

The role of microbial genomics in delivering the UK's national action plan for confronting antimicrobial resistance 2024–29



Tess Johnson*, Lewis C E Mason*, Hayley J Wilson, James R Price, Katie L Hopkins, Marie Anne Chattaway, Alistair Leanord, Olga Francino Marti, Rivie Mayele-Tamina, Stephanie Johnson, Paul Flowers, Willem van Schaik, Kate S Baker



Antimicrobial resistance (AMR) is a major threat to human and animal health, in addition to environmental resilience. Countries set the agenda on their national action against AMR in the form of National Action Plans (NAPs), with the UK's latest NAP released in May, 2024. Advances in genomics have strengthened our ability to work towards NAP priorities; however, to date, no mapping of the role genomics plays in contributing to specific goals within the NAP has been undertaken. The UK Research and Innovation-funded Transdisciplinary Antimicrobial Resistance Genomics Network brought together a range of stakeholders to discuss the role of genomics for action on AMR and to deliver policy priority-led research, as outlined in the UK NAP 2024–29. We report our discussions in this Personal View, with key roles for genomics, including informing targeted stewardship in health-care settings, supporting AMR literacy, and supporting effective antimicrobial innovation. However, changes in infrastructure, communication, and cross-sector coordination are needed to support implementation.

Introduction

Antimicrobial resistance (AMR) is one of the major threats to human and animal health, in addition to environmental resilience, in the coming decades. Bacterial AMR alone was associated with nearly 5 million deaths in 2019.¹ To address the threat of AMR, the WHO Global Action Plan (GAP) on AMR calls for all countries to develop strategies in the form of their own National Action Plan (NAP),² which almost 90% of countries have now developed.³ NAPs vary greatly in their stringency and in the effectiveness of their implementation globally, but they can include policies regarding improving AMR awareness; strengthening the evidence base through surveillance; supporting water, sanitation, and hygiene measures; optimising antimicrobial use; and supporting antimicrobial innovation.

The first UK NAP for AMR spanned 2019–24,⁴ with the UK 5-year AMR strategy preceding this plan in 2013.⁵ Successful outcomes of the first UK NAP included a reduction in antimicrobial use in animal husbandry, improvements in surveillance systems, and a pilot payment scheme for antimicrobials used by the National Health Service.⁶ The second UK NAP on AMR, *Confronting antimicrobial resistance 2024–29*,⁶ sets the agenda for confronting AMR in the UK from 2024 to 2029 with nine strategic outcomes organised across four themes (table 1).

Technological developments since the release of the GAP in 2015, including advances in genomics, have strengthened the UK's ability to work towards these themes. Genomics has transformed our knowledge and understanding of AMR emergence and the transmission of resistant pathogens. In the last 15 years, there has been an expansion in genomics expertise, political support, and technological capacity across the UK, in both research and clinical and public health contexts.^{7–9} Use of genomics to generate phylogenetic trees, to establish pathogen relatedness, identify AMR determinants (genes and mutations) among samples, and infer transmission networks allows us to

target interventions (eg, hospital deep cleans, incident management team convening, and health protection educational campaigns) effectively.

Furthermore, metagenomics allows for pathogen-agnostic sequencing, which could be used for tailoring antimicrobial innovations to promising drug targets. Finally, plasmid sequencing allows for tracking of resistance among species and in local settings for improved infection control measures, potentially bringing health and economic benefits. With genomics knowledge, we can implement these interventions and better deliver on the themes of the UK NAP 2024–29. Indeed, within the NAP, the UK academic community was noted as conducting world leading research on surveillance and genomics, and genomics was noted as an enabling technology. However, an explicit mapping of the role of genomics in delivering the UK NAP outcomes and against the ten identified research priorities has not taken place, and genomics knowledge is not currently gathered and organised to allow for delivery on the interventions described therein.

