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Research Article

Gut microbiota analysis of marsh crocodile (*Crocodylus palustris*) of Vishwamitri River

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Abstract—A study was conducted to establish baseline information regarding the microbiome composition of the Marsh crocodile (Crocodylus palustris) gut flora through DNA isolation and sequencing of scat samples. Metagenomics, focusing on microbial communities within ecosystems, was employed to analyze the diverse microbiota, including bacteria, viruses, archaea, and eukaryotes. These microorganisms are ubiquitous and inhabit various environmental niches, such as soil, air, and water, and also form symbiotic relationships with host organisms, including their skin, lungs, and gastrointestinal tracts. Traditional bacterial biochemical identification approaches were found to be labor-intensive due to the inability to culture certain microbes. The use of One Codex software facilitated the analysis of the Marsh crocodile scat community, revealing a rich diversity comprising 84 phyla, 75 classes, 150 orders, 326 families, 1104 genera, and 3025 species. The gut microbiome is recognized for its significant impact on host health. In this study, Firmicutes predominated, comprising 50.07% of the phylum, followed by Proteobacteria, Actinobacteria, and Bacteroidetes. Notably, Firmicutes, including Bacilli, Gammaproteobacteria, and Clostridia, were associated with high levels of fecal coliforms in the aquatic environment inhabited by Marsh crocodiles.
Keywords: gut flora, microbiome, Firmicutes, Marsh crocodile, DNA isolation.

1. Introduction

India, known for its cultural icons such as snake charmers and elephants, has recently garnered attention as a nation significantly populated by crocodiles. Among the three crocodilian species inhabiting India, the Mugger or Marsh crocodile (Crocodylus palustris) is the most prevalent.[1]Crocodylus palustris, widely distributed across the country, is of particular interest compared to the other two species, Crocodylus porosus (Estuarine or Saltwater Crocodile) and Gharial (Gavialis gangeticus), due to its characteristic features. All three species enjoy legal protection in India, though they face various threats such as habitat loss, pollution, and human activities like hunting and the pet trade, leading to environmental degradation.[2] Despite these challenges, crocodilian populations remain substantial in India and neighboring countries like Pakistan, Nepal, Sri Lanka, Bangladesh, Bhutan, and Myanmar. However, Bhutan and Myanmar have reported their extinction due to habitat loss[3]. Recent reports from Bangladesh indicate the persistence of Mugger populations in their native habitats[4,5,6].

Metagenomics, a discipline investigating microbial diversity within ecosystems, encompasses the study of microbiomes comprising bacteria, viruses, archaea, and eukaryotes.[7,8] These microorganisms are omnipresent, existing in diverse environmental niches such as soil, air, water, and within mixnismal body parts including the skin, lungs, and gastrointestinal tract. Understanding microbial diversity and functional capabilities within specific habitats is pivotal for elucidating microbial evolution and ecology[9]. Traditional approaches to microbial diversity studies, involving bacterial biochemical identification and culture-dependent methods, pose significant scientific and technological limitations, including laborious processes and challenges associated with identifying non-culturable bacteria[10]. Consequently, researchers have endeavored to develop novel methods for studying microbial diversity[11].

The term "metagenome" encompasses two main approaches: structural metagenomics, which examines the structure of uncultivated microbial populations to understand interactions between individual components, and functional metagenomics, which identifies genes through the generation of expression libraries followed by activity-based screenings.[12,13]. Studies often employ 16S rRNA gene investigations as a metagenomic approach, which can elucidate metabolic pathways and the functional potential of microbiomes. Sanger sequencing technology has historically facilitated microbial diversity analysis in metagenomic studies[14]. Environmental factors such as temperature,

salinity, water quality, and dissolved oxygen significantly influence fish biological functions, including reproduction and growth.[15] Organisms adapt to environmental variations by altering protein-coding DNA sequences, thereby affecting gene expression and individual fitnes[16].

