



# PHAMILIA

A Journal by  
**Ibadan Bacteriophage Research Team**

Issue: #002, DECEMBER, 2022



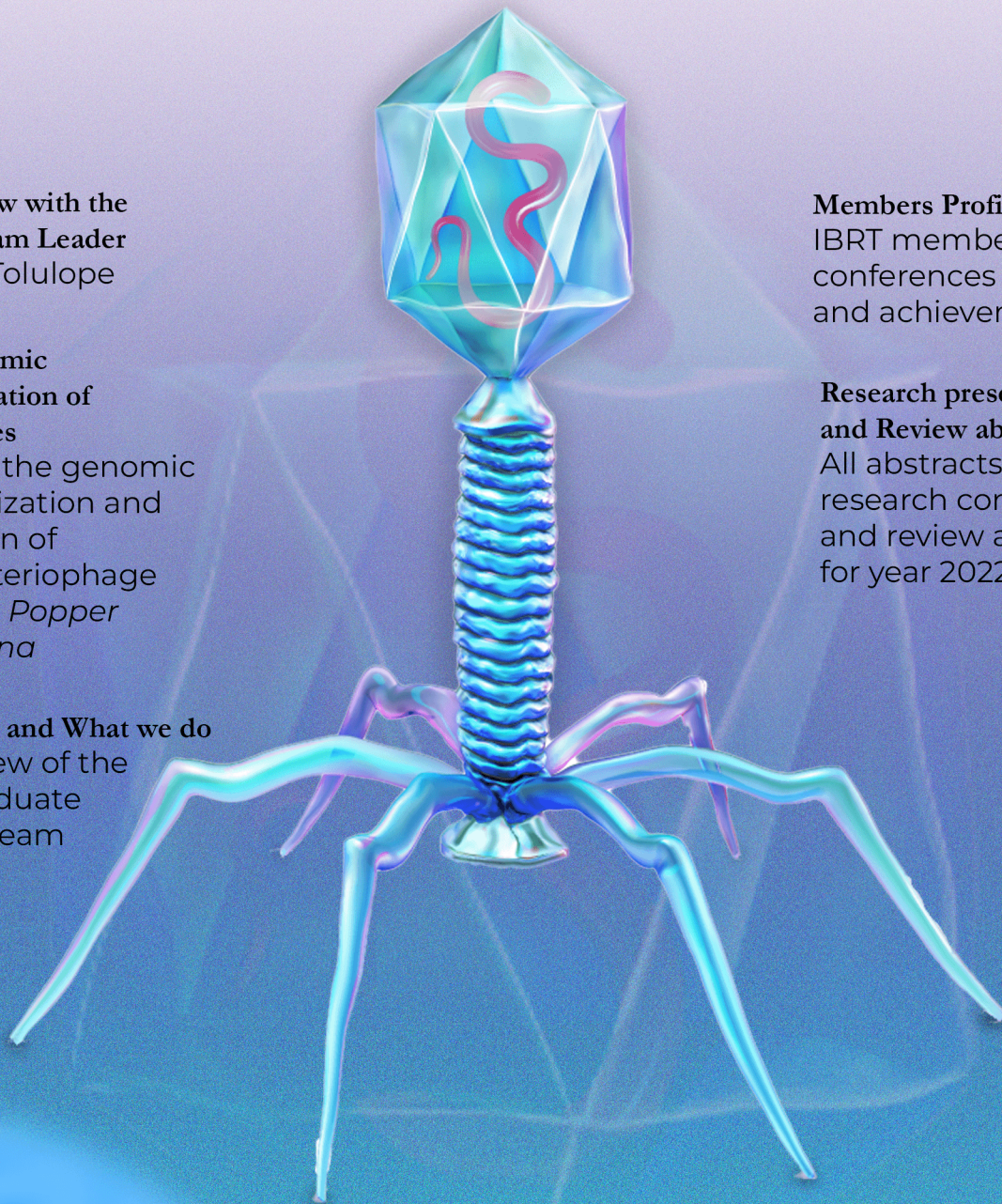
**An Interview with the  
Pioneer Team Leader**  
Oduselu Tolulope

**Novel genomic  
characterization of  
three phages**  
Report of the genomic  
characterization and  
annotation of  
mycobacteriophage  
*Gretchen*, *Popper*  
and *Sedona*

**Who we are and What we do**  
An overview of the  
Undergraduate  
research team

**Members Profiles**  
IBRT members profiles,  
conferences attended  
and achievements

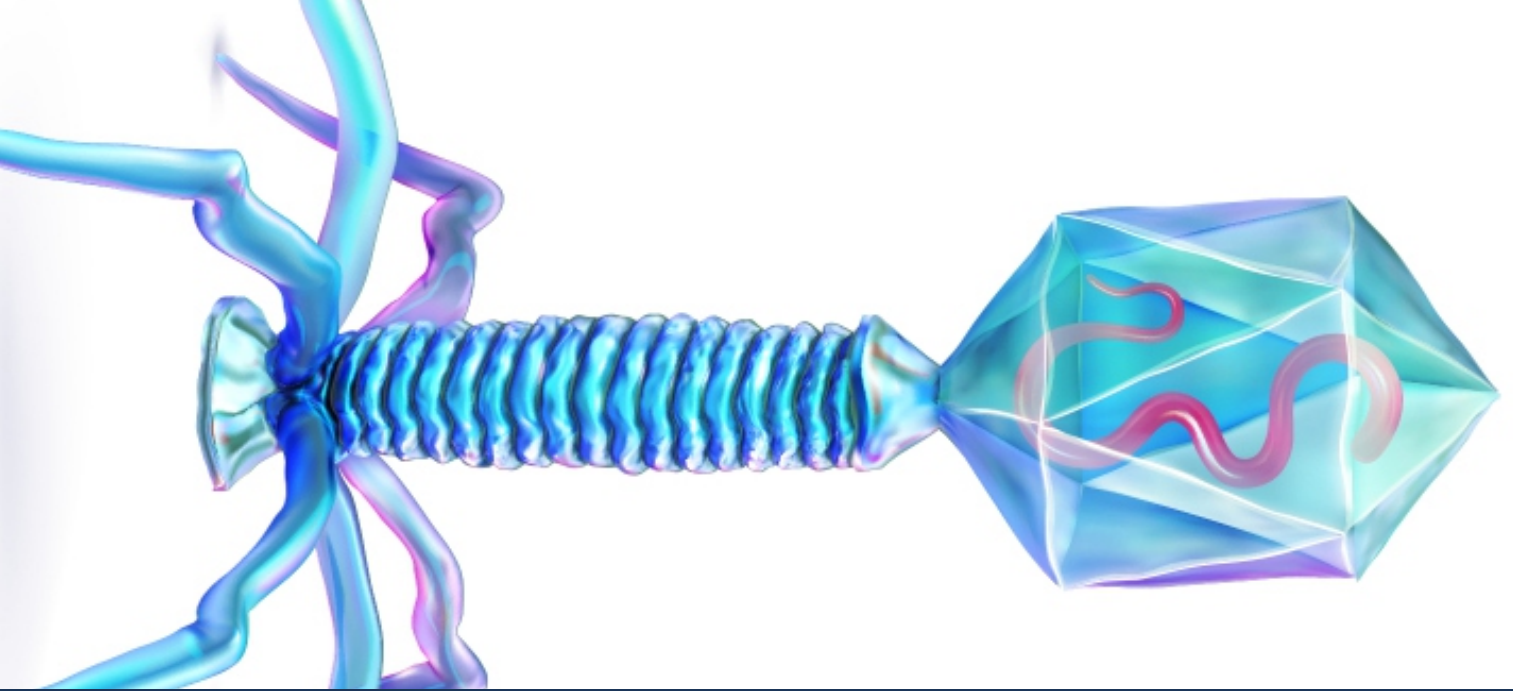
**Research presentations  
and Review abstracts**  
All abstracts of original  
research conducted  
and review abstracts  
for year 2022





*"the inquisitive passion for  
scientific research comes first,  
and it's all that matters"*

Daramola Oluwasegun Isaac



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# WHO WE ARE AND WHAT WE DO



The Ibadan Bacteriophage Research Team is an undergraduate research organization based at Nigeria's premier university, the University of Ibadan. The team was founded in the year 2018 by a team of 8 Faculty members led by Prof. O.G Ademowo, after the successful registration of the department of Biomedical Laboratory Science of the University under the Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Sciences (SEA-PHAGES) project in collaboration with the Hughes Howard Medical Institute (HHMI) and University of Pittsburgh.

Today, the team prides itself in being the most successful undergraduate research organization at the University of Ibadan and in sub-Saharan Africa, with a vibrant early-career research community sustained by active faculty mentorship. The team has grown to become a force to be reckoned with in the field of bacteriophage biology and antimicrobial resistance, with numerous international collaborations and research engagements. In the 2022 research year, the team expanded its reach by delving into cancer research and metagenomics, alongside its bacteriophage research origin.

The team which consists of 31 members is focused on teaching all of its members the use of bioinformatic approaches to microbial



genome studies and actively engaging the local and international community in its work through scientific review articles, IBRT Phamilia Journal, conference presentations, hosting the annual IBRT World Phage Week Webinar Series, and science advocacy through active social media engagement. The team extends its reach outside the host department through collaborative projects such as the Faculty of Basic Medical Sciences Research and the Ibadan Enterovirus Project.

Two bacteriophage research-based journals and three webinars hosted to commemorate the World phage week later, the mission at Ibadan Bacteriophage Research remains the same: *'To build an undergraduate research community of early career researchers who are enthusiastic about bacteriophage biology and its prospective use as alternative antimicrobial therapy'.*

The Phamilia journal aims to extend the frontiers of learning by dissemination of our research findings and also to serve as an archive of our research which is essential in the ever-continuous process of scientific exploration.

# Faculty's Piece

It is with pleasure that I write the foreword message of the second edition of the Ibadan Bacteriophage Research Team (IBRT) Journal (PHAMILIA), first as the faculty head of the research team and as a mentor to a highly formidable, enthusiastic, and talented group of undergraduate students of the College of Medicine, University of Ibadan, Nigeria. The Ibadan Bacteriophage Research Team (IBRT) started in 2018 by co-opting volunteers among the Biomedical Laboratory Science students who were interested in devoting extra time for research under the Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Sciences (SEA-PHAGES) project, in collaboration with the Howard Hughes Medical Institute and the University of Pittsburgh. The students took semester classes in basic bioinformatics and bacteriophage biology and proceeded to successfully annotate and characterize the genomic

features of a novel bacteriophage named *IDAHO*. The team has since characterized seven more novel bacteriophages and uploaded their genomic details to the National Center for Biotechnology Information (NCBI) repository with assigned accession number.

The successes of IBRT are a testament to the place of pride that the University of Ibadan holds among other higher institutions of learning in the nation and the world at large. Team members have showcased their research acumen through diverse research presentations at local and international conferences and established membership in the Surveillance and Epidemiology of Drug-Resistant Infections Consortium (SEDRIC). IBRT also expanded its research reach beyond bacteriophage research by establishing subgroups in the fields of metagenomics research, cancer and transcriptomics research as well as AMR research.



**Prof. O.G. Ademowo**

**Faculty Head**



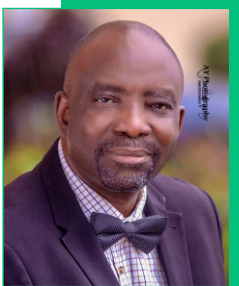
. It is gratifying that the team members have also received notable recognitions by international organizations such as the Microbiology Society and the European Society of Clinical Microbiology and Infectious Diseases, and won notable awards, including an early career travel grant awarded by the International Society for Viruses of Microbes for the previous Research Team Head in 2022.

Beyond the firm and rich research history of the team, IBRT continues to forge ahead in its plan to further expand the team, promote undergraduate research participation, both at the university and national levels, and maintain a status as a research organization to reckon with in the field of bacteriophage biology, in Nigeria and Africa.

PHAMILIA 2.0 is sure to be an interesting read for all bacteriophage biology enthusiasts all over the world. Readers will also be introduced to the world of the University of Ibadan's pride research team, which has undoubtedly created the most successful undergraduate research training model through guided adventure-based learning in a research field largely unexplored in the African research space. I welcome you all to get familiar with our outstanding research successes through this second edition of the PHAMILIA Journal.

