Journal of Current Medical Research and Opinion
Received 18-01-2024| Revised 20-01-2024| Accepted 08-02-2024| Published Online 12-02-2024

DOI: https://doi.org/10.52845/CMRO/2024/7-2-6 ISSN (O) 2589-8779 | (P) 2589-8760
CMRO 07 (02), 2102-2106 (2024)
Original Articles

# Staphylococcus aureus: Molecular Genetic Bioinformatics and Evolutionary Relationships

**Mohja Aref Sadkhan[1], Hawraa Riyadh Abd Alhassan[2], Muhammad Hammoud Nasser[3], Ghufran Ali Soued[4], Adian Ali Kadhim[5], Basim Mohammed Karim[6], Khetam Ali Abd[7], Zainab Hussein Hazam[8], Zahraa Naeem Hashem[9], Safa Ali Hadi[10]**

[1]University of Thi_Qar, College of Science/ Department of pathological analyzes
[2]Thi Qar University/ College of Science/ Department of Pathological Analysis
[3]Dhi Qar University/ College of Science/ Department of Pathological Analysis
[4]Dhi Qar University/ College of Science/ Department of Pathological Analysis
[5]Dhi Qar University/ College of Science/ Department of Pathological Analysis
[6]Dhi Qar University/ College of Science/ Department of Pathological Analysis
[7]University of Thi-Qar, College of Science/ Department of pathological analyzes
[8]University of Thi-Qar, College of Science/ Department of pathological analyzes
[9]University of Thi-Qar, College of Science/ Department of pathological analyzes
[10]University of Thi-Qar, College of Science/ Department of

**Abstract**

Staphylococcus aureus is a type of Gram-positive bacteria, usually living on human skin, in the nasal cavity or in the respiratory tract. This type of bacteria has several characteristics: coagulation-positive, DNA decoding, and its consumption of mannitol-type sugar. Although it does not always cause disease, one of the diseases caused by this type of germ is toxic shock syndrome, which leads to severe illness accompanied by fever, a widespread red rash with the effect of other organs in the body. Recently, new types of antibiotic-resistant Staphylococcus aureus have emerged, the most important of which is methicillin-resistant Staphylococcus aureus, which is an RNA component of the 30s subunit of the prokaryotic ribosome (SSU rRNA). It is related to the TTS of Shine-Dalgarno tuberculosis and provides most of the SSU structure. The genes encoding it are referred to as the 165 rRNA gene and are used in reconstructing strains due to the slow evolutionary rates of this region of the gene Genetics Multiple sequences of the 16s rRNA gene can exist within a single bacterium To identify the bacteria in a given sample, this procedure uses 165 rRNA gene sequencing, which is currently the most cost-effective method for comprehensive determination of bacterial taxonomy and relative quantitative performance. Alternative methods include targeted.

**Keywords:** Bioinformatics, Staphylococcus aureus, Genetic, Relationships



## Introduction:

Staphylococcus aureus is a major bacterial human pathogen that causes a wide variety of clinical manifestations.[1] Infections are common both in community-acquired as well as hospital-acquired settings and treatment remains challenging to manage due to the emergence of multi-drug resistant strains such as MRSA (Methicillin-Resistant Staphylococcus aureus). [2] [3] S. aureus is found in the environment and is also found in normal human flora, located on the skin and mucous membranes (most often the nasal area) of most healthy individuals.[1] S. aureus does not normally cause infection on healthy skin; however, if it is allowed to enter the bloodstream or internal tissues, these bacteria may cause a

variety of potentially serious infections.[1] Transmission is typically from direct contact. However, some infections involve other transmission methods.[4] The emerging clinical importance of *Staphylococcus aureus* and coagulase-negative staphylococci (5) in connection with the expanding number of staphylococcal subspecies described requires accurate identification to the subspecies level. Currently, the genus *Staphylococcus* is divided into 36 species and 21 subspecies. Staphylococcal subspecies not included in the databases of commercial identification systems, as well as phenotypic variants (e.g., small-colony variants), are often misidentified (6). The usefulness of genotypic identification of staphylococcal subspecies by using partial 16S rDNA sequences in comparison with phenotypic tests (7). However, the partial 16S rDNA sequences used were not discriminative enough to differentiate all staphylococcal subspecies. This study was aimed to show the genetic relatedness among several S. aureus strains collected from GenBank.

## Genetic bioinformatics

With the widespread adoption of next generation sequencing technologies by the genetics community and the rapid decrease in costs per base, exome sequencing has become a standard within the repertoire of genetic experiments for both research and diagnostics. Although bioinformatics now offers standard solutions for the analysis of exome sequencing data, many challenges still remain; especially the increasing scale at which exome data are now being generated has given rise to novel challenges in how to efficiently store, analyze and interpret exome data of this magnitude. In this review we discuss some of the recent developments in bioinformatics for exome sequencing and the directions that this is taking us to. With these developments, exome sequencing is paving the way for the next big challenge, the application of whole genome sequencing (8).

