



PHAMILIA

A Journal by

Ibadan Bacteriophage Research Team

Issue: #001, NOVEMBER, 2021

An interview with the
Faculty Team Head
- Prof Ademowo

All conference papers
presented classified
by the conference

Appreciation of IBRT'S
work by HOD

Guest write ups from
International Community

Excerpts from
our Review Papers

Profile of all team
members and what
they have achieved
through IBRT

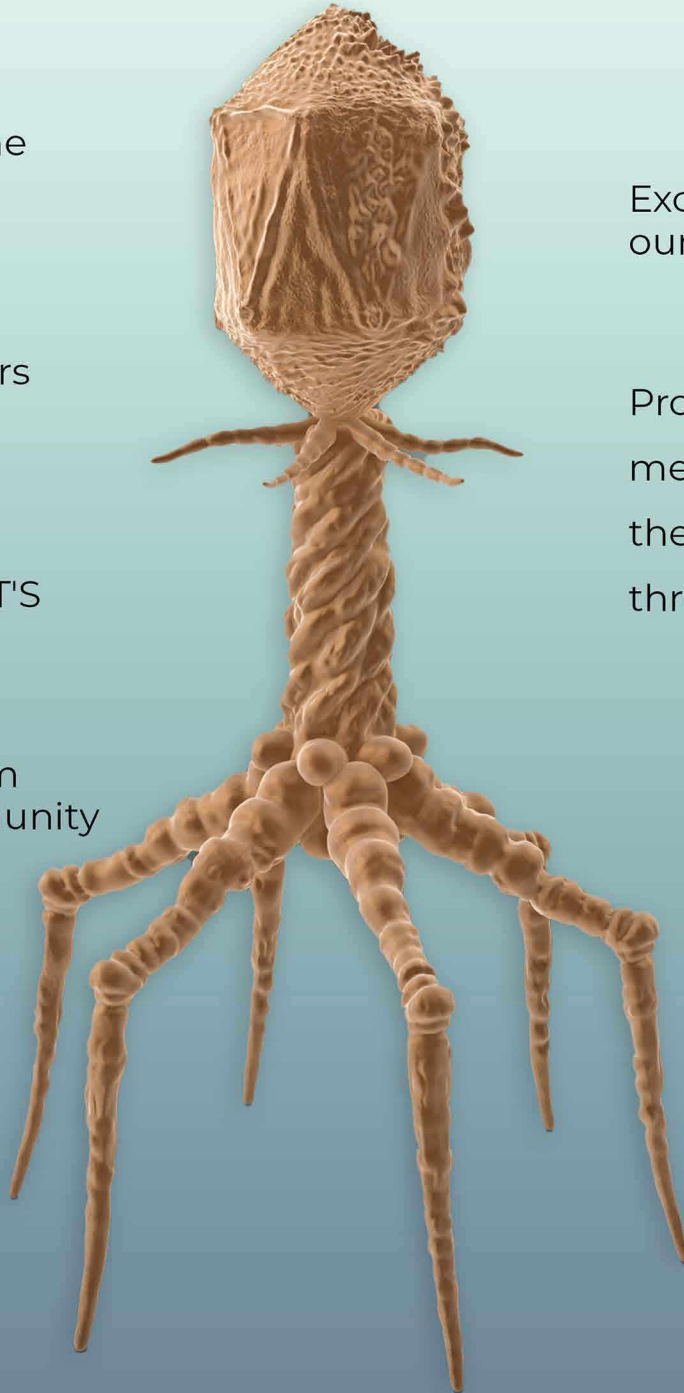


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Faculty Team



Prof. O.G Ademowo



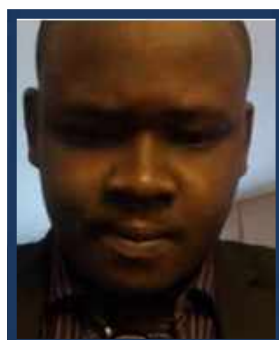
Prof. J.I Anetor



Dr. M.O Adewumi



Dr. A.S Bakarey



Dr. T.O.C Faleye



Mrs. Ini Adebisi



Mrs. V.O Ogunleye



Mr. M.K Raifu

Foreword

I got to know about Ibadan Bacteriophage Research team at the Seventh Unibadan Conference of Biomedical Research (UCBR-7) where four scientific presentations were made by undergraduate students of our Faculty. I was impressed by the scientific importance of their presentations (which centered on genomic research) that I had to inquire about them.

It is therefore with great delight that I write this foreword to celebrate a team of undergraduate students, whose vision has ultimately redefined undergraduate studies, not only in the Faculty of Basic Medical Sciences of this University, but also gives an idea of the extent of involvement and direction the Faculty should go in the area of mentoring. I therefore congratulate the team of Faculty members, ably led by Prof. O.G. Ademowo, who initiated this project as a way of nurturing young brilliant minds through active research engagement.

It has always been my desire over the years in the academia to find young, brilliant minds who would look beyond the immediate limitations and strive to break new grounds in pursuit of academic excellence. The Ibadan Bacteriophage Research Team project will definitely achieve this aim. It is worth mentioning that this undergraduate research team is hosted in the Department of Biomedical Laboratory Science and the initiators have in mind to establish a collaboration with the Howard Hughes Medical Institute and the University of Pittsburgh, through the Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Sciences project. The commencement of this project at the university in 2018 marked the beginning of bacteriophage research at the university. While it seemed rather unlikely that such a novel research field would be sustained by undergraduate students, the Faculty team maintained the drive and today, the success story of this project has been nothing short of amazing.

Team members have showcased their research acumen through diverse research publications in local and international journals, as well as abstract publications presented at the reputable scientific conferences. The successes of IBRT are a testament of the place of pride the University of Ibadan holds amongst the other higher institutions of learning in the nation and all over the world. The Ibadan Bacteriophage Research Team publication, PHAMILIA will surely be an interesting read for all bacteriophage biology enthusiasts all over the world, who desire to get familiar with the emerging role of bacteriophage biology in combatting antimicrobial resistance amongst all other novel concepts of bacteriophage biology. Readers will also be opened to the world of the University of Ibadan's pride research team, which has created undoubtedly the most successful undergraduate research training model, through guided adventure-based learning in a research field largely unthreaded in the African research space. So, from the Faculty of Basic Medical Sciences of Nigeria's premier and best ranked University, I welcome all readers to get familiar with our outstanding research successes through PHAMILIA.

Prof. Samuel B. Olaleye

*Professor of Gastrointestinal Physiology and Inflammation
and Dean, Faculty of Basic Medical Sciences
College of Medicine, University of Ibadan*



INTRODUCTORY REMARK FOR IBRT

PHAMILIA JOURNAL



The decision to undertake the Ibadan Bacteriophage Research Team Journal project “PHAMILIA” was born out of a desire to detail the team’s journey over the years. The journey of the Ibadan Bacteriophage Research Team has been one full of exciting turns. Under the supervision of the Faculty Team headed by the founder and coordinator of the project, Professor O.G Ademowo, the team has deployed her unique guided, adventure-based learning model, reinforced by a vibrant mentor-mentee relationship to great success. The Phamilia journal is a testament to the immense strides made by the team to bring greater visibility to bacteriophage research in Nigeria. It also provides an imitable training model for early-career research engagement among undergraduate students.

The Ibadan Bacteriophage Research Team began in 2018 with the registration of the University of Ibadan as a 13th cohort member of the Howard Hughes Medical Institute early career research project in conjunction with the University of Pittsburgh, named Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Sciences (SEA-PHAGES). As of the time of registration, the University of Ibadan became the second Nigerian university to be registered under the project after the University of Lagos. The team formerly named The Ibadan Phage Hunters Team began with 11 members of the 2015/2016 class of the Biomedical Laboratory Science department. What started as a team of young bacteriophage enthusiasts with very little knowledge of bacteriophages and computational tools for genome analysis has become a full-fledged research group with affiliate research projects such as the Ibadan Enterovirus Project and the Faculty of Basic Medical Sciences Research Hub. The team has completed the annotation of six bacteriophage genome sequences, all of which are accessible on the NCBI database. The team boasts of more than 20 publications in various areas of bacteriophage research such as genomic characterization of bacteriophage genomes, bacteriophage-based alternative antimicrobial therapy, use of phage-derived enzymes for therapeutic use, bacteriophage interaction with eukaryotic cells, etc. Some of these articles also focus on in-silico models for disease studies, antimicrobial resistance, and many more. These range of topics have been studied by the group and presented across local and international conferences.

The story of the Ibadan Bacteriophage Research Team cannot be complete without due acknowledgment of the faculty team who have given their full support to see the vision of undergraduate engagement in active research process come to fruition. Special appreciation to the dean of the Faculty of Basic Medical Sciences, University of Ibadan, Professor S.B Olaleye, the head of the Department of Biomedical Laboratory Science, University of Ibadan, Dr. Mabel Charles-Davies, and other members of staff who have given an enabling environment for the project to be sustained over the years. We say a very big thank you to all of our international partners and sponsors such as the Howard Hughes Medical Institute (HHMI), Graham Hatfull Group (University of Pittsburgh), Baylor Tailor Laboratory at Baylor College of Medicine, Phase Genomics, Africa Phage Forum, Indian Bacteriophage Research Consortium, Phage Directory and many more, who have relentlessly given their unreserved support to the team. Special mention must be made for 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.

ODUSELU Tolulope John
Team Lead



LETTER FROM THE EDITOR

The Ibadan Bacteriophage Research Team, with its focused mission to build an undergraduate research community of early career researchers who are enthusiastic about bacteriophage biology and its prospective use as alternative antimicrobial therapy, has continued to grow and make incredible waves in the global research community. After being formed just

three years ago, the team has grown to become what is now known as one of the most vibrant undergraduate research projects of the University of Ibadan, with recognitions both locally and internationally. We have therefore deemed it fit to put forth the history, achievements, articles, projects and so on, into a journal, coupled with guest write-ups from other colleagues around the world, to put on display the strides of the team on this research path, largely untreaded in the African research space.

This journal would not have been possible without a fantastic editorial team, that put in lots of efforts, to bring the Phamilia vision to a reality. We hope you enjoy this issue of Phamilia, as it reflects the hardwork and dedication of the Faculty team, Team leaders, members, researchers, amongst many others.

For more information about the team, visit ibadanphageresearchteam.org. You can also follow us on Twitter @IbadanPhageTeam.

Best,

OYEBAMIJI Toba.

Editor-in-Chief.

Phage Leaders



ODUSELU Tolulope John
Team Lead



TAIWO
Anjolaoluwa .E.



DARAMOLA
Oluwasegun .I.



AYODELE Ifeoluwa .E.



OYEBAMIJI Toba .O.



OMOLOLA
Comfort .M.



ADEDEJI Roqeeb .O.



ADESANYA
Oluwafolajimi .A.



AKOMOLAFE
Ayobami .O.



ATOYEBI Abigail .N.



OJEBOLA
Babatunde .M.

Editorial Team



OYEBAMIJI Toba
Editor-in-Chief



ATOYEBI Abigail



ODUSELU Tolulope



OWOEYE Williams



OMOLOLA Comfort



An Interview with the Faculty Team Head

For every historical event that occurs, there are always two narratives: the original and the others. The Ibadan Bacteriophage Research Team (IBRT) has been basking in the floodlight of attention of late, writing their name on the fine sands of time in the research community. While they are building new shelves to accommodate the tons of commendations that have been coming their way, it is expedient to hear a first-hand narrative from the horse's mouth about how the trailblazing team was conceived. In this interview, IBRT's Correspondent, Williams Owoeye, had a coffee chat with the academic giant that brought the vision to life, Professor O.G. Ademowo. Only that there isn't actual coffee; just conversations flowing both ways over a laptop and the aroma of freshly-printed thesis papers.

Williams: To us, you are well known as a father-figure but for the benefit of our audience, can you kindly introduce yourself, sir.

Prof Ademowo: Well, I am Olusegun George Adeomowo, a Professor of Pharmacology and Therapeutics at the Institute for Advanced Medical Research and Training of the College of medicine. I also have joint appointment with the department of Pharmacology and Therapeutics where I am involved in training of both undergraduate and postgraduate students of the University.

Williams: All right sir. Thank you. A bit more about your personality now: the father figure attributes that is welcoming and easily approachable by students is somewhat a rarity among academic administrators. So can you just tell us the personal philosophy that is behind these attributes?

