RESEARCH ARTICLE

Molecular characterization of \textit{Pseudomonas aeruginosa} isolates from Sudanese patients: A cross-sectional study [version 1; peer review: 1 approved with reservations, 1 not approved]

Reem H. Amoon\textsuperscript{1}, Amna H. Abdallha\textsuperscript{1}, Ahmed Osman Sharif\textsuperscript{1}, Ehssan H. Moglad\textsuperscript{1}, Hisham N. Altyb\textsuperscript{2}, Salaheldein G. Elzaki\textsuperscript{3}, Mohamed A. Salih\textsuperscript{4}

\textsuperscript{1}Departement of Microbiology and Parasitology, Medicinal and Aromatic Plants Research Institute, National Centre for Research, Khartoum, Sudan
\textsuperscript{2}Medical Microbiology, College of Medical Laboratory Science, Sudan University of Science and Technology, Khartoum, Sudan
\textsuperscript{3}Department of Epidemiology, Molecular Epidemiology Laboratory, Tropical Medicine Research Institute, National Centre for Research, Khartoum, Sudan
\textsuperscript{4}Department of Biotechnology, Africa City of Technology, Khartoum, Sudan

Abstract

\textbf{Background:} 16S rRNA gene sequence analysis is a robust tool for characterization of new pathogens in clinical specimens with suspected bacterial disease. The aim of this study was to characterize \textit{Pseudomonas aeruginosa} isolated from clinical specimens by sequencing the 16S rRNA gene.

\textbf{Methods:} Forty bacterial isolates were obtained from different clinical specimens (wound, urine and sputum) using enrichment selective media and biochemical tests to characterize and identify the bacteria as \textit{P. aeruginosa}. DNA was extracted from \textit{P. aeruginosa} using the Chelex method. A universal primer was used to amplify 16S rRNA genes by a conventional PCR technique. The amplified PCR products were sequenced, and the sequences were viewed by Finch TV program version 1.4.0. The identity and similarity of the nucleotide sequence of the isolated strains was detected by comparing them with published sequences using BLASTn. Phylogenetic trees were constructed using Phylogeny.fr software.

\textbf{Results:} Sequence analysis by BLASTn displayed high similarity and identity with \textit{P. aeruginosa} from China KX461910, Australia JN609194 and with other \textit{P. aeruginosa} isolates from the GenBank database.

\textbf{Conclusions:} Our observation of isolates from different origin sites, further show the utility of 16s rRNA PCR amplification. This reveals the high specify of the primers and accuracy of the PCR. Thus, 16S rRNA sequencing can be used to identify genetically atypical \textit{P. aeruginosa} isolates from different origins.

\textbf{Keywords} Pseudomonas aeruginosa, 16S rRNA, Alignment, PCR, phylogenetic tree, Blast, Sudan.

Open Peer Review

Reviewer Status

Invited Reviewers

<table>
<thead>
<tr>
<th>Invited Reviewers</th>
<th>report</th>
<th>report</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Giuseppe Comi, University of Udine, Udine, Italy</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2 Juan Alfonso Ayala Serrano, Universidad Autónoma de Madrid-CSIC, Madrid, USA</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Any reports and responses or comments on the article can be found at the end of the article.
Introduction

*Pseudomonas aeruginosa* is a gram-negative bacterium that is found widely in the environment and engages in various forms of interactions with eukaryotic host organisms. It is an opportunistic pathogen that is widely spread in humans, giving rise to a broad spectrum of infections in community and healthcare facilities. Due to the extended spread of *P. aeruginosa* habitat, the control of the organism in a hospital setting is very difficult, and makes it practically impossible to prevent contamination. The major threat is the infection of patients who are immuno-compromised or those in burns, neonatal and cancer wards. Infection of *P. aeruginosa* is still one of the main causes of death among the critically ill and patients with impaired immune systems in spite of the development of newer and stronger antibiotics.

Sequencing of 16S rRNA worldwide has provided interesting and useful information. For instance, with the use of 16S rDNA sequencing, 215 novel bacterial species, 29 of which belong to novel genera, have been discovered from human specimens in the past 7 years of the 21st century (2001–2007). One hundred of the 215 novel species, 15 belonging to novel genera, have been found in four or more subjects. In Sudan, there is deficient data on sequencing about bacteria; therefore it is important to investigate what kinds of bacteria affect Sudanese people. Consequently, the objective of this study was to isolate and characterize *P. aeruginosa* from samples obtained from Sudanese patients by sequencing the 16SrRNA gene.

Methods

Clinical isolates

This was cross sectional laboratory based study, conducted in Khartoum state in the period from January to April 2016. The study was approved by the Ethical and Scientific Committee of the Medicinal and Aromatic Plants and Traditional Medicine Research Institute, National Center of Research, Khartoum, Sudan (approval number 03-16) which ensures that all ethical considerations for conducting the research in a way that protects patient’s confidentiality and privacy are followed. Informed consent was obtained from the hospital laboratories (laboratory manager) after providing them with the ethical approval to collect samples during routine procedures from the microbiology laboratories. Participants’ privacy and confidentiality was protected for all samples; personal information was not of great value in the current study and was thus not taken. Consequently, the Ethical and Scientific Committee waived the need for patient consent.