## Bioinformatic tools for identifying disease gene and SNP candidates

As databases of genome data continue to grow, our understanding of the functional elements of the genome grows as well. Many genetic changes in the genome have now been discovered and characterized, including both disease-causing mutations and neutral polymorphisms. In addition to experimental approaches to characterize specific variants, over the past decade, there has been intense bioinformatic research to understand the molecular effects of these genetic changes. In addition to genomic experimental assays, the bioinformatic efforts have focused on two general areas. First, researchers have annotated genetic variation data with molecular features that are likely to affect function. Second, statistical methods have been developed to predict mutations (9).

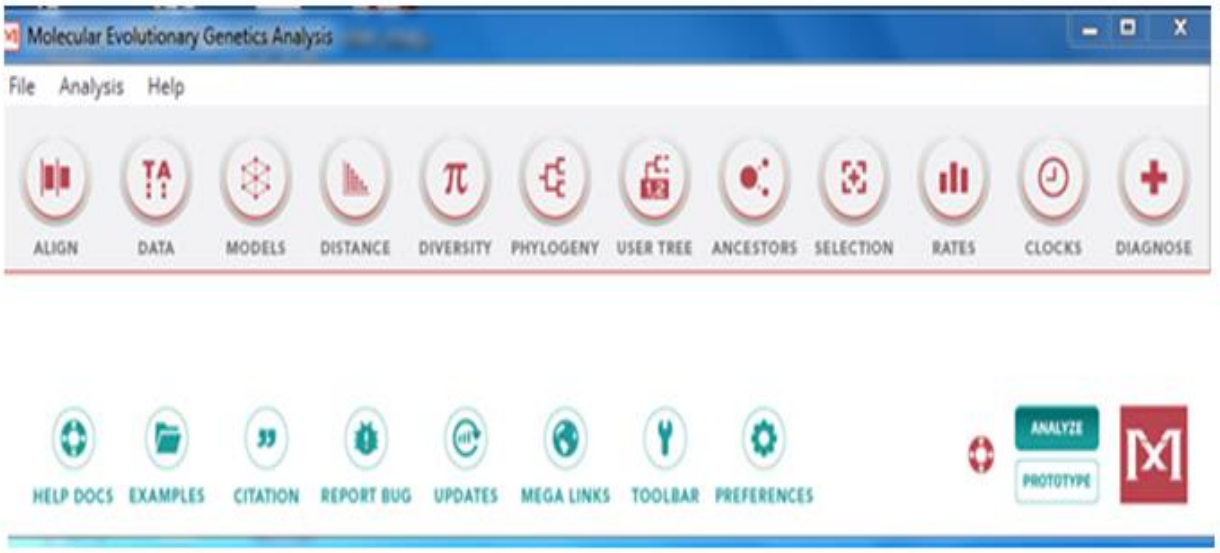
## Methods:

## Samples collection

*S. aureus* samples were collected from GenBank in form of Fasta file. Key words used to select the strains were “Staphylococcus aureus”, “16sRNA gene”, “2019 or 2020 or 2021” and “Iraq- Basrah, Thi-Qar”. Nucleotides sequences of *S. aureus* strains were implemented in Mega X software and analyzed using UPGMA tools to construct the phylogenetic tree. The pairwise relatedness was calculated to show the relationships between the strains using numerical data.

**Fig. 1 website of NCBI and the search strand of GenBank.**

**Fig. 2 the main screen of Mega x software**




**Results:**

Eight strains of *S. aureus* were selected from both Thi-Qar and Basrah provinces. A strain of Baghdad was added as control (out-group). Results from Mega x software showed that there is a genetic relatedness between the strains of both Basrah and Thi-Qar Fig. 3, Except one strain from Thi-Qar appeared down the tree as out-group.