Prof Ademowo: Well, I think part of what's brought about this attribute of mine is what I can find when I look back at my upbringing and the kind of association that I always find myself or that I decide to put myself in. You know, when we were growing up, we grew up in the communal kind of life whereby we don't discriminate against anybody whether you are the son of Imam or a Pastor or whatever. All of us together, we went to public schools. We didn't have private schools then. So whether it is the son of the high, the low, the mighty, we were all mingling together? So for me, as a person, I think that has been part of me. So, fortunately, when I came in as an undergraduate in the University of Ibadan, I continued with that kind of life. We didn't even know how to discriminate within ourselves. So I think that kind of spirit continues to be with me, and became like my guiding principle. So I always love when I have people around me, and I also like defending people who I think are weak, or that are lower in rank, in age; I want to see how I can help them to come up. That's just me.

Williams: Now, moving to other topics now. IBRT has grown to be a prodigy that is known locally and internationally in the research world. Now can you briefly take us down memory lane, how this pacesetting vision was conceived?

Prof Ademowo: Yes. That's a good one. You see, IBRT when it came up was actually because of our collaboration with HHMI that is Howard Hughes Medical Institute. I must tell you that the first time that I tried to get involved with HHMI, I would say it was not successful. That was like, maybe 10 or 15 years before IBRT started. Then I submitted a proposal to get involved in some kind of research partnership with them but somehow it didn't work. Maybe, for some reason, I can't

remember very well. And then when the issue of the bacteriophage research came up, I wrote to them, they were receptive to it. And then they said, okay, we should write our own proposal, which we did. And they were very happy with us; to the fact that we're going to be able to do justice to what we have put down and I'm sure we have not disappointed them. And so, now as I started, we gathered people together and formed our own team. And then we thought, okay, how about the student team, which must be undergraduates. That was the first challenge that we had: which category of students are we going to even use? So then I thought of different categories of students, I thought of students in Biochemistry, Medicine and Surgery, Biomedical Laboratory Science (BMLS)... So finally, I zeroed down on BMLS, because of the kind of training that they have, that is the nature of work they are supposed to be doing. So they are likely going to embrace it more. I looked at the Medicine and Surgery students, well, maybe they may not have so much time because they are more focused on their clinical area when it gets to a stage. And so I look at that and I said, well, it might not be too smooth with them. As for the Biochemistry students, I looked at them and I said, well, they are mainly on the main campus; they are not on the clinical side here (in the University College Hospital). So because of the logistics, that was why I didn't feel too comfortable with them. So I zeroed down on BMLS students, I'm not regretting that.

Williams: Now looking at all these history and antecedents. If you had the opportunity to travel back in time, when all this started, is there anything you would love to change the about the whole thing?

Prof Ademowo: Ah, that's a good one. So that's like asking, what are the kind of challenges that we had in a way. You know part of what has to do with this programme is that we needed to introduce a course of its own. So this course was supposed to teach the rudiments of bacteriophages, Introduction to Bioinformatics and other things like that. But the procedure of setting up a new course, not an entire programme, a new course, you have to first of all go to the curriculum committee of the department, then to the faculty, from faculty to the College (of Medicine), and then from College you take it to the Senate for approval. You even first of all had to go to curriculum committee of the Senate and then to Senate proper. So these take some time, it can even take years. Meanwhile we have to start the programme as quickly as possible. So what we did was said "Okay since we have existing courses, we can look at those courses to see which one can we attach this courses to the outline of the course?" So we deliberately chose MLS 301 (Introduction to Medical Lab. Science). We put it there as an extension of MLS 301. But that aspect is not compulsory; it's only meant for volunteers. We had it done that way and then we introduce it to students. So those that felt they wanted to do it, they did it. You are free when you finish your normal course. If you like, you come for the extension course, if you don't like then you don't come if you think it's an extra work for you. And which is not an offence rather is it a sin that you say "No, I am not going to partake in it". So you see, that in itself is a challenge because we are not even able to examine the course. So maybe if we had examined it maybe the students will likely be more serious with it. But I must say that I'm not even regretting because the people that volunteered, you see the enthusiasm in them, you see how they have been doing excellently well. So one is also not regretting that because it means that those who are really doing it are doing it because of love they have (for the program) from the bottom of their heart. So it's not as if I'm regretting it, but what I'm saying here is that while we did it in a different way from what is expected, but we still got the same results.

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IBRT has done the
faculty proud, the
University proud, and
in fact, also Nigeria,
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Williams: So on a scale of 1 – 10, how well do you think IBRT has been performing so far and what would be the reason why you'll be given this particular score?

Prof Ademowo: Hmm. Very good question. This question I like so much, because I feel on top of the world; I feel that our sense of judgement was very, very correct. We didn't misjudge when we were actually choosing the category of students that we chose. IBRT is performing wonderfully well. And I will score IBRT... with every sense of responsibility, I want to score IBRT 90% for its performance. I don't want to say 100%. I must say that IBRT has done us proud. It's not only the group that they have done

proud, they have done the department proud. IBRT has done the faculty proud, the University proud, and in fact, also Nigeria, as a nation, and indeed Africa because of their initiatives; because of their conduct and general achievements. This is something that we should be very proud of. I must say that I think we are not being fair enough to IBRT by not actually projecting it well: the projection we give it is not commensurate with its achievements.

Williams: Alright, so let's now narrow it down a bit to specifics. What would you consider to be like the biggest news you've heard so far about the impact of the team?

Prof Ademowo: Well, that's a million dollar question because everything looks super to me. First of all, there is this one that is sustainable which is there forever which is the fact that you have been able to submit 6 isolates to the Genbank. I mean, this means that it will always be in that database forever. So even in the next 10, 20, 30, 40, 50, 100 years, when all of us would have gone beyond it will still be there. So that is a great achievement. I will say that is the greatest achievement. And I know we're still going to do more. So the other achievement that I can also say is this international programmes that the IBRT has been involved in at the international levels, leading Africa and ensuring that the name of the University of Ibadan, and indeed Nigeria is written in gold by trying to get involved in all these international collaborations whereby they are being recognised by European institutions as an excellent group. I don't want to say Centre of Excellence now but if I could actually borrow that for the group, I would say.

Williams: Sir, you know in every journey there are always the ups and then the downs. So is there any low moment or are there any low moments in this exciting journey you will love to share?

Prof Ademowo: Yes, I must say that the worry that I have is that we are supposed to have started our wet lab aspect of the programme. But somehow, we have some hiccups here and there that have not made us to start. Sometimes I ask myself, it's like we have an inertia that we're finding difficult to surmount. And, you know, sometimes you think that money is the only thing that will cause that kind of delay, but in this case, our problem is not money; that doesn't mean that we have unlimited funding, but at least we still have some fund that we can commit to that but somehow because of one reason or the other; you know, distractions here and there and then came COVID; the unstable university calendar. Every-

Everything conspired together to ensure that we have not yet started. So this is the only regret that I have but what I know is that we're going to surmount it and I believe that shortly, we should be able to start something.

Williams: It's like the next question I wanted to ask has been kind of answered, but then I will still ask all the same just in case you have something different to add. So if you had all the resources right now, at this moment, what will be the thing you will do to give the team a boost?

Prof Ademowo: The resources? I don't really understand that question

Williams: I mean resources maybe in terms of funding, the right people or the right moves to make. Let me say if you have the power that is needed make something happen. So what will be that thing you will do to give the team a boost?

Prof Ademowo: Okay, yeah. Well I have spoken about the wet lab aspect, which I will not only want us just to start alone but I also want us to widen. In fact, I want it to even go beyond. I want IBRT to be the lead research arm of the University in that area. I will also love the opportunity of actually taking members of the team to see the place of our collaborators at Pittsburgh in Virginia. So, one member of the team ought to have gone along with me to the US in 2019. Even though all expenses were paid for but there was this policy of not giving young people Visas to the US then because of the policy of the then President Trump but all these have changed. Unfortunately COVID has overtaken all of us. So this is another area that I would have loved to help to boost the morale of people working there but I think that is still doable. So a good number will be taken to visit the US and make presentations or learn some new ways of doing things at the same time.

Williams: So finally, now, some words of encouragement generally to our audience, and then specifically to undergraduates all round that will be reading the journal.

Prof Ademowo: Yes, my message is that I will say that everybody should see themselves as people whose value is more than what they themselves think about them, or what others think about them when they see them for the first time. So what I'm trying to say here is that you should try and bring out the creative instinct in you at all times where you have the opportunity; when have the enabling environment to do so. Honestly, I was beaten hands down by the performance of members of the IBRT. I never expected that level of performance and you know, what marvels me the most is that it's not only one person. It is like everybody is like that. I know that everybody is on a spectrum. Of course, everybody cannot have the same score. But the performance of everybody is up there. They are on the top percentile. So that is the way I see it. And my candid advice is that people should also try to go the extra mile. Don't limit yourself. Try and put in extra effort, this will ensure you can never be a failure. If you put in an extra effort, your value can only increase, there is no other way than that. So, once you have those kinds of opportunities, please just use them because if we had created the opportunity for the IBRT and they don't use it. Of course, they will never see that potential in themselves.

Williams: Thank you very much sir, it has been a very wonderful and insightful session. Thank you very much for your time.

IBRT TEAM PROFILING

STANDARD NAMING FORMAT FOR CONFERENCES

1. 7th UNIBADAN Conference on Biomedical Research (UCBR-7)
2. 11th International Symposium of SEA Researchers.
3. 12th International Symposium of SEA Researchers.
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. IBRT World Phage Week 2021 Webinar.

STANDARD NAMING FORMAT FOR PUBLICATIONS.

1. Olusegun G Ademowo, John I Anetor, Olubusuyi M Adewumi, Temitope O Faleye, Adeleye S Bakarey, Olatimbo V Ogunleye, Ini Adebisi, Muideen K Raifu, Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo (2019), SEA-PHAGES 2018-2019 Session: The Ibadan Phage Hunters Experience, 11th Annual SEA Symposium Abstract (Page 109).

2. Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo, Muideen K Raifu, Ini Adebisi, Olatimbo V Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, Olusegun O Ademowo (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108).

3. Tolulope J Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>

4. Adesanya, O., Oduselu, T., Akin-Ajani, O., Adewumi, O. M., & Ademowo, O. G. (2020). An exegesis of bacteriophage therapy: An emerging player in the fight against anti-microbial resistance. *AIMS microbiology*, 6(3), 204–230. <https://doi.org/10.3934/microbiol.2020014>

5. Tolulope J. Oduselu et al. (2020), "Expanding the Frontiers of Bacterial diagnosis through Bacteriophage Biotechnology", *Tropical Journal of Natural Product Research (TJPNR)*.

6. Abdelrahman, F., Easwaran, M., Daramola, O. I., Ragab, S., Lynch, S., Oduselu, T. J., Khan, F. M., Ayobami, A., Adnan, F., Torrents, E., Sanmukh, S., & El-Shibiny, A. (2021). Phage-Encoded Endolysins. *Antibiotics (Basel, Switzerland)*, 10(2), 124. <https://doi.org/10.3390/antibiotics10020124>

7. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>

8. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafolajimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbachidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>

9. Tolulope Oduselu, J., Oluwafolajimi Adesanya, A., Isaac Daramola, O., Ayobami Akomolafe, O. and Moses Adewumi, O. Expanding the Frontiers of Bacterial Diagnosis through Bacteriophage Biotechnology. Presented at International Bio-technology Conference, Exhibition and Workshop.

10. Comfort M. Omolola, Roqeeb O. Adedeji, Anjolaoluwa E. Taiwo, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Adopting Phage Therapy for Treatment of Secondary Bacterial Infections in COVID-19 Patients. Presented at 13th World Congress of Microbiology and Clinical Research.

11. Abdulmujeeb Opatola, Williams T. Owoeye, Benjamin A. Adediran, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Effects of Alteration in the Gut Microbiota by Bacteriophages. Presented at 13th World Congress of Microbiology and Clinical Research.

12. Tolulope J. Oduselu, Oluwasegun I. Daramola, Anjolaoluwa E. Taiwo, Ayobami J. Akomolafe, Ifeoluwa E. Ayodele, Toba O. Oyebamiji, Oluwafolajimi A. Adesanya, Abigail N. Atoyebi, Olubusuyi M. Adewumi, and Olusegun G. Ademowo. Bacteriophage Therapy Resurgence: Designing a Workable Framework to combat associated regulatory hurdles, presented at Webinar of Clinical Pharmacy and Clinical Research 2021.

13. Abdulmujeeb Opatola, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Physics of Viral Infection by Bacteriophages. Presented at 27th International Phage Virus Assembly Conference.

