Partneriaeth Genomeg Cymru
Genomics Partnership Wales

Poster Abstracts

1

Shaping the Future of Pathogen Genomics Research in Wales: Public, Workforce and System Perspectives

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The expansion of pathogen sequencing services in Wales and the increasing use of genomics in public health practice create new opportunities to strengthen prevention research and disease surveillance. Public Health Wales (PHW) is uniquely positioned in coordinating and advising national outbreak response and health security. We aim to identify the public health genomics research priorities for PHW and explore how research can be embedded across specialist teams. Using a mixed-methods approach, the work brings together public involvement activities, workforce engagement and partnership working to understand future research opportunities, current capability and areas for development. It also explores how PHW can strengthen collaboration with universities, Genomics Partnership Wales and other partners to support impactful research. Early findings show strong public support for research that improves prevention, preparedness and response to infectious disease threats, alongside expectations for transparency, trust and appropriate governance. By integrating public, workforce and partner perspectives, this work will inform organisational research priorities and identify practical opportunities to strengthen research capacity, collaboration and innovation. The findings will support a coordinated approach to pathogen genomics research, helping maximise its contribution to public health in Wales.

2

Nutritional and Genetic Risk Factors in Mild Cognitive Impairment

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Mild cognitive impairment (MCI) represents a critical window in which modifiable factors may help delay progression to Alzheimer's disease (AD). Nutritional status and genetic susceptibility are increasingly recognised as influential components of cognitive vulnerability, yet evidence on their combined effects remains inconsistent. This research integrates findings from a systematic review and a multi cohort analysis to evaluate whether blood based nutritional biomarkers and APOE ε4 jointly shape clinical conversion from MCI to AD. The systematic review synthesised evidence and identified consistent associations between higher vitamin D, selenium, and antioxidant levels and better cognitive outcomes. Although some nutrient–gene interactions were reported, findings were limited by small samples, highlighting the need for large, genotyped cohorts. The multi cohort analysis addressed this gap using data from AIBL & NACC cohorts. APOE ε4 carriers progressed significantly faster across both cohorts, confirming strong genetic acceleration of decline. Nutritional factors exerted independent effects: lower BMI predicted faster conversion, consistent with the late life obesity paradox, while baseline vitamin B12 deficiency aligned with slower decline. Nutrient–gene interaction terms were consistently non significant, and simplified models using independent main effects achieved high predictive accuracy.

3

Bugs and antibiotic resistance in hospital sink traps.

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Hospital sink traps have been recognised as a reservoir for antibiotic resistant hospital-acquired infections, yet their microbial community structure and resistance potential remain incompletely characterised. In this study we sampled sink traps (n = 75) from three augmented care units in a North Wales hospital. We assessed their bacterial communities using shotgun metagenomics, to identify bacterial taxa and the resistance mechanisms they carry. We also utilised cultivation-based techniques to identify potential pathogens, by using selective and non-selective media. Media included those selective for ESBL and carbapenemase producing gram Gram-negative bacteria. Recovered isolates were identified using MALDI-TOF MS. Carbapenem resistance capacity was assessed by disk diffusion. The most abundant recovered isolates were non-aeruginosa Pseudomonas, alongside species of Enterobacterales. A total of 25% of isolates showed resistance to meropenem. Metagenomic analysis revealed bacterial diversity and included emerging pathogens. Genomes demonstrated a range of resistance mechanisms. Combining cultivation with shotgun metagenomics provides a broader picture of sink trap biofilm inhabitants than either approach alone, uncovering a diverse array of emerging resistant pathogens. These findings highlight the need for more comprehensive surveillance of sink traps to deliver feasible, targeted strategies for mitigating their role in hospital-acquired infections.

4

Longitudinal Surveillance of Candida auris in Wastewater Using Quantitative Real-Time PCR

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Candida auris is an emerging, multidrug-resistant fungal pathogen of significant global public health concern, associated with high mortality rates and persistence within healthcare environments. Conventional clinical surveillance methods are known to underestimate the true prevalence of C. auris colonisation, highlighting the need for complementary population-level monitoring approaches. Wastewater-based epidemiology (WBE) has demonstrated considerable utility for community-scale surveillance of infectious agents, yet its application to fungal pathogens remains largely unexplored. This study aimed to establish and apply a TaqMan quantitative PCR (qPCR) assay for the detection and quantification of C. auris DNA in municipal wastewater. Samples were collected from nine sampling points across three sites in North Wales between January 2023 and December 2025 as part of the PATH-SAFE surveillance programme. The qPCR assay demonstrated excellent analytical performance, and positive detections were confirmed by amplicon sequencing. The findings provide proof-of-concept that C. auris DNA can be detected in community wastewater, supporting the potential of WBE as a complementary surveillance tool for this high-consequence pathogen. The temporal pattern of detections suggests links to healthcare facility activity within the catchment area. Further work is needed to improve assay sensitivity, increase sampling resolution, and correlate wastewater signals with clinical case data.