In this Personal View, we map genomics to the UK NAP to help the research and clinical communities align their use of genomics with policy-led priorities. Informing this work, we held discussions at a stakeholder workshop of the UK Research and Innovation-funded Transdisciplinary Antimicrobial Resistance Genomics Network (TARGetAMR). TARGetAMR was initiated in 2024 with the goal of reducing the burden of AMR through genomics and runs monthly seminars, offers project seed-funding, engages with policy and public stakeholders, and hosts larger-scale events, often in collaboration with other UK transdisciplinary AMR networks. In a 3-h online workshop held in June, 2025, potential genomic contributions across the four themes were discussed, alongside the ten research priorities identified within Outcome 7 of Theme 3 in the NAP (table 1). The stakeholders in attendance represented various expertise and sectors: patient and public

Lancet Microbe 2026

Published Online
<https://doi.org/10.1016/j.lanmic.2026.101372>

*Contributed equally

Ethox Centre, Nuffield Department of Population Health, University of Oxford, Oxford, UK (T Johnson PhD, S Johnson MBChB PhD); National Institute for Health Research (NIHR) Health Protection Research Unit (HPRU) in Gastrointestinal Infections, University of Liverpool, Liverpool, UK (L C E Mason BBS PhD), Department of Genetics, University of Cambridge, Cambridge, UK (L C E Mason, Prof K S Baker); Warwick Medical School, University of Warwick, Coventry, UK (L C E Mason); Foundation for Genomics and Population Health, Wort's Causeway, Cambridge, UK (H J Wilson PhD); Department of Global Health and Infection (J R Price MBBS PhD) and Centre of Infection and Antimicrobial Research (J R Price), Brighton and Sussex Medical School, Brighton, UK; Antimicrobial Resistance and Healthcare Associated Infections Reference Unit (K L Hopkins PhD) and Antimicrobial Resistance & Healthcare-Associated Infections Division (K L Hopkins), UK Health Security Agency (UKHSA), London, UK; West Midlands Health Tech Innovation Accelerator (K L Hopkins), NIHR HPRU in Public Health Genomics (M A Chattaway PhD, Prof W van Schaik PhD), and Department of Microbes, Infection and Microbiomes, School of Infection, Inflammation and Immunology (R Mayele-Tamina MBA, Prof W van Schaik), University of Birmingham, Birmingham, UK; Gastrointestinal Bacteria Reference Unit, UKHSA, London, UK (M Anne Chattaway); School of Infection and Immunity,

College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, UK (Prof A Leanord PhD); Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Spain (Prof O Francino Marti PhD); Department of Psychological Sciences and Health, University of Strathclyde, Glasgow, UK (Prof P Flowers PhD)
Correspondence to: Prof Kate S Baker, Department of Genetics, University of Cambridge, Cambridge CB2 3EH, UK kb827@cam.ac.uk

Outcomes	
1. Reducing the need for, and unintentional exposure to, antimicrobials	1. Infection prevention and control management 2. Public engagement and education 3. Strengthened surveillance
2. Optimising the use of antimicrobials	4. Antimicrobial stewardship and disposal 5. Antimicrobial resistance workforce
3. Investing in innovation, supply, and access	6. Innovation and influence 7. Using information for action 8. Health disparities and health inequalities
4. Being a good global partner	9. Antimicrobial resistance diplomacy

Table 1: The four themes and nine outcomes stipulated within the UK National Action Plan, Confronting antimicrobial resistance 2024–29

involvement and engagement workers, policy makers, multidisciplinary researchers, clinical scientists, practitioners, bioethicists, and others (appendix p 1). We outline the outcomes of the discussion, and the further work envisaged in key areas, to ensure that the potential of genomics is harnessed to deliver the goals of the NAP.

Mapping genomics to NAP deliverables

The first portion of the discussion focuses on the role of genomics in contributing to the delivery of the nine outcomes (arranged across the four themes) of the NAP.

Theme 1: reducing the need for, and unintentional exposure to, antimicrobials

The first outcome in the first theme of the UK NAP is infection prevention and control (IPC) management in hospital settings. Genomics can contribute to achieving this outcome in several ways. Since 2010, the UK's capacity to use genomics for hospital-based surveillance has increased, leading to, for instance, better tracking of transmission and possibilities for intervention in transmission pathways, and more potential for targeted implementation of IPC in hospitals with high transmission of multidrug-resistant pathogens or those where there is substantial circulation of resistance determinants. Genomics can also contribute to breaking down barriers between hospital and non-hospital health-care settings, by tracking transmission across community and hospital reservoirs. Yet, to effectively use genomics to inform IPC, further development is needed in several areas (panel 1).

The second outcome for the first theme of the UK NAP relates to public engagement and education. Public understanding of genomics, its potential uses, benefits, and risks, is poor. Clinical, policy, and public trust and support in the use of genomics is paramount to its success. However, to achieve this aim, further development is needed in relation to several aspects (panel 2).

