Seventh Annual Research Meeting of the Noguchi Memorial Institute for Medical Research: Bacterial Infections and Antimicrobial Resistance

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SUMMARY

Antimicrobial resistance (AMR) is rapidly advancing, surpassing the development of new control measures and posing significant threats to patient care, public health, agriculture, economic growth, and global security, particularly in Sub-Saharan Africa. Bacterial infections, responsible for about 7.7 million deaths annually, are often caused by AMR bacteria. The WHO has identified several bacteria, including *Staphylococcus aureus, Streptococcus pneumoniae, Escherichia coli, Klebsiella pneumoniae*, and *Mycobacterium tuberculosis*, as priority pathogens for global surveillance due to their resistance to common antimicrobials.

At the 2022 Annual Research Meeting (ARM) of the Noguchi Memorial Institute for Medical Research, University of Ghana, the prevalence of AMR among humans, animals, and the environment in Ghana was highlighted. Studies revealed the widespread presence of the blaCTX-M gene in *K. pneumoniae* and *E. coli* from surgical site infections in Accra, posing significant public health threats. Additionally, global clones of Carbapenemase-producing *E. coli* with resistance to fluoroquinolones and other antibiotics were reported.

Research also noted the lack of data on AMR bacteria in water for human use, finding high levels of coliforms and AMR bacteria in drinking water and lettuce irrigated with contaminated water. Whole genome sequencing of bacterial pathogens from febrile patients revealed multi-drug resistant *Salmonella spp*. Continuous AMR surveillance and advanced genomic tools are recommended to generate detailed data for better treatment decisions and surveillance strategies.

Keywords: Bacterial infections, antimicrobial resistance, Extended Spectrum Beta-Lactamase, Ghana
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INTRODUCTION

Antimicrobial resistance (AMR) is occurring alarmingly, outrunning the rate at which new control measures are being developed. This situation threatens patient care, public health, agriculture, economic growth, and global security. A greater proportion of this global health menace is found in Sub-saharan Africa.[1] Bacterial infections are a leading cause of death (about 7.7 million deaths; an eighth of all global deaths) and are often caused by AMR bacteria species. Owing to the significant resistance burdens associated with these infections, the WHO has listed several bacteria species as priority pathogens for global surveillance, for example, *Staphylococcus aureus, Streptococcus pneumoniae, Escherichia coli, Klebsiella pneumoniae* and *Mycobacterium tuberculosis.*[2,3]

These organisms frequently carry a wide range of resistance genes, making them less susceptible to commonly used antimicrobial agents.[4]
Research findings presented at the 2022 Annual Research Meeting (ARM) of the Noguchi Memorial Institute for Medical Research, University of Ghana, provided information on the high prevalence of AMR bacteria among humans, animals, and the environment in Ghana. General recommendations were for continuous surveillance of AMR bacteria species in humans, animals, food, water, and the environment.

Ms Felicia Amoa Owusu and colleagues reported on the distribution of the blaCTX-M gene, which encodes Extended Spectrum Beta-Lactamase (ESBL) in *K. pneumoniae* and *E. coli* isolated from surgical site infections in Accra, Ghana. The study emphasised the common occurrence of the *blaCTX-M* gene among the isolates investigated. The presence of *blaCTX-M* represents significant public health threats since isolates harbouring this gene often carry extra resistance genes, making them non-susceptible to several antimicrobials.[5,6] Along the same lines, Dr Anthony Ablordey and colleagues reported on the molecular epidemiology of Carbapenemase-producing *E. coli* ST410 and ST131 in Ghana. They highlighted the finding of global clones and the occurrence of resistance determinants for fluoroquinolone, 3rd-generation cephalosporin (CTX-M-15 blaCTX-M-14 and blaCTX-M-27), and oxacillinase-181 carbapenemase-producing diarrheagenic Escherichia coli in Ghana.

Mr. Daniel Kwaku Baka and colleagues highlighted the paucity of data on antimicrobial susceptibilities of AMR bacteria from water for human use. The presentation focused on the quality of food and water for human consumption. Assessment of microbial quality of drinking water samples showed unacceptable levels of coliforms and the presence of AMR bacteria. A recommendation was made for enhanced monitoring of bacteria pathogens from drinking water sources. Quarcoo and colleagues also presented ESBL-producing *E. coli* in lettuce irrigated with water from different sources in Ghana. The findings highlighted the need to assess the microbial quality of irrigation water for vegetable production as it tends to contain faecal contaminations. Public education on safer farming practices and preparing vegetables before consumption were highlighted.

Whole genome sequencing of bacterial pathogens recovered from febrile patients showed the occurrence of multi-drug resistant strains of *Salmonella spp* circulating in our settings, which was previously unnoticed. Ms. Clara Yeboah and colleagues presented this. Further, insights into genomic surveillance of commonly isolated bacteria species in Ghana were shared by Dr Beverly Egyir and the team. Resistance to last-line antimicrobials and global epidemic clones were detected among *E. coli*, *K. pneumoniae*, *P. aeruginosa*, and *S. aureus* recovered from clinical sources. The findings underpin the need for continuous AMR surveillance and the utilisation of robust tools like whole genome sequencing to generate granular data to inform treatment decisions and surveillance strategies in the country.

CONCLUSION

In conclusion, AMR presents a rapidly advancing threat, surpassing the pace of developing new control measures. This escalating issue significantly impacts patient care, public health, agriculture, economic growth, and global security, particularly in Sub-Saharan Africa. The seventh ARM of the NMIMR highlighted the high prevalence of AMR bacteria in Ghana among humans, animals, and the environment. The presentations advocate for sustained and rigorous AMR monitoring, utilising robust methodologies like whole genome sequencing to generate detailed data for managing and mitigating AMR's impact in Ghana and beyond. Collaborative efforts and support from various stakeholders and funding bodies remain critical in effectively addressing this global health challenge.

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