14. Toba O. Oyebamiji, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Role of Bacteriophages in Neurodegenerative Disorders. Presented at 27th International Phage Virus Assembly Conference.

15. Ayobami J. Akomolafe, Oluwasegun I. Daramola, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Use Case of Bacteriophages in Gene Therapy. Presented at 27th International Phage Virus Assembly Conference.

16. Anjolaoluwa E. Taiwo, Babatunde M. Ojebola, Praise L. Alabi, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Use of Bacteriophage Polymerase in the removal of bacterial biofilms. Presented at 27th International Phage Virus Assembly Conference.

17. Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebi A.N, Raifu M.K, Adebiyi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

18. Oduselu T.J, Adedeji R.O, 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 (2021). Computational Analysis of *Gordonia* Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

19. Adediran B.A, Opatola A.D, Alabi P.L, Ojediran M.A, Owoeye W.T, Oduselu T.J, 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 (2021). Anti-CRISPR System: Unravelling the Dynamics of Bacteria-Bacteriophage Evolution, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

20. Daramola O.I, Akomolafe A.J, Adedeji R.O, Inyang E.S, Iyede T.O, Adepoju O.D, Oduselu T.J, 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 (2021). The Use of Endolysins as alternative Antimicrobial Therapy, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

21. Ifeoluwa E. Ayodele, Tolulope J. Oduselu, and Olubusuyi M. Adewumi (2021). Adopting Sewage water testing for SARS-COV-2 surveillance, presented at 14th World Congress on Microbiology and Clinical Research

22. Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebi A.N, Raifu M.K, Adebiyi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021). Transcriptomic Analysis of SARS-CoV-2 infected lung tissues, presented at BioAcCES Conference 2021, Rockefeller University.

LEADERS

1. Name: **Tolulope John Oduselu**

Level: 500 level

Conferences:

- IBRT World Phage Week Webinar 2020.
- 7th UNIBADAN Conference on Biomedical Research.
- 11th International Symposium of SEA Researchers
- 12th International Symposium of SEA Researchers
- 27th International Phage Virus Assembly Conference.
- International Biotechnology Conference, Exhibition and Workshop.
- 14th World Congress of Microbiology and Clinical Research
- ISCB Africa Workshop on Bioinformatics Adventure.
- CRM Computational Modelling of Cancer Biology and Treatment Workshop
- Webinar on Clinical Pharmacy and Clinical Research 2021.
- International Synthetic Biology and Biosecurity Conference in Africa 2021.
- BioACCES Conference 2021, Rockefeller University.



Publications:

1. Oduselu Tolulope, Taiwo Anjolaoluwa, Faleye Temitope, Adewumi Olubusuyi, Ademowo Olusegun et al (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108). •
2. Olusegun G Ademowo, John I Anetor, Olubusuyi M Adewumi, Temitope O Faleye, Adeleye S Bakarey, Olatimbo V Ogunleye, Ini Adebisi, Muideen K Raifu, Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo (2019), SEA-PHAGES 2018-2019 Session: The Ibadan Phage Hunters Experience, 11th Annual SEA Symposium Abstract (Page 109).
3. Oluwafolajimi O. Adesanya, Tolulope J. Oduselu et al (2020), "An exegesis of bacteriophage therapy: An emerging player in the fight against anti-microbial resistance", AIMS Microbiology, 6(3): 204-230. DOI: 10.3934/microbiol.2020014 •
4. Tolulope J. Oduselu et al. (2020), "Expanding the Frontiers of Bacterial diagnosis through Bacteriophage Biotechnology", Tropical Journal of Natural Product Research (TJPNR). •
5. Oduselu, T., & Adewumi, O. (2020). Ibadan Bacteriophage Research Team: A SEA-PHAGES team with a difference. Capsid & Tail, (102). Retrieved from <https://phage.directory/capsid/ibadan-bacteriophage-research-team>. •
6. Abdelrahman, F., Easwaran, M., Daramola, O. I., Ragab, S., Lynch, S., Oduselu, T. J., Khan, F. M., Ayobami, A., Adnan, F., Torrents, E., Sanmukh, S., & El-Shibiny, A. (2021). Phage-Encoded Endolysins. Antibiotics (Basel, Switzerland), 10(2), 124. <https://doi.org/10.3390/antibiotics10020124>
7. Tolulope J. Oduselu et al. (2021). Impact of the SEAPHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>
8. Tolulope J. Oduselu et al. (2021). Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothraki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>

9. Benjamin A. Adediran et al. (2021). Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>
10. Tolulope J. Oduselu et al. (2021). Bacteriophage Therapy Resurgence: Designing a Workable Framework to combat associated regulatory hurdles, presented at Webinar of Clinical Pharmacy and Clinical Research 2021
11. Tolulope J. Oduselu et al. (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
12. Tolulope J. Oduselu et al. (2021) Computational Analysis of Gordonia Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7)

INTEREST:

Bacteriophage Biology, Antimicrobial Resistance, Computational and Microbial Genomics, Transcriptomic Analysis.

2.Name: **Ayodele Ifeoluwa Emmanuel**

Level: 500

Conferences:

- 14th World Congress on Microbiology and Clinical Research
- 27th International Phage Virus Assembly Conference.
- IBRT World Phage Week 2020
- 12th International Symposium of SEA Researchers



Publications:

- 1.Ifeoluwa E. Ayodele et al. (2021). Adopting Sewage water testing for SARS-COV-2 surveillance, 14th World Congress on Microbiology and Clinical Research
- 2.Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebe A.N, Raifu M.K, Adebiyi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
- 3.Tolulope J Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebe, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>
- 4.Oduselu T.J, Adedeji R.O, Akomolafe A.J, Daramola O.I, Olatinwo S.O, Adesanya O.A, Inyang E.S, Taiwo A.E, Atoyebe A.N, Iyede T.O, Ayodele I.E, Omolola C.M, Ojobola B.M, Lazarus F.U, Adepoju O.D, Oyebamiji T.O1,2, 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 (2021). Computational Analysis of Gordonia Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest:

Bioinformatics, Phage genomics, Genetic engineering, Anti-microbial resistance.

3. Name Atoyebi Abigail Nanayaa

Level: 500 level.

Conferences

- 27th International Phage Virus Assembly Conference.
- IBRT World Phage Week 2020
- 12th International Symposium of SEA Researchers



Papers

1. Tolulope J. Oduselu, Oluwasegun I. Daramola, Anjolaoluwa E. Taiwo, Ayobami J. Akomolafe, Ifeoluwa E. Ayodele, Toba O. Oyebamiji, Oluwafolajimi A. Adesanya, Abigail N. Atoyebi, Olubusuyi M. Adewumi, and Olusegun G. Ademowo (2021). Bacteriophage Therapy Resurgence: Designing a Workable Framework to Combat Associated Regulatory Hurdle. Presented at 2nd Clinical Conference on Clinical Pharmacy and Clinical Research.
2. Oduselu T.J, Adedeji R.O, 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^{1,2}, 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 (2021). Computational Analysis of Gordonia Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
3. Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebi A.N, Raifu M.K, Adebisi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
4. Tolulope J. Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>

Areas of interest: Cancer research, Antimicrobial therapy

4. Name: **Comfort Modupeoluwa OMOLOLA**

Level: 500

Conferences:

- 3rd World Conference on Clinical Research and Microbiology (Microbiology expo 2020)
- 27th International Phage Virus Assembly Conference 2021.
- IBRT World Phage Week 2021
- 12th International Symposium of SEA Researchers



Papers

1. Comfort M. Omolola, Roqeeb O. Adedeji, Anjolaoluwa E. Taiwo, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Adopting Phage Therapy for Treatment of Secondary Bacterial Infections in COVID-19 Patients. Presented at 13th World Congress of Microbiology and Clinical Research.

2. Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo, Muideen K Raifu, Ini Adebisi, Olatimbo V Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, Olusegun O Ademowo (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108).
3. Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebi A.N, Raifu M.K, Adebisi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
4. Oduselu T.J, Adedeji R.O, 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, Adebisi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021). Computational Analysis of Gordonia Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest: Bacteriophages, Antimicrobial resistance

5. Name: **Oluwafolajimi Adesanya**

Level: 6th year

Conferences:

- 2021 SEA Symposium



Papers

1. Adesanya, O., Oduselu, T., Akin-Ajani, O., Adewumi, O. M., & Ademowo, O. G. (2020). An exegesis of bacteriophage therapy: An emerging player in the fight against anti-microbial resistance. *AIMS microbiology*, 6(3), 204–230. <https://doi.org/10.3934/microbiol.2020014>
2. Tolulope J Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>
3. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafolajimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbechidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>
4. Tolulope Oduselu, J., Oluwafolajimi Adesanya, A., Isaac Daramola, O., Ayobami Akomolafe, O. and Moses Adewumi, O. Expanding the Frontiers of Bacterial Diagnosis through Bacteriophage Biotechnology. Presented at International Biotechnology Conference, Exhibition and Workshop.

Areas of interest:

Clinical Microbiology, Bacteriophage Therapy, Virology, Antimicrobial Resistance

6. Name - **Daramola Oluwasegun Isaac**

Level - 400L

Conferences

- GCURS 2020
- Phage Virus Assembly
- UBCR-7



Papers

1. Daramola O.I, Akomolafe A.J, Adededeji R.O, Inyang E.S, Iyede T.O, Adepoju O.D, Oduselu T.J, 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 (2021). The Use of Endolysins as alternative Antimicrobial Therapy, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
2. Tolulope J. Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>
3. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adededeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>
4. Abdelrahman, F., Easwaran, M., Daramola, O. I., Ragab, S., Lynch, S., Oduselu, T. J., Khan, F. M., Ayobami, A., Adnan, F., Torrents, E., Sanmukh, S., & El-Shibiny, A. (2021). Phage-Encoded Endolysins. *Antibiotics* (Basel, Switzerland), 10(2), 124. <https://doi.org/10.3390/antibiotics10020124>
5. Tolulope J Oduselu, Roqeeb O Adededeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafolajimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbechidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>
6. Tolulope Oduselu, J., Oluwafolajimi Adesanya, A., Isaac Daramola, O., Ayobami Akomolafe, O. and Moses Adewumi, O. Expanding the Frontiers of Bacterial Diagnosis through Bacteriophage Biotechnology. Presented at International Biotechnology Conference, Exhibition and Workshop.

Areas of Interest:

Microbial and Computational Genomics, Bacterial Pathogenesis, Host-Pathogen interaction, Antimicrobial Resistance, Phage Biology, Data Modeling

7. Name: **Akomolafe Ayobami Joseph**

Level: 400 level

Conferences

- 12th sea-phages symposium 2021
- Phage virus Assembly 2021



Papers

1. Ayobami J. Akomolafe, Oluwasegun I. Daramola, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Use Case of Bacteriophages in Gene Therapy. Presented at 27th International Phage Virus Assembly Conference.
2. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafo-laimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbechidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>
3. Tolulope Oduselu, J., Oluwafolajimi Adesanya, A., Isaac Daramola, O., Ayobami Akomolafe, O. and Moses Adewumi, O. Expanding the Frontiers of Bacterial Diagnosis through Bacteriophage Biotechnology. Presented at International Bio-technology Conference, Exhibition and Workshop.
4. Daramola O.I, Akomolafe A.J, Adedeji R.O, Inyang E.S, Iyede T.O, Adepoju O.D, Oduselu T.J, Raifu M.K, Adebisi I, Ogun-leye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021). The Use of Endolysins as alterna-tive Antimicrobial Therapy, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
5. Tolulope J. Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>

Area of Interest:

Data Science/ AI, Molecular biology, Computational studies

8. Name: **Roqeeb Olamide ADEDEJI**

Level: 400level

Conferences attended:

- 7th Unibadan Conference of Biomedical Research.
- Phage Virus Assembly 2021



Papers

1. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafo-laimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbechidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>

2. Comfort M. Omolola, Roqeeb O. Adedeji, Anjolaoluwa E. Taiwo, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Adopting Phage Therapy for Treatment of Secondary Bacterial Infections in COVID-19 Patients. Presented at 13th World Congress of Microbiology and Clinical Research.
3. Oduselu T.J, Daramola O.I, Taiwo A.E, Akomolafe A.J, Ayodele I.E, Oyebamiji T.O, Adesanya O.A, Adedeji R.O, Omolola C.M, Atoyebi A.N, Raifu M.K, Adebisi I, Ogunleye V.O, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021) Early Career Research Engagement in Genomic Research: The Ibadan Bacteriophage Research Team Model, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
4. Oduselu T.J, Adedeji R.O, 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, Adebisi I, Ogunleye V.I, Faleye T.O.C, Bakarey A.S, Adewumi O.M, Anetor J.I, and Ademowo O.G (2021). Computational Analysis of Gordonia Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
5. Daramola O.I, Akomolafe A.J, Adedeji R.O, Inyang E.S, Iyede T.O, Adepoju O.D, Oduselu T.J, 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 (2021). The Use of Endolysins as alternative Antimicrobial Therapy, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest:

Viral Genomics, Viral epigenetics, Bacteriophage therapy, Genetic engineering, Bioinformatics, Computational Biology.

