISL_1	18518	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-16
hCoV-19Morocco112020 EPI_ISL_1	20939	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-17
hCoV-19Morocco122020 EPI_ISL_1	12194	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-18
hCoV-19Morocco132020 EPI_ISL_1	15281	Severe acute respiratory syndrome-related coronavirus	SARS-CoV-2 International A_B Diversity	https://app/typingtool/cov/job/10784617-be9c-44bc-98dc-81acdd8baf65/sequence-19

The phylogenetic analysis depicted in the circular dendrogram highlights the evolutionary relationships between SARS-CoV-2 sequences from Morocco (Figure 2) and other coronaviruses, including bat SARS-CoV ZXC21/ZC45, bat SARS-CoV HKU3, SARS-related coronaviruses, SARS-CoV-1, and an outgroup. The Moroccan SARS-CoV-2 sequences cluster predominantly within the SARS-CoV-2 branch, showcasing their close genetic similarity and evolutionary proximity. Notably, these sequences form distinct sub-clusters within the SARS-CoV-2 clade, reflecting the diversity of circulating variants. The inclusion of bat and SARS-related coronaviruses, along with the outgroup, underscores the broader context of coronavirus evolution and zoonotic spillover. This phylogenetic representation emphasizes the genetic distinction of SARS-CoV-2 from related coronaviruses while also illustrating the lineage-specific variations observed in the Moroccan isolates.

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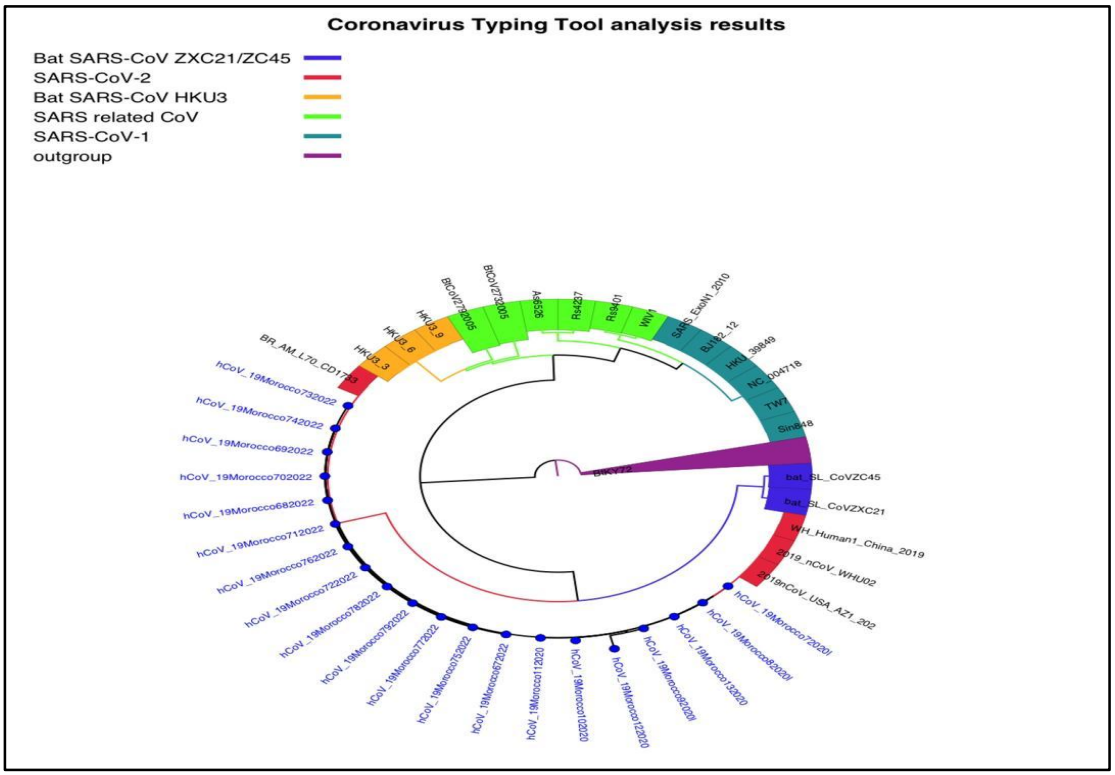

Figure 2: Phylogenetic exploration of Morocco samples: overview of links with global coronaviruses.