# FACULTY TEAM

Professor O.G Ademowo  
**Faculty Head**



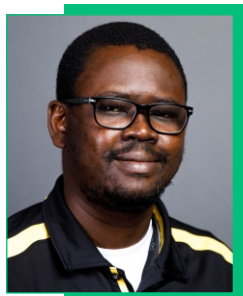
Prof. J.I Anetor



Dr. M.O Adewunmi



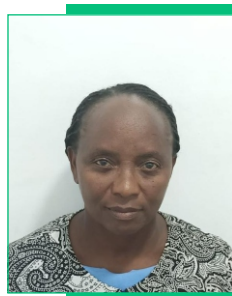
Dr. A.S Bakarey



Dr. T.O.C Faleye



Mrs. Ini Adebisi



Mrs. V.O Ogunleye



Mr. M.K Raifu



# PHAGE LEADERS



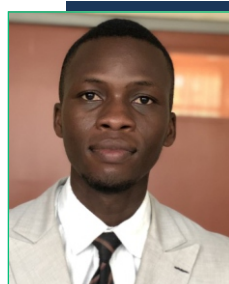
**DARAMOLA**  
Oluwasegun Isaac  
IBRT Team Lead &  
AMR Subgroup Head



**ADEDEJI**  
Roqeeb  
BRH Head & Cancer  
Subgroup Head



**AKOMOLAFE**  
Ayobami  
Metagenomics Subgroup  
Head & Head of  
Recruitment



**ADEDIRAN**  
Benjamin  
Bacteriophage Subgroup  
Head & Year 1 Training



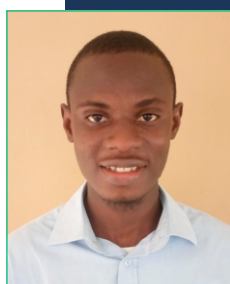
**AKINFEMISOYE**  
Oluwaseun  
Head of Team Strategy



**OWOEYE**  
Williams  
Head of Team Publicity

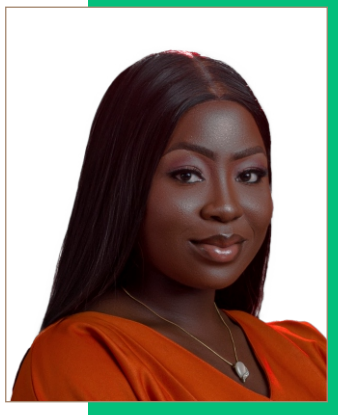


**OJEDIRAN**  
Mercy Adedamola  
Head of Finance



**OPATOLA**  
Abdulmujeeb  
Head of Orientation,  
Evaluation & Monitoring

# EDITORIAL TEAM



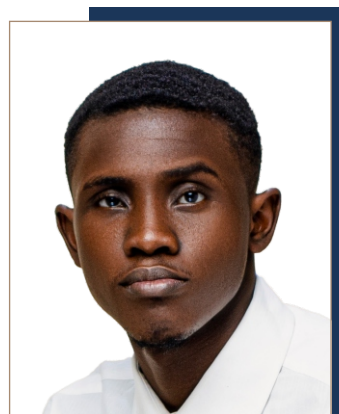
**AKINFEMISOYE**  
**Oluwaseun**



**OWOEYE**  
**Williams**



**DARAMOLA**  
**Oluwasegun**



**IBIYINKA**  
**Joshua**



**ADAMS**  
**David**



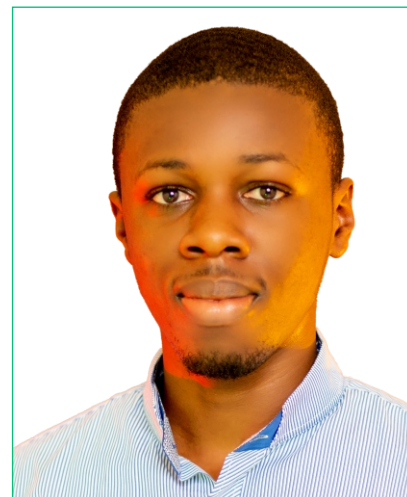
**AGBOOLA**  
**RIDWAN**

# Team Lead's Piece

Since the start of the 2022 research year, the Ibadan Bacteriophage Research Team (IBRT) has proven itself as a team with a vision and a mission and forged ahead to fulfill them. This has been the reality since its inception in 2018: from being a SEA-PHAGES participating group at the University of Ibadan to becoming the University's first voluntary undergraduate research training project. This was all achievable following the well-structured outline of leadership laid out by the previous team leaders, the student-driven, adventure-based learning model, and the enormous benefit of a vibrant mentee-mentor relationship from the team's faculty advisors and faculty project coordinator, Professor O.G. Ademowo. We also had the great and undeniable support of the global bacteriophage community.

The 2022 research year was a year filled with challenges and the overcoming of them. The decision to establish and sustain the team's "PHAMILIA" journal was born out of the desire to detail the team's journey over the years. And in this second edition, Phamilia 2.0 portrays the effort of research-inclined undergraduates and presents the continuous growth of the team as one of the most vibrant undergraduate research projects of the University of Ibadan. Phamilia is a testament to the immense strides made by the team to bring greater visibility to bacteriophage research in Nigeria.

This year, IBRT completed the annotation and characterization of two novel bacteriophages, making a total of eight phage genome sequences attributable to the team in the NCBI repository. We have sustained and maintained active research engagement with the affiliate research projects that forked from the team: the Ibadan Enterovirus project and the Faculty of Basic Medical Sciences Research Hub. The team recruited and trained 13 new undergraduate intakes with avid interest in bacteriophage science, and launched its bi-monthly twitter space discussion. This year, IBRT also expanded its research reach by establishing subgroups in the fields of metagenomics research, cancer and transcriptomics research, AMR studies, alongside bacteriophage biology and computational genomics research.



**D A R A M O L A**  
Oluwasegun Isaac

**IBRT Team Lead**



The team presented research findings at key international genome conferences this year and established membership in the Surveillance and Epidemiology of Drug-Resistant Infections Consortium (SEDRIC). IBRT conducted research in the fields of bacteriophage biology, metagenomics, computational genomics, antimicrobial resistance, and transcriptomics research, and this journal details the findings of our research, coupled with guest features from other colleagues around the world, to display the strides of the team on this research path, largely untrodden in the African research space. We proceeded to host the 3rd annual edition of the IBRT World Phage Week Webinar Series to commemorate the International World phage day, bringing vast international phage enthusiasts across different continents to educate participants on the Emerging Prospects in Bacteriophage Use and Phage Clinical Phage Therapy.

The story of the Ibadan Bacteriophage Research Team cannot be complete without the due acknowledgement of the faculty team, who have given their full support to see the vision of undergraduate engagement in active research processes come to fruition. We also say a very big thank you to all of our international event partners and sponsors, such as the Howard Hughes Medical Institute (HHMI), Graham Hatfull Group (University of Pittsburgh), JAFRAL Ltd., the Black Microbiologists Association (BMA), Phage Directory, Phage Pro, Phase Genomics, and many more, who have relentlessly given their unreserved support to the team. A special mention should be made to Jessica Sacher and Jan Zheng (founders of Phage Directory), who have followed the journey of the team and provided the platform for international exposure and networking for the team in the global bacteriophage community.

**Daramola Oluwasegun Isaac**

Student Team Lead

Ibadan Bacteriophage Research Team

# EDITOR-IN-CHIEF'S LIVE

Dear reader,

Welcome to the annual edition of The Phamilia Journal, featuring the best research work of the Ibadan Bacteriophage Research Team (IBRT) published in 2022. The Ibadan Bacteriophage Research Team (IBRT) has worked tirelessly this year to explore fields of scientific research and document our work which have been published in this undergraduate research journal alongside the work of other gifted researchers; and we couldn't be prouder of the incredible work we've done.

We are honored to publish Phamilia 2.0, with papers on a wide array of topics; from complete phage genome sequence annotation and characterization to research findings unveiling hypervirulent and hypermucoidy drug-resistant isolates in multi-drug resistant *Klebsiella pneumoniae*.

2022 has been and continues to be a big year for IBRT, from change in leadership which left the new leaders with big shoes to fill, to exploration of new grounds in cancer and



metagenomics. We've had to deal with new, exciting and challenging things and I'm glad to say that we were able to rise to the occasion as a team, and we have made the best of every card that has been thrown our way.

I have been a part of IBRT for three years now, and I'm continually impressed by the hard work and dedication of all of the faculty team members, leaders and IBRT members to keep this journal running. We always have new projects in the works and I can't wait for them to come to life in order to enable us share even more of our work with you, but for now I hope you enjoy this edition of our best research and articles from 2022.

This journal is a team effort which I am privileged to have spear headed, special thanks to the fantastic team lead, amazing members of the editorial team, gifted researches and everyone who contributed to the success of this publication.

For more information about the team, please visit [ibadanbacteriophageteam.org](http://ibadanbacteriophageteam.org). We welcome feedbacks at [ibadanbacteriophageresearchteam@gmail.com](mailto:ibadanbacteriophageresearchteam@gmail.com)

Also, kindly follow us on our official handles on social media platforms listed below:

Twitter: IbadanPhageTeam

LinkedIn: Ibadan Bacteriophage Research Team

Best Wishes,

Oluwaseun Akinfemisoye

**Editor-in-chief, Phamilia 2.0.**



# IBRT TEAM PROFILING

## CONFERENCES

1. 7th UNIBADAN Conference on Biomedical Research (UCBR-7)
2. 12th International Symposium of SEA Researchers, 2021
3. 13th International Symposium of SEA Researchers, 2022
4. 27th International Phage Virus Assembly Conference
5. 13th World Congress of Microbiology and Clinical Research
6. 14th World Congress of Microbiology and Clinical Research
7. 2021 IBRT World Phage Week Webinar Series
8. 2022 IBRT World Phage Week Webinar Series
9. Wellcome Connecting Science Genome Informatics Conference, 2022
10. Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes, 2022

## PUBLICATIONS

Adedeji R.O, Oduselu T.J, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebi A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojebola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O, Raifu M.K, Adebiyi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G. **Computational Analysis of Gordonia Bacteriophage Sedona.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbechidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Complete Genome Sequence Annotation of Arthrobacter Bacteriophage Popper.** *13th International Symposium of SEA Researchers, 2022*

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebisi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **Genomic outlay of blood-isolated *Klebsiella pneumoniae* reveal hypervirulent and hypermucoidy drug-resistant isolates.** *Wellcome Connecting Science - Genome Informatics Conference, 2022*

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Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owwoye, W.T., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adedeji, Roqeeb O, Oduselu, Tolulope J, Adewumi, Olubusuyi M, Anetor, John I, Bakarey, Adeleye S, Ademowo, Olusegun G. (2022) **Transcriptomic Analysis of Chimeric Antigen Receptor (CAR) T-cell Targeting Epithelial Cell Adhesion Molecule (EpCAM)**

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvellous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebisi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (*Mandrillus leucophaeus*)**

Opatola, Abdulmujeeb D, Alabi, Praise L, Olatoye, Marvellous R, Ojediran, Mercy A, Daramola, Oluwasegun I, Adewumi, Olubusuyi M, Ademowo, Olusegun G. (2022) **Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples**

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Adams O. David, Adedeji Roqeeb, Oluwasegun I. Daramola, Adeleye S. Bakarey, Olubusuyi M. Adewumi, and Olusegun G. Ademowo. (2022) **Phage Cocktails: A Biological Control for Foodborne Pathogens**



# LEADERS



**DARAMOLA**

Oluwasegun Isaac

Level: 500

## CONFERENCES

1. Gulf Course Undergraduate Research Symposium, 2020
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# LEADERS



**A D E D E J I**

Roqeeb Olamide

Level: 500

## CONFERENCES

1. 27th International Phage Virus Assembly Conference, 2021
2. 7th UNIBADAN Conference on Biomedical Research, 2021
3. 12th International Symposium of SEA Researchers, 2021
4. 13th International Symposium of SEA Researchers, 2022
5. 2021 IBRT World Phage Week Webinar Series
6. 2022 IBRT World Phage Week Webinar Series
7. Australian Bioinformatics and Computational Biology Society

## 2022 PUBLICATIONS

Adedeji R.O, Oduselu T.J, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebi A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojebola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O, Raifu M.K, Adebiyi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G. **Computational Analysis of Gordonia Bacteriophage Sedona**. *13th International Symposium of SEA Researchers, 2022*

Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbechidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Complete Genome Sequence Annotation of Arthrobacter Bacteriophage Popper**. *13th International Symposium of SEA Researchers, 2022*

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome**. *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adedeji, Roqeeb O, Oduselu, Tolulope J, Adewumi, Olubusuyi M, Anetor, John I, Bakarey, Adeleye S, Ademowo, Olusegun G. (2022) **Transcriptomic Analysis of Chimeric Antigen Receptor (CAR) T-cell Targeting Epithelial Cell Adhesion Molecule (EpCAM)**

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (Mandrillus leucophaeus)**

Adams O. David, Adedeji Roqeeb, Oluwasegun I. Daramola, Adeleye S. Bakarey, Olubusuyi M. Adewumi, and Olusegun G. Ademowo. (2022) **Phage Cocktails: A Biological Control for Foodborne Pathogens**