9. Name: **Taiwo Anjolaoluwa Emmanuel**

Level: 500 Level

Conferences

- 27th International Phage Virus Assembly Conference.
- IBRT World Phage Week 2020
- 12th International Symposium of SEA Researchers
- 7th UNIBADAN Conference on Biomedical Research.



Papers

1. Anjolaoluwa E. Taiwo, Babatunde M. Ojebola, Praise L. Alabi, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Use of Bacteriophage Polymerase in the removal of bacterial biofilms. Presented at 27th International Phage Virus Assembly Conference.
2. Comfort M. Omolola, Roqeeb O. Adedeji, Anjolaoluwa E. Taiwo, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Adopting Phage Therapy for Treatment of Secondary Bacterial Infections in COVID-19 Patients. Presented at 13th World Congress of Microbiology and Clinical Research.
3. Olusegun G Ademowo, John I Anetor, Olubusuyi M Adewumi, Temitope O Faleye, Adeleye S Bakarey, Olatimbo V Ogunleye, Ini Adebisi, Muideen K Raifu, Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo (2019), SEA-PHAGES 2018-2019 Session: The Ibadan Phage Hunters Experience, 11th Annual SEA Symposium Abstract (Page 109).
4. Tolulope J Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O

Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>

10. Name: Oyebamiji Toba Oluwatimileyin

Level: 500 Level

Conferences

- 27th International Phage Virus Assembly Conference.
- IBRT World Phage Week 2020
- 12th International Symposium of SEA Researchers

Papers

1. Toba O. Oyebamiji, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Role of Bacteriophages in Neurodegenerative Disorders. Presented at 27th International Phage Virus Assembly Conference.

2. Olusegun G Ademowo, John I Anetor, Olubusuyi M Adewumi, Temitope O Faleye, Adeleye S Bakarey, Olatimbo V Ogunleye, Ini Adebisi, Muideen K Raifu, Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo (2019), SEA-PHAGES 2018-2019 Session: The Ibadan Phage Hunters Experience, 11th Annual SEA Symposium Abstract (Page 109).

3. Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo, Muideen K Raifu, Ini Adebisi, Olatimbo V Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, Olusegun O Ademowo (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108).

4. Tolulope J Oduselu, Oluwasegun I Daramola, Anjolaoluwa E Taiwo, Ayobami J Komolafe, Ifeoluwa E Ayodele, Toba O Oyebamiji, Oluwafolajimi A Adesanya, Abigail N Atoyebi, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, and George O Ademowo (2021). Impact of the SEA-PHAGES programme on the Ibadan Bacteriophage Research Team, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/601/>

Area of interest:



11. Name: Ojebola Babatunde Michael

Level: 500 level

Conferences:

- Phage virus assembly

Papers

1. Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo, Muideen K Raifu, Ini Adebisi, Olatimbo V Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, Olusegun O Ademowo (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108).



2.Oduselu T.J, Adedeji R.O, 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 (2021). Computational Analysis of Gordonina Bacteriophage Sedona, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest: Bacteriophage therapy

MEMBERS

2018/2019

Name: **OLATINWO Samuel**

Level: 500

Conferences:

- Phage Virus Assembly
- SEA-PHAGES symposium 2021



Paper

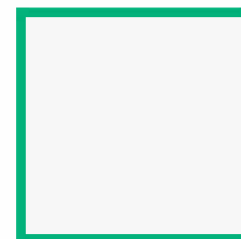
1.Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo, Muideen K Raifu, Ini Adebiyi, Olatimbo V Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, Olusegun O Ademowo (2019), Cluster FE-like Bacteriophages infect a range of Bacteria and can be Lysogenic, 11th Annual SEA Symposium Abstract (Page 108).

Areas of interest: Bacteriophage biology, Gene annotation

Name: **Adepoju Odunayo Deborah**

Level: 400

Conferences: Nil



Papers

1.Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafo-laimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbechidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothraki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>

Name: **Ayeni Damilola Precious**

Level: 400

Conferences: Nil

Papers: Nil

Areas of interest: Bacteriophage Therapy



Name: **Temitayo Oluwadamilare IYED**

Level 400 level

Conferences:

- World phage week
- Africa phage forum



Paper

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>
2. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafolajimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbachidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>

Areas of interest: Bioinformatics

Name: **Inyang, Emem Samuel**

Level: 400

Conferences: Nil



Papers

1. Tolulope J Oduselu, Roqeeb O Adedeji, Ayobami J Akomolafe, Oluwasegun I Daramola, Iyede O Temitayo, Oluwafolajimi A Adesanya, Emem S Inyang, Ogochukwu M Mgbachidinma, Gloria N Igbor, Temitayo O Iyede, Odunayo D Adepoju, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Complete Genome Sequence Annotation of Microbacterium Bacteriophage Dothra-ki, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/600/>
2. Daramola O.I, Akomolafe A.J, Adedeji R.O, Inyang E.S, Iyede T.O, Adepoju O.D, Oduselu T.J, 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 (2021). The Use of Endolysins as alternative Antimicrobial Therapy, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest: Bioinformatics

2020/2021

Name: **Awojide mayowa Margaret**

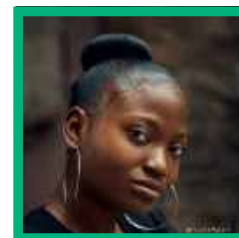
Level: 300level

Conferences:

- Phage virus assembly 2021

Papers

Areas of interest: Bacteriophage biology.



Name: **Adediran Benjamin Adesumbo**

Level: 300

Conferences attended:

- Phage Virus Assembly 2021
- 7th Unibadan Conference of Biomedical Research
- 3rd World conference on clinical research and microbiology

Papers

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>
2. Adediran B.A, Opatola A.D, Alabi P.L, Ojediran M.A, Owoeye W.T, Oduselu T.J, 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 (2021). Anti-CRISPR System: Unravelling the Dynamics of Bacteria-Bacteriophage Evolution, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).
3. Abdulmujeeb Opatola, Williams T. Owoeye, Benjamin A. Adediran, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Effects of Alteration in the Gut Microbiota by Bacteriophages. Presented at 13th World Congress of Microbiology and Clinical Research.

Areas of interest: Computational studies



Name: **Opatola ABDULMUJEEB Damola**

Level: 300

Conferences attended:

- 3rd World conference on clinical research and microbiology (microbiology expo 2020)
- Phage Virus Assembly 2021
- 7th Unibadan Conference of Biomedical Research

Papers

1. Abdulmujeeb Opatola, Williams T. Owoeye, Benjamin A. Adediran, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Effects of Alteration in the Gut Microbiota by Bacteriophages. Presented at 13th World Congress of Microbiology and Clinical Research.
2. Abdulmujeeb Opatola, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. The Physics of Viral Infection by Bacteriophages. Presented at 27th International Phage Virus Assembly Conference.
3. Adediran B.A, Opatola A.D, Alabi P.L, Ojediran M.A, Owoeye W.T, Oduselu T.J, 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 (2021). Anti-CRISPR System: Unravelling the Dynamics of Bacteria-Bacteriophage Evolution, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interests: Bacteriophages, Quantum Mechanics and Evolution.

Name : **Alabi Praise Lois**

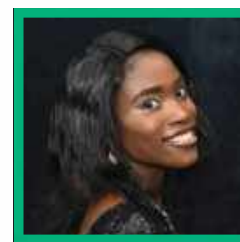
Level: 300

• **Conferences:** Phage virus Assembly 2021

Papers:

1. Adediran B.A, Opatola A.D, Alabi P.L, Ojediran M.A, Owoeye W.T, Oduselu T.J, 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 (2021). Anti-CRISPR System: Unravelling the Dynamics of Bacteria-Bacteriophage Evolution, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest: Bacteriophages



Name: **Olatoye Marvellous Rotimi**

Level: 300

Conferences attended:

- Sea phage symposium,
- Phage Virus assembly 2021

Papers

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>

Area of Interest: Bacteriophage, Medical Microbiology



Name - **Ojediran Mercy Adedamola**

Level - 300

Conferences attended -

- 12th SEAPHAGES Symposium 2021
- Phage Virus Assembly

Papers

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owoeye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebiyi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>

2. Adediran B.A, Opatola A.D, Alabi P.L, Ojediran M.A, Owoeye W.T, Oduselu T.J, 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 (2021). Anti-CRISPR System: Unravelling the Dynamics of Bacteria-Bacteriophage Evolution, presented at UNIBADAN Conference on Biomedical Research (UCBR-7).

Areas of interest: Computational Studies, Phage Biology, Cancer research



Name: **Olaomito Mayowa Anthony**

Level: 300

Conferences

- Phage virus assembly 2021

Papers

Areas of interest: Bacteriophages



Name - **Adams David Oluwatimilehin**

Level - 300

Conferences

- SEAPHAGES Symposium 2021
- Phage Virus Assembly



Papers

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owioye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>

Areas of interest: Phage Biology

Name: **OWOEYE, Williams Timilehin**

Level: 300

Conferences attended:

- SEAPHAGES Symposium 2021
- Phage Virus Assembly



Papers

1. Benjamin A Adediran, David O Adams, Abdulmujeeb D Opatola, Marvellous R Olatoye, Praise L Alabi, Williams T Owioye, Mercy A Ojediran, Monsurat A Sulayman, Oluwasegun I Daramola, Roqeeb O Adedeji, Ayobami J Akomolafe, Temitayo O Iyede, Oluwafolajimi A Adesanya, Comfort M Omolola, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Tolulope J Oduselu, Muideen K Raifu, Ini Adebisi, Veronica I Ogunleye, Temitope O Faleye, Adeleye S Bakarey, Olubusuyi M Adewumi, John I Anetor, George O Ademowo. Computational Analysis of Gordonia Bacteriophage Phishy Genome Sequence, 12th Annual SEA Symposium Abstract. Retrieved from <https://seaphages.org/abstracts/summary/599/>

2. Abdulmujeeb Opatola, Williams T. Owioye, Benjamin A. Adediran, Tolulope J. Oduselu, and Olubusuyi M. Adewumi. Effects of Alteration in the Gut Microbiota by Bacteriophages. Presented at 13th World Congress of Microbiology and Clinical Research.

Area of Interest: Bioinformatics

LAZARUS FAVOUR UCHEMADU

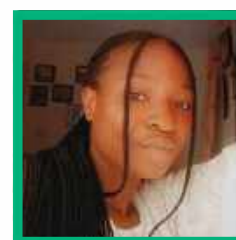
Level: 500

Conferences:

World Phage Week 2020

Papers

1. Olusegun G Ademowo, John I Anetor, Olubusuyi M Adewumi, Temitope O Faleye, Adeleye S Bakarey, Olatimbo V Ogunleye, Ini Adebisi, Muideen K Raifu, Tolulope J Oduselu, Anjolaoluwa E Taiwo, Ifeoluwa E Ayodele, Oluwatimileyin T Oyebamiji, Nanayaa A Atoyebi, Modupeoluwa C Omolola, Uchemadu F Lazarus, Adefola L Jose, Elijah M Akinlolu, Babatunde M Ojebola, Olakunle S Olatinwo (2019), SEA-PHAGES 2018-2019 Session: The Ibadan Phage Hunters Experience, 11th Annual SEA Symposium Abstract (Page 109).



Phage-Encoded Endolysins

Due to the global emergence of antibiotic resistance, there has been an increase in research surrounding endolysins as an alternative therapeutic. Endolysins are phage-encoded enzymes, utilized by mature phage virions to hydrolyze the cell wall from within. There is significant evidence that proves the ability of endolysins to degrade the peptidoglycan externally without the assistance of phage. Thus, their incorporation in therapeutic strategies has opened new options for therapeutic application against bacterial infections in the human and veterinary sectors, as well as within the agricultural and biotechnology sectors. While endolysins show promising results within the laboratory, it is important to document their resistance, safety, and immunogenicity for in-vivo application.