The third, and final, outcome in the first theme is strengthened surveillance, and although genomics is key to this outcome, there was minimal discussion on this topic, as we felt that the evidence for genomics was very strong for this topic and research gaps had been previously identified elsewhere.¹²

Theme 2: optimising the use of antimicrobials

In the second theme of the UK NAP, the first outcome relates to antimicrobial stewardship and disposal, including better clinical decision making and diagnostic support. Genomics has expanded the range of tools available to support clinical decision making, offering an insight into genotypes and presence of AMR genes or mutations that could inform tailored patient treatment and decisions about antimicrobial prescription. However, the use of genomics in this area is also constrained in several ways (panel 3).

The second outcome of the theme was AMR workforce. An agreement was reached that increasing genomics literacy and capability among the AMR workforce would help to capitalise on the benefits offered, although more research is needed to understand people's beliefs about, and trust in genomics, and how they think genomics could help with their work.

Theme 3: investing in innovation, supply, and access

The leading outcome of innovation and influence in Theme 3 responds to the demand for new tools, technologies, and interventions for tackling AMR. Genomics can contribute greatly in a high-income setting such as the UK, with knowledge that is essential for several areas of innovation, including identification of drug and diagnostic targets, and vaccine design. For example, historical genomic surveillance datasets can be used to evaluate the potential utility of new products (eg, new antimicrobials or vaccine targets) even years after sequence data has been collected, as was done for *Neisseria gonorrhoeae* during 2024–25.¹⁴ Assuming future effective implementation of national routine surveillance, genomics can also provide information on global distributions of AMR burden, to target efforts to improve access and supply of antimicrobials wherever needed, based on regional susceptibility data. The ease of reuse of genomic data among experts offers an advantage over traditional culture methods, which cannot be readily shared and reanalysed for a multitude of different ends at a later point (and therefore, is restricted in its contribution to future innovation). However, to deliver on the promises of genomics to support this theme, we propose that some research efforts are prioritised (panel 4).

A second outcome is using information for action and relates largely to evidence generation and use. This outcome includes the creation of UK-wide AMR research networks, of which TARGeAMR is one, but also outlines ten priority research questions, which are further discussed in a separate section later. Notably, however, this step highlights the urgent need for researchers to work backwards from stakeholder engagement and policy-led

For more on TARGeAMR, see <https://www.targetamr.org.uk/>
See Online for appendix

Panel 1: Areas in need of further development for effective use of genomics to inform infection prevention and control

1. Researchers need to have an awareness of the genomics literacy of infection prevention and control professionals, collaborating with them and communicating bidirectionally to promote uptake of pathogen-sequencing systems. This step includes cogeneration of data and reports that are actionable and can inform interventions for outbreaks of resistant infections, locally, nationally, and globally.
2. There exists an opportunity to more broadly disseminate, within the UK, examples of best practices from other countries such as the AusTrakka system in Australia,¹⁰ highlighting examples wherein genomics knowledge has informed diagnostics, interventions, and policy changes to address the spread of antimicrobial resistance.
3. Monitoring mechanisms need to be implemented to quantify the added value, in terms of patient benefits, health-care costs, and reduction of unnecessary use of antimicrobials, genomics-informed diagnostics, and infection prevention and control interventions.
4. Implementation barriers need to be addressed, including the cost, timeliness, and data linkage of genomics in hospital settings, to ensure that surveillance and incident investigation can be conducted effectively.

Panel 2: Areas in public engagement and education that need development for use of genomics

1. Direct engagement with health workers is necessary to ensure that the training and education of new workers is being updated to improve knowledge on the potential uses of genomics to support the identification of appropriate uses and misuses of antimicrobials in clinical settings (without the need for heavy involvement of bioinformaticians). A gap analysis should be conducted to understand national variations in education and training, and the development of workforce competencies. This analysis would additionally support adherence to the national Good Practice Guidelines on the recording of antimicrobial resistance on the Medical Certificate of Cause of Death.¹¹
2. The public, too, needs to be consulted as their genomics literacy increases, to understand what antimicrobial resistance genomics means to them, its acceptability, and other considerations, and identify what results are appropriately communicated.
3. Communication between researchers and policy makers is often underdeveloped, as are the regulatory and ethical frameworks that surround this interaction. A shared language, legal clarity, and sense of purpose is needed to support better policy engagement.

questions such as those outlined in the NAP, which was the main motivator to gather a group of stakeholders for this Personal View. We want to highlight the essential need for researchers to collaborate with stakeholders in academia and outside academia at an early stage of research, to facilitate translation from research to practice.