5

Complete Genome Assembly of Trichophyton interdigitale Reveals Extensive Structural Variation and Pathogenicity-Associated Genetic Adaptability

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Abstract - Richophyton interdigitale is a prevalent dermatophyte causing chronic skin and nail infections with rising antifungal resistance. Despite clinical importance, high-quality genomic resources for this species remain limited, with current assemblies being highly fragmented and lacking comprehensive characterization of genetic diversity and virulence mechanisms. This study aimed to generate the first complete, high-quality genome assembly of T. interdigitale and characterize structural variation, heterozygosity, and pathogenicity factors using Oxford Nanopore long-read sequencing. We achieved a near-complete genome assembly comprising 7 contigs (22.31 Mb, N50=4.4 Mb) with exceptional quality metrics including 99.7% BUSCO completeness, representing an enhanced improvement in contiguity over existing assemblies. Functional annotation identified 6,273 predicted genes with 86.4% receiving functional assignments. Comparative genomics confirmed 94.7% average nucleotide identity to T. mentagrophytes and 89.2% to T. rubrum, establishing phylogenetic relationships and species-specific features. This complete genome represents the highest quality Trichophyton assembly to date and reveals unprecedented genetic complexity underlying dermatophyte pathogenesis. This assembly provides a robust foundation for investigating genetic adaptability mechanisms potentially contributing to persistent infections and treatment resistance.

6

Before the Wards: Building Genomic and Interprofessional Confidence Through MDT Emulation

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Background: Multidisciplinary Team (MDT) meetings sit at the heart of cancer care, requiring professionals to synthesise clinical, radiological and genomic information for the benefit of patients. Undergraduate curricula offer limited chances to experience this before students meet it in professional practice. Aims: Evaluate whether an emulated colorectal cancer MDT session involving Medicine, Physician Associate and Biomedical Science students changes their understanding of MDT processes, genomic decision-making and related knowledge.
Methods: Year 2/3 students (n=54 pre, n=32 post; unpaired, anonymised) took part in an emulated colorectal cancer MDT covering staging and genomic testing (Lynch syndrome, APC-Wnt, KRAS therapy) scaffolded around a Medical Case Based Learning scenario. Questionnaires measured self-reported understanding (Likert) and knowledge pre/post; retention follow-up ongoing.
Results: Composite self-reported understanding rose significantly, 3.81 to 4.37/5 (Mann-Whitney U, $p=3.75\times10^{-6}$, d=1.21), with the largest gain in understanding how MDT decisions are reached (3.40 to 4.39/5, $p=6.34\times10^{-7}$). Knowledge scores rose descriptively, 38.5% to 45.0%. Evaluation was strongly positive (mean 4.3–4.4/5), with students consistently valuing genomic and specialist input.
Conclusions: Emulation offers a feasible route to genomic literacy and interprofessional confidence well before students first encounter these decisions in clinical settings.

7

The Wales Cancer Biobank: evolution of bioresourcing to serve both patients and the evolving multimodal appetite of the cancer research community in Wales

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The WCB holds extensive cancer sample archives collected over 20 years. Its approval and consent model enables direct linkage between biosamples and patients' NHS e health records, creating richly linked clinical–biological datasets for research. With rapid advances in AI, big data, and genomics transforming cancer research, biobanks must evolve to meet new data needs. Therefore WCB are therefore responding to this by developing Wales' first national Bioresource, expanding the multimodal data available to researchers. Biological sample provision remains WCB's core function, distinguishing it from other national biobanks that limit sample access. Several projects are enhancing WCB's cancer data infrastructure, including establishing pipelines to genomic diagnostic data via AWMGS, creating a histopathology image databank to support AI diagnostics, and acquiring radiological imaging datasets. Strong PPIE initiatives are modernising (digitising) consenting processes through iConsenting, with plans to broaden these digital consent procedures nationally. Together, these developments demonstrate WCB's collaborative approach with academic, NHS, and industry partners, supporting research aligned with CReSt priority themes and delivering improved resources for cancer patients

8

Driving National Collaboration in Advanced Therapy Research and Delivery

Lin Amor, Advanced Therapies Wales

Advanced Therapies Wales is the only programme of its kind in the UK, providing a national focal point for expertise & support. Established in 2019 with a statement of intent from Welsh Government it has become a central point for resources, clinical activity & industry ambition. It offers a one-Wales approach with a unified strategy to enable patient access. The Delivery Plan for Advanced Therapies in Wales was written in 2024 on behalf of the Welsh advanced therapies ecosystem, with its delivery coordinated & facilitated through the ATW Programme. It captured the steps required to progress the development of the advanced therapies sector across Wales, over the subsequent five years ensuring alignment with National policies, objectives and ambitions. The Delivery Plan is centred around 4 key goals and 3 cross cutting themes. There has been significant progress for the advanced therapies sector in Wales over the last year, driven by a shared commitment to innovation, equity, and collaboration. Wales has moved from participating to leading.