# LEADERS



**AKOMOLAFE**

Ayobami Joseph

Level: 500

## CONFERENCES

1. 27th International Phage Virus Assembly Conference, 2021
2. 12th International Symposium of SEA Researchers, 2021
3. 13th International Symposium of SEA Researchers, 2022
4. 2021 IBRT World Phage Week Webinar Series
5. 2022 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Adedeji R.O, Oduselu T.J, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebi A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojebola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O, Raifu M.K, Adebiyi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G. **Computational Analysis of Gordonia Bacteriophage Sedona**. *13th International Symposium of SEA Researchers, 2022*

Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbechidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Complete Genome Sequence Annotation of Arthrobacter Bacteriophage Popper**. *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (*Mandrillus leucophaeus*)**

Akomolafe J. Ayobami, Adams O. David, Iyede O. Temitayo, Inyang S. Emem, Oluwasegun I. Daramola, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Complex Interaction of Host Immune System and Clinical Therapy Phages**

# LEADERS



**A D E D I R A N**

Benjamin Adesumbo

Level: 400

## CONFERENCES

1. Phage Virus Assembly 2021
2. 7th UNIBADAN Conference on Biomedical Research (UCBR-7)
3. 13th World Congress of Microbiology and Clinical Research
4. 2021 IBRT World Phage Week Webinar Series
5. Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes, 2022

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Benjamin Adediran, Zainab Kuku, Emmanuel Adebayo, Oluwasegun Daramola, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **The role of crRNA sequence selection in CRISPR/Cas9-based engineering of T4 Phages.** *Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebisi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (Mandrillus leucophaeus)**



# LEADERS



O P A T O L A

Abdulmujeeb Damola

Level: 400

## CONFERENCES

1. 7th UNIBADAN Conference on Biomedical Research (UCBR-7)
2. 27th International Phage Virus Assembly Conference
3. 13th World Congress of Microbiology and Clinical Research
4. 2021 IBRT World Phage Week Webinar Series
5. 2022 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **Genomic outlay of blood-isolated Klebsiella pneumoniae reveal hypervirulent and hypermucoidy drug-resistant isolates.** *Wellcome Connecting Science - Genome Informatics Conference, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Opatola, Abdulmujeeb D, Alabi, Praise L, Olatoye, Marvellous R, Ojediran, Mercy A, Daramola, Oluwasegun I, Adewumi, Olubusuyi M, Ademowo, Olusegun G. (2022) **Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples**

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**

# LEADERS



**O J E D I R A N**

Mercy Adedamola

Level: 400

## CONFERENCES

1. 12th International Symposium of SEA Researchers, 2021
2. 13th International Symposium of SEA Researchers, 2022
3. 27th International Phage Virus Assembly Conference
4. 2021 IBRT World Phage Week Webinar Series
5. 2022 IBRT World Phage Week Webinar Series
6. Wellcome Connecting Science Genome Informatics Conference, 2022

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **Genomic outlay of blood-isolated Klebsiella pneumoniae reveal hypervirulent and hypermucoidy drug-resistant isolates.** *Wellcome Connecting Science - Genome Informatics Conference, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Opatola, Abdulmujeeb D, Alabi, Praise L, Olatoye, Marvellous R, Ojediran, Mercy A, Daramola, Oluwasegun I, Adewumi, Olubusuyi M, Ademowo, Olusegun G. (2022) **Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples**

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adediji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (*Mandrillus leucophaeus*)**

Ojediran Mercy, Olatoye Marvellous, Alabi Praise, Daramola Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. (2022) **The Incorporation of Proteomics Analysis in AMR Studies**



# LEADERS



O W O E Y E

Williams Timilehin

Level: 400

## CONFERENCES

1. 12th International Symposium of SEA Researchers, 2021
2. 13th International Symposium of SEA Researchers, 2022
3. 27th International Phage Virus Assembly Conference
4. 2021 IBRT World Phage Week Webinar Series
5. 2022 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adededeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adededeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

# LEADERS



**AKINFEMISOYE**

Oluwaseun Dorcas

Level: 500

## CONFERENCES

1. 12th International Symposium of SEA Researchers, 2021
2. 13th International Symposium of SEA Researchers, 2022
3. 2021 IBRT World Phage Week Webinar Series
4. 2022 IBRT World Phage Week Webinar Series

# Existing Members



A D A M S

David Oluwatimelehin

Level: 400

## CONFERENCES

1. 12th International Symposium of SEA Researchers, 2021
2. 13th International Symposium of SEA Researchers, 2022
3. 27th International Phage Virus Assembly Conference

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (Mandrillus leucophaeus)**

Akomolafe J. Ayobami, Adams O. David, Iyede O. Temitayo, Inyang S. Emem, Oluwasegun I. Daramola, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Complex Interaction of Host Immune System and Clinical Therapy Phages**

Adams O. David, Agboola A. Ridwan, Okunade O. Peace, Taiwo A. Jesutofunmi, Daramola I. Oluwasegun, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Exploiting Receptor-binding Proteins (RBP)s for Clinical Therapeutics Purposes**

Adams O. David, Adediji Roqeeb, Oluwasegun I. Daramola, Adeleye S. Bakarey, Olubusuyi M. Adewumi, and Olusegun G. Ademowo. (2022) **Phage Cocktails: A Biological Control for Foodborne Pathogens**



**A L A B I**

Praise Lois

**Level: 400**

## CONFERENCES

1. 13th International Symposium of SEA Researchers, 2022
2. 27th International Phage Virus Assembly Conference

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adediji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome.** *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adediji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **Genomic outlay of blood-isolated *Klebsiella pneumoniae* reveal hypervirulent and hypermucoidy drug-resistant isolates.** *Wellcome Connecting Science - Genome Informatics Conference, 2022*

Opatola, Abdulmujeeb D, Alabi, Praise L, Olatoye, Marvellous R, Ojediran, Mercy A, Daramola, Oluwasegun I, Adewumi, Olubusuyi M, Ademowo, Olusegun G. (2022) **Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples**

Ojediran Mercy, Olatoye Marvellous, Alabi Praise, Daramola Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. (2022) **The Incorporation of Proteomics Analysis in AMR Studies**



I Y E D E

Temitayo Oluwadamilare

Level: 500

## CONFERENCES

2021 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Adedeji R.O, Oduselu T.J, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebi A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojebola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O, Raifu M.K, Adebiyi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G. **Computational Analysis of *Gordonia* Bacteriophage Sedona.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbechidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Complete Genome Sequence Annotation of *Arthrobacter* Bacteriophage Popper.** *13th International Symposium of SEA Researchers, 2022*



Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository*, 2022

Akomolafe J. Ayobami, Adams O. David, Iyede O. Temitayo, Inyang S. Emem, Oluwasegun I. Daramola, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Complex Interaction of Host Immune System and Clinical Therapy Phages**



**O L A T O Y E**

Marvellous Rotimi

Level: 400

## CONFERENCES

1. 13th International Symposium of SEA Researchers, 2022
2. 27th International Phage Virus Assembly Conference
3. 2021 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Computational Analysis of Microbacterium Bacteriophage Gretchen Genome**. *13th International Symposium of SEA Researchers*, 2022

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owoeye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository*, 2022

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **Genomic outlay of blood-isolated *Klebsiella pneumoniae* reveal hypervirulent and hypermucoidy drug-resistant isolates.** *Wellcome Connecting Science - Genome Informatics Conference, 2022*

Opatola, Abdulmujeeb D, Alabi, Praise L, Olatoye, Marvellous R, Ojediran, Mercy A, Daramola, Oluwasegun I, Adewumi, Olubusuyi M, Ademowo, Olusegun G. (2022) **Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples**

Ojediran Mercy, Olatoye Marvellous, Alabi Praise, Daramola Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. (2022) **The Incorporation of Proteomics Analysis in AMR Studies**

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (*Mandrillus leucophaeus*)**



**I N Y A N G**

Emem Samuel

Level: 500

## CONFERENCES

1. 2021 IBRT World Phage Week Webinar Series

## 2022 PUBLICATIONS

Adedeji R.O, Oduselu T.J, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebi A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojebola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O, Raifu M.K, Adebiyi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G. **Computational Analysis of *Gordonia* Bacteriophage Sedona.** *13th International Symposium of SEA Researchers, 2022*

Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbechidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. **Complete Genome Sequence Annotation of Arthrobacter Bacteriophage Popper**. *13th International Symposium of SEA Researchers, 2022*

Daramola, O.I., Adams, D.O., Alabi, P.I., Adedeji, R.O., Adediran, B.A., Akomolafe, A.O., Inyang, E.S., Iyede, T.O., Ojediran, M.A., Olatoye, M.R., Opatola, A.D., Owwoye, W.T., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Bianmat Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*

Akomolafe J. Ayobami, Adams O. David, Iyede O. Temitayo, Inyang S. Emem, Oluwasegun I. Daramola, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Complex Interaction of Host Immune System and Clinical Therapy Phages**

Akomolafe, Ayobami J, Adams, David O, Inyang, Emem S, Oluwasegun, Daramola I, Ifeoluwa, Ayodele, Ojediran, Mercy, Olatinwo, Samuel, Adediran, Benjamin, Ernesto, Dibia, Olatoye, Marvelous, Adedeji, Roqeeb, Iyede, Temitayo O, Oduselu, Tolulope J, Adebiyi, Ini, Ogunleye, Veronica I, George, Uwem, Faleye, Temitope O, Bakarey, Adeleye S, Adewumi, Olubusuyi M, Anetor, John I, Ademowo, Olusegun G. (2022) **Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (Mandrillus leucophaeus)**



**ONIFADE**

Yemi-Mubaraqat

Level: 500

## CONFERENCES

1. 2022 IBRT World Phage Week Webinar Series
2. 13th International Symposium of SEA Researchers, 2022

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**



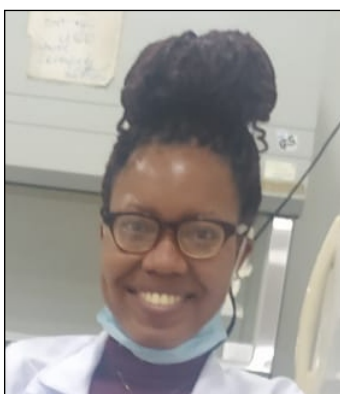
**A D E P O J U**

Odunayo Deborah

Level: 500

## CONFERENCES

1. 13th International Symposium of SEA Researchers, 2022
2. 2022 IBRT World Phage Week Webinar Series



**A Y E N I**

Damilola Precious

Level: 500

## CONFERENCES

1. 13th International Symposium of SEA Researchers, 2022
2. 2022 IBRT World Phage Week Webinar Series



**A W O J I D E**

Mayowa Margaret

Level: 400

## CONFERENCES

1. 27th International Phage Virus Assembly Conference
2. 13th International Symposium of SEA Researchers, 2022
3. Wellcome Connecting Science Genome Informatics Conference, 2022



**OLAOMITO**

Mayowa Anthony

Level: 400

## CONFERENCES

1. 27th International Phage Virus Assembly Conference
2. 12th International Symposium of SEA Researchers, 2021



# IBRT New Intakes



**OLUDIPE**

Oluwaseyi John

Level: 300

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**



**ANIMASAHUN**

Favour Mobolade

Level: 400

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

- Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**
- Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*



**A R O K O Y O**  
Oluwashoyinfunmi  
Level: 500

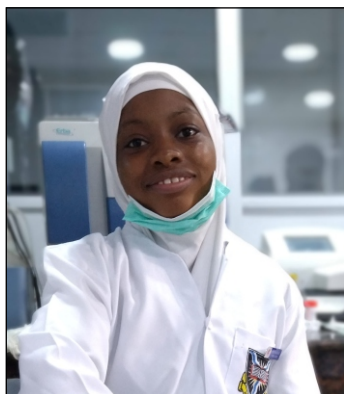
## CONFERENCES

- 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*



**K U K U**

Zainab Oreoluwa

Level: 400

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022
2. WCS Genome Informatics Conference
3. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Benjamin Adediran, Zainab Kuku, Emmanuel Adebayo, Oluwasegun Daramola, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **The role of crRNA sequence selection in CRISPR/Cas9-based engineering of T4 Phages.** *Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes, 2022*

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*



**T A I W O**

Jesutofunmi Abosedo

Level: 400

## CONFERENCES

- 13<sup>th</sup> International Symposium of SEA Researchers, 2022
- 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adams O. David, Agboola A. Ridwan, Okunade O. Peace, Taiwo A. Jesutofunmi, Daramola I. Oluwasegun, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Exploiting Receptor-binding Proteins (RPBs) for Clinical Therapeutics Purposes**



**ADEDAMOLA**

Adedoyin

Level: 400

## CONFERENCES

1. 2021 World Phage Week Webinar
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebisi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*