The third outcome for Theme 3 relates to health disparities and health inequalities. We feel that the ability of genomics “to make something previously invisible, visible” was pertinent here as genomics has indeed been successful in detecting and investigating transmission in minoritised communities,^{15,16} and in uncovering the links between drug-resistant infections in humans and non-human reservoirs of AMR. The potential for genomics to better address health inequalities is also investigated further in priority research question 2 of Outcome 7, Theme 3 (table 2).

Theme 4: being a good global partner

The final theme of the UK NAP relates to global AMR and the role of the UK in addressing the shared problem under the sole outcome of AMR diplomacy. Global genomic surveillance has the potential to strengthen public health responses to the emergence of resistance and prevent spread elsewhere, and to support efforts to improve diagnostics and access to treatments for better clinical care.

There are a range of examples of the effective use of globally sourced genomic data to understand the global spread of AMR across the One Health Triad¹⁷ and to support the prevention of food-borne disease.¹⁸ Yet, such effective use relies on some aspects, which are discussed in panel 5.

Mapping to the research priorities of Outcome 7 in Theme 3

Outcome 7 (using information for action) of Theme 3 in the UK NAP also outlines a series of ten high-priority research questions (table 2). The TARGeTAMR stakeholder group also considered how genomics could contribute to addressing each of these research questions to identify where, and how, UK genomics researchers can serve the delivery of the UK NAP.

Research question 1: what is the cost of AMR?

There is a need for more work to be undertaken to evaluate the economic value and cost-effectiveness of genomics for surveillance and diagnostics of AMR across health systems, particularly in comparison to other methodologies. Genomics can help to quantify AMR by mapping resistance determinants across organisms and support efforts to quantify the cost of AMR. However, it is important not to ignore the less well-examined costs of AMR or genomic surveillance itself. For instance, AMR determinants in the

Panel 3: Challenges faced in the use of genomics in antimicrobial stewardship and disposal

1. Although genomics offers the potential for rapid identification and prediction of antimicrobial susceptibility phenotypes, we are still reliant on culture-based diagnostics for accurate diagnosis of infections. This reliance reduces the potential benefit offered by genomics, at least until further validation work is completed—eg, to refine relationships between genotype and phenotype sufficiently to allow genomics to be used as a stand-alone diagnostic tool, as currently used for the diagnostics of *Mycobacterium tuberculosis*,¹³ HIV, and hepatitis C.
2. Wherever assays have been primarily developed commercially with little consultation with public health bodies, their utility in public health is often suboptimal. There is a need for improved partnership between innovators, researchers, and clinical and public health delivery to ensure that novel antimicrobial resistance determinants are continuously considered in commercially developed assays.
3. The potential benefit of reduced turn-around times from genomic diagnostics is also low while phenotypic testing is still necessary, and interpretation of genomic data requires specialised expertise, perhaps necessitating delegation of this task to a unique role within a clinical diagnostic laboratory. Substantial infrastructural and logistical changes would be needed to create change in this area. Routine sequencing runs and genomic data analyses can be undertaken in research settings, to characterise infectious agents by genomics. However, translating these protocols to clinical laboratories requires accreditation of assays for patient management, timescales that allow for clinical intervention, enhanced expertise in genomics, including data analysis, and distinct infrastructure (eg, sequences and high-performance computing clusters). Considering such implementation at clinical diagnostic laboratories raises questions about feasibility and fundability at scale, and whether services should be centralised or local.

Panel 4: Research efforts needed for use of genomics for innovation and influence

