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Convergence of surveillance blind spots with antimicrobial resistance hotspots

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Antimicrobial resistant pathogens that are detected and reported cause an estimated 700,000 deaths per year.¹ The global distribution of antimicrobial resistance (AMR) means that future generations can expect to stay in hospital longer, have increased treatment complications and be at greater risk of dying following surgical procedure.^{2,3} The economy will also suffer from escalating healthcare costs and loss of productivity due to excess morbidity and premature mortality.^{1,4} An appropriate response relies on accurate data; however, it is becoming increasingly clear that the true burden of infection is significantly greater than what is reported through clinical surveillance data. Indeed, resource-constrained and geographically isolated regions have limited infrastructure, resources and are often outside of surveillance reach. This surveillance blind spot limits health services' ability to provide early warning signs and response at regional, national and international level. The consequences of delayed disease response are now, more than ever, recognised in the context of the current pandemic.

Globally, Australia is considered a low-AMR region with a reported national average of 10% resistance for eight priority bacteria.¹ However, this omits the striking geographical variation of AMR across the country, with as much as 56% of *Staphylococcus aureus* clinical isolates resistant to methicillin and an emergence of inducible-clindamycin co-resistance in northern Australia.⁵ Accurate geographical and temporal changes of AMR are invaluable for guiding empiric treatment, particularly in light of high community MRSA in regional Australia.^{5,6} Persistent clusters of AMR hotspots are converging with surveillance blind spots in regional Australia and to effectively contain this threat, we need innovative, region-specific solutions.

To address this surveillance blind spot, a geospatial surveillance tool called *HOTspots* was developed specifically targeting northern Australia.⁵ *HOTspots* is an analytical platform that uses spatial epidemiology to deliver synthesised data to clinicians on evolving antimicrobial susceptibility by region. Health providers with access to rapid molecular tests that identify the infecting organism and resistance determinants within hours of patient presentation can make an informed decision about antibiotic selection. However, in the absence of such tools, the health provider must rely on population-level susceptibility data, their expertise and available treatment guidelines. The *HOTspots* tool provides at point of care, AMR data by region that are accurate for local needs and up-to-date. Health providers can choose the region of interest (i.e. where patient may be residing), and visualise maps and graphs of the combinations of pathogens with AMR important for empiric treatment. *HOTspots* is currently being deployed in clinical settings as an interactive and secure surveillance system that provides ongoing automated synthesis of AMR across community clinics and hospitals in northern Australia.

HOTspots is a longitudinal surveillance platform that has the capacity to perform a vital role in public health, informing the allocation of resources and facilitating the evaluation of region-specific and population-level infection prevention strategies. In addition to detection of AMR hotspots, the platform permits an epidemiological surveillance function by capturing vital statistics (age, sex) and measures of economic impact, which are currently being developed.

A current limitation of *HOTspots* is that it is a passive system reporting data on phenotypic AMR isolated from clinical infections. It does not capture patients who do not seek

healthcare or are not diagnosed, which is important in regional and rural settings. It is currently only available for northern Australia and plans for expanding beyond this region are being developed.

The strength of *HOTspots* is the large geographical coverage of previously unsurveyed regions. It directly assesses the population-at-risk and empowers decision makers to lead and manage AMR more effectively by providing timely and region-specific evidence. Additionally, the geospatial visualisation of AMR data from both primary and tertiary healthcare sectors, and from various sites of infection (i.e. blood, urine, skin) held in an easily accessible tool will innovate communication and information for action.

Future growth of *HOTspots* and other AMR surveillance platforms should focus not only on individual user needs and representations of graphs, but on the context of available data. Centralised access to reliable and timely antibiotic utilisation data,⁷ disease-specific estimates of morbidity and mortality^{3,4} are the minimum information needs required to take strategic action on AMR. While culture-based systems examine the ability of bacteria to grow in the presence of each antibiotic at varying concentrations, microbiology labs are increasingly able to generate molecular data that identify genetic mutations that bacteria have developed or acquired to counteract the effects of the particular antibiotic. Complementing culture-based surveillance with molecular data can overcome some of the challenges faced in remote parts of Australia where transport distances and climate pose limits on the viability of samples for culture. Genetic variation by geography and cluster detection, as it relates to *Neisseria gonorrhoeae*⁸ or others and monitoring commensal bacterial flora of healthy populations⁹ should continue to be developed. Finally, valuation of the economic cost of AMR is important for decision making and should be estimated accurately.¹⁰ If AMR action is to be sustained it needs to be properly resourced, it has to be part of the national agenda. That means AMR surveillance and activities must be embedded in government planning and budget at all levels.

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References

1. Organisation of Economic Co-operation and Development. *OECD Health Policy Studies: Stemming the Superbug Tide: Just A Few Dollars More*. Paris (FRA): OECD Publishing; 2018.
2. Cassini A, Hogberg LD, Plachouras D, et al. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and the European Economic Area in 2015: A population-level modelling analysis. *Lancet Infect Dis*. 2019;19(1):56-66.
3. Lee XJ, Stewardson AJ, Worth LJ, Graves N, Wozniak TM. Attributable length of stay, mortality risk and costs of bacterial healthcare-associated infections in Australia: A retrospective case-cohort study. *Clin Infect Dis*. 2021;72(10):e506-e514.
4. Wozniak TM, Bailey EJ, Graves N. Health and economic burden of antimicrobial-resistant infections in Australian hospitals: A population-based model. *Infect Control Hosp Epidemiol*. 2019;40(3):320-7.
5. Wozniak TM, Cuningham W, Buchanan S, et al. Geospatial epidemiology of *Staphylococcus aureus* in a tropical setting: An enabling digital surveillance platform. *Sci Rep*. 2020;10(1):13169.
6. Tong SY, Varrone L, Chatfield MD, Beaman M, Giffard PM. Progressive increase in community-associated methicillin-resistant *Staphylococcus aureus* in indigenous populations in northern Australia from 1993 to 2012. *Epidemiol Infect*. 2015;143(7):1519-23.
7. Bishop JL, Schulz TR, Kong DCM, James R, Buising KL. Similarities and differences in antimicrobial prescribing between major city hospitals and regional and remote hospitals in Australia. *Int J Antimicrob Agents*. 2019;53(2):171-6.
8. Whiley DM, Trembizki E, Buckley C, et al. Molecular antimicrobial resistance surveillance for *Neisseria gonorrhoeae*, Northern Territory, Australia. *Emerg Infect Dis*. 2017;23(9):1478-85.
9. Hendriksen RS, Munk P, Njage P, et al. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. *Nat Commun*. 2019;10(1):1124.
10. Wozniak TM, Barnsbee L, Lee XJ, Pacella RE. Using the best available data to estimate the cost of antimicrobial resistance: A systematic review. *Antimicrob Resist Infect Control*. 2019;8:26.

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