



# Tackling antimicrobial resistance through optimisation of high-throughput technologies: A focus on developing countries

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Antimicrobial resistance (AMR) is a public health menace occurring in both the hospital setting and general environments of every country around the world. Even more worrisome, AMR has the ability to launch a post-antibiotic era. That is, no antibiotics will be efficacious enough to handle infectious diseases of microbial origin if nothing is done to mitigate it early on.

AMR occurs when bacteria change over time and no longer respond to antibiotics; thus, infections become untreatable, leading to severe illness, long hospitalisations, death and economic loss.<sup>1,2</sup>

According to a recent report by Hooban et al., by 2050, 10 million deaths per year will be caused by AMR.<sup>3</sup>

Antibiotics are used in both human and animal medicine, and in most cases, they are used at sub-inhibitory levels that are not lethal enough to kill the infecting bacteria. This can happen, for example, when patients do not finish their course of treatment.

Consequently, the surviving bacteria strains go on to develop resistance mechanisms against the exposed antimicrobial agents. AMR bacteria and genes evolve continuously as a natural mechanism to ward off the antimicrobial onslaughts of antimicrobial agents. The irrational use in both hospital milieus and the general environment makes it easy for AMR bacteria and genes to evolve and spread between humans and animals and the environment.

More worrisome is the fact that the rate at which bacteria evolves resistance to available antibiotics is faster than the development of novel antimicrobial agents in countering this global crisis of AMR.

Self-medication is one major factor driving the spread of AMR in most parts of the world, especially in places where there is less-controlled use of antibiotics in human or animal health.

In Nigeria, for example, a majority of people who are being treated for malaria (caused by Plasmodium – a protozoan) will most often be given antibacterial agents targeting the pathogen that causes typhoid fever (Salmonella) in addition to the anti-malarial drug.

Such phenomenon will result in the evolution of AMR that allows bacteria to become resistant following undue exposure of the pathogen to antibiotics.

In sub-Saharan Africa alone, AMR causes 27.3 deaths per 100,000 people, making it a super-region for



death due to AMR pathogens.<sup>2</sup> Low- and middle-income countries (LMICs), particularly those in the sub-Saharan West African region, are predominantly vulnerable to the fallouts of the AMR menace.

In most LMICs, healthcare facilities are in a deplorable state, and infection disease control practices are not as strong as in most developed countries. To further exacerbate the AMR crises in LMICs, environmental sanitation and water supply systems are still in a pitiable state, and the use of antibiotics, particularly in poultry, livestock and other agricultural practices, is not controlled.

The availability of pharmacies that dispense antibiotics to anyone willing to buy, even without a doctor's prescription backed with a good laboratory result of pathogen isolation and susceptibility test result, is another fundamental factor fueling the AMR crisis in LMICs.

A further major challenge to tackling AMR is understanding resistance burden and how AMR genes are mobilized.<sup>4,5</sup> Mobile genetic elements such as plasmids that are present in pathogenic bacteria help to facilitate the transmission of AMR genes between organisms in a particular environment.

To be able to make informed, location-specific healthcare policy decision that are sustainable to tackle the menace of AMR, particularly in LMICs, it is important for all stakeholders in the healthcare sector to understand the disease burden of AMR in a "One Health" context. This is crucial if we are to win the war against AMR. After all, the health of humans, animals and the environment are interconnected.

To achieve this, we must build and develop sustainable, novel diagnostic interventions that could be easily implemented in LMICs to monitor/track and possibly mitigate the evolution and community spread of AMR.

To better understand the molecular mechanisms underpinning AMR in priority resistance patho-

gens (e.g., *Klebsiella*, *Pseudomonas*, *Acinetobacter*, *Escherichia coli* & *Staphylococcus*, etc.), novel and advanced high-throughput molecular biology techniques such as functional metagenomics approaches and whole genome sequencing must be developed and optimised to enable prompt detection and reporting of AMR from clinical and environmental samples by clinical microbiologists in LMICs. This is particularly the case in Africa, with the overarching goal being the reduction of the disease burden of AMR, as well as ensuring the optimisation of the use of antibiotics in human and animal health in LMICs and across the globe.

Most AMR genes and strains may be circulating in an unknown environment. The available culture and sensitivity techniques currently being used in most regions in LMICs needs an upgrade to include sustainable genomics techniques that could be optimized to meet the needs of various regions in terms of tracking and mitigating AMR early on.

High-throughput technologies such as functional metagenomics and whole genome sequencing are innovative but expensive. Despite their costs, these approaches both have the capacity to transform the face of healthcare research in the LMICs, particularly in the early detection and reporting of AMR occurring in the environment before they transform into a clinical problem.

### Conclusions

With the optimisation and implementation of innovative high-throughput technologies to track and monitor AMR in LMICs, new insights into the trends of AMR in the various regions can be uncovered. Even more so, these innovative high-throughput technologies have the potential to help reveal hotspots of drivers of AMR in diverse milieus, as well as help scientists and healthcare professionals understand the abundance and diversity of AMR genes and

strains circulating in their regions.

This is particularly useful for tackling AMR in LMICs – where the disease burden of AMR is high and little to nothing is done to holistically address and possibly end the menace in the region.

The availability and widespread distribution and implementation of high-throughput technologies for the on-spot tracking and monitoring of AMR in LMICs will help to drastically reduce the disease burden of AMR and improve lives in the region.

Some of the notable direct benefits of these innovative technologies include improved health outcomes and saved lives, as well as strengthened AMR knowledge in LMICs.

Such technologies also help inform scientists about trends in AMR in the region, assist policymakers to implement programs to mitigate AMR, and extend the current overall knowledge base of AMR.

Moreover, training laboratory personnel and microbiologists across the African continent to use these high-throughput technologies will improve current AMR protocols in hospitals and communities, and hopefully save lives in the process.

### References

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