1. The use of genomics for innovation needs to be supported by sufficient accompanying metadata to contextualise the genomic data. Further work is needed to coordinate data-collection efforts, standardise procedures, and ensure that demographic, health, and other data are used ethically and effectively alongside genomics data for future innovation. This process could also require there to be more types of data collected within a more efficient and integrated system with higher interoperability, for instance, long-term follow-up to assess outcomes for individuals with drug-resistant infections. Long-term follow-up of this data will bolster assessments of clinical utility of pathogen genomics, and these assessments support further policy development.
2. In a world with high global mobility, the predictive value of genomics in addressing future antimicrobial resistance surveillance needs to be explored. Such exploration will require continuous globally coordinated surveillance systems, across humans, animals, and the environment, as well as the collection and association of genomic data and information on phenotypic susceptibilities—both already existing, accessible data, and that which are newly produced—with possible treatment strategies in National Health Service platforms to be made openly accessible.
3. The use of genomic data to inform the efforts of academic and commercial partners developing new antimicrobials is essential to incentivise their innovation. Continuing genomic surveillance of antimicrobial resistance determinants across microbial species can be used to inform efforts to assess the potential of future resistance development against novel antimicrobials and the potential for using whole-genome sequencing for characterisation of novel antimicrobial resistance mechanisms to new antimicrobials.

environment should not be neglected, nor should human long-term or lifetime burdens, such as the effects of childhood microbiome on disease resilience (eg, for non-communicable diseases such as heart disease) across the life course. The effects of AMR in this space are currently unknown but can only be investigated with genomics. Understanding and addressing them could bring associated benefits that lower health-care costs.

Research question 2: what is the relationship between AMR and health disparities?

Through a better understanding of the pathogens and genotypes associated with resistance, and the implementation of genomic surveillance on a global scale, associations between AMR burden and broader health disparities can be drawn. However, it is important that efforts do not stop at examining these disparities, and that attention is

also given to efforts to address AMR in the fairest way possible. Fairness might be considered with respect to whose AMR burden is addressed (by comparing AMR against other potential threats to populations' health and wellbeing) and in terms of ensuring that burdens associated with interventions against AMR are equitably distributed. Through the ability to infer transmission at a fine scale, genomics is an invaluable tool for investigating and assessing the burden of infectious disease and AMR in minoritised communities among lower-income, middle-income, and higher-income countries. However, this utility is contingent on accounting for factors such as country-specific subvariants and the implications of conducting surveillance in one country and a clinical trial in another country with a different subvariant.¹⁹ Such considerations are crucial for a just transition towards a future in which AMR has been addressed with global and regional health

Priorities in Theme 3 Outcome 7: using information for action

- 1 What is the cost of AMR?
- 2 What is the relationship between AMR and health disparities?
- 3 How to influence public awareness and behaviour on AMR?
- 4 How to address AMR in international settings?
- 5 What are the basic drivers and effects of AMR, and how does it spread?
- 6 How can we prevent AMR from spreading?
- 7 How can we optimise the use of antimicrobials?
- 8 What methods can be used to prevent, treat, and manage infections without antimicrobial medicines?
- 9 How can we drive innovation of new products for tackling AMR?
- 10 How can we ensure what is known to work is implemented?

AMR=antimicrobial resistance.

Table 2: Summary of the ten research priorities of Theme 3 Outcome 7: using information for action in the UK National Action Plan, Confronting antimicrobial resistance 2024–29

disparities in mind. Concurrently, the advent of genomics in the area highlights existing disparities that will exacerbate differences in disease burden across many countries, due to insufficient access to the infrastructures, training, and health-care funding required to support use of genomics in some low-income and middle-income countries (LMICs).

Research question 3: how to influence public awareness and behaviour on AMR?

Genomics has historically been difficult to communicate to public audiences; however, increasing genomics literacy among the public, particularly in the wake of the COVID-19 pandemic, creates greater opportunities for genomics to be used in informing public awareness and behaviour. For example, describing genomics analysis as fingerprinting bugs can support discussions with patients about tailoring care with appropriate treatments and improve understanding of public health decisions. Working with bioartists can also support communication and awareness.²⁰ Research on how genomics knowledge can influence the awareness and behaviour of actors in other industries (eg, agriculture) surrounding AMR is also important. Genomics can be used to provide compelling evidence that could support behavioural change across communities.

Research question 4: how to address AMR in international settings?