2. Materials and method

Sample collection The Crocodile scat sample was collected in an air-tight plastic bag from the Vishwamitri river bank. Sample fig.1 Scat analysis Scat analysis was done by the proper hand shorting method. During analysis, different type of material was observed and collected from the scat. DNA extraction Sample preparation

1. Add 0.8 ml of 1XSS buffer to 1 ml of sample and mix. 2. Centrifuge for 1 minute at 12000 rpm in a microfuge tube and discard 1 ml of supernatant. 3. Add 1 ml of 1XSSC buffer again, vortex, and centrifuge at 12000 rpm for 1 minute, and remove all of the supernatant. 4. Add 370 microliter of 0.2 M sodium acetate to each pellet and mix by inverting the tube briefly. 5. Add 25 microliter of 10% SDS and 5 microliter of proteinase K (20 mg/ml). mixed by inverting the tubes briefly and incubated for 1 hour at 55°C. 6. Add 100 microliter of phenol-chloroform-isoamyl alcohol and mix for 30 seconds. 7. Centrifuged for 2 minutes at 12000 rpm in a microcentrifuge tube. 8. Collect the aqueous layer (top layer) carefully in a new microcentrifuge tube, add 1 ml of cold 100% ethanol, mix, and incubate for 15 minutes at -20°C. 9. Centrifuged for 2 minutes at 12000 rpm in a microcentrifuge. The supernatant was removed by draining the tubes. 10. Add 180 microliters 1 X TE buffer, vortex, and incubate at 55°C for 10 minutes. 11. Add 20 microliter of 2 M sodium acetate and mix. 12. Add 500 microliter of cold 100% ethanol mixed. Centrifuged for 1 minute at 12000 rpm in a microcentrifuge. 13. Decant supernatant and rinsed the pellet with 1 ml of 70% ethanol. Centrifuged for 1 minute at 12000 rpm in microcentrifuge. 14. Decant supernatant, dry the pellet in a speed-vac for 10 minutes, or until dry at room temperature. 15. Resuspend the pellet by adding 200 microliter of 1X TE buffer. Incubate overnight at 55°C, vortex periodically to dissolve the genomic DNA.

3. Results and Discussion

Result DNA Visualization isolated DNA was visualized by 0.8% Agarose gel electrophoresis (Bio-Rad) using 0.5 X TEA buffer at 60-65 voltage for approximately 45 minute to 1 hour. The Image of the gel was captured in the gel documentation system to check the quality of the DNA. Fig.-2. 16s metagenomics report of marsh crocodile scat sample: Qualitative and quantitative analysis of gDNA. DNA was isolated from given sample by Qiagen gDNA kit[17]. The quality of gDNA was checked on 0.8% agarose gel (loaded 5□l) for the single intact band. The gel was run at 110 V for 30 mins. 2□l of the sample was loaded in BioTek Epoch to determine the A260/280 ratio. The DNA was quantified using a Qubit dsDNA HS Assay kit(life Tech). 1□ of each sample was used for determining concentration using a Qubit 2.0 Fluorometer. Preparation of libraries for run chemistry: the amplicon library was prepared as per the 16s Metagenomics sequencing library preparation protocol. primer for amplification of the hyper-variable region of 16rDNA gene of bacteria and archaea:primer set V2-4-8.primer set V3-6,7-9 software for community metagenomics analysis by One Cordex: The one cordex data platform works with the dual goals of analyzing microbial reference data against the largest possible collection of microbial reference genomes, as well as presenting those results in a formate that is consumable by applied end-users.one codex identifies microbial sequences using a “k-mer based” taxonomic classification algorithm through a web-based data platform, using a reference database that currently includes approximately 40, 000 bacterial, viral,fungal,protozoan genomes. The data were analyzed with standard instructions provided by the developer (Minot et al.,2015) DNA isolation from the crocodile scat sample was done by using the 1X SS buffer method. DNA visualization the isolated DNA from the crocodile scat sample was visualized as a single compact DNA band by using the 0.8% agarose gel electrophoresis. Fig.3 Quantification of gDNA using Qubit Flurometer dsDNA Assay lane sample Concentration No. (ng/□l) 1 Crocodile scat sample 40 community metagenomic study with one Codex: one codex database classified the sequence into 84 phyla, 75 classes, 150 orders, 326 families, 1104 genera, and 3025 species. community metagenomices study with one codex : all results of the metagenomices study with one codex are given in Fig. 5,6,7,8,9,10. The community of crocodile scat samples was analyzed by the softwere one codex. the phylum lavel analyzed showed 87 phyla of which the highly abundant phyla was Firmicutes 596522 (50.07%), followed by proteobacteria 268260 (22.52%), Actinobacteria 55653 (4.67%) and Bacteroidetes 5290 (0.44%). The Class level analysis showed a high abundance of Bacilli 479480 (40.25%), followed by Gammaproteobacteria 244885 (20.55%), Clostridia 87946 (7.38%), and Actinobacteria 46456 (3.9%). The Order level analysis reported 150 Orders in which the most abundant was Bacillales 453906 (38.1%), followed by Enterobacterales 114056 (9.57%), Pseudomonadales 110728 (9.29%) and Clostridiales 87295 (7.33%). At the family level, a total of 326 Families were identified, and from that the highly abundant was Bacillaceae 175461 (14.73%) followed by Pseudomonadaceae 103920 (8.72%), Enterobacteriacesae 46062 (3.87%), and Morganellaceae 44764 (3.78%). At the genus level high abundance of Bacillus 146362 (12.28%) followed by Pseudomonas 103454 (8.68%), Proteus 40575 (3.41%), and Clostridium 38845 (3.26%). At the species level, Escherichia coli was reported most abundant from the total 3025 species followed by Bacillus sp.UFRGS-B20 9088 (0.76%), Clostridioides dif cile 4813 (0.4%), and Salmonella enterica 2470 (0.21%). Krona-based interactive chat was generated by one codex software for in-depth analysis of data. The one codex generated the Krona-based interactive chart for depth analysis of the relative abundance and confidence within the complex hierarchies of all the microbes present in the Crocodile scat sample. Fig.13,14,15