Endolysins are bacteriophage-encoded enzymes, which act by hydrolyzing the host cell wall and subsequently allowing the release of bacteriophage progenies. Endolysins are gaining importance in recent years due to their broad lytic activities against Gram-positive and Gram-negative bacterial cells. The lytic activity of endolysins is classified into different types, namely; (a) acetylmuramidases, (b) transglycosylases, (c) glucosaminidases, (d) amidases, and (e) endopeptidases. Endolysins are involved in peptidoglycan degradation during cell lysis, which is regulated by different phage lytic enzymes and holins. The lytic activity of endolysins may be mitigated by development by resistance mechanisms by bacteria and also by the actions of host immune response. The structure of endolysins is dependent of their origin and it determines what group of bacteria they lyse. Majority of endolysins have a modular configuration with two N-terminal enzymatically active domains (EADs) linked by a short, flexible linker region to a C-terminal cell wall-binding domain (CBD). This configuration is common to Gram-positive phages and mycobacteriophages. Endolysins acting on Gram-negative bacteria have a simple globular configuration.

The structure of endolysins is dependent of their origin and it determines what group of bacteria they lyse. Majority of endolysins have a modular configuration with two N-terminal enzymatically active domains (EADs) linked by a short, flexible linker region to a C-terminal cell wall-binding domain (CBD). This configuration is common to Gram-positive phages and mycobacteriophages. Endolysins acting on Gram-negative bacteria have a simple globular configuration.

The discovery and study of phage-encoded endolysins have brought great attention to their possible therapeutic alternatives as antibacterial agents. Phage proteins like endolysins rarely develop resistance among their bacterial hosts, mostly due to the horizontal gene transfer among phage–host systems over a long time; thus, reducing the burden of resistance. The applications of endolysins extends to many other industries such as agriculture, veterinary, food, and biotechnology. However, the adoption of endolysins has been limited to research and model systems in many of these industries.

In the wake of the urgent need to develop alternatives to conventional antibiotics for therapeutic use, bacteriophages have been considered as plausible alternatives. However, their

use as antimicrobial agents might be limited or totally hindered due to limitations they pose which include: reduced activity due to immune system response, the possible emergence of bacterial resistance against bacteriophages, and health safety issues. As promising as endolysins are in the fight against antimicrobial resistance, their ultimate approval as therapeutics for the public is highly hinged on these three factors; immunogenicity, which is how the immune system of the body will respond to them, their safety profile on human health, and the possibility of bacteria building resistance against endolysins. Such factors require clinical trials on endolysins for a better insight into these concerns.

Research endeavors over the years have raised strong recommendations for the synergetic approach to bacterial treatment via endolysin–antibiotics combination. Early research work by Beveridge and colleagues describe the role of Gram-negative bacteria outer membrane in shielding bacterial peptidoglycan cell wall from exogenous treatment. To perform a successful administration of any therapeutic agent to the target site of infection, there are some issues to be considered, including the administration route and suitable delivery systems that maintain the treatment's stability and activity. Currently, the administration of phage-derived enzymes can be applied via different routes including injections (intravenous, and intraperitoneal), topical applications (creams, ointments, and gels), transnasal, vaginal, and oral delivery systems. Preclinical and clinical trials for therapeutic endolysins are in progress. Most of these studies involving endolysins are targeting different routes of infections caused by *S. aureus*.



Endolysins are an attractive option as they show lytic potential against numerous bacterial species of concern within veterinary and human medicine and show advantages within the agricultural and biotechnology sector. Additionally, endolysins show promising advances against biofilm formation. Interestingly, the recent exploration of resistance, safety, immunogenicity, and the synergy with antibiotics has advanced the research of endolysins further. Endolysins are the best alternative therapeutic approach to cure and treat multi-drug resistant bacteria. Up to now, many endolysins are reported which show good results in treating antibiotic-resistant bacteria. New strategies are needed to develop universal chimeric lysin, to cross the Gramnegative bacterial outer membrane barrier, and to overcome these immunological responses against endolysin. While endolysins are proving to be advantageous as novel therapeutics, further research is required to consider their formulation and engineerability towards clinical trials.

Expanding the frontiers of bacterial diagnosis through bacteriophage biotechnology

In a bid to achieve microbial diagnostic precision and reduce diagnostic turn-around time, the development of technologically advanced novel techniques has been on the rise. There is a gradual phasing out of traditional diagnostic methods such as culture plating and antibody-based assays from the mainstay of bacterial diagnostics in clinical settings by more specific and highly sensitive molecular techniques. Asides from being technically demanding and cost-ineffective, these molecular methods have themselves not fulfilled the most essential diagnostic criterion of distinguishing between viable and dead bacterial cells.

The use of bacteriophages as bio-recognition elements for bacterial detectors offers numerous advantages in terms of cost, ease of accessibility, and high specificity binding of bacteriophages to their bacterial host. The unique ability of bacteriophages to exhibit binding specificity for only their target host makes them ideal candidates for use as bio-recognition elements in bacterial detection. Bacteriophage host binding is profoundly strong, multivalent, and specific. The enormous attributes of robustness, low reagent cost, and relative ease of accessibility due to the ubiquitous nature of bacteriophages make the design of novel bacteriophage-based detectors easily achievable. Bacteriophages have been shown to have numerous advantages in rapid bacterial detection as they are resistant to the denaturation effects of harsh conditions posed by organic solvents and high temperatures. They are considered more sensitive than conventional diagnostic systems because they can distinguish between viable and dead bacterial cells, a critical diagnostic criterion in which traditional diagnostic techniques and molecular-based methods have fallen short.

Bacteriophages offer numerous design options for bacterial detection systems beyond use as recognition elements. They can be used as immobilized bio-sorbents on sensing layers such as the surface plasmon resonance technique, which measures real-time changes in resonant frequency to determine bacterial count. Design of bacteriophage-based detection systems is aided by the relative ease of modifying the bacteriophage genome to increase phage-bacteria complex identification through the incorporation of fluorescent proteins, affinity tags, and chemical labels. Biotechnological advancements further give bacteriophage use the leading edge as genetic modification of bacteriophage genome through the fluorescent gene insertion produces reporter bacteriophages. These recombinants can produce detectable fluorescent signals through intracellular lytic action, strictly in metabolically active bacteria cells. Fluorescent labelled enzyme-active and cell wall binding domains of bacteriophages also offer better alternatives to the use of antibodies as diagnostic markers because they are resistant to pH and temperature sensitivities. Overall, bacteriophage-based detection systems are less prone to detection errors and significantly reduce diagnostic time while also attaining high test sensitivity.

3RD WORLD CONGRESS ON MICROBIOLOGY AND CLINICAL RESEARCH

Adopting Phage Therapy for Treatment of Secondary Bacterial Infections in COVID-19 Patients.

Comfort M. Omolola¹, Roqeeb O. Adedeji¹, Anjolaoluwa E. Taiwo¹, Tolulope J. Oduselu¹, and Olubusuyi M. Adewumi².

¹ Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Nigeria.

² Department of Virology, College of Medicine, University of Ibadan, Nigeria.

The global health threat posed by the COVID-19 pandemic has put immense pressure on antimicrobial treatment. The supportive treatment regimen adopted as palliative care for COVID-19 patients include the administration of antibiotics, to relieve symptoms such as cough and sore throat presented in the early stages of the SARS-CoV-2 infection. This alongside the use of azithromycin for the treatment of COVID-19 patients due to its immunomodulatory function further exacerbates the already fragile nature of antimicrobial resistance as a silent, yet dangerous health concern. Experimental studies have shown the high prevalence of secondary bacterial infections in elderly COVID-19 patients and patients with underlying health conditions. Such infections defy conventional antibiotic treatment, as they are often caused by multi-drug resistant bacterial strains, which are causative organisms of common nosocomial infections. They have been identified as causes of comorbidity and mortality in numerous viral respiratory infections and are significant contributors to the severity in many COVID-19 cases. Secondary bacterial infections worsen the prognosis of COVID-19 patients while also aggravating the concerns of antimicrobial resistance due to continuous antibiotics use. Bacteriophage therapy as an alternate antimicrobial option offers the advantage of host specificity binding, relatively low production cost, rare occurrence of bacterial resistance to treatment, and experimentally proven success in combatting numerous multidrug-resistant strains. While regulatory concerns regarding the full adoption of bacteriophage use for bacterial treatment still exist, it is without a doubt a viable treatment option worth urgent consideration.

Keywords: Bacteriophage, Antibiotics, Secondary bacterial infection.

Word Count: 238words.

3RD WORLD CONGRESS ON MICROBIOLOGY AND CLINICAL RESEARCH

Effects of Alteration in the Gut Microbiota by Bacteriophages

Abdulmujeeb Opatola¹, Williams T. Owoeye¹, Benjamin A. Adediran¹, Tolulope J. Oduselu¹ and Olubusuyi M. Adewumi².

¹ Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Nigeria.

² Department of Virology, College of Medicine, University of Ibadan, Nigeria.

The maintenance of the equilibrium amongst microbes in the human gut and the body at large plays a very important role in homeostatic regulation and maintenance of the body's physiology. An alteration in this delicate homeostatic balance is considered a triggering factor of the pathogenesis of different diseases. While the role of bacteriophages as possible human pathogens has often been overlooked due to their existence as normal microbial entities in the human gut, emerging evidences from human metagenome and phagobiota proteome analyses using animal models suggest otherwise. Bacteriophages can disrupt the gut microbiota equilibrium by killing beneficial bacteria, causing dysbiosis, which results in the maladaptation of the gut microbial composition. Increased number of prophages or free lytic phages that become virions, following lysogenic induction in the gut, result in an imbalance in the gut microbiota. Experimental evidences suggest the direct interaction of bacteriophages with eukaryotic cells via transcytosis through epithelial cells, enable bacteriophages to disperse to isolated regions such as the human brain. Bacteriophage association with prion-like domains, which interact with eukaryotic proteins result in protein misfolding, a mechanism which has been implicated in the pathogenesis of autoimmune and neurodegenerative disorders such as Parkinson's disease, Alzheimer, etc. While it is true that bacteriophages mainly infect prokaryotic cells, the experimental studies showing the impact of bacteriophages on gut microbiota suggest that the possible pathogenic effect of bacteriophages on humans cannot be overlooked. Further studies will contribute greatly to our understanding of the pathogenesis, diagnosis, treatment, and prevention of several diseases.

Keywords: bacteriophages; microbiota; dysbiosis; virions.

Word Count: 250 words.

CLINICAL PHARMACY & CLINICAL RESEARCH 2021

Title: Bacteriophage Therapy Resurgence: Designing a Workable Framework to Combat Associated Regulatory Hurdles

Name: Tolulope J. Oduselu

Affiliation: Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan

Oluwasegun I. Daramola, Anjolaoluwa E. Taiwo, Ayobami J. Akomolafe, Ifeoluwa E. Ayodele, Toba O. Oyebamiji, Oluwafolajimi A. Adesanya, Abigail N. Atoyebi, Olubusuyi M. Adewumi, and Olusegun G. Ademowo.

Abstract

The declaration of a global health emergency on the prevalence of antimicrobial resistance and its projected impact on human health was believed to be a clarion call for all health stakeholders. With mortality rate estimated to be over 10 million deaths per annum globally by 2050, one would wonder what the global health situation might be during the lag phase before the projected peak antimicrobial resistance severity is reached. There exist empirical evidences substantiating the fact that the world is fast running out of options in her antibiotics war-chest. Scientific evidences have leaned towards the resurgence of phage therapy, an age-long treatment option whose early fortunes succumbed to the enticing prospects of antibiotics use. Attention has been drawn to the use of bacteriophages and phage derived products such as endolysins as antimicrobial agents, to combat the numerous strains of antibiotic resistant bacterial agents. These therapeutic approach takes advantage of the natural properties of bacteriophages as bacterial predators, which exert specific antimicrobial action against bacterial host. With recent advancements in genetics and computational biology, host specificity ranges can be further broadened to cover more strains of bacterial species and also afford genomic alterations to improve lytic action and overcome numerous resistant strategies mustered by bacteria to evade phage infection. The ultimate advantage of phage therapeutics is the little or no impact of phages on eukaryotic cell genome.