Genomics is an indispensable tool for surveillance and can be used to monitor the spread of AMR elements and pathogens across various scales and compartments, including across geographical locations, the One Health Triad,¹⁷ and among diverse bacterial hosts. Building capacity for genomic surveillance in LMICs is hampered by competing priorities for health budgets, and the high price and poor availability of genomics equipment and consumables. However, routine genomic surveillance in high-income countries could be leveraged to support remote

Panel 5: Areas to be addressed to ensure effective global use of genomics

1. Ensuring equitable access to genomics capabilities and expertise, alongside a willingness to contribute towards interventions that might not produce short-term visible benefit for the UK population (although many interventions still produce short-term benefits, including enabling individuals to receive appropriate, and perhaps, personalised treatment), but that are beneficial in the long term by helping to address antimicrobial resistance.
2. Developing stronger methods to uncover directionality of transmission of antimicrobial resistance among different reservoirs and geographical locations and implementing these understandings on a global scale.
3. Development of robust, ethical data-sharing frameworks among stakeholders, to address long-standing sociopolitical and ethical concerns regarding cross-border data and sample sharing.

surveillance in LMICs, which often have higher infectious disease and AMR burdens, and to strengthen partnerships.¹

Research question 5: what are the basic drivers and effects of AMR, and how does it spread?

Genomics is a crucial tool for monitoring the transfer of AMR across several reservoirs in the One Health Triad.¹⁷ In fact, it is the only technology able to differentiate between AMR emergence and spread.²¹ Innovative genomic and environmental metagenomic methods can also further enhance AMR surveillance. Genomics has a great capacity to characterise the drivers of AMR encoded as recognised resistance determinants. As a starting point, an important initial priority is to improve environmental surveillance to support the development of risk-assessment frameworks for focusing efforts on reservoirs that are key to the emergence of known and novel resistance mechanisms.

Research question 6: how can we prevent AMR from spreading?

Examining surveillance uses of genomics and how it informs public health measures against AMR is key to ensuring that it is effective and trustworthy. As genomics capacity develops, improved understanding of the directionality of AMR spread among hospitals and communities, and the complexities of spread via mobile genetic elements (particularly plasmids and the molecular clock of their evolution) allows for the design and targeting of measures that effectively prevent spread. By elucidating the flow of AMR through One Health systems, genomics is crucial for identifying key points for intervention to prevent spread, and for identifying hotbeds of evolution and emergence.

Research question 7: how can we optimise the use of antimicrobials?

Informing clinical care via accurate diagnosis and avoiding the inappropriate use of antimicrobials is essential to prevent the emergence of AMR. This aim can be supported

through genomic diagnostic tools. Genomic analyses can help to characterise relationships among antimicrobial use and resistance not only at the level of the pathogen, the individual patient, or a hospital system, but also across food production systems and countries. Genomics can also be used to design and deploy innovative diagnostics for clinical decision making, but only when implementation strategies are feasible and account for limitations in time, clinical laboratory capacity, training, and other operational considerations. A top research priority is how validated genomic diagnostic tools can be developed without the need for companion diagnostics for confirmation, as such diagnostics will add time and costs. Such tools will, in turn, require implementation-strengthening efforts via the development of genomics workforce competencies that can either be adapted into existing clinical scientist-training programmes or the training of a genomics-microbiologist workforce that can operate in clinical settings.

Genomics can also be used to identify novel targets in AMR pathogens for both drug targeting and vaccine design, and to select and screen natural populations for potential resistance. Although metagenomics has the potential to contribute to this goal, more work is needed to help clinicians to understand whether an organism is innocuously colonising or is causing disease in an individual.²² There is also a need to achieve genotypic validation of resistance phenotypes or clinical resistance among contemporary bacterial populations, and to develop improved systems for ongoing curation of AMR determinant databases, to keep pace with novel mechanisms of resistance.

In addition, it was recognised that genomics can expand our understanding of resistant clones and resistance genes that circulate among animal and environmental reservoirs. If these are related to the strains causing infections in humans, a strong evidence base can be built for the development of targeted policies around the reduction of antimicrobial use in veterinary medicine.

Research question 8: What methods can be used to prevent, treat, and manage infections without antimicrobial medicine?

The genomic epidemiology and phylogeny of pathogens, wherein data regarding bacterial genomics (eg, AMR and virulence genes or mutations and mobile genetic elements) are combined with patient demographic information (age group, gender identity, other legally protected characteristics, and infection risk-associated behaviours) can inform targeted public health interventions for preventing communicable infection in those identified to be at a higher risk. The directionality and potential source(s) of outbreaks can be identified through high-resolution genomic epidemiology, aiding in the prevention, treatment, and management of infections through targeted public health interventions, pertinent in successfully eliminating the transmission of hepatitis C virus and HIV. Hence, by being an unrivalled molecular epidemiological tool for characterising transmission pathways, genomics can identify the

flow of AMR for targeting through preventive disease management.