A total of 40 isolates of *P. aeruginosa* (all samples available) were obtained from three hospitals in Khartoum State (Al Ribat Hospital, Bahri Hospital and Souba Hospital).

The bacterial isolates were collected from sputum culture, urine culture and wound infection because these types of cultures were dominant. Standard biochemical tests were performed on all samples for the isolation and identification of the bacterial isolates and were performed at the Medicinal and Aromatic Plants and Traditional Medicine Research Institute (MAPTMRI), Department of Microbiology. *P. aeruginosa* presence was confirmed in all 40 samples. All media required for biochemical tests were obtained from LAB M, UK and Laboratories Flow Media, Sudan.

DNA extraction

Bacterial DNA was isolated by the Chelex-based protocol for all samples without deviation from the methodology.

Conventional polymerase chain reaction (PCR)

All bacterial genomic DNA were used as templates for PCR amplification of the 16S rRNA gene. The two primers used were 27F (5’ AGAGTTTGATCCTGGCTCAG-3’) and 1495R (5’ CTACGGCTACCTTGTTACGA-3’) for forward primer and reverse primer, respectively (Macrogen, South Korea). The 25μL PCR reaction mixture (Intro Biotechnology, South Korea) contained 1μL DNA, 1x reaction buffer (10x) with 3mM MgCl2, 2.5U i-Taq DNA polymerase (5 U/μL), 2.5mM dNTPs, 1μL of 10 pmol of each primer, and 1x of gel loading buffer, followed by completing the volume to 25μL with nuclease free water. Thermal cycling conditions were as follows: 94°C for 5 min; 30 cycles of denaturation (94°C for 1 min), annealing (58°C for 1 min), extension (72°C for 2 min); final extension at 72°C for 10 min. PCR was performed on a Bio-Rad (DNA engine/Dyad Peltier) automatic thermal cycler. Duplicate PCR of every sample were carried out for confirmation. PCR products (5μl) were analyzed by gel electrophoresis in 1.0% agarose stained with ethidium bromide. The results were photographed under ultraviolet light machine (Transilluminator; Uvite, UK) to detect the specific amplified product by comparing it with 100 base pairs standard DNA ladder (Figure 1) and the remains from PCR products were store at -20°C until sequencing.

Sequencing of 16S rRNA gene

Isolates were packaged according to the International Air Transport Association guidelines and shipped with authorized permission to Macrogen Company (Seoul, South Korea). Purification and standard forward sequencing of 16S rRNA were done by ABI Genetic Analyzer (Applied Biosystems). We randomly selected 20 isolates only for DNA sequencing due to the limitation of resources.
Bioinformatics analysis

The chromatogram sequences were visualized using Finch TV program version 1.4.0. The nucleotide sequences of the 16S rRNA gene were searched for sequences similarity using online BLASTn. Highly similar sequences (accession numbers KX108935.1, KT943978.1, JN609194.1, KX214108.1, KU672378.1, and FJ648815.1) were retrieved from NCBI GenBank and subjected to multiple sequence alignment using BioEdit software version 7.2.5. Newick format was withdrawn from ClustalW, to create phylogenetic trees in Phylogeny.fr software. MEGA6 software version 0.06 was used for confirmation of phylogenetic trees.

Results

A total of 40 clinical isolates were identified as P. aeruginosa by conventional methods, including growth characteristics, colony morphology, and biochemical tests. The results revealed that P. aeruginosa were dominant in wound infection cultures (42.5%), followed by (32.5%) from urine cultures and (25%) from sputum cultures.

The 16SrRNA in the isolates was amplified by PCR. In total, 20 were sent for characterization by sequencing of PCR products. 5 out of these 20 had a clear chromatogram, leading to further sequence analysis. Sequence analysis by BLASTn revealed 100% identity with P. aeruginosa from Iran (KX108935.1), China (KT943978.1), Austria (KX214108.1), India (KU672378.1), South Africa (KU764451.1), and slightly different from a sample from Australia (FJ648815): there was one substitution of A to G in position 148 (Figure 2). The phylogenetic tree of the 16S rRNA gene and other 16S rRNA genes obtained from the database revealed that the tree is classified into two branches. All isolates have a common ancestor. The isolate 120 is at the upper branch, isolate 113 and isolate 114 are sister groups, as shown in Figure 3.

![Figure 2](image-url)

Figure 2. BioEdit multiple sequence alignment of the five isolates and other selected strains. The isolates had 100% identify with samples from Iran, China, Austria, India, and South Africa. There was one substitution of A to G in position 148 from a sample from Australia (FJ648815).