**AGBOOLA**

Ridwan Mayowa

Level: 300

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*

Adams O. David, Agboola A. Ridwan, Okunade O. Peace, Taiwo A. Jesutofunmi, Daramola I. Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Exploiting Receptor-binding Proteins (RPBs) for Clinical Therapeutics Purposes**



**O K U N A D E**

Peace Oluwaseun

Level: 300

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022.
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adams O. David, Agboola A. Ridwan, Okunade O. Peace, Taiwo A. Jesutofunmi, Daramola I. Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Exploiting Receptor-binding Proteins (RPBs) for Clinical Therapeutics Purposes**

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*





A D E B A Y O

Emmanuel Oluwabamiji

Level: 300

## CONFERENCES

1. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Benjamin Adediran, Zainab Kuku, Emmanuel Adebayo, Oluwasegun Daramola, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo. **The role of crRNA sequence selection in CRISPR/Cas9-based engineering of T4 Phages.** *Wellcome Connecting Science - CRISPR and Beyond: Perturbations at Scale to Understand Genomes, 2022*



A D E D E J I

Dorcas Anuoluwapo

Level: 500

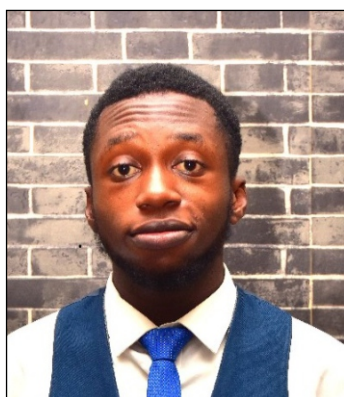
## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers, 2022
2. 2022 IBRT World Phage Week Webinar

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation.** *National Center for Biotechnology Information (NCBI) Repository, 2022*

Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**



**A J A Y I**  
Oluwasanmi Michael

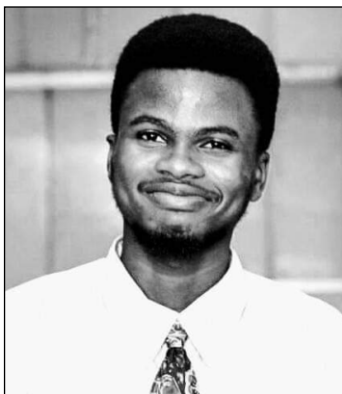
**Level: 500**

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers 2022
2. 2022 World Phage Week Webinar

## 2022 PUBLICATIONS

Adams O. David, Agboola A. Ridwan, Okunade O. Peace, Taiwo A. Jesutofunmi, Daramola I. Oluwasegun, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo. (2022) **Exploiting Receptor-binding Proteins (RPBs) for Clinical Therapeutics Purposes**



**RANTI**

Daniel

Level: 400

## CONFERENCES

1. 2022 World Phage Week Webinar
2. 13<sup>th</sup> International Symposium of SEA Researchers, 2022

## 2022 PUBLICATIONS

Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*



**ADEGBITE**

Adesubomi

Level: 300

## CONFERENCES

1. 13<sup>th</sup> International Symposium of SEA Researchers 2022
2. 2022 World Phage Week Webinar

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- Adediran, B.A., Adebayo, E.O., Adedamola, A., Adedeji, D.A., Adegbite, A., Agboola, R., Animasahun, F.M., Ayeni, D.P., Kuku, Z., Okunade, P.O., Oludipe, O.J., Onifade, Y., Ranti, D., Taiwo, J., Daramola, O.I., Raifu M.K., Adebiyi I., Ogunleye V.I., Faleye T.O.C., Bakarey A.S., Adewumi O.M., Anetor J.I., and Ademowo O.G. **Gordonia Phage Salvador Complete Genome Annotation**. *National Center for Biotechnology Information (NCBI) Repository, 2022*
- Abdulmujeeb D. Opatola, Adedoyin Q. Adedamola, Oluwaseyi J. Oludipe, Favour M. Animashaun, Adesubomi A. Adegbite, Mubaraqat Y. Onifade, Dorcas A. Adedeji, Oluwashoyin P. Arokoyo, Oluwasegun I. Daramola, Olubusuyi M. Adewumi, Olusegun G. Ademowo. (2022) **Functionality of the Presence of tRNA in Phages**

# INTERVIEW WITH ODUSELU TOLULOPE

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**ESCMID 30 under 30  
Young Scientist awardee**

**Research Analyst,  
Ibadan Enterovirus Project**



**Pioneer Team Leader  
and Head of Research,  
Ibadan Bacteriophage  
Research Team**

**ISVM/VOM Early Career  
Research awardee**

# INTERVIEW WITH ODUSELU TOLULOPE

In the first issue of Phamilia, we had an interview with Prof. O.G Ademowo, the founder of IBRT where he shared the backstory to the creation of the research group. Knowing the narrative would be incomplete without sampling the perspective of students that were a part of this pacesetting feat, Williams Owoeye, Head of Communication and Publicity for IBRT spoke with Tolulope Oduselu, the pioneer Team Lead of IBRT. In this interview, he shared with us the uncertainties that characterized that period of infancy. In addition, he also shared some insights into the evolution of IBRT over the 4 years of its existence.

**Can you kindly introduce yourself so the audience can know you better?**

**Tolulope:**

My name is Tolulope John Oduselu and I am a member of the BMLS 2k18. I hail from Ijebu Ode, Ogun state and I had my primary and secondary school education there. I had a very wonderful childhood with two older male siblings. My siblings are brilliant, and my parents were teachers, so when it came to academics, I had that motivating and disciplined environment from the start. Despite this, growing up was very interesting because I enjoyed all the mischief childhood could offer. I was able to maintain a good academic record throughout secondary school. There were many highs, a few lows and opportunities to take up leadership positions in the course of the six years. I had fairly good grades in the WAEC and NECO examinations, so I was pretty confident medicine and surgery was the way for me. I will blame it in part on Ben Carson, if you know what I mean. God had other plans and University of Ibadan ensured that was the case. I believe the eventual choice of Biomedical Laboratory Science redefined a lot for me over the years and today, I have no regrets.

**Thank you for that concise introduction. I'd like to move to the part that pertains to IBRT. Can you give us a short overview of how the IBRT story started from a student's perspective since we've had the perspective of a faculty member in the previous issue?**

**Tolulope:**

The SEA-PHAGES program was introduced to us in 2018 during a Chemical Pathology class by Prof J. I Anetor. He really did not give the full details of the programme but he mentioned that it would be a good engagement for those looking to pursue a career in Medical Microbiology and Virology.



Afterwards, a few of us were called over to the IAMRAT building for a proper introduction to the faculty team, headed by Prof. O.G Ademowo. We had a virtual meeting with representatives of SEA-PHAGES at the University of Pittsburgh. Quite frankly, that was about the second time I was hearing the word “Bacteriophage”. We were called 'Ibadan Phage Hunters', we had a mission to hunt and characterize viruses we were told could be found anywhere and everywhere.

Due to the lag in the SEA-PHAGES calendar compared to the University calendar, My colleagues and I had to commence bioinformatics training (Taiwo Anjolaoluwa, Oyebamiji Toba, Ayodele Ifeoluwa, Comfort Omolola, Ojebola Tunde, Atoyebi Abigail to mention a few) carried laptops to IAMRAT seminar room without the faintest clue of what to use it for. Our instructors, Dr. M.O Adewumi, Dr. A.S Bakarey, and Dr. T.O.C Faleye introduced us to bioinformatic tools which we had never heard before. We obviously knew that foreign scientists (at least in movies) make use of computational models to study biological systems but nothing prepared us as 300 level students of a Nigerian university for what we were about to be exposed to. The program was designed to be driven by student interest and our instructors maintained that approach. Fortunately for us, there was an ongoing ASUU strike so we had time on our hands. We thoroughly studied the tool guide and tried to understand the features of the software. Some of us literally crashed the software on our systems along the way.

Thankfully, It all paid off in the end because we completed the first bacteriophage genome characterization (Phage Idaho) and had it successfully submitted to NCBI GenBank.

**Being the pioneer team lead of IBRT, you've seen a lot happen in the team. Is there a point you can reference as that defining point for the success story IBRT has come to record?**

**Tolulope:**

Definitely. It was 2020. All that is now known to be IBRT today began in August 2020 during the course of the global pandemic. We all had that sense of satisfaction in undertaking a characterization project and seeing it through to the conference abstract presentation stage and having it published on NCBI. We knew we could do better with time and more dedication and so we were willing to follow it up. We had numerous consultations with the faculty team on how to design the project to meet our peculiar research needs. We studied the organizational structure of successful organizations like Dokita, Dentiscope, Physioray, and Panacea Project. We wanted a well-structured research organization that could enable active early career research engagement alongside academic pursuit for members. The consultation took that long because there was no model organization like what we wanted at the university back then.

We began test-running the new design with the BMLS 2k19 class members. They were strictly taught by previous members of the team from scratch up until the characterization project for Phage Dothraki was complete. With that success, we knew we could push for more new ideas. In 2019, we tried the phage isolation process but it was cut short due to the global pandemic. Since we had time and the world was becoming virtual, we started pushing new ideas to the faculty team in August 2020. We rebranded the team name, the team logo, the leadership structure, we introduced a virtual teaching structure using recorded teaching videos, we started writing review articles and short publications, we expanded our reach to the global phage community through the World Phage Week Webinar, amongst other things.

**Let us now link the antecedents with the current reality. If we are to look at IBRT with you as team lead and IBRT now, what are the key differences you observe?**

**Tolulope:**

Hmm, A whole lot has changed over the course of the years. I think one thing that I'd like to point out is that IBRT makes a conscious effort at maintaining an upward trajectory in learning and I think that is one key difference between IBRT and perhaps any other student organization in the University of Ibadan and across different universities. We place a high value on learning and maintaining our learning curve. As much as we are learning, we are ensuring engagement from all our members and we do well to engage our immediate community as well. Secondly, I will admit that the traction, attention, and exposure have increased due to the nature of the work that has been done over the years. So, I would say that the system is better defined now.

**Indeed a lot of growth has happened in IBRT including the transition from a bacteriophage research-inclined group to one that now explores other research fields such as cancer, antimicrobial resistance, and metagenomics. This appears audacious. What can you say is the motivation behind the switch into these other fields?**

**Tolulope:**

During the leadership transitory period, the past Phage Leaders Forum met with the founder, Prof O.G Ademowo. During the course of our discussion, Prof Ademowo asked us what we wanted the team to be like in the years to come. He advised us to design a 10-year team development plan in order to maintain a smooth transition and continuity. This advice was the major push for us to go big, and it influenced the aspect you mentioned. In addition, when I was team lead at IBRT, I had often thought that over time, the team might not do well- if there is no diversity of interests. I

thought that over time, the team might not do well- if there is no diversity of interests. I also knew we have to have an identity other than being a SEA-PHAGES team.

We had the vision to create a training programme for early career research for undergraduates at the BMLS department and we desired that the model would be used as a template for other organizations at the University of Ibadan and even in other universities in Sub-Saharan Africa. We knew we had much ground to cover in bacteriophage biology and computational genomics but we also anticipated that with time, new interests in cancer research, antimicrobial resistance, etc. would be developed by members. Our invitation from the Enterovirus Team, at the Department of Virology, University of Ibadan to study novel bacteriophages in faecal samples of non-human primates encouraged us to integrate the metagenomic sub-group. This model has proven to be successful with the BAMSSA Research Hub. The secret like I mentioned earlier remains perfecting understanding by teaching others what you have learnt. The more we learnt and taught, the more we got better and realized new knowledge.

### **Looking at the way things are now and when you were the pioneer leader of IBRT, is there anything you wish you had done differently?**

#### **Tolulope:**

Absolutely nothing and here is my reason. I think the current leadership is doing a lot more wonderful work than what was done in the past. Perhaps it is not as publicized as what it was during the growth phase. I think the current leadership is handling a much more delicate phase than what we had then. In the past, like the sigmoid curve of bacterial growth, the active phase had so much going on for the team. It seemed we could not do anything wrong but that wasn't the case. The leaders would laugh when they read this because we made so many mistakes and had many failed projects too. The success compensated for the failings and because we were learning, we didn't bother much. The internal structure was not too clear as well so that affected us a little. But like I said, it is far better now. The new leaders have been able to manage their phase properly.

### **So where do you see IBRT in the next five years?**

#### **Tolulope:**

I think in the next five years, IBRT would still be able to maintain the growth trajectory and definitely would have been able to isolate our own indigenous bacteriophage. That's like a major thing for us. Of course, I'm hoping that we will be able to continue all the programs we have put in place and be able to introduce new ones as the demand comes. But overall, I see IBRT maintaining its place as the leading early career research organisation at the university, breaking new ground in bacteriophage biology and doing so well in computational genomics as well.