Research question 9: how can we drive innovation of new products for tackling AMR?

Innovation is a key area that genomics can contribute to and could be enhanced by using machine learning and artificial intelligence to predict drug susceptibilities and resistance emergence. Genomic studies used during development of new technologies can derisk new therapeutic agents and diagnostic tools (eg, by the investigation of distribution or conservation or variation in relevant target genes or proteins), resulting in a greater effectiveness of the product, and therefore, supporting trust in health care and public health interventions against AMR. Genomics can also aid in assessing the areas in which the greatest health burdens of AMR fall, and thus, contribute to innovation, investment planning, and equity. Improved communication among public health institutions (who need to undertake verification of industry-designed products before use to inform public health) and genomic technology industry partners (who are continually developing new technologies) needs to be coordinated, to ensure continued future support for products that have undergone years of industrial development and verification in public health laboratories.

Research question 10: how can we ensure what is known is implemented?

Ensuring the implementation of effective measures to address AMR is an area wherein collaboration between social science and humanities is essential. However, these transdisciplinary efforts in the field of implementation science are rare. Behavioural and implementation scientists, medical sociologists, bioethicists, and other experts can support efforts to ensure that interventions against AMR based on genomics knowledge are socially and ethically acceptable, as well as effective. They can also apply implementation models to assess and fill gaps, and identify training needs and other areas for development.

Conclusions

Genomics can address AMR across all themes of the UK NAP. However, this capacity is restricted by some gaps in research, particularly in the implementation of genomics across a range of sectors and settings, across the One Health Triad. This cross-cutting topic was raised during the TARGetAMR stakeholder meeting, with specific highlighted issues, including: paucity of effective implementation for monitoring the effectiveness of using genomics knowledge to inform targeted IPC; suboptimal sharing of genomics knowledge to inform updates to assays for effective diagnosis; gaps in understanding of the real-world needs of front-line workers and patients, and acceptability of genomic testing for informing care; and limitations around global access to the genomics capabilities and expertise needed to effectively pursue global AMR surveillance in both clinical and non-clinical settings. If the

themes outlined in the UK NAP are to be moved forward by 2029, the thriving community of AMR genomics experts in the UK needs to be harnessed and expanded. This effort needs to include not just genomics scientists but also transdisciplinary research communities, coming together with stakeholders in the industry, policy, clinical practice, and public advocacy groups, to address UK NAP priorities.

Contributors

TJ, SJ, PF, WvS, and KSB conceptualised the study, conducted the investigation, and sourced funding. RM-T was responsible for project administration. TJ and LCEM wrote the original draft. All authors contributed to reviewing and editing.

Declaration of interests

TJ, WvS, and KSB declare funding from UK Research and Innovation (UKRI; only declaration related to this work). WvS further declares consulting for Cepheid. KLH declares financial support for contracted evaluations from Merck, Shionogi, Pfizer, and Paion. LCEM declares previous support from National Institute for Health and Social Care Research (NIHR). All other authors declare no competing interests.

Acknowledgments

This study was funded by UKRI (BB/Z515620/1). MAC is affiliated to the NIHR Health Protection Research Unit in Gastrointestinal Infections at University of Norwich and Public Health Genomics at University of Birmingham in partnership with UK Health Security Agency (UKHSA), in collaboration with University of Newcastle, and is based at UKHSA. The views expressed are those of the authors and not necessarily those of the National Health Service, NIHR, Department of Health and Social Care, or UKHSA.