It is saddening that the resurgent attention to the prospects of bacteriophage therapeutics has not culminated into the formulation of a well-defined framework for phage use in many countries. The non-existence of such a framework can be attributed to little or no knowledge about phage therapeutic potentials. While the historical records of clinical successes of bacteriophage use have been nothing short of outstanding, regulatory concerns regarding the adherence of such trials to modern, standardized practices make them of little relevance. The compassionate administration of bacteriophages in chronically ill patients, whose conditions have defied all clinically approved treatments have been well reported. The success of compassionate use has aided the calls for a more holistic framework for the use of bacteriophages in human treatment. Studies have shown that the regulatory hurdles associated with bacteriophage use largely exist due to the absence of pragmatic framework, which caters for the peculiarities of biological status of bacteriophages. A well-tailored framework would explore possible establishment of safety protocols and quality assessment in bacteriophage design as well as provide proper outlay for the legal nuances associated with tailored phage treatment. The framework would also provide protocols for bacteriophage design on a commercial scale and address legal issues that might arise due to patency of the phage products. The existence of such a framework would aid translational research in bacteriophage biology and better the prospects of phage use in bacterial treatment. If the wheels of governmental interest can be steered in the favor of bacteriophage use, as an alternative or complementary antimicrobial option, perhaps the current hurdles of regulation and widespread acceptance would easily be overcome.

GULF COAST UNDERGRADUATE RESEARCH SYMPOSIUM, RICE UNIVERSITY

Comparative Genomic and Phylogenetic Analysis of Staphylococcal Cassette Chromosome mec (SCCmec) in Methicillin Resistant Staphylococcus aureus

Daramola, Oluwasegun I1, Adewumi, Moses O2

1. Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Nigeria

2. Department of Virology, College of Medicine, University of Ibadan, Nigeria.

Abstract

The Staphylococcal Cassette Chromosome mec (SCCmec) is the defining feature of Methicillin-Resistant Staphylococcus aureus (MRSA). SCCmec is a mobile genetic element carrying the mec gene complex which encodes the resistance feature of Staphylococcus aureus to β -lactam agents and semi-synthetic penicillins, and the cassette chromosome recombinase, ccr complex, which encodes genes for the excision, integration and mobilization of SCCmec around the bacterial chromosome. Since the recent discovery of novel SCCmec types, little has been reported about the comparative analysis of SCCmec variants. This study used genomic and phylogenetic analysis to compare 40 SCCmec regions spanning all 13 types recognized by the International Working Group on the classification of SCC Elements (IWG-SCC), using archived genome databases from NCBI.

An evaluation of the mec classes in SCCmec showed that all SCCmec types encoded the conventional mecA, except type XI which encoded a mecC variant. A combination of 72 ccr classes was analyzed to visualize the diversity of ccr in SCCmec. ccr variants of novel SCCmec type XII and XIII showed high nucleotide homology, which formed the novel allo-type ccrC2. mecC variant of type XI revealed ccr subtype B composition highly similar to early-identified SCCmec type III mecA. This report would help extend the understanding of SCCmec mobile genetic features, region comparison and characteristics of SCCmec types in MRSA.

INTERNATIONAL BIOTECHNOLOGY CONFERENCE, EXHIBITION & WORKSHOP 2020, COVENANT UNIVERSITY

Expanding the Frontiers of Bacterial Diagnosis through Bacteriophage Biotechnology.

Tolulope Oduselu, J.1, Oluwafolajimi Adesanya, A.2, Isaac Daramola, O.1, Ayobami Akomolafe, O.1 and Moses Adewumi, O.3

Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Ibadan1

Department of Medicine, College of Medicine, University of Ibadan, Ibadan2

Department of Virology, College of Medicine, University of Ibadan, Ibadan3

Corresponding Author: johntolu98@gmail.com

ABSTRACT

Growing demand for real-time bacterial diagnostic approaches in clinical and industrial settings has necessitated technologically advanced techniques which are gradually phasing out traditional plating techniques. Biotechnology amidst its diverse uses allows for the harnessing of bacteriophage natural properties in the development of novel precision diagnostics at a lower cost. Recombinant bacteriophages expressing fluorescent reporter genes can be adopted as bio-recognition elements for their specific bacterial pathogen. The resulting intracellular lytic phage replication produces weak detectable fluorescent signals which can then be measured by a luminometer. The technique can successfully distinguish between viable and dead bacterial cells in real-time making it less prone to errors due to false-positive case detection associated with real-time PCR amplification. Bacteriophage high specificity binding to host-pathogen allows for the shortening of diagnostic time and increase test sensitivity range. Bacteria presence is detectable even in small aliquots of collected samples. A drawback however is the need for the design of recombinant bacteriophages specific for each bacteria of interest. Bacteriophage based assays can prove pivotal in the development of novel, cost-effective diagnostic techniques that would revolutionize bacterial diagnosis.

Keywords: Bacteriophage, Fluorescent reporter genes, Biotechnology

PHAGE VIRUS ASSEMBLY, 2021

The Physics of Viral Infection by Bacteriophages

Abdulmujeeb Opatola¹, Tolulope J. Oduselu¹, and Olubusuyi M. Adewumi².

**¹ Department of Biomedical Laboratory Science, College of Medicine,
University of Ibadan, Nigeria.**

² Department of Virology, College of Medicine, University of Ibadan, Nigeria.

The rising need to solve the problem of antimicrobial resistance has necessitated the study of bacteriophage use as alternative antimicrobial therapy. Bacteriophages infect their microbial hosts by injecting their DNA into the cytoplasm of the host cell. This is followed by replication to form virions, which can be integrated into the host cell genome during lysogeny or ultimately burst out of the host cell during the lytic cycle. Recent developments in the fields of cryoelectron microscopy, x-ray crystallography, spectroscopy, etc., have helped to reveal more detailed information on the progression phages during infection. This complex mechanism is simply explained using the concept of equilibrium of forces. Studies show that the release of phage DNA into the host cell results from an “injection force”, caused by the internal pressure exerted by the enclosed DNA within the phage capsid. The internal pressure is as a result of strong bending stress and repulsive forces between closely-linked negatively charged chains of the DNA. Opposing the injection force is the resisting force of the capsid strength, which keeps the viral DNA enclosed within its protein coating. A balance of these forces termed viral metastability helps to keep the viral DNA intact within its capsid enclosure. A distortion of this delicate balance is integral in successful host cell infection by bacteriophages. Studies have also suggested that at the later stage of DNA injection, there is a manifestation of self-diffusion after the internal pressure force has been exhausted. Further studies on these dynamics are integral in understanding what alterations can be used to interfere with phage-host cell interaction. It would also afford the development of novel techniques to genetically engineer bacteriophages that are efficient against antimicrobial resistant strains.

Keywords: Bacteriophages, Physics, Injection force, Viral metastability, Capsid strength, Diffusion, Colloidal system.

PHAGE VIRUS ASSEMBLY, 2021

THE ROLES OF BACTERIOPHAGES IN NEURODEGENERATIVE DISORDERS

Toba O. Oyebamiji¹, Tolulope J. Oduselu¹, and Olubusuyi M. Adewumi².

¹Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Nigeria.

²Department of Virology, College of Medicine, University of Ibadan, Nigeria.

Bacteriophages are viruses that infect bacterial cells and typically hijack the host cellular machinery for their replication. It has always been a general notion that bacteriophages do not infect eukaryotic cells and rightly so, this has been the premise for the safety of bacteriophage use as alternative antimicrobial therapy in humans. Emerging evidences of the role of bacteriophages in the human gut and the possible dissemination to other parts of the body provides a plausible explanation for the discovery of bacteriophages in the cerebrospinal fluid [1]. Bacteriophages have been identified as players in a multi-faceted neurodegenerative pathway, characterized by protein structure reconfiguration, altered inflammatory responses, and an associated autoimmune cascade. Neurodegenerative disorders such as Alzheimer's, Parkinson's, amyotrophic lateral sclerosis, etc. have been known to be a result of the formation of neurotoxic aggregates, triggered by protein misfolding. The pathogenesis of these prion-mediated disorders has been associated with alterations in the gut microbiota, which influence the central nervous system function through the gut-brain axis [2]. The process of neurodegeneration has been widely studied in Alzheimer's disease, an age-dependent disease of the brain, characterized by problems of progressive impairments in memory, language, reasoning, behavior, and visuospatial skills. M13 bacteriophages have been shown to bind beta-amyloid and α -synuclein proteins, leading to plaque disaggregation and neurofibrillary tangles. A similar pathogenic mechanism was also recently reported for Parkinson's disease [3]. While the overall mechanism of this pathogenic process has not been extensively studied, it becomes necessary that more attention be given to the study of these mechanisms and what genetic modifications would be required to halt such processes, seeing that there is growing acceptance of bacteriophage therapy in the antimicrobial resistance era.

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PHAGE VIRUS ASSEMBLY, 2021

The Use-Case of Bacteriophages in Gene Therapy

Ayobami J.Akomolafe¹, Oluwasegun I. Daramola, Tolulope J. Oduselu, and Olubusuyi M. Adewumi.

¹Biomedical Laboratory Science, College of Medicine, University of Ibadan.

²Department of Virology, College of Medicine, University of Ibadan, Nigeria.

The diversity of bacteriophage use cases is fast growing owing to the development of novel bacteriophage technologies, which transcend the conventional therapeutic use against bacterial hosts. Bacteriophages provide numerous advantages in eukaryotic gene therapy as phage genome alteration allows for the display of foreign genetic entities such as antibodies, vaccines, and drugs via phage display, which can then be successfully targeted against specific cells and tissues. Peptides specific to tissue receptors of interest are fused into the phage coat protein gene, to be expressed on the phage capsids. The phage in fused peptides are then taken up by receptor-mediated endocytosis. Bacteriophage-based gene delivery system is often challenged by the impact of host degradative pathways, which prevent the genetic cargo from reaching the nuclear target. Studies have however shown that this pathway can be safely evaded through genetic modification processes, which prevent recognition by cellular proteasomes and lysosomes. The receptor binding specificity of the displayed peptides confer protection on non-receptor bearing cells. The bacteriophage-based gene delivery systems have been shown in numerous studies to be more potent and less debilitating in use compared to other viral and non-viral vector systems. Their harmless impact on eukaryotic cells offer substantial gene protection while their considerable smaller genome affords ease of manipulation for customized delivery. Furthermore, experimental studies have ruled out the possibility of immunogenic or oncogenic impact of phages on their targeted cells, a much likely occurrence found in the use of other vector types. The use of bacteriophage-based gene delivery vehicle remains a promising treatment option for the design of novel cures for cancers and inherited disorders.

PHAGE VIRUS ASSEMBLY, 2021

THE USE OF BACTERIOPHAGE DEPOLYMERASE IN THE REMOVAL OF BACTERIAL BIOFILMS

Anjolaoluwa E. Taiwo¹, Babatunde M. Ojebola¹, Praise L. Alabi¹, Tolulope J. Oduselu¹, and Olubusuyi M. Adewumi².

¹Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, Nigeria.

²Department of Virology, College of Medicine, University of Ibadan, Nigeria.

The growing concern of antimicrobial resistance as a global pandemic threat has been largely attributed to the emergence of diverse genetic mechanisms, which confer protection on bacterial cells. The continued sophistication of bacterial cell cooperative group behavior, resulting in biofilm formation has also been identified as a major contributing factor. More than 80% of chronic bacterial infections have been attributed to the formation of biofilms, which are complex polymeric networks held in place by extracellular polymeric substances (EPS). Bacterial cells (one or more species) can be immobilized within these matrices, conferring a considerable degree of resilience to the immune system, antibiotics as well as provide mechanical stability for surface adhesion to living tissues, medical equipment, prosthetics, etc.[1] While it was initially believed that bacteria had a predominant planktonic existence, the growing knowledge of bacterial cell to cell communication via quorum sensing unravels the dynamics of synchronous gene expression amongst bacterial cells, in response to bacterial cell population density.[2] Bacteriophages do not only offer the advantage of lytic action on targeted bacterial hosts but contain enzymatic domains, encoded within structural genes such as tail-spike proteins, to degrade biofilm EPS. These EPS degrading enzymes known as Depolymerases (grouped as hydrolases, lyases, and triacylglycerol lipases) exhibit specific binding to capsular polysaccharides, exopolysaccharides, and O-polysaccharides derived from lipopolysaccharides and upon degradation, the phage receptor sites on the host bacterium become exposed for bacteriophage binding. They have been shown not only to degrade the biofilm matrix but also, inhibit the formation of new ones. Interestingly, only a small fraction of bacteriophages have been shown to encode for this enzyme but with advancements in synthetic biology, genetically modified phages that code for this enzyme can be synthesized. The therapeutic potential of bacteriophage depolymerases will be brought to the fore in the coming years, as efforts towards combatting chronic and recurrent bacterial infections increase.[3]

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UNIBADAN CONFERENCE FOR BIOMEDICAL RESEARCH 2021

ANTI-CRISPR SYSTEM: UNRAVELLING THE DYNAMICS OF BACTERIA -BACTERIOPHAGE EVOLUTION.