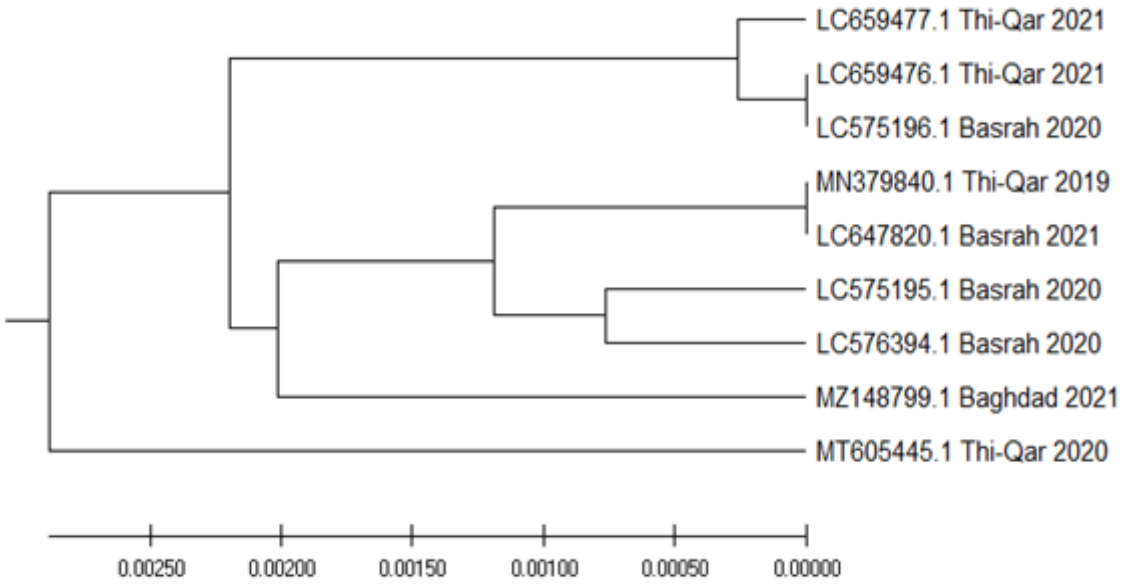



**Fig. 3 Evolutionary relationships of *S. aureus***

The evolutionary history was inferred using the UPGMA method [1]. The optimal tree with the sum of branch length = 0.01218485 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [2] and are in the units of the number of base substitutions per site. The analysis involved 9 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1460 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [3].

**Table 1. The pairwise of genetic relatedness**

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| LC659477.1_Thi-Qar_2021 | | | | | | | | |
| LC659476.1_Thi-Qar_2021 | 0.0010 | | | | | | | |
| MT605445.1_Thi-Qar_2020 | 0.0078 | 0.0071 | | | | | | |
| MN379840.1_Thi-Qar_2019 | 0.0015 | 0.00045 | 0.0064 | | | | | |
| LC647820.1_Basrah_2021 | 0.0015 | 0.00045 | 0.0055 | 0.0000 | | | | |
| LC575196.1_Basrah_2020 | 0.0000 | 0.0000 | 0.0062 | 0.0006 | 0.0209 | | | |
| LC575195.1_Basrah_2020 | 0.0054 | 0.0037 | 0.0046 | 0.0028 | 0.0022 | 0.00355 | | |
| LC576394.1_Basrah_2020 | 0.004 | 0.0029 | 0.0034 | 0.0022 | 0.00220 | 0.00636 | 0.00153 | |
| MZ148799.1_Baghdad_2021 | 0.004 | 0.0032 | 0.0047 | 0.0025 | 0.00563 | 0.00612 | 0.00269 | 0.00521 |

**Discussion:**

In Phylogenetic analysis, alignment of nucleotide sequencesis a major consideration, particularly in studies of genesfrom divergent taxa. It seems obvious to state that thephylogenetic analysis of sequences begins with theappropriate alignment of the data themselves, yet alignmentremains one of the most difficult and poorly understood facets of molecular data analysis (10). In this study, we found that the S. aureus isolates transfer between the populations of Basrah and Thi-Qar located southern of Iraq.

**References:**


1. Lowy FD. Staphylococcus aureus infections. N Engl J Med. 1998 Aug 20;339(8):520-32. [PubMed[
2. Centers for Disease Control and Prevention (CDC). Outbreaks of community-associated methicillin-resistant Staphylococcus aureus skin infections--Los Angeles County, California, 2002-2003. MMWR Morb Mortal Wkly Rep. 2003 Feb 07;52(5):88. [PubMed[
3. Boucher HW, Corey GR. Epidemiology of methicillin-resistant Staphylococcus aureus. Clin Infect Dis. 2008 Jun 01;46 Suppl 5: S344-9. [PubMed[
4. Rasigade JP, Vandenesch F. Staphylococcus aureus: a pathogen with still unresolved issues. Infect Genet Evol. 2014 Jan; 21:510-4. [PubMed]
5. von Eiff C, Peters G, Heilmann C. Pathogenesis of infections due to coagulase-negative staphylococci. *Lancet Infect Dis*. 2002; 2:677–85. 10.1016/S1473-3099(02)00438-3 [PubMed] [CrossRef] [Google Scholar]
6. Seifert H, Wisplinghoff H, Schnabel P, von Eiff C. Small colony variants of *Staphylococcus aureus* and pacemaker-related infection. *Emerg Infect Dis*. 2003; 9:1316–8. [PMC free article] [PubMed] [Google Scholar]
7. Becker K, Harmsen D, Mellmann A, Meier C, Schumann P, Peters G, et al. Development and evaluation of a quality-controlled ribosomal sequence database for 16S ribosomal DNA-based identification of *Staphylococcus* species. *J Clin Microbiol*. 2004; 42:4988–95. 10.1128/JCM.42.11.4988-

4995.2004 [PMC free article] [PubMed] [CrossRef] [Google Scholar]

8. Lelieveld SH, Veltman JA, Gilissen C. Novel bioinformatic developments for exome sequencing. Hum. Genet. Springer Verlag; 2016. p. 603–14 .
9. Mooney SD, Krishnan VG, Evani US. Bioinformatic tools for identifying disease gene and SNP candidates. Methods Mol. Biol. Humana Press Inc.; 2010. p. 307–19.
10. Hsu HW, Su HY, Huang PH, Lee BL, Liu HJ, Sequence andphylogenetic analysis of P10- and P17-encoding genes of avianreovirus. Avian Dis. 2005; 49(1):36-42.