## Any parting words?

### **Tolulope:**

That will be just to appreciate all the pioneer members of IBRT. There is a way the mind works such that you might just want to focus on one person and it is one of the reasons I try to avoid a narrative that focuses on a person. IBRT is more than just one person and everyone (both past and current members) have contributed to what we have today. My big appreciation to the Faculty team led by Prof. Ademowo. No write-up can be exhaustive enough to appreciate the entire faculty team. All past and current Heads of Department of BMLS, members of teaching and non-teaching staff are also greatly appreciated. I must also dedicate special mention to Joshua Ibiyinka who designed the IBRT graphic portfolio to what we have today. Special thanks to members of the pioneer phage leaders forum, Taiwo Anjola, Ayodele Ifeoluwa, Atoyebi Abigail, Comfort Omolola, Oyebamiji Toba, Adedeji Roqeeb, Daramola Isaac, Adesanya Folajimi and Akomolafe Ayobami.

# SEA-Symposium 2022



# Computational Analysis of Microbacterium Bacteriophage Gretchen Genome

**Benjamin A. Adediran, David O. Adams, Abdulmujeeb D. Opatola, Marvellous R. Olatoye, Praise L. Alabi, Williams T. Owoeye, Mercy A. Ojediran, Oluwasegun I. Daramola, Roqeeb O. Adedeji, Temitayo O. Iyede, Oluwafolajimi A. Adesanya, Comfort M. Omolola, Tolulope J. Oduselu, Muideen Raifu, Ini Adebiyi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Olusegun G. Ademowo**

Microbacterium bacteriophage Gretchen (accession number: [OK040779](https://phagesdb.org/phages/Phishy/)) was isolated by the University of Pittsburgh in the year 2019 (<https://phagesdb.org/phages/Phishy/>). The bacteriophage was grown on *Microbacterium paraoxydans* NWU1 bacterial host, sequenced via Illumina genome sequencing and revealed an approximate shotgun coverage of 2183X. It has a genome length of 47463 base pairs, G+C content of 69.6%, and a 3' sticky overhang of 11 bases. Sequence alignment carried out on NCBI BLASTn (<https://blast.ncbi.nlm.nih.gov/BlastAlign.cgi>) and phagesdb.org (<https://phagesdb.org/blast/>) revealed 84% - 98% nucleotide sequence identity with other temperate phages belonging to cluster EH, with the closest member to Gretchen being Percival ([MH271308](https://phagesdb.org/phages/Phishy/)). Other notable phages with marked genome identities included Floof (accession number: [MH271298](https://phagesdb.org/phages/Phishy/)), IAmGroot (accession number: [MK880124](https://phagesdb.org/phages/Phishy/)), and GardenState (accession number: [MT952845](https://phagesdb.org/phages/Phishy/)). Auto-annotation of the genome was carried out using Glimmer and GeneMark in-built predictors in DNA Master and RAST server (<https://rast.nmpdr.org/>), both predicting 77 protein-coding features. ARAGORN (<http://www.ansikte.se/ARAGORN/>) and tRNASCAN-SE identified gene 76 to code for a tRNA. Visual inspection of the genome sequence was done using both DNA Master and Artemis, while manual inspection for start site refinement was carried out using DNA Master, Starterator, and Phamerator. Assignment of putative functions was done on NCBI Protein BLAST, HHPred (<https://toolkit.tuebingen.mpg.de/tools/hhpred>) and Uniprot (<https://www.uniprot.org/blast/>) databases. Of the 77 manually validated protein features, 72 were forward oriented genes and 4 were reversed oriented genes. Whilst none of the reversed oriented genes was assigned any putative function, Forty-eight percent of the forward oriented genes were assigned putative functions comprising of Structural and assembly proteins, Tape measure proteins, Minor tail proteins, HNH Endonuclease, Membrane Protein, Endolysin, DNA Binding Protein, Tail Assemble Chaperone and Scaffolding Proteins.

# Complete Genome Sequence Annotation of *Arthrobacter* Bacteriophage Popper

**Oluwasegun I. Daramola, Tolulope J. Oduselu, Oluwafolajimi A. Adesanya, Ayobami J. Akomolafe, Iyede O. Temitayo, Roqeeb O. Adedeji, Odunayo D. Adepoju, Ogochukwu M. Mgbachidinma, Gloria N. Igbor, Emem S. Inyang, Muideen Raifu, Ini Adebisi, Veronica I. Ogunleye, Temitope O.C. Faleye, Adeleye S. Bakarey, Olubusuyi M. Adewumi, John I. Anetor, and Oluwasegun G. Ademowo**

*Arthrobacter* bacteriophage Popper (accession number: [MZ274308](#)) was originally isolated by the University of Pittsburgh in the year 2017. The bacteriophage has a linear genome with a 3' sticky overhang of 12 bases and was isolated on *Arthrobacter globiformis* B-2979 host. It has a genome length of 41822 base pairs, an approximate shotgun coverage of 1204X, and a G+C content of 65.24%. Whole-genome sequence alignment carried out on [NCBI-BLASTn](#) and [phagesdb.org](#) revealed high nucleotide sequence identity with other phages belonging to cluster FF. Notable genome similarities include Nandita (accession number: [MH834621](#)), Zaheer (accession number: [MZ150784](#)), and Ryan (accession number: [MH834627](#)). The visual comparison of the FF cluster identity was created using Blast Ring Image Generator (BRIG) and Artemis Comparison Tool (ACT). Pairwise similarity sorting of bacteriophage genomes using Phamerator revealed very close gene synteny amongst the cluster FF phages.

Auto-annotation of the genome was carried out using GeneMark and Glimmer in-built gene predictors in DNA Master and [RAST](#) server, and both predicted 69 protein-coding features. [ARAGORN](#) and [tRNAscan-SE](#) analysis identified gene 36 as a tRNA. Visual inspection of the genome was conducted using both DNA Master and Artemis, while manual inspection for start site refinement was carried out using DNA Master, Starterator, and Phamerator. Putative protein functional assignment was identified using NCBI BLASTp, HHPred, and UniProt. The genome structural organization comprised of Eighty-eight percent forward transcribed genes and Twelve percent reverse-transcribed genes, out of the 69 manually validated protein-coding features. Sixty-three percent of the protein-coding features were assigned putative functions. Seventy-nine percent of proteins with coding features were forward-transcribed genes, comprising virion structural and assembly proteins, and lytic cycle proteins; Lysin A and Holin. The reverse-transcribed genes accounted for 21% of assigned putative functions, comprising lysogenic cycle proteins integrase, DNA Binding, Lipase, and Membrane proteins.

# Annotation and characterization of *Gordonia* bacteriophage Sedona

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*Gordonia* bacteriophage Sedona belongs to cluster DE, sub-cluster DE1, which is made up of 36 members with average genome length of 58,733 base pairs and an average G+C content of 67.6% (<https://phagesdb.org/subclusters/DE1/>). Sedona was originally isolated from an unenriched soil sample by the University of Pittsburgh team in 2019. The phage was grown on *Gordonia terrae* 3612 isolation host and sequencing information shows approximate shotgun coverage of 1264X. It has circularly permuted ends, a G+C content of 67.4%, and a genome length of 59,571 base pairs (<https://phagesdb.org/phages/Sedona/>). Like other members of the sub-cluster DE1, Sedona exhibits a lytic cycle, evidenced by the presence of lytic proteins Lysin A and B. NCBI-BLASTn (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) whole-genome sequence alignment revealed considerable nucleotide similarities between Sedona and other sub-cluster DE1 members, with the closest relative being phage Bibwit (<https://www.ncbi.nlm.nih.gov/nucore/MH976508>). The overall nucleotide similarity is revealed on the generated Phamerator and BLAST Ring Image Generator (BRIG) maps.

Auto-annotation carried out using Glimmer and GeneMark predictors on DNA Master predicted 84 protein-coding features, which was also confirmed by auto-annotation created on RAST server (<https://rast.nmpdr.org/>). Manual inspection and start site refinement using conserved start site predictions from Starterator index (<http://phages.wustl.edu/starterator/>), gene synteny on Phamerator, and six-frame translation inspection on DNA Master and Artemis resulted in the deletion of gene 47, a reverse transcribed gene with very poor supporting information. Ninety-nine percent of the predicted protein-coding features are forward transcribed genes, with a single exception of gene 36 (33689 to 34162 bp), which codes for an HNH-Endonuclease. Putative functional assignment carried out on NCBI BLASTp, Uniprot, and HHPred successfully assigned putative functions to Forty-two percent of the predicted gene features. Some of the predicted protein functions include Helix-turn Helix DNA Binding protein, HNH Endonuclease, RNA Ligase, Terminase, Portal protein, and Tape Measure protein..

Papers

Papers

Papers

Papers



# COMPLEX INTERACTIONS OF HOST IMMUNE SYSTEM AND CLINICAL THERAPY PHAGES

Akomolafe J. Ayobami<sup>1,2</sup>, Adams O. David<sup>1,2</sup>, Iyede O. Temitayo<sup>1,2</sup>, Inyang S. Emem<sup>1,2</sup>, Oluwasegun I. Daramola<sup>1,2</sup>, Muideen Raifu<sup>1,3</sup>, Ini Adebisi<sup>1,4</sup>, Veronica I. Ogunleye<sup>1,4</sup>, Temitope O.C Faleye<sup>1,5</sup>, Adeleye S. Bakarey<sup>1,2,3</sup>, Olubusuyi M. Adewumi<sup>1,5</sup>, John I. Anetor<sup>1,6</sup>, and Olusegun G. Ademowo<sup>1,3,7</sup>

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A recurring challenge in the fight against bacterial infections is the resistance developed against antibiotics; once a novel discovery to fight bacteria. Although not devoid of its challenges and limitations, bacteriophage (phage) therapy has been considered an alternative to antibiotics in the fight against bacterial infections and antimicrobial resistance. A limitation to the successful use of phages therapeutically is the likelihood of reduced activity due to host immune system response. Specifically, recent studies have confirmed an innate immune system-induced host-phage interaction with the capacity to take up phages and their particles. Phages and phage particles also trigger the production of cytokines, which are crucial for maintaining immunological and innate responses. Aside from the innate immune system-induced host-phage interaction, an interaction of clinical therapy phages with the adaptive immune system also triggers the humoral response. Several studies have shown that administering phages to immunocompetent subjects results in the production of anti-phage antibodies, which neutralize serum phage load, lowering its effectiveness but ultimately not influencing the therapeutic efficacy of the phage cocktail. The titer level of the anti-phage antibodies has been demonstrated to depend on the route of administration, with a high titer observed for local administration routes and a low titer observed with orally administered cocktails. Also, it has been reported that phage proteins elicit varying degrees of immunogenic responses from one another. These emphasize the need for further research into the complex reactions between phages and the host immune system to assure safe use of bacteriophages as therapeutic agents against bacterial infections.

Word count = 252 words

# Genomic Surveillance For Antimicrobial-Resistant Determinants From Blood-Isolated *Klebsiella Pneumonia* Samples

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Daramola, Oluwasegun I<sup>1</sup>, Adewumi,  
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*Klebsiella pneumoniae* is a priority antimicrobial-resistant (AMR) pathogen and a leading cause of bloodstream infection around the world. The prevalence of more extended spectrum beta-lactamase (ESBLs) and carbapenemase-producing isolates pushes for urgent therapeutic strategies. Adequate surveillance of these multi-drug resistant (MDR) strains is predominantly lacking in Nigeria and Africa, and this hinders attempts to achieve effective control strategies nationwide. Archived clinical *K. pneumoniae* genomes of different sequence types (n = 164 blood-isolated samples from Nigeria) were retrieved from genome data deposited to the PathogenWatch repository. Relevant clinical information (antimicrobial resistance genes, virulence genes, sequence types (STs)) was extracted using Kleborate, a *K. pneumoniae*-specific genomic surveillance and genotyping tool.

Overall, 63 distinct STs were identified from the isolates. All isolates exhibit multi-drug resistance to different antibiotic classes. Resistance to antibiotic classes of Penicillins (98%), Aminoglycosides (88%), Sulfonamides (85%), Trimethoprim (81%) and third generation Cephalosporins (80%) were most prevalent across the isolates, and significant population of isolates resistant to Carbapenems, Fluroquinolones, Phenicol and Tetracyclines were also recorded. In particular, all isolates carried many additional AMR genes conferring resistance to major MDR classes, including ESBLs (73%), Carbapenemases (7%), and otherwise (20%), respectively. AMR determinant genes with the most prevalent frequency in isolates resistant to different antibiotic classes include CTM-M-15 (98%), drfA1 (95%) and sul2 (94%), respectively.