Adediran B.A^{1,2}, Opatola A.D^{1,2}, Alabi P.L^{1,2}, Ojediran M.A^{1,2}, Owoeye W.T^{1,2}, Oduselu T.J^{1,2},
Raifu M.K^{1,3}, Adebiyi I^{1,4}, Ogunleye V.O^{1,4}, Faleye T.O.C^{1,5}, Bakarey A.S^{1,2,3}, Adewumi O.M^{1,5},
Anetor J.I^{1,6}, and Ademowo O.G^{1,3,7}

1 Ibadan Bacteriophage Research Team, University of Ibadan.

2 Department of Biomedical Laboratory Science, University of Ibadan.

3 Institute for Advanced Medical Research and Training, University of Ibadan.

4 Department of Medical Microbiology, University of Ibadan.

5 Department of Virology, University of Ibadan.

6 Department of Chemical Pathology, University of Ibadan.

7 Department of Pharmacology and Therapeutics, University of Ibadan.

The discovery of the Clustered Regularly Interspaced Palindromic Repeats and CRISPR associated proteins (CRISPR-Cas) genome-editing tool has immensely revolutionized the field of genome engineering, as efforts to unravel the possibilities of its use in achieving novel biotechnological advancements are being made. This potent genome editing tool was first identified as a bacterial host defense mechanism against bacteriophages. The CRISPR-Cas system functions by identifying short fragments of foreign DNA, which are then incorporated into the CRISPR locus separated by short palindromic repeats. It was initially believed that the only mechanism by which bacteriophages escape this bacterial immune system is through the acquisition of point mutations. This has however been invalidated by the mechanism of primed adaptation, which allows CRISPR locus to acquire new spacers in response to the appearance of escape mutants. Studies have identified the role of anti-CRISPR proteins in bacteriophages, encoded by nucleotide regions of 150-450 bp. These can interact directly with the bacterial host CRISPR system resulting in the suppression of phage DNA binding and cleavage, inhibition of CRISPR locus primed adaptation, suppression of CRISPR guided RNA (crRNA) processing for CRISPR-Cas complex activation, and the blockage of Cas protein expression. This discovery sheds more light on the continued evolutionary contention that exists between bacteria and bacteriophages. The mechanism of self targetting has been proposed to explain how bacteria bearing anti-CRISPR locus within their prophage regions escape destructive crRNA when targeted. This also has significant implications on the use of CRISPR genome editing, as anti-CRISPR proteins can now be engineered to function as regulatory switches in genome re-engineering. The extent of the evolutionary advantage of these proteins on bacteriophages and bacteria is yet to be known. It is however clear that increased knowledge on the mechanism of their action would prove pivotal in expanding the CRISPR toolbox.

Word Count: 298 words.

UNIBADAN CONFERENCE FOR BIOMEDICAL RESEARCH 2021

COMPUTATIONAL ANALYSIS OF GORDONIA BACTERIOPHAGE SEDONA

Oduselu T.J^{1,2}, Adedeji R.O^{1,2}, Akomolafe A.J^{1,2}, Daramola O.I^{1,2}, Olatinwo S.O^{1,2}, Adesanya O.A^{1,3}, Inyang E.S^{1,2}, Taiwo A.E^{1,2}, Atoyebi A.N^{1,2}, Iyede T.O^{1,2}, Ayodele I.E^{1,2}, Omolola C.M^{1,2}, Ojebola B.M^{1,2}, Lazarus F.U^{1,2}, Adepoju O.D^{1,2}, Oyebamiji T.O^{1,2}, Raifu M.K^{1,4}, Adebisi I^{1,5}, Ogunleye V.I^{1,5}, Faleye T.O.C^{1,6}, Bakarey A.S^{1,2,4}, Adewumi O.M^{1,6}, Anetor J.I^{1,7}, and Ademowo O.G^{1,4,8}

1 Ibadan Bacteriophage Research Team, University of Ibadan.

2 Department of Biomedical Laboratory Science, University of Ibadan.

3 Department of Medicine, University of Ibadan.

4 Institute for Advanced Medical Research and Training, University of Ibadan.

5 Department of Medical Microbiology, University of Ibadan.

6 Department of Virology, University of Ibadan

7 Department of Chemical Pathology, University of Ibadan

8 Department of Pharmacology and Therapeutics, University of Ibadan

Gordonia bacteriophage Sedona belongs to cluster DE, sub-cluster DE1, which is made up of 36 members of an 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 Pittsburg 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/nuccore/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 42% 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.

Word Count: 296 words.

UNIBADAN CONFERENCE FOR BIOMEDICAL RESEARCH 2021

EARLY CAREER RESEARCH ENGAGEMENT IN GENOMIC RESEARCH: THE IBADAN BACTERIOPHAGE RESEARCH TEAM MODEL

Oduselu T.J^{1,2}, Daramola O.I^{1,2}, Taiwo A.E^{1,2}, Akomolafe A.J^{1,2}, Ayodele I.E^{1,2}, Oyebamiji T.O^{1,2}, Adesanya O.A^{1,3}, Adedeji R.O^{1,2}, Omolola C.M^{1,2}, Atoyebi A.N^{1,2}, Raifu M.K^{1,4}, Adebiyi I^{1,5}, Ogunleye V.O^{1,5}, Faleye T.O.C^{1,6}, Bakarey A.S^{1,2,4}, Adewumi O.M^{1,6}, Anetor J.I^{1,7}, and Ademowo O.G^{1,4,8}

1 Ibadan Bacteriophage Research Team, University of Ibadan.

2 Department of Biomedical Laboratory Science, University of Ibadan.

3 Department of Medicine, University of Ibadan.

4 Institute for Advanced Medical Research and Training, University of Ibadan.

5 Department of Medical Microbiology, University of Ibadan.

6 Department of Virology, University of Ibadan.

7 Department of Chemical Pathology, University of Ibadan.

8 Department of Pharmacology and Therapeutics, University of Ibadan.

The commencement of the SEA-PHAGES program at the Department of Biomedical Laboratory Science, University of Ibadan in 2018 marked the beginning of undergraduate research engagement in bacteriophage biology and computational studies at the University of Ibadan. A team of 7 faculty members led by Prof. O. G. Ademowo founded the Ibadan Bacteriophage Research Team (IBRT), which has grown to become a full-fledged undergraduate research community where active research in bacteriophage genomics is supervised by seasoned faculty members. The team runs a voluntary-based sessional course work of hands-on laboratory experimentation in bacteriophage isolation and genome characterization. Team members undertake a six-week hybrid training program in the use of genome annotation softwares including DNA Master, Artemis, Artemis Comparison Tool, Starterator, Phamerator for genome characterization project. They are also taken through the rudiments of scientific research writing and literature review. The team has published four fully characterized bacteriophage sequences, all accessible on the NCBI and actinobacteriophage databases (phages Idaho- MK757448, Dothraki- MT451985, Sedona- MW822146, and Phishy- MW862986). We have also published three review papers on the use of whole phages and phage-derived products in microbial therapeutics and diagnosis and presented over 15 conference abstracts at local and international conferences. IBRT has become the leading undergraduate research organization in sub-Saharan Africa, with international recognition from the European Society of Clinical Medicine and Infectious Disease. Team members belong to international organizations including British Society of Antimicrobial Chemotherapy, the International Society of Virus of Microbes, American Society of Microbiology. Its training model was successfully adopted to pioneer the Faculty of Basic Medical Science undergraduate research hub. The adventure-based, all-inclusive training model adopted by IBRT has brought unprecedented outcomes in active undergraduate engagement. It allows students to build mentor-mentee relationships in areas of their research interest, while also providing a community that supports their academic pursuits.

Word Count: 299 words

UNIBADAN CONFERENCE FOR BIOMEDICAL RESEARCH 2021

THE USE OF ENDOLYSINS AS ALTERNATIVE ANTIMICROBIAL THERAPEUTICS

Daramola O.I^{1,2}, Akomolafe A.J^{1,2}, Adedeji R.O^{1,2}, Inyang E.S^{1,2}, Iyede T.O^{1,2}, Adepoju O.D^{1,2}, Oduselu T.J^{1,2}, Raifu M.K^{1,3}, Adebisi I^{1,4}, Ogunleye V.O^{1,4}, Faleye T.O.C^{1,5}, Bakarey A.S^{1,2,3}, Adewumi O.M^{1,5}, Anetor J.I^{1,6}, and Ademowo O.G^{1,3,7}

1 Ibadan Bacteriophage Research Team, University of Ibadan.

2 Department of Biomedical Laboratory Science, University of Ibadan.

3 Institute for Advanced Medical Research and Training, University of Ibadan.

4 Department of Medical Microbiology, University of Ibadan.

5 Department of Virology, University of Ibadan.

6 Department of Chemical Pathology, University of Ibadan.

7 Department of Pharmacology and Therapeutics, University of Ibadan.

The recent upsurge in the incidences of multi-drug resistant infections and a continuous decline in the production of new antibiotics has resulted in increased concerns for the development of alternative approaches to antimicrobial therapy. The early warning signs of a large-scale bacterial resistance, most likely to result in a global pandemic were jettisoned, as the inappropriate practice of antibiotics misuse and abuse continued unabated. Advances in the field of bioengineering have however opened opportunities for novel antimicrobial therapeutics to be explored. Endolysins, which are phage-encoded hydrolytic enzymes with the ability to degrade bacterial peptidoglycan cell walls have been proposed as potential therapeutic alternatives. Owing to bacteriophage host specificity interaction, endolysins exhibit bactericidal action which does not disrupt the host's normal microbiota. Recent studies have revealed elevated levels of antibacterial activity from actions of purified endolysins on bacterial cell walls than the use of whole bacteriophages. Also, a significant increase in antimicrobial activity against resistant bacteria strains has been reported from the synergistic combination of endolysins with antibiotic doses. Studies have revealed a lower propensity for bacterial resistance development to endolysins compared to conventional antibiotics. Endolysins offer a new therapeutic strategy against multi-drug resistant bacteria while also eliminating the limitations surrounding the use of whole phages as alternative antimicrobial therapy. Genetic engineering provides a platform for the development, manufacture, and remodeling of endolysins to suit diverse antibacterial therapeutic needs in medical and veterinary fields.

Word Count: 233 words

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Transcriptomic Analysis of SARS-CoV-2 Infection of Lung Tissues

Oduselu, Tolulope J^{1,2}, Daramola, Oluwasegun I^{1,2}, Taiwo, Anjolaoluwa E^{1,2}, Akomolafe Ayobami J^{1,2}, Ayodele Ifeoluwa E^{1,2}, Oyebamiji, Toba O^{1,2}, Adesanya, Oluwafolajimi A^{1,3}, Adedeji, Roqeeb O^{1,2}, Omolola, Comfort M.^{1,2}, Atoyebi, Abigail N.^{1,2}, Raifu, Muideen K^{1,4}, Adebiyi, Iniolouwa^{1,5}, Ogunleye, Veronica O.^{1,5}, Faleye, Temitope O.C^{1,6}, Bakarey, Adeleye S^{1,2,4}, Adewumi Olubusuyi M^{1,6}, Anetor John I^{1,7}, and Ademowo Olusegun G^{1,4,8}

1 Ibadan Bacteriophage Research Team, University of Ibadan.

2 Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan.