Phylogenetic

The phylogenetic analysis comparing SARS-CoV-2 sequences from Morocco and Mauritania reveals notable similarities and distinctions in the evolutionary patterns of the virus in these two regions. While Moroccan sequences form distinct sub-clusters within the SARS-CoV-2 clade, reflecting intra-regional diversity, the Mauritanian sequences also cluster tightly within the SARS-CoV-2 clade but exhibit a slightly more homogeneous distribution. Both datasets highlight the genetic proximity of the sequences to the SARS-CoV-2 lineage, distinct from bat SARS-CoV and SARS-related coronaviruses. This comparison underscores the shared evolutionary trajectory of the virus in North Africa while reflecting regional variations in viral diversity and potential transmission dynamics. These findings provide critical insights into the genomic evolution and transmission dynamics of SARS-CoV-2 in the region.

4. Discussion

Analysis of SARS-CoV-2 genomic data in the distinct geographical contexts of Mauritania and Morocco highlights crucial elements concerning genomic surveillance and the evolution of virus variants, underlining its fundamental role in pandemic management. In both countries, the Omicron variant dominates, although there are notable differences in the sub-variants circulating.

In Mauritania, Omicron (BA.5) accounts for 27.8% of samples analyzed, followed by the Delta variant (B.1.617.2), which remains at 22.2%, despite its overall decline. The fact that Delta still persists at a relatively high rate in this country suggests either local resistance, or persistence of this variant due to specific epidemiological or health management factors [10]. The situation in Morocco is different, where Omicron (BA.2) dominates with 40%, and there is also a significant presence of Omicron sub-variants, such as BA.1, accounting for 25% of samples. A residual presence of the Gamma variant is also noted in 5% of Moroccan samples, which could indicate a local introduction or persistence of older variants, or a delay in the circulation of new variants [10].

The differences in variant dynamics between these two countries highlight the importance of genomic monitoring. In Mauritania, the diversity of variants is wider, with a marked coexistence of Omicron, Delta and other sub-variants such as Alpha. This may reflect a more complex history of virus circulation, including imported cases and diverse local transmissions. On the other hand, although Omicron is dominant in Morocco, the small but significant persistence of the Gamma variant suggests the continued presence of older variants, which could also be linked to geographical factors or specific public health measures [11].

The study of mutations and clade diversity in both countries highlights the rapid evolution of the virus, with Omicron diversifying genetically to partially escape immune recognition. This phenomenon enables Omicron to maintain its prevalence and gradually replace earlier variants such as Delta. The dominance of Omicron, particularly the BA.2 and BA.5 sub-variants, is in line with global trends where Omicron has supplanted other variants due to its increased transmissibility and partial immune evasion [14]. The absence of Delta in the data marocaines could be linked to local pandemic management strategies, such as sanitary measures, vaccination and travel restrictions. These measures may have has led to reduced circulation of the Delta variant, favoring the rapid emergence of Omicron. This highlights the importance of continuous monitoring of variants to anticipate their evolution and adapt health strategies in line with epidemiological trends [16].

Another important dimension of the analysis lies in the disparities observed in surveillance efforts between the two countries. Morocco benefits from wider sampling and a greater capacity to track and identify local strains, in contrast to Mauritania, which has a richer but still insufficiently sampled genetic diversity. This represents an opportunity for more in-depth research, particularly in under-sampled areas, to identify intermediate strains and better understand the origin of viruses circulating in these regions. It is therefore essential to invest in genomic surveillance infrastructures and improve data collection strategies in countries such as Mauritania [17]. The importance of regional and international collaboration is also emphasized, particularly to better understand the origins and evolutionary trajectories of coronaviruses. This analysis of genetic diversity in Mauritania and Morocco shows that understudied regions can play a key role in the global understanding of viral dynamics. Extended surveillance would not only enable us to detect the emergence of new variants of concern, but also to adapt health interventions to the evolution of strains. These efforts are all the more necessary in view of the possibility of the emergence of new virus strains, which requires a rapid response on an international scale [18].

