

**THE UNIVERSITY OF HONG KONG  
SCHOOL OF BIOLOGICAL SCIENCES**

*Postgraduate Student Public Seminar*

**“Microbiome Characteristics and Nitrogen Transformation Reactions on  
Angkor Sandstone Monuments”**

**Mr. Xinghua DING**

*PhD Student, School of Biological Sciences, HKU*  
(Supervisors: Dr. Aixin Yan & Prof. Ji-Dong Gu)

**on Thursday 27 January, 2022 at 9:30 am  
Room 6N-11, Kadoorie Biological Sciences Building**

**Abstract**

Stone cultural heritages are threatened by deterioration caused by natural and anthropogenic processes, among which microorganisms are involved. Metagenomic analysis of the Angkor sandstone monuments was carried out by applying whole-genome shotgun sequencing (WGS) techniques. Detailed taxonomic and biochemical descriptions of the stone-dwelling microbiome were retrieved from this metagenomic dataset. At the same time, the accumulation of nitrate has been widely observed on the Angkor monuments. The ammonia oxidizing bacteria (AOB), archaea (AOA), and complete ammonia oxidizing bacteria (Comammox) were further examined from Angkor monuments by DNA-based metagenomics and RNA-based functional gene reverse-transcriptional (RT)-qPCR quantification. The metagenomic results showed the AOA and Comammox bacteria were abundant ammonia oxidizers together with the dissimilatory nitrate reduction to ammonium (DNRA) which could drive internal recycling between ammonia and nitrate to support the stone microbiome. The activity of this internal cycle is confirmed by the significantly high enrichment of stable isotope  $^{15}\text{N}$  of nitrate in the microbial biofilms on the Angkor monuments. And the transcript analysis of *amoA* gene by RNA-based RT-qPCR revealed that AOA were much more active than AOB in the microbiome on these Angkor monuments.

Bioinformatics meta-analysis was further conducted on metagenomes of stone monuments in different climatic regions to obtain the distribution characteristics of key community members in stone-dwelling microbiome on stone deterioration processes under different climatic conditions of the world. The results of this large data analysis are in good agreement with those obtained in Cambodia and further expanded insights were also enlightened for other climate types. Higher microbial diversity is found in dry than humid regions, but the high abundance of AOA was detected in humid regions.

Angkor sandstone monuments attract millions of visitors worldwide and are an important contributor to the local economy. The growth of tourism poses public health-related risks, because these popular sites become vectors for transmitting microorganisms from humans, animals, and the ecosystem to amplify pathogenicity and resistome diffusivity. The microbiome and resistome profiling of selected geo-ecologically variable Angkor monuments revealed that pathogens and resistome of the microbiome are impacted by anthropogenic factors. A group of antibiotic-resistant genes (ARGs) with high dispersal ability was found on these monuments, suggesting a latent health-related risk of pathogens and antibiotic resistance genes transmission on the Angkor monuments with a high density of tourism activity.

In summary, this study provides new information of stone-dwelling microbiome on historically important stone monuments, identified biochemical reactions driving by the specific microbes involved in biodeterioration, and dispersal of pathogenicity within the microbiome onto these stone cultural heritages by tourism for sustainable management.

--- ALL ARE WELCOME ---