Figures and Tables

Figure 1 Scat sample of Marsh crocodile

Figure 2 Gel electrophoresis

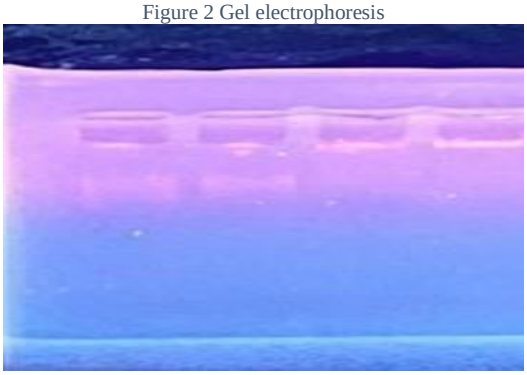


Figure 3DNA bands of Marsh crocodile sample

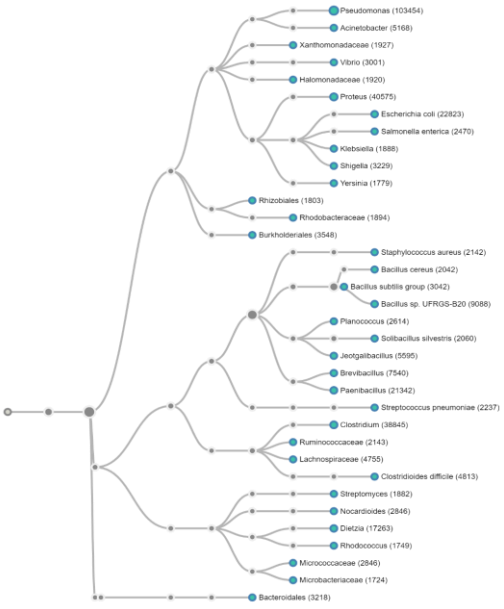


Figure 4 Taxonomic chart of classified read

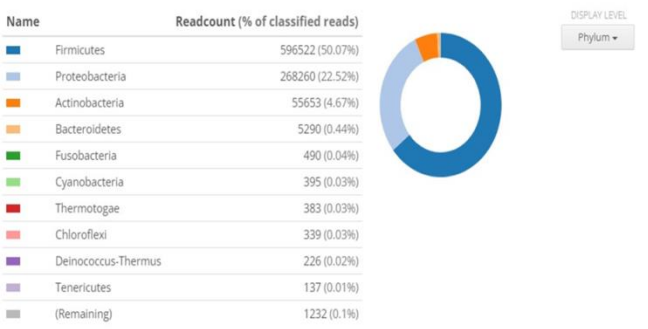


Figure 5 % classified reads of phyla from sequence

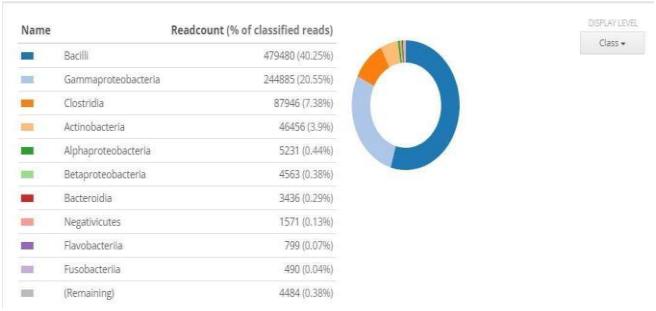


Figure 6 % classified reads of Class from sequence

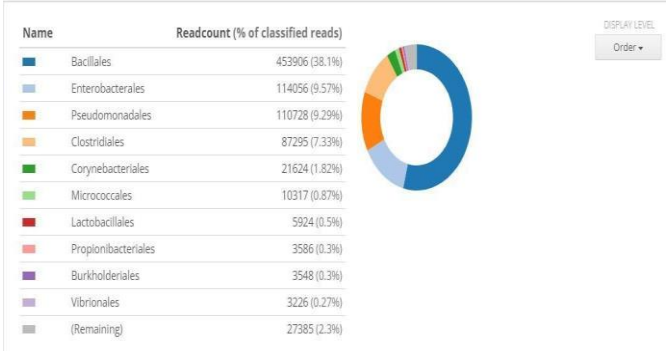


Figure 7% classified reads of Orders from sequence

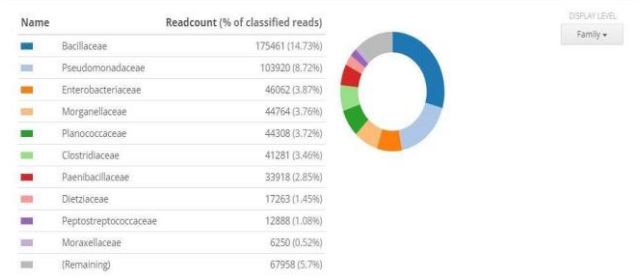