Across blood isolated *K.pneumoniae* of varying sequence types and strain identities in Nigeria, the population are vastly MDR. Evidence from this genomic surveillance suggests high prevalence of multiple AMR gene determinants in *K.pneumoniae* isolates, hence, implies the significant emergence of MDR *K.pneumoniae* causing bloodstream infections in Nigeria.

Acknowledgement – This work was supported in part by the HHMI-SEAPHAGES Early career research grant by Prof. O.G Ademowo for the University of Ibadan, and the Ibadan Bacteriophage Research team.

# Genomic outlay of blood-isolated *Klebsiella pneumoniae* reveals hypervirulent and hypermucoviscous drug-resistant isolates

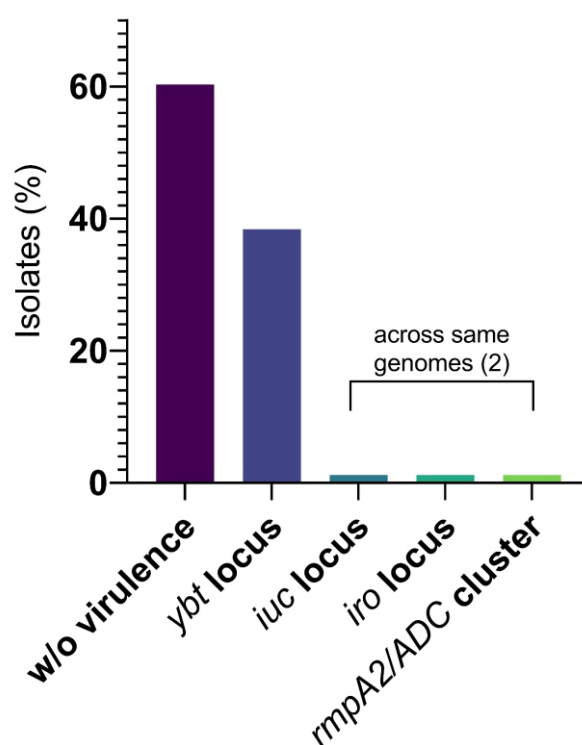
Wellcome Connecting Science -  
Genome Informatics Conference

Oluwasegun Daramola, Mercy Ojediran, Abdulmujeeb Opatola, Alabi Praise, Marvellous Olatoye, Muideen Raifu, Ini Adebiyi, Veronica Ogunleye, Temitope Faleye, Adeleye Bakarey, Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo

**INTRODUCTION:** Polysaccharide capsules and iron-scavenging siderophore systems are known to confer key bacterial virulence factors, as the ability to upregulate capsule production and acquire iron is essential for bacteria during host infection. High-virulent *Klebsiella pneumoniae* determinants include the *ybt* locus, which encodes the yersiniabactin module and is mobilized by integrative conjugative elements (ICEKps), the *iro* and *iuc* loci, which encode salmochelin and aerobactin gene clusters respectively and are located on virulent plasmids, and *rmp* genes that upregulate capsule gene expression for the hypermucoviscous phenotype.

**AIM:** Adequate genomic surveillance of multi-drug resistant (MDR) strains with virulent determinants is predominantly lacking in Nigeria, and this hinders attempts to achieve effective control strategies of virulence spread.

**METHOD:** Archived clinical *K. pneumoniae* genomes of different sequence types (n = 164 blood-isolated samples from Nigeria) were retrieved from genome data deposited to the PathogenWatch repository. Relevant clinical information (antimicrobial resistance genes, virulence genes, sequence types (STs)) was extracted using Kleborate, a *K.pneumoniae*-specific genomic surveillance and genotyping tool. AntiSMASH was employed to identify biosynthetic gene



**RESULTS:** Of the 164 isolates, 63 (38.4%) contained yersiniabactin biosynthesis genes, and 2 (1.2%) isolates both possessed the salmochelin and aerobactin biosynthesis genes. The *ybt* locus-containing isolates were identified to be heavily resistant to at least six antimicrobial drug classes, suggesting the elevated population of hypervirulent drug-resistant *K.pneumoniae* isolates in Nigeria. The two isolates (genome names ERR4783064 and ERR4783437) with the *iuc* and *iro* loci also contained hypermucoid phenotypes, evident by the presence of *rmpADC* and *rmpA2* genes. Importantly, we discovered that these isolates share highly similar metadata and could have a related origin. Secondary metabolite analysis on these two isolates confirmed siderophoric gene clusters for aerobactin with a 100% similarity score. We identified 63 distinct STs from the isolates. Owing to the content of virulent determiners, ST86 was identified as the most virulent MDR high-risk clone in the collection.

**CONCLUSION:** Genomic surveillance of these blood-isolated genomes indicates the ease of spread of virulent mobile genetic elements (MGE), even in multi-drug resistant *K.pneumoniae* in Nigeria, and further investigation into the virulence of isolates from other sample sites needs to be pursued. Evidence from this genomic analysis suggests the prevalence of virulent MGE spread, with the possible gradual progression of hypermucoviscous isolates in Nigeria.



## The role of crRNA sequence selection in CRISPR/Cas9-based engineering of T4 Phages

Wellcome Connecting Science -  
CRISPR and Beyond:  
Perturbations at Scale  
to Understand Genomes

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Olubusuyi Adewumi, John Anetor, and Olusegun Ademowo

The bioengineering of bacteriophages in recent times has faced the limitation of effectively achieving high-rate synthetic phages with wider host specificity range. Various studies to incorporate the CRISPR/Cas9 system into T4 genome editing have revealed that extensively modified bases present, mainly the possession of hydroxymethylcytosine and glycosylated genomes, resulted in significant contradiction to the action of Cas9 endonucleases. However, the CRISPR RNA (crRNA), which contains a short segment of RNA that identifies the query sequence in the foreign genetic elements and a CRISPR repeat sequence, contributes to the successful engineering of T4 synthetic phages. The overall pathway of mutant phage synthesis is hinged on the accurate cleavage of the desired region in the genome by a potent crRNA, creating a gap to be filled by the targeted mutant sequence imported by the donor plasmid. Importantly, approaches to genetically editing the T4 phage genome identified potent crRNAs using three specific score methods: the Protospacer adjacent motif (PAM) sites; the Zhang specificity score; and the Doench activity score. Upon a crRNA cleavage in the T4 genome, the dual plasmid system, containing the donor plasmid and the CRISPR/Cas9-crRNA plasmid, creates a site for the homologous recombination of the desired mutant sequence, resulting in an engineered T4 phage genome. A comprehensive assemblage and sorting of potent crRNAs resolves the host specificity limitation in exploring phage bioengineering. The synthesis of mutant T4 phages using a library of crRNAs could be potentially applied to other characterized phages with more efficient scoring methods in selecting potent crRNAs to foster phage bioengineering and therapy use.

# Transcriptomic Analysis of Chimeric Antigen Receptor (CAR) T-cell Targeting Epithelial Cell Adhesion Molecule (EpCAM)

Australian Bioinformatics and  
Computational Biology Society

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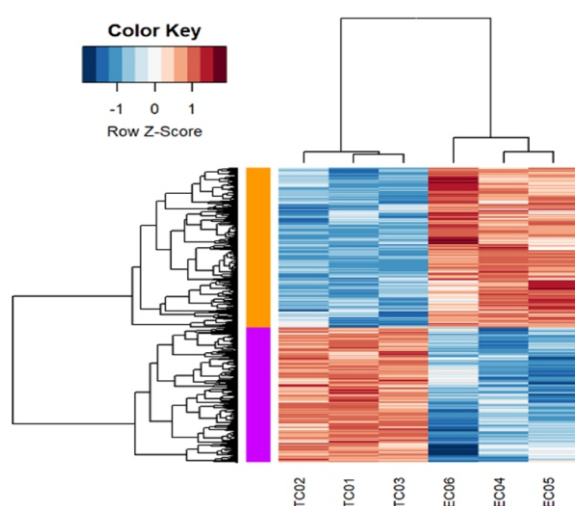
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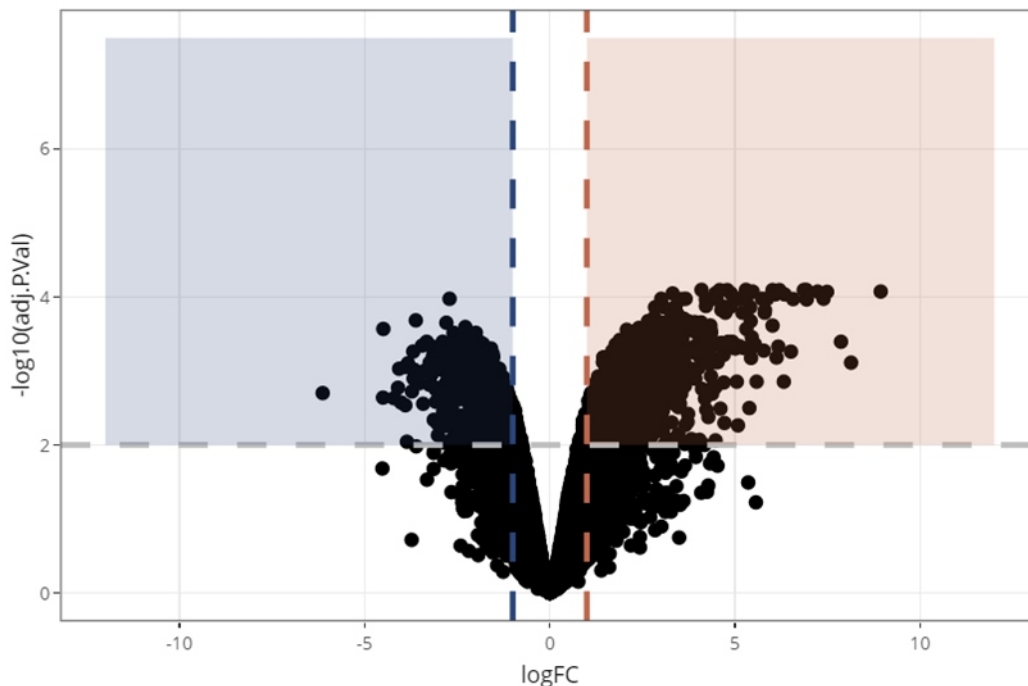
## Abstract

Chimeric Antigen Receptor (CAR) T-cells targeting Epithelial Cell Adhesion Molecule (EpCAM) have demonstrated unparalleled potential in the treatment of hematological and solid tumors, however, there are cases of severe toxicities, antigen escape, restricted T-cell trafficking and reduced tumor infiltration which has been attributed to adverse reactions, tumor relapse and limited therapeutic efficacy. Understanding the transcriptomic landscape of EpCAM targeted CAR-T cells may help inform advancements that will address these treatment inefficiencies. Transcriptomic profiling was carried out using 3 EpCAM CAR-T cells as the perturbation group and 3 normal human T-cells as the control group. Transcriptomic analysis was carried out using publicly available paired-end RNA sequences (GSE162796). Quality of the sequences was assessed using FASTQC, while pseudoalignment was done using Kallisto. Differential expression analysis was conducted using EgdeR, and expression of genes with a log Fold Change (logFC) greater than 1 was used to determine differential expression. Pathway and Gene Ontology analysis were carried out using GSEABase and Limma-Camera.



***Heatmap showing 2809 differentially expressed genes that were clustered using Pearson correlation***

Our analysis outlined a total of 2,809 differentially expressed genes (with KLF2 and MK167 being the most downregulated and upregulated genes, respectively) and 760 enriched genes. From the enriched pathways, we identified downregulation of genes involved in T-cell Receptor complex (TRBV and TRBJ genes), and Chemotaxis (ITGA4, ZFP36, GPR183, CXCR6). Upregulated genes were involved in cell growth and division (TOP2A, RAD51, MK167, NCAPG), cytokinesis (KIF20A, PLK1, IFIH), cytokine mediated signaling (HIPK1, TRAF6, IL27RA), apoptotic signaling (PHLDA3, CYP1B1, ATAD5), and inflammatory response (TUSC2, FYN, IL17RC). This study revealed the downregulation of some genes necessary for efficient immune response (honing, antigen recognition and processing) which may be responsible for antigen escape, limited T-cell trafficking, and reduced tumor infiltration, while others (apoptotic and inflammatory signaling pathways) were rather upregulated, contributing to the observed secondary effects. These findings suggest that the reduced tumor infiltration and clearing capacity of EpCAM CAR-T cells can be due to the downregulation of chemotactic genes, and the increased predisposition of CAR-T cell therapy to secondary effects stems from the upregulation of genes mediating inflammatory response. It also unravels possible novel gene targets (such as CXCR6 which has been shown to promote antitumor activity) which can enhance efficacy and reduce secondary effects of EpCAM CAR-T cell therapy.