![Figure 3](image-url)

Figure 3. Phylogenetic tree of the 16S rRNA gene and other 16S rRNA genes. The tree is classified into two branches. All isolates have a common ancestor. The isolate 120 is at the upper branch, isolate 113 and isolate 114 are sister groups.
Discussion

*P. aeruginosa* can cause various clinical infections. In the present study, 42.5% of isolates were identified from wound infection. Beside the highly preserved conserved primer binding sites, 16S rRNA gene sequences include hypervariable regions with high conservation that have the ability to characterize species-specific signature sequences beneficial to the characterization of bacteria. The present results agree with Didelot et al., who reported that 16S rRNA gene sequencing is now common in medical microbiology as a quick and inexpensive alternative to phenotypic approaches of bacterial identification. We investigated the phylogenetic affiliation of the pseudomonads and reexamined the 16S rRNA sequence data available in public databases. According to an alignment of 16S rRNA sequences, we identified *P. aeruginosa*-specific signature sequences.

16S rRNA sequencing can be used to identify genetically atypical *P. aeruginosa* isolates from different origins. Our observation of 40 isolates from 40 samples, further showed the utility of 16s rRNA PCR amplification. This reveals the high specificity of the primers and accuracy of the PCR. Sequencing of the 16S (rRNA) gene was used as an effective tool for determining phylogenetic relationships between bacteria. The features of this molecular target make it valuable and useful for bacterial detection and identification in the clinical laboratory.

Conclusions

In conclusion, 16S rRNA-based PCR assay and sequencing is highly specific, sensitive and reliable for identification of *P. aeruginosa* and its differentiation from other genotypically closely related *Pseudomonas* species. DNA sequencing of the 16S rRNA gene has been used as an effective tool to study bacterial phylogeny and taxonomy relationships between bacteria and for bacterial detection.

Data availability

The results of the nucleotide sequences of the 16S rRNA gene were submitted in the GenBank database. Accession numbers: KX650648, KX650649, KX650650, KX650651 and KX650652.

Competing interests

No competing interests were disclosed.

Grant information

The author(s) declared that no grants were involved in supporting this work.

Acknowledgments

The authors are grateful to Africa City of Technology, Medicinal and Aromatic Plants and Traditional Medicine Research Institute (MAPTMRI), Microbiology and Parasitology department, National Center for Research, Khartoum, Sudan and department Epidemiology, Molecular Epidemiology Laboratory Biology, Tropical Medicine Research Institute, National Centre for Research, Khartoum, Sudan for their kind support.

References


Page 5 of 9


Open Peer Review

Current Peer Review Status:  

Version 1

Reviewer Report 02 January 2019

https://doi.org/10.5256/f1000research.16686.r42041

© 2019 Ayala Serrano J. This is an open access peer review report distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Juan Alfonso Ayala Serrano
Laboratorio de División Celular Bacteriana y Resistencia a Antibióticos, Centro de Biología Molecular “Severo Ochoa, Universidad Autónoma de Madrid-CSIC, Madrid, USA

Manuscript deals with the characterization of Pseudomonas clinical isolates by PCR and 16S rRNA gene sequencing. Only twenty isolates were used for sequence comparison, and actually only five sequences are compared by BLAST and deposited on Genbank DATABASE. Authors claim that sequencing of 16S rRNA gene is useful for Pseudomonas identification, but this fact has been shown in hundred of papers. It is not a novelty. Moreover, no other molecular analysis is done with the isolates, as for example, identification of resistance mechanisms. In addition, isolates were already identified as Psedomonas aeruginosa by biochemical methods. A more useful analysis would be to take the full number of isolates and without previous identification, characterize them as P. aeruginosa.

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
No

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Not applicable

Are all the source data underlying the results available to ensure full reproducibility?
Partly

Are the conclusions drawn adequately supported by the results?
Partly
**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Molecular Microbiology. Peptidoglycan characterization, Antibiotic resistance, betalactamases

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Reviewer Report 29 October 2018

https://doi.org/10.5256/f1000research.16686.r39641

© 2018 Comi G. This is an open access peer review report distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Giuseppe Comi
Department of Food Science, University of Udine, Udine, Italy

The paper at the moment is only a description of a group of Pseudomonas aeruginosa. The strains come from different areas, the genomic study was made by a Korean lab. What did the authors want to say or to communicate with the paper?

The paper is interesting, and gives additional data about the *P. aeruginosa* species. However:

- Reading the paper I cannot find the aim and the meaning of the work. It would be better to explain the aim of the paper.
- It would be better to explain the aim of the paper.
- Additional literature to explain the aim and the meaning of the work must be included.
- What is the meaning of the results?
- How can the results be used?
- Material and methods must be better written.
- What did the authors do? The collected data and applied a software and no other skills.
- The conclusion must be improved.

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
Yes
Are sufficient details of methods and analysis provided to allow replication by others?  
Yes

If applicable, is the statistical analysis and its interpretation appropriate?  
I cannot comment. A qualified statistician is required.

Are all the source data underlying the results available to ensure full reproducibility?  
Yes

Are the conclusions drawn adequately supported by the results?  
Partly

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.