Figure 8% classified reads of Family from sequence

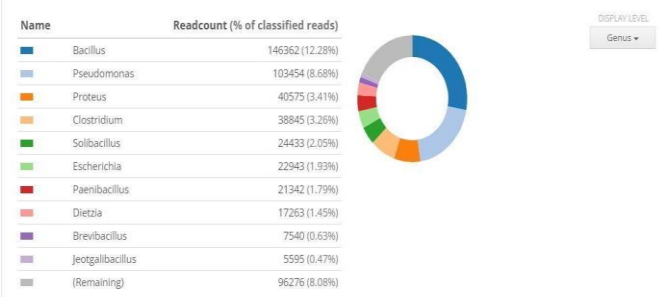
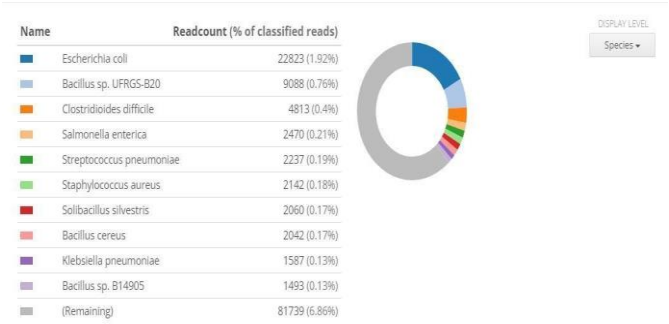


Figure 9 % classified reads of Genera from sequence



Name	Readcount (% of classified reads)
Escherichia coli	22823 (1.92%)
Bacillus sp. UFRGS-B20	9088 (0.76%)
Clostridioides difficile	4813 (0.4%)
Salmonella enterica	2470 (0.21%)
Streptococcus pneumoniae	2237 (0.19%)
Staphylococcus aureus	2142 (0.18%)
Solibacillus silvestris	2060 (0.17%)
Bacillus cereus	2042 (0.17%)
Klebsiella pneumoniae	1587 (0.13%)
Bacillus sp. B14905	1493 (0.13%)
(Remaining)	81739 (6.86%)