***Volcano plot of the upregulated (red) and downregulated (blue) genes in EpCAM CAR-T cells relative to Normal T cells***

# Taxonomic Diversity and Genomic Characterization of Bacteriophage Sequences in Fecal Sample of Drill Monkey (*Mandrillus leucophaeus*).

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## Abstract

The study of microbial biodiversity within environmental samples at the genome level has witnessed significant progress in recent years due to advances in sequencing technology and bioinformatic methods. Metagenomic shotgun analysis is fast becoming the primary means of discovering novel viruses. This study was designed to unravel the taxonomic diversity of bacteriophages within the gut microbiome and characterize the genome of complete and near-complete novel bacteriophages from the metagenome assembly of faecal samples obtained from Drill Monkeys (*Mandrillus leucophaeus*) housed in a sanctuary in Cross River State, Nigeria. The short read sequences assembled using MetaSPAdes yielded 2,175,670 bp and 499 contigs. The quality of the assembled file was assessed using QUAST v4.4 and CheckV; the latter was used to check the completeness of the viral contigs. vConTACT2 was used to assess viral taxonomic diversity, while VirSorter2, viralVerify, MetaPhinder, and RAST Server were used to narrow viral contig selection to probable phage sequences for downstream characterization. Manual annotation was conducted using DNA Master, while putative protein functional assignment was done via comparison with NCBI, HHPRED, and IMG/VR databases.

A total of 2,804 viral genomes, classified under two viral orders, Caudovirales and Ligamenvirales, were identified by vConTACT2. Viruses with unassigned orders accounted for 60.3% of the total. This was not unexpected as a significant fraction of viruses have not been associated with definite host cells. Twelve contigs were identified as novel, complete and near complete phage sequences from the assembly, two members of the siphoviridae family and ten members of the microviridae family. Our findings confirm that the gut microbiome environment of non-human primates is a rich reserve of novel bacteriophages, which can be explored for bacteriophage therapy in treating antimicrobial-resistant infections.

**Acknowledgement – Ibadan Enterovirus Team.**

# The Incorporation of Proteomics Analysis in AMR Studies

**Mercy Ojediran, Marvellous Olatoye, Alabi Praise, Oluwasegun Daramola, Ini Adebisi, Veronica Ogunleye, Temitope Faleye and Olusegun Ademowo**

Antimicrobial resistance (AMR) is a major global health threat due to the misuse of antimicrobial therapeutic drugs. In the past years, AMR studies have mainly been limited to the genomic level; however, the recent incorporation of proteomics is a major advancement in antimicrobial resistance studies. Proteomics studies identify the genome and measure proteins from microbes in a quantitative manner. Various studies incorporating proteomics in studying the interactions between bacteria and antibiotics have extensively revealed how bacteria initially susceptible to antibiotics reversibly become resistant to those antibiotics. The overall pathway of proteomic analysis hinges on the analysis of the total protein content of cells after sub-lethal contact between selected antibiotics and isogenic resistant and susceptible bacterial strain. Studies have revealed that proteomic analysis was employed to uncover antibiotic hydrolyzing proteins known as beta-lactamases as the main mechanism of resistance to beta-lactams. A separate study using proteomics identified key virulence and resistance-conferring proteins abundant in susceptible isolates. Proteomics analyses have also been reported to determine biochemical alterations in resistant strains exposed to sub-lethal concentrations of antibiotics by quantifying their protein expression and fold of expression changes. This method enabled the creation of a protein repository involved in drug resistance biochemical processes. The effective incorporation of proteomics can further result in a translated approach to AMR surveillance and studies.

# Functional Microarray for Differential Expression Analysis of Colorectal Cancer: A Meta-Analysis

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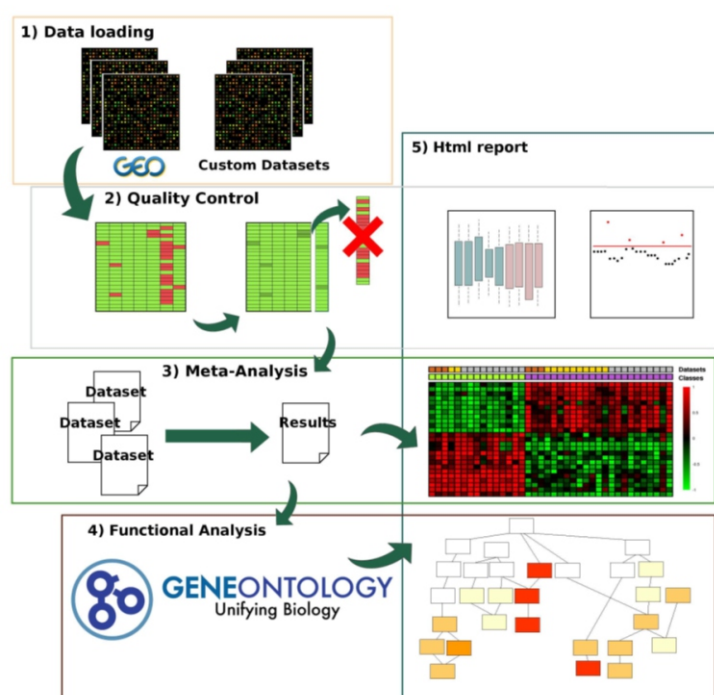
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Colorectal cancer (CRC) is one of the most prevalent cancer types around the world; it is the third most diagnosed and the second most fatal. Several factors have been found to contribute to this cancer including mutations in nucleic acid metabolism. A look into this meta-analysis will help us see the differential expression analysis of colorectal cells from healthy and diseased patients respectively. The meta-analysis was based on functional microarray analysis, an effective tool for detecting the expression of thousands of genes at the same time. It was carried out on the following micro-array samples: GSE156355, GSE44076, and GSE79794. The number of control samples in the GSE156355, GSE44076, and GSE79794 datasets were 6, 148, and 10, and the number of perturbation samples was 6, 98, and 26 respectively.

These datasets were analyzed using ImaGeo (<https://imageo.genyo.es>). The random-effect model was used and the percentage of missing values allotted was 10%. Also, the adjusted p-value was set to 0.05.



**Figure 1. Pipeline of ImaGEO Analysis.**

It begins with data selection. A quality control based on the percentage of missing values. Meta-analysis is performed with an enrichment analysis of the differentially expressed genes.



Our results showed that 4583 significant genes were differentially expressed in GSE156355, 12238 genes in GSE44076, and 451 genes in GSE79774. From a representative heat map of the top 100 differentially expressed genes in the samples, it was observed that the TIMP1, NOX4, KRT17, and BGN genes were significantly upregulated, and OTC, VDR, KRT20, TMEM61, CLDN8 genes were significantly downregulated. The enriched biological processes include nucleic acid metabolism, nucleobase-containing compound metabolism, and cellular aromatic compound metabolism. For molecular function, nucleic acid binding, DNA binding, and catalytic activity were enriched. Nuclear and chromosomal cellular components were also enriched. This meta-analysis was able to determine the genes that were differentially expressed, significantly upregulated, and downregulated in the datasets. TIMP1 is upregulated in cytokine activity, protein binding and zinc ion binding. Also, for NOX4, it is upregulated in the stress fiber and integral component of the membrane under cellular component. For the downregulated genes, taking OTC for example, it functions in protein binding but not as much as TIMP1, it also regulates cell growth biologically. An in-depth study of these genes may provide novel insight into the treatment of CRC through chemotherapy in the future.

# Plasmids and Prophages are not Main Genetic Element Drivers Influencing the Resistance Pattern in Common Pathogenic Type Strain Organisms

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## INTRODUCTION:

ESKAPE organisms (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*), and other common enteric organisms; *Escherichia coli*, *Shigella flexneri* and *Salmonella enterica* are among the leading organisms with increased resistance to various antibiotic therapy due to the antimicrobial resistance genes (ARGs) they carry. Prophages and plasmids are mobile genetic elements that have been proven to play a role in the mobility of ARGs in pathogenic organisms. Bacteria type strains are reference nomenclature species types essential in understanding bacteria phylogeny and genomic evolution.

## AIM:

This study aims to determine the role of plasmids and prophages in the transfer of ARGs among the type strain genomes of some selected ESKAPE organisms and common enteric bacteria.

## METHOD:

We retrieved the FASTA files of type strain genomes of 8 organisms from the American Type Culture Collection (ATCC) Genome Portal. Prophage regions were identified using Plasmidfinder. Resfinder and ARGs identifier on the ATCC Genome Portal were used to identify the ARGs and their locations in the genome sequences. Only prophages and plasmids proven intact were recorded.

**RESULT:** Across 7 type strain genomes, 33 intact prophage regions were identified, with *Shigella flexneri* possessing the highest count (n = 17) while *Acinetobacter baumannii* had no intact prophage. 18 plasmids were identified across 5 genomes. *Pseudomonas aeruginosa*, *Enterococcus faecium* and *Acinetobacter baumannii* had no plasmid count. Importantly, we identified 28 ARGs across all genomes, with each genome possessing at least 1 ARG, except for the *Shigella flexneri* type strain. No ARGs were found within the plasmids. However, we discovered the presence of CAT (Chloramphenicol Acetyltransferase), a detoxifier of the antibiotic Chloramphenicol obtained in *Pseudomonas aeruginosa* located within an intact prophage region of the organism.

**CONCLUSION:** This study reveals that plasmids and prophages are not mainly responsible for the resistance pattern of the selected type strain, hence other genetic elements could play more significant role in ARG presence in these genomes.

Keywords: Antimicrobial Resistance genes (ARGs), Type strains, Prophages, Plasmids

# Exploiting Receptor-binding Proteins (RPBs) for Clinical Therapeutics Purposes

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The primary determinant for phage specificity is the receptor-binding protein (RBP) that mediates virion binding to bacterial structural components such as polysaccharides matrix, proteins, pili or flagella. The nature of the interaction of phages and their host grants phages their high host specificity. Studies have shown that the antimicrobial and therapeutic efficacy of bacteriophages is currently limited, mostly due to rapid emergence of phage resistance through the development of mechanisms to prevent phage adsorption, and the inability of most phage isolates to bind and infect a broad range of pathogenic bacteria strains. Recent attempts to improve phage infectivity consult the bioengineering of phage receptor binding proteins. A phage cocktail composed of wild-type phages each targeting a particular cohort of pathogenic strains can be used to circumvent the limited host range of a single phage.

Practically, a phage cocktail may become unnecessary for those pathogenic species with low clonal diversity across the epidemiological strains, or for which polyvalent phages with broad-host spectrum are available. The high specificity of RBPs has inspired the bioengineering of phages with swapped tail fibers. Trading tail fibers by homologous recombination is to only recombine the RBP gene(s) of an infecting phage or electroporated phage genome with a cytosolic RBP template featuring the desired host range. Several studies have shown that RBP engineering based on homologous recombination is inefficient due to its low recombination frequency ranging from  $10^{-10}$  to  $10^{-4}$ , necessitating a laborious and time-consuming screen. This low frequency is due to bacterial and plasmid DNA degradation during phage infection, as well as a lack of selectable markers. In addition, phages are generally lethal for their hosts, limiting the opportunities for efficient engineering of their genomes. The low recombination frequency particularly hinders the engineering of phages in multiple, non-contiguous loci of the phage genome. Further studies to understand the function and location of these phage receptors, which is a desirable step in the characterization of all phages used therapeutically, can unravel innovative ways to use phage therapy.

# Functionality of the Presence of tRNA in Phages

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Phages have compact genomes which consist mainly of coding regions. They rely on their host's cellular machinery to execute their cellular functions. Nevertheless, genes involved in DNA replication, transcription and translation have been found in viral genomes, especially tRNA encoding genes. The essence of these tRNA genes in phages is somewhat intriguing and has inspired few research studies. Codon and amino acid usage hypotheses have been posited to explain the functionality of the presence of these tRNA genes. Codon usage suggests that tRNA genes in phages are retained if they correspond to codons more common in phage genomes compared to their hosts whilst amino acid usage posits that they are retained if the amino acids encoded by the tRNA genes are more common in the phage genomes compared to its bacterial hosts. These hypotheses have been tested by comparative genomic analysis of phages and their hosts' genomes. However, significant association between codon usage and retention of tRNA in phages has been shown by a master equation model which simulates the acquisition and loss of tRNAs by phages using likelihood comparisons (Bailly-Bechet *et al.*, 2007). In spite of this, a recent comparative analysis of mycobacteriophage genomes has suggested that amino acid usage explains the presence of tRNA in mycobacteriophages better than codon usage (Delesalle *et al.*, 2016). Moreover, it was suggested that the functions of tRNA in phages may be associated with their growth rate in their hosts, ability to infect more hosts, and even their virulence ability as lytic phages are found to contain more tRNA genes than temperate ones. These findings present the need for further studies to explicitly evaluate tRNA retention between and within (sub)clusters of phages and elucidate their functionality.