3 Department of Medicine, College of Medicine, University of Ibadan.

4 Institute for Advanced Medical Research and Training, College of Medicine, University of Ibadan.

5 Department of Medical Microbiology, College of Medicine, University of Ibadan.

6 Department of Virology, College of Medicine, University of Ibadan.

7 Department of Chemical Pathology, College of Medicine, University of Ibadan.

8 Department of Pharmacology and Therapeutics, College of Medicine, University of Ibadan.

Understanding the host transcriptional changes associated with SARS-CoV-2 virus infection helps to unearth the underlying mechanisms of the viral pathogenesis, identify differentially expressed gene signatures that account for some of its characteristic symptoms, identify molecular biomarkers of altered biological processes in infected persons, and novel drug targets, which can be of therapeutic relevance. In this study, normalized gene counts of publicly available RNA sequence data of nine lung tissues (4 infected and 5 control samples) were obtained as GEO datasets from the NCBI repository (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE150316>). The gene counts were subjected to principal component analysis to examine the global patterns of disparity between the control and infected samples. Differentially expressed genes were visualized using clustergram analysis and volcano plot while gene ontology analysis was carried out to identify altered biological processes, molecular functions, and cellular components. L1000CDS2 and L1000FWD queries were used to identify drugs and small molecules, capable of reversing and mimicking gene expression signatures. The result of the analysis showed significant upregulation of genes associated with cell-mediated and humoral immune responses, antigen-mediated receptor signaling, complement activation cascade, and phagocytic activity. There was a downregulation of transcription factor activity, which showed significant impact on the type-I and type-III interferon signaling activity of infected cells. Protein kinase activity, hemostatic regulation, angiogenesis, and apoptotic processes were all found to be significantly downregulated. The observed profile confirms the plausible occurrence of chronic inflammatory responses, acute respiratory distress syndrome, multiple organ dysfunction, and disseminated coagulopathy associated with severe cases of the SARS-CoV-2 infection.

EXPLORING THE PROSPECTS OF IN-SILICO MODELLING IN STUDYING HUMAN DISEASES

Tolulope J. Oduselu^{1,2}, Oluwatosin R. Owolabi^{1,3}, Marvellous O. Salami^{1,3}, Angel Umez^{1,3}, John C. Duruson^{1,4}, Onifade Mubaraqat. Y^{1,2}, Oluwatimilehin D. Atiye^{1,2}, Sherifat O. Ojekunle^{1,3}, and Olugbuyiro O. Success^{1,4}

1 Faculty of Basic Medical Sciences Student Association Research Hub.

2 Department of Biomedical Laboratory Science, University of Ibadan.

3 Department of Biochemistry, University of Ibadan.

4 Department of Physiology, University of Ibadan.

It is undeniable that biomedical research has profited immensely from technological advances. Biological processes which have seemed largely elusive due to phenotypic variations and ethical hindrances can now be elucidated by the adoption of in-silico models. In-silico systems attempt to simulate in-vivo biological processes and cellular functions, through the use of complex pattern recognition and statistical parameters, which can then be altered to mimic genomic perturbations and sub-cellular changes in human diseases. They can interpret differential expression signatures in normal and diseased cells, making it easy to identify the genetic basis of differing phenotypes. In-silico study models have been proven to be more cost-effective and can be conducted repeatedly without concerns of ethical guidelines governing clinical research. They also allow the visualization of complex molecular interactions and identification of biological pathways, which can be targeted for therapeutic purposes. Upon the identification of novel drug targets, molecular docking for the modeling of drug-protein interactions can be conducted, thus, making translational research effective and hitch-free. It is noteworthy that in-silico models function to simply complement laboratory experimentation and not replace it. The enormous volume of biological data generated via modern technologies can only be utilized when well-structured computational-based models are adopted.

Word Count: 218 words.

Guest Write ups from International Community

PHASE GENOMICS WRITE UP

Accurate viral genome reconstruction and host attribution with proximity-guided metagenomics

Metagenomics has become a driving force in the study of environmental viromes, contributing vastly to our knowledge of viral diversity and enabling functional characterization. Increasing sequencing read depth and decreasing cost have enabled routine recovery of metagenomes from human and animal microbiomes, and environmental samples. However, metagenome deconvolution and assembly pipelines rely on a priori knowledge, statistical assumptions, and binning algorithms, as shotgun sequencing data lacks genomic contiguity information. These analysis methods cannot tell with certainty which sequences originated from which cell in a complex microbial community. This leaves metagenome-assembled genomes (MAGs) incomplete and contaminated. In addition, conventional binning approaches are unable to accurately associate mobile genetic elements, such as bacterial plasmids, viruses or bacteriophages, or integrons and transposons, with their hosts. Inversely, this means that bona fide hosts for the viruses in metagenomic samples remain largely unidentified, leaving huge gaps in our understanding of the biological and ecological roles of these viruses.

The Phase Genomics ProxiMeta™ Metagenome Deconvolution Platform employs proximity ligation (Hi-C) technology to capture physical interactions between sequences within the same cell. The ProxiMeta™ analysis pipeline tool augments metagenomic binning with this additional layer of linkage information to reconstruct more, high-quality bacterial and viral genomes, and enable specific and sensitive host attribution of DNA viruses (phages). As the "perfect predators" of microbial communities, phages and DNA viruses impact the genomic plasticity of their hosts and ecosystems, with functional impacts all the way up the proverbial food chain. As such, the ProxiMeta™ Platform is a powerful tool for emerging applications, such as viral therapy and fecal microbiota transplants.

Title: Isolation and identification of bacteriophage against salmonella typhi

Running Title: Lytic phages against Salmonella typhi

Authors

Dennis Kotti Makuani^{1,2}, Jane Maurine Gati² Ivy Jepkurui Mutai¹, Atunga Nyachieo¹

Authors Affiliations

¹Institute of Primate Research Department of Reproductive Health and Biology, Phage Biology Section, P.O Box 24481, 00502 Karen, Nairobi.

²Technical University of Kenya, Department of Biochemistry and Biotechnology, P.O Box 52428 00200, Nairobi, Kenya.

Abstract

Introduction: The genus Salmonella, like many other bacteria, has been frequently reported as resistant to commonly used antibiotics in treating diseases. Therefore, the current spread of antibiotic resistance genes in bacteria raises doubts about the effectiveness of antibiotics in the future. One possible alternative to antibiotics is the use of bacteriophages (phages) as antimicrobial agents to control antibiotic-resistant pathogenic Salmonella typhi. Phages have been reported in various studies as a new, safe, and effective bio-control method for treating infectious diseases caused by drug resistant bacteria. The primary goal of this study was to isolate phages using a standard S. typhi bacterium and test it on a clinical S. typhi isolate for host range to determine the effectiveness of phages on multi-drug resistant infections.

Methodology: Phages specific to Salmonella typhi were isolated from sewage sample collected from Nairobi River through phage enrichment. The presence of phages was determined by spot test method following 10-fold dilution of the enrichment filtrate using soft agar (0.4%) overlay method. Plaque assay was used in purification and quantitation of phages. The in vitro antimicrobial potential of lytic phage was determined by dispensing 10 µl of phage to an MDR Salmonella typhi lawn on an agar plate and incubated overnight at 37°C. Additionally, the efficacy of phages in different concentrations was also studied through plaque assay. Presence of clear patched zones indicated the potential of phages in treatment of MDR infections.

Results: From the Nairobi River waste water, one phage with complete lysis and 2mm in size was picked and purified. On host range activity, the isolated phage was effective on lysing an MDR S. typhi. On the effect of varying phage concentrations with dilutions (from 10⁻³, 10⁻⁵ and 10⁻⁷), it was evident that the phage titre was decreasing and hence the lytic activity though still efficacious in lysing the bacteria.

Conclusion:

This study shows that our environment harbors lytic phages that can be isolated and used in the treatment of MDR infections.

Keywords: multi-drug resistance, lytic phages, waste water, bacterial infections, Kenya

THE AFRICAN PHAGE FORUM

A Collaborative Network of African phage researchers to promote and sensitize phage research in Africa.

Vision: To improve human lives through phage research.

Mission Statement: To provide a platform that encourages scholarship, collaboration and mentorship among researchers and for the advancement of phage research in Africa.

Who are we? We are African phage researchers in early and mid-career level, brought together while seeking solutions to the common challenges we were facing as phage scientists in the developing world/third world. In our quest we realized that there are more phage scientists in Africa, working in isolation and facing the same challenges. To this end we formed the platform; African Phage Forum (APF) for phage researchers in Africa to engage (share ideas, experiences, resources, opportunities) and network with a common goal of improving human life through phage research.

What we will do?

Motivate and mentor phage research students (undergraduate/postgraduate) in African Universities:

- Share affordable protocols for efficient phage experimental processes
- Link to affordable commercial phage research service providers e.g. for sequencing, TEM etc
- Form North-South collaborations for possible support on phage research services e.g TEM

Encourage and work towards South-South multidisciplinary collaborative work among phage scientists in a bid to solve problems tailored to African context.

Bridging phage research and policy implementation at national levels, using research-based evidence to improve development policy, programs and practice.

For more, join us via the WhatsApp link

<https://chat.whatsapp.com/LsPBzD5dkYqHokjOx5iDH8>

Co-ordinators

Dr. Emmanuel Nnadi – Plateau State University, Nigeria.

Dr. Rita Nakayinga – Kyambogo University, Uganda

Dr. Juliah Khayeli – Jomo Kenyatta University of Agriculture and Technology, Kenya



THE INTEGRATION OF MICROBIAL GENOMIC STUDIES IN COMBATTING GROWING CONCERNS OF ANTIMICROBIAL RESISTANCE

Roqeeb O. Adedeji^{1,2}, Olumide K. Ariyibi^{1,2}, Stephen Odeleye^{1,3}, Marvellous Badmus^{1,2}, Favour O. Animasahun^{1,2}, Marvellous O. Salami^{1,3}, Aishat A. Ibitoye^{1,4}, Sogo O. Akinleye^{1,2}, and Tolulope J. Oduselu^{1,2}

¹ Faculty of Basic Medical Sciences Student Association Research Hub.

² Department of Biomedical Laboratory Science, University of Ibadan.

³ Department of Biochemistry, University of Ibadan.

⁴ Department of Physiology, University of Ibadan.

The World Health Organisation in the year 2018 declared antimicrobial resistance to be a global health concern and mortality is projected to reach its height in the year 2050, with more than 50 million deaths per annum. If the global scale of the COVID-19 pandemic is anything to go by, rising concerns to prevent similar outcomes with the AMR crisis through the design of alternative antimicrobial therapy are thus justifiable. Environmental pressures due to antimicrobial misuse and abuse have contributed significantly to mutational changes, which have increased microbial virulence. These have also resulted in the acquisition of genetic features, which aid microbial evasive mechanisms. To effectively address this growing health concern, there is an urgent need for the integration of genomic characterization as a routine protocol in microbial studies. Genomic information helps to understand the overall architecture of microbial genomes, understand the mechanisms of the acquisition of antimicrobial-resistant genes through horizontal gene transfer, lysogenic induction of prophage regions which contribute to overall host defense mechanisms, and the elucidation of synchronous gene expression in microbial biofilms through quorum sensing. This technologically driven research approach has been widely explored as a complement for laboratory experimentation in many developed countries but has struggled to find room for routine use in developing countries, largely due to inadequate research funding and very little technical know-how of its use. Addressing the growing concerns of antimicrobial resistance requires more concerted research efforts and the adoption of genomic studies in microbial research would go a long way in achieving this goal.

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Appreciation of IBRT'S work by HOD



Department of Biomedical Laboratory Science

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Faculty of Basic Medical Sciences,
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University of Ibadan, Ibadan, Nigeria.



Email: bmls@com.ui.edu.ng
Website: www.com.ui.edu.ng
Phone: +2348128515470

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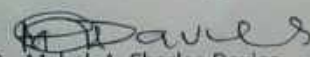
CONGRATULATORY REMARKS FOR IBRT PHAMILIA JOURNAL

On behalf of the entire staff of the Department of Biomedical Laboratory Science, College of Medicine, University of Ibadan, I congratulate the entire members of Ibadan Bacteriophage Research Team (IBRT) on the success of the maiden edition of the team's journal "PHAMILIA".

My congratulatory remarks also go to notable scientists and researchers who have been mentoring these young students' scientists to attain this feat. The team demonstrated high level of innovation and competence during the 7th Unibadan Conference. The research efforts of this team had uplifted the department locally and internationally.

There is no doubt that availing these young student scientists the opportunity of writing scientific papers for publication in the Phamilia Journal will immensely prepare them for the challenges ahead in writing scientific papers for local and international publications.

Best Wishes


Dr. Mabel A. Charles-Davies
Ag. Head, Department of Biomedical Laboratory Science.

CHEMICAL PATHOLOGY Dr I. O. Omotosho PhD, MSc, FIMLSCH, AIBMS (UK)	HAEMATOLOGY/BLOOD TRANSFUSION SCIENCE Mrs Oluwaseyi E. Bamisaye, MSc	HISTOPATHOLOGY Mr Onyegbula K. C. Msc Dr (Mrs) Racheal O. Folann, PhD Mr Adenuga A. D. Msc	MEDICAL MICROBIOLOGY
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Photo Gallery