Figure 10 % classified reads of Species from sequence

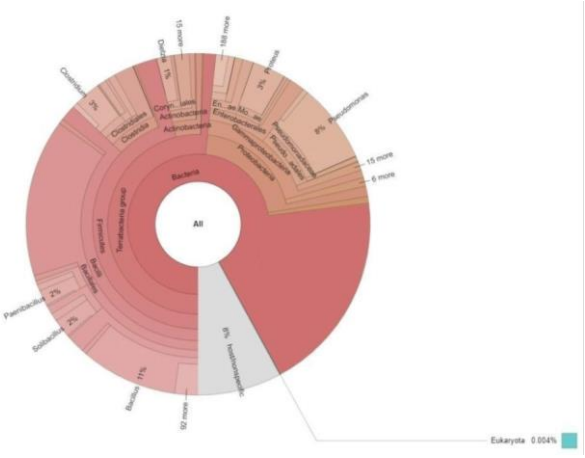


Figure 11Top Kingdom Diversity Classification in Sample

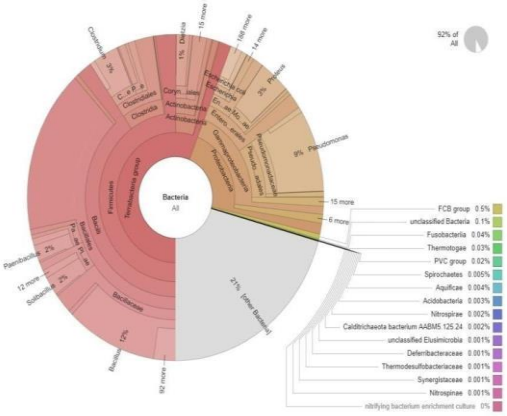


Figure 12 Top Phylum Diversity Classification in Sample

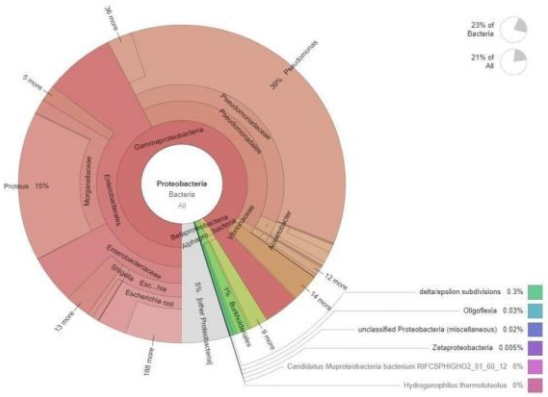


Figure 13 Proteobacteria class Diversity Classification in Sample

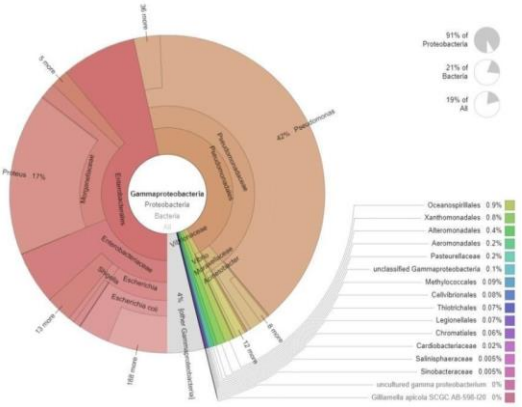


Figure 14 Gammaproteobacteria class diversity classification of sample

4. Conclusion and Future Scope

EThe gut microbiome was accepted to play a crucial role in the health of the host. This study of metagenomics evaluation scat of a Crocodile (Crocodylus palustris) revealed that the microbiota of the gut of a Crocodile (Crocodylus palustris) was dominated by phylum Firmicutes, followed by Proteobacteria, Actinobacteria, and Bacteroidetes mainly. Which, Firmicutes phylum consists of Bacilli, Gammaproteobacteria, and Clostridia across a high load of fecal coliforms in their aquatic environment. Nonetheless, despite constantly being exposed to many potential pathogens, crocodilians do not seem to be susceptible to infection by these organisms, either systemically or through their skin, via lesions or wounds suggesting that these species possess potent antimicrobial abilities in their immune system or gut microbiome.

Data Availability
None

Conflict of Interest
None

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Authors' Contributions

Author-1 conducted a literature review and conceptualized the study. Author-2 contributed to protocol development, obtained ethical approval, and conducted data analysis. Author-3 drafted the initial manuscript. All authors critically reviewed, edited, and approved the final version of the manuscript.

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