# Antimicrobial Resistance: The Need for A Different Approach

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*Staphylococcus aureus* was the first ever bacteria to show resistance to penicillin. Utilizing its ability to produce penicillinase (a specific type of beta-lactamase), *S. aureus* harnessed the enzymatic characteristics of penicillinase to hydrolyze the cyclic amide bond in the beta-lactam ring of penicillin, rendering the antibiotic capability of the drug ineffective. Overtime, the misuse of antibiotics influenced the rise of Antimicrobial Resistance (AMR) in many pathogens.

In 2020, It was observed that over 70% of patients infected with COVID-19 received antimicrobial treatments (1). This was owing to the fact that some COVID-19 symptoms greatly resembled symptoms from infections caused by bacteria which resulted in inappropriate prescriptions and a number of COVID-19 patients acquired secondary co-infections which required antimicrobial drugs. Nevertheless, both situations only favored the rise in antimicrobial resistance.

One recent unexpected complication affecting the progress in containing the pestilence of antimicrobial resistance caused by COVID-19 is the genetic modification of resistant bacteria strains. It was discovered in a study that *Pseudomonas aeruginosa* a biofilm forming opportunistic pathogen which causes chronic infection in immunocompromised patients became genetically adapted to COVID-19. This adaptiveness was seen to have activated the rise in a morphological variant. Utilizing the differential gene expression analysis, it was indicated that this variant strain formed excessive biofilm (a thin protective resistant layer of microbes that acts as a barrier against antibiotics) by reducing flagellar formation and overproducing extracellular matrix components such as CdrA, alginate and Pel which created this biofilm that enhanced antimicrobial resistance –(2).

It is evident that our 20<sup>th</sup> century traditional approach of eliminating bacteria using antibiotics has only produced resistance.



However, is the problem really the use of antibiotics or the dogma that requires the killing of microbes? It can be seen that our fundamental approach of killing bacteria has failed because microbes will often evolve to ensure their survival. The failure of antibiotics has led to the production of other alternatives to antibiotic. Unfortunately, these other alternatives also implement the bacteria-elimination-approach. How good are the outcomes of these alternatives over antibiotics in regard to antimicrobial resistance?

In our fight against microbes, a plethora of alternatives to antibiotics has emerged. One of the alternatives gaining a lot of attention is the use of bacteriophages. Bacteriophages are viruses that prey on bacteria. Their physical structure which consist of a polyhedral head, a short collar and a helical tail enables them to pierce the bacterium's membrane and inject their genetic material into the cell which result in the hijacking of the bacteria leading to a massive production of more bacteriophages and finally the lysing of the bacterial cell. The advantages of utilizing bacteriophages supersede that of antibiotics in so many ways. Some of the ways by which bacteriophages stand out is their ability to increase in numbers when needed (this is termed

auto “dosing”), this ensures the administration of just a single dose. They also have minimal disruption of normal flora. Bacteriophages display little to no toxicity, they do not affect human and animal cells hence they are safer. With the potential to clear biofilms, bacteriophages could be our best alternative to antibiotics. Nevertheless, as promising as the utilization of bacteriophages may seem, they are also targets to resistance.

It has been observed that bacteria possess the ability to gain resistance against bacteriophages either through the modification of the structure of their surface phage receptor to prevent the absorption of bacteriophage, or by hindering the access of the phage to the receptor through the production of an excess extracellular matrix (3). Notwithstanding, regardless of the method taken, the goal of preventing the entrance of the phage by the bacteria has been achieved.

Since most of the modification done by the bacterium cell is to prevent the entrance of bacteriophages, another alternative in line with the elimination of bacteria has been developed which is the implementation of the phage lytic

enzymes known as Endolysins rather than the whole virion. Endolysins hydrolyze the peptidoglycan layer on the bacterium, resulting in a sudden drop in turgor pressure and osmotic lysis to cause cell death. Unfortunately, the use of endolysins can actually be counterproductive. Considering the fact that they are proteinaceous, the administration of the treatment through the oral route poses a great problem. Employing the oral route, endolysins are made vulnerable to different pH levels and enzymatic reactions in the digestive system. In order to by-pass this problem, endolysins are now given as intravenous injections to allow the drug to be administered straight into the blood stream. On the contrary, this route also poses a great risk as injection site could leave patient vulnerable to secondary bacterial infection.

Another alternative that has been created in line with the bacteria-elimination-approach is the utilization of Proteobiotics. These small oligopeptides inhibit bacteria virulence by interrupting bacteria cell-to-cell communication. This reduces the growth of harmful bacteria leading to their death. However, since proteobiotics are produce by probiotics, there is a higher likelihood for proteobiotics to trigger allergic reactions

in the human body .

It is therefore obvious that the bacteria-elimination-approach will always have an obstacle. Resistance will always emerge, and treatment options will continue to dwindle. To protect our future from antimicrobial resistance, the answer is already around us. For years, we have been living peacefully with microbes that do not produce toxin, and we can do the same for the ones that do. Rather than striving to kill harmful bacteria, we can channel all our effort into disarming these microbes to halt their production of toxins. Some promising mechanisms that can disarm bacteria are already in development. One of them includes the use of Musin in mucus to regulate how microbes behave and reorder their identity. It has been discovered that Musin can suppress the antagonist characteristics of microbes —". Once these microbes are prevented from producing toxins, they become harmless to us which stops us from looking for methods to kill them and in essence ends the endless cycle of microbe resistance.

## REFERENCES

- Destoumieux-Garzón, D., Duquesne, S., Peduzzi, J., Goulard, C., Desmadril, M., Letellier, L., Rebuffat, S., Boulanger, P., 2005. The iron-siderophore transporter FhuA is the receptor for the antimicrobial peptide microcin J25: role of the microcin Val11-Pro16 beta-hairpin region in the recognition mechanism. *Biochem. J.* 389, 869876. <https://doi.org/10.1042/BJ20042107>
- Lansbury, L., Lim, B., Baskaran, V., Lim, W.S., 2020. Co-infections in people with COVID-19: a systematic review and meta-analysis. *J. Infect.* 81, 266275. <https://doi.org/10.1016/j.jinf.2020.05.046>
- Qu, J., Cai, Z., Liu, Yumei, Duan, X., Han, S., Liu, J., Zhu, Y., Jiang, Z., Zhang, Y., Zhuo, C., Liu, Yang, Liu, Yingxia, Liu, L., Yang, L., 2021. Persistent Bacterial Coinfection of a COVID-19 Patient Caused by a Genetically Adapted *Pseudomonas aeruginosa* Chronic Colonizer. *Front. Cell. Infect. Microbiol.* 11.
- Wheeler, K.M., Cárcamo-Oyarce, G., Turner, B.S., Dellos-Nolan, S., Co, J.Y., Lehoux, S., Cummings, R.D., Wozniak, D.J., Ribbeck, K., 2019. Mucin glycans attenuate the virulence of *Pseudomonas aeruginosa* in infection. *Nat. Microbiol.* 4, 21462154. <https://doi.org/10.1038/s41564-019-0581-8>
- Williams, N.T., 2010. Probiotics. *Am. J. Health-Syst. Pharm. AJHP Off. J. Am. Soc. Health-Syst. Pharm.* 67, 449458. <https://doi.org/10.2146/ajhp090168>

# Phage Cocktails: A Biological Control for Foodborne Pathogens

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Foodborne pathogens contamination in foods and their formation of biofilms in food processing facilities are the primary bacterial cause of a significant number of foodborne outbreaks and infections. Foodborne illness acquired from the consumption of contaminated food remains a serious threat to human health and economics. Conventional control measures such as chemical disinfectant, chemical preservatives, biocides, and heat treatment are frequently used against varying food pathogens, in food products and to reduce biofilms. However, these measures run the risk of negatively affecting the taste of food products and reducing the nutritional availability. Also, antibiotics were once considered as an effective method to reduce the pathogens burden in both farms and industries, but the surge of prevalent resistant cases proved it unsuitable. Due to these limitations, one major approach considered to eliminate food product pathogens involves the use

Phages are obligate viral parasites of bacteria, which through interactions with unique bacterial surface receptors infect specific prokaryotes. As such, phages exhibit extreme host-specificity, which enables the selective targeting of certain bacterial genera or species. Phages may be classified as virulent (lytic) and temperate (lysogenic) depending on their life cycle. However, studies have shown that lytic phages are the most suitable for food applications. Phages only infect bacteria, and elicit little harm to eukaryotic cells, thereby affording a high degree of safety. Also, studies have shown that phage-based products have received regulatory approval from the Food and Drug Administration (FDA). Although, since bacteria and phage have co-evolved for billions of years, bacteria have developed multiple defense systems against phage. This requires the continual provision of new promising phages with relatively broad lytic range and high lytic activity for practical application in which phage cocktails (products containing more than one phage with different host specificities) can be used. Phage cocktail could be modified to contain additional phages specific to resistant bacteria, in case resistance does arise. Further studies regarding phage resistance mechanism and modification of phage cocktail to combat resistant bacteria should be looked into for better understanding on how to use phage cocktail in controlling foodborne pathogens.

# ANTIBIOTIC AND BACTERIOPHAGE SUSCEPTIBILITY OF DIARRHOEIC ESCHERICHIA COLI CLINICAL ISOLATES FROM MULAGO HOSPITAL MICROBIOLOGY LABORATORY IN KAMPALA DISTRICT

**Research Conducted By: Suubi Ivy Grace Chimulwa BBLT, MSc.c,  
Makerere University in fulfillment of Bachelor of  
Biomedical Laboratory Technology degree**

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## **Introduction:**

Antimicrobial resistance is a threat to global health and various strains of pathogenic bacteria. *Escherichia coli* associated with various infections in different host species, are increasingly developing resistance to existing drugs. Hence the need for exploration of alternative strategies for management of associated bacterial infections. One of such strategies include utilization of bacteriophages.

## **Objective:**

This study aimed at determination of the antibiogram of diarrheic *E. coli* isolates and to isolate and partially characterize the specific bacteriophages against them.

## **Method:**

Thirty confirmed diarrheic *E. coli* isolates were collected from Mulago Hospital Microbiology laboratory and their antibiotic susceptibility patterns determined by the Kirby- Bauer method.

Bacteriophages were sourced from sewage effluent obtained from Mulago Hospital and other different sewage collection centers around Kampala. Phage isolation was achieved by both direct and pre-enriched phage treatments using the spot assay test following the double agar overlay method. Phage purification was achieved by the plaque method, which was followed by host range, efficiency analyses and effect of temperature and pH on phage infectivity and stability

## **Results:**

Resistance to antimicrobial agents was common among all the isolates. The isolates showed high level of resistance to sulfamethoxazole-trimethoprim (100%), amoxicillin and ampicillin (93.3% each) and tetracycline (90%) but were highly susceptible to gentamicin (83.3%) and Cefixime (73.3%). Five phages specific to *E. coli*, coded as P1A, P1B, P2, P3 and P4; were isolated. Phage isolates, P1A, P2 and P4 exhibited activity against nine, eight and 10 of the 30 *E. coli* isolates that is 30%, 26.7% and 33.3% inhibition respectively.

Phages P1A and P4 registered desirable characteristics for therapy with better multiplicity of infection, efficacy of plating and stability studies in vitro on the different isolates than on the original bacterial host that was for their isolation. All the phage isolates were preserved by keeping in SM buffer at refrigeration temperature as well as freeze-drying in 10% skimmed milk.

**Recommendation:**

The combined inhibitory effect of all the isolated phages should be examined to evaluate the formulation of a cocktail. The molecular characterization of the phages should be performed to evaluate the possibility of undesirable characteristics such as antibiotic resistance.



# Picture Gallery







**IBRT** International BioReactor Technology

**2022 WORLD PHAGE WEEK**

Theme: Emerging Prospects in Bacteriophage Use and Clinical Phage Therapy

Date: 28th & 29th October, 2022

Day 1: 28th Oct, 2022

Day 2: 29th Oct, 2022

Prof. Martha Clarke (PhD)  
Prof. of Microbiology  
University of Leicester

Dr. Tolulope Odusele (PhD)  
Postdoctoral Research Fellow  
Environmental Health Engineering  
Arizona State University

Prof. Don Iredell (PhD)  
Director and Chief Investigator  
Phage Australia Unit of Infectious  
and Immunology, University of Sydney

Dr. Adenuga Oyedele (PhD)  
& Toy Odudu  
Principal Investigator, and  
Research Fellow, Institute  
of Biomedical Research (IBR)

Issue 197 | October 14, 2022

**World Phage Week 2022**

Oluwasegun Isaac Daramola Williams Timilehin Owioye

This week, Oluwasegun Isaac Daramola and Williams Timilehin Owioye explain why you should join them in celebrating another



# OUR ROADMAP