References

- Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet* 2022; **399**: 629–55.
- WHO. Global action plan on antimicrobial resistance. Jan 1, 2016. <https://www.who.int/publications/i/item/9789241509763> (accessed Aug 10, 2025).
- WHO. Global antimicrobial resistance and use surveillance system (GLASS) report. Dec 9, 2022. <https://www.who.int/publications/i/item/9789240062702> (accessed Aug 10, 2025).
- Department of Health and Social Care. UK 5-year action plan for antimicrobial resistance 2019 to 2024. Jan 24, 2019. <https://www.gov.uk/government/publications/uk-5-year-action-plan-for-antimicrobial-resistance-2019-to-2024> (accessed Aug 10, 2025).
- Department of Health and Social Care. UK 5 year antimicrobial resistance strategy 2013 to 2018. Sept 10, 2013. <https://www.gov.uk/government/publications/uk-5-year-antimicrobial-resistance-strategy-2013-to-2018> (accessed Aug 10, 2025).
- Department of Health and Social Care. The Scottish Government. Welsh Government, Department for Environment, Food & Rural Affairs, Department of Health (Northern Ireland), Department of Agriculture, Environment and Rural Affairs (Northern Ireland). UK 5-year action plan for antimicrobial resistance 2024 to 2029. May 8, 2024. <https://www.gov.uk/government/publications/uk-5-year-action-plan-for-antimicrobial-resistance-2024-to-2029> (accessed Aug 10, 2025).
- NHS England. Accelerating genomic medicine in the NHS. Oct 12, 2022. <https://www.england.nhs.uk/long-read/accelerating-genomic-medicine-in-the-nhs/> (accessed Aug 10, 2025).
- Hannah A. How genomics is transforming healthcare in the UK. 2022. <https://onenucleus.com/how-genomics-transforming-healthcare-uk> (accessed Feb 5, 2026).
- Wellcome Sanger Institute. Genomics campus expansion to boost science in UK and health globally. May 5, 2023. <https://wellcome.org/news/genomics-campus-expansion-boost-science-uk-and-health-globally> (accessed Aug 10, 2025).
- Webb JR, Andersson P, Sim E, et al. Implementing a national programme of pathogen genomics for public health: the Australian Pathogen Genomics Program (AusPathoGen). *Lancet Microbe* 2025; **6**: 100969.
- Fletcher A. National Medical Examiner's Good Practice Series No. 9. Recording antimicrobial resistance on the Medical Certificate of Cause of Death. <https://www.rcpath.org/static/5677cccb-e4c2-450d-aaea199035bc3828/bd98e91c-f134-49b0-965c7076b0a8f5bf/Good-Practice-Series-Recording-antimicrobial-resistance-on-the-Medical-Certificate-of-Cause-of-DeathFinal.pdf> (accessed Aug 10, 2025).
- Baker KS, Jauneikaite E, Hopkins KL, et al. Genomics for public health and international surveillance of antimicrobial resistance. *Lancet Microbe* 2023; **4**: e1047–55.
- UK Health Security Agency. *Mycobacterium tuberculosis* whole-genome sequencing and cluster investigation handbook. Sept 5, 2022. <https://www.gov.uk/government/publications/tb-strain-typing-and-cluster-investigation-handbook/mycobacterium-tuberculosis-whole-genome-sequencing-and-cluster-investigation-handbook> (accessed Aug 10, 2025).
- Murray-Watson RE, Grad YH, St Cyr SB, Yaesoubi R. Personalizing the empiric treatment of gonorrhoea using machine learning models. *PLoS Digit Health* 2024; **3**: e0000549.
- Baker KS, Dallman TJ, Behar A, et al. Travel- and community-based transmission of multidrug-resistant *Shigella sonnei* lineage among international orthodox Jewish communities. *Emerg Infect Dis* 2016; **22**: 1545–53.
- Chen MY, Williamson DA. Sexually transmitted outbreaks and genomic surveillance. *Lancet Infect Dis* 2022; **22**: 1409–11.
- Djordjevic SP, Jarocki VM, Seemann T, et al. Genomic surveillance for antimicrobial resistance — a One Health perspective. *Nat Rev Genet* 2024; **25**: 142–57.
- Food Standards Agency. Pathogen Surveillance in Agriculture, Food and Environment (PATH-SAFE) Programme. April 10, 2025. <https://www.food.gov.uk/our-work/pathogen-surveillance-in-agriculture-food-and-environment-path-safe-programme> (accessed Aug 10, 2025).
- Phillips LT, Bradshaw D, Packer S, et al. Direct-acting antiviral treatment outcomes in people infected with endemic compared to epidemic hepatitis C virus subtypes in England. *J Infect* 2025; **90**: 106465.
- Breedlove B. Repurpose and reuse: artistic perspectives on antimicrobial resistance. *Emerg Infect Dis* 2019; **25**: 198–99.
- Baker S, Thomson N, Weill FX, Holt KE. Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. *Science* 2018; **360**: 733–38.
- Zhou Y, Wylie KM, El Feghaly RE, et al. Metagenomic approach for identification of the pathogens associated with diarrhea in stool specimens. *J Clin Microbiol* 2016; **54**: 368–75.

© 2026 The Author(s). Published by Elsevier Ltd. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).