The study of SARS-CoV-2 genomic data in other North African countries, such as Algeria and Tunisia, reveals similar trends. In Algeria, a sequencing study of 36 genomes in 2021 showed the diversity of circulating variants, with a marked presence of Delta and Alpha. In Tunisia, an analysis of 1,359 samples identified 48 distinct lineages, including variants of concern such as Alpha, Beta, and Delta, across several waves of infection. These results confirm the rapid evolution of the virus and the need for continued monitoring of variants to better manage the pandemic and its consequences [10], [20]. In Europe, Omicron variants also dominate, notably the BA.2, BA.5 and XEC sub-variants, which have supplanted Delta due to their greater transmissibility. The XEC sub-variant, which appeared in Germany in 2024, quickly demonstrated its ability to spread across Europe. These sub-variants are also associated with less severe forms of the disease, contributing to less severe waves despite their rapid spread. This phenomenon is important in assessing the management of epidemic waves and in adapting health policies [21], [22].

Finally, the results of this analysis underline the urgent need to strengthen genomic surveillance capacities in order to better prevent future pandemics. Proximity of North African countries with animal reservoirs, such as bats, increases the risk of the emergence of new zoonotic pathogens. This calls for coordinated efforts to monitor wildlife, strengthen laboratory infrastructures and develop effective zoonosis prevention policies

[23]. In sum, these findings call for a global, regional and coordinated approach to genomic surveillance to better understand viral dynamics and protect global public health.

5. Conclusion

This comparative analysis of SARS-CoV-2 genomic data in Mauritania and Morocco highlights the complexity of viral evolution and the critical role of genomic surveillance in pandemic management. Omicron variants, particularly subvariants BA.2 and BA.5, dominate in both regions, although regional dynamics reveal subtle differences, such as the persistence of the Delta variant in Mauritania and the presence of the Gamma variant in Morocco. These findings align with global trends, particularly in Europe, where Omicron subvariants continue to spread due to their increased transmissibility and ability to partially evade immunity. The regional disparities in variant circulation reflect varying public health measures, surveillance capabilities, and epidemiological histories. The ongoing evolution of SARS-CoV-2 underscores the need for continuous genomic surveillance to adjust public health strategies and prevent future waves. These results also emphasize the importance of regional cooperation in genomic surveillance to track viral mutations and contribute to global pandemic preparedness. Additionally, in-depth research and better data collection in under-sampled regions, such as Mauritania and Algeria, could enrich the understanding of virus evolution, thus enabling more effective responses to future outbreaks.

Authors contributions

MSEK (Med Salem Sid'Ahmed El Kehel) was involved in the conception and design of the study, collected patient data, participated in the analysis and interpretation of results, and contributed to the preparation of the initial draft of the manuscript. RB (Rihab Boustine) contributed to the conception and design of the study and was involved in the analysis and interpretation of the results. MN (Mouad NAJIH) participated in the analysis and interpretation of the results. AB(Ahmed El Bara) and SM (Sidi Mohamed Ahmed) was responsible for the collection of patient data in Mauritania. HB(Hind BERRADI) was involved in the analysis and interpretation of the results, as well as in reviewing and editing the main text of the manuscript. MME (Moulay Mustapha ENNAJI)supervised the study, ensuring its direction and integrity, and contributed to the conception and design of the study and the final editorial changes of the manuscript and coordination between authors. All authors have reviewed and approved the final version of the manuscript. All authors have participated sufficiently in the work and agreed to be accountable for all aspects of the work.

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