9

How patient and public voices are integral to our work

Midlands-Wales ATTC/ATW - Lin Amor, NHS Wales JCC- Hannah Crocker, Midlands-Wales ATTC/ATW - Rebecca Curtis, Midlands-Wales ATTC/ATW - John Lewis

Midlands-Wales Advanced Therapies Treatment Centre (MW-ATTC) are part of the Advanced Therapies Treatment Centre Network (ATTC) who address the unique and complex challenges of bringing advanced therapy medicinal products (ATMPs) to patients. Advanced Therapies Wales (ATW) is the only programme of its kind in the UK, providing a national focal point for ATMP expertise and support, and co-lead the MW-ATTC. Friends of Cymru Sickle Cell and Thalassaemia (FOCST) invited us to attend their community education and engagement event. The aim was to build a framework of knowledge about two new advanced therapies which were soon to be available in standard care. By bringing together patients, clinical experts, clinical psychologists, carers and members of supporting voluntary organisations the hope was to find a shared language, discuss issues of importance and learn more. People with lived experience and their loved ones asked questions and shared their stories with us. We took away key messages which we integrated into our work: We formulated the agenda for our annual symposium event to ensure patient voices were at the fore; We co-produced a new ATW website with patient and public representatives ensuring information was presented in clear language in an accessible format. We also formulated a list of current and future projects to develop this workstream further.

10

Optimising Glaucoma Pathways in NHS Wales : Integrating Genomic Risk Stratification through a Quality Improvement Approach

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Glaucoma remains a leading cause of irreversible blindness in Wales, with outcomes closely linked to timely detection and consistent monitoring. Emerging genomic evidence highlights inherited susceptibility and risk-associated variants that may enable earlier identification of individuals at increased risk. However, the practical integration of genomic insight into routine ophthalmology services remains limited. This service-focused perspective explores how genomic risk stratification could be embedded within glaucoma pathways in NHS Wales using structured quality improvement methodology. By analysing existing referral, triage, and follow-up processes, opportunities can be identified to align genetic risk indicators with clinical decision-making, surveillance intervals, and patient communication. Integrating genomic data alongside established parameters—such as intraocular pressure, optic nerve assessment, and visual field analysis—may support more personalised and preventative models of care. Applying improvement principles ensures that innovation is implemented safely, equitably, and sustainably. The strategic incorporation of genomics within glaucoma services has the potential to enhance early intervention, reduce avoidable progression, and optimise resource allocation as precision medicine becomes increasingly embedded across NHS Wales.

11

Developing and Evaluating an Interactive Science Communication Tool for Epigenetics Education and Public Engagement

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Background & Aims: Effective public engagement is critical in genomics and health sciences to foster trust, communicate research value, and inspire future scientists. This project designed and evaluated an interactive communication tool to improve epigenetics literacy among A-level students and the public.
Methods: A three-section digital tool was deployed: (1) a pre-questionnaire assessing baseline knowledge, (2) an educational presentation using visual design and analogies (e.g., DNA structure) to make complex concepts accessible, and (3) a post-questionnaire gathering quantitative and qualitative public feedback.
Results: Prior to the session, 82.4% of participants had little to no knowledge of epigenetics. Post-presentation analysis demonstrated clear impact, with 58.9% showing measurable improvement in understanding. Qualitative feedback praised the visual analogies and provided actionable insights to further condense text and optimize design.
Conclusion & Impact: This initiative provides a proven, lay-accessible model for genomic education and Patient & Public Involvement and Engagement (PPIE). Future work will leverage this approach to inspire students toward genomic research and health communication careers.

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Carbapenemase-producing organisms in wastewater and wastewater-impacted aquatic environments.

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Antimicrobial resistance (AMR) poses a serious threat to global public health. Carbapenemase-producing organisms (CPOs are associated with high mortality and limited treatment options. While AMR has historically been studied in clinical settings, the One Health framework has positioned the environment as a critical reservoir and dissemination pathway for AMR. Using digital polymerase chain reaction (dPCR), metagenomics and whole-genome sequencing (WGS), we are investigating the distribution of CPOs in Welsh wastewater networks. We hypothesise that hospital wastewater represents a primary source of CPOs entering the broader wastewater network and that they persist through conventional wastewater treatment, finally entering the receiving water bodies. Findings from this study will serve as an early warning tool for public health risk monitoring, contribute to the design of effective mitigation strategies, and provide evidence to support delivery of the National Action Plan for AMR.

13

An in-silico pipeline for miRNA therapeutic identification, ranking and functional assessment in solid tumour cancers

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MiRNA therapeutics could correct the dysregulated gene networks underpinning cancer, but miRNA pleiotropy makes candidate selection difficult and raises off-target concerns, and existing databases lack integration and disease-specific context. We present an in-silico pipeline that integrates differential expression, validated and predicted miRNA-mRNA pairs, tissue expression filtering, cancer hallmark enrichment, the oncogene/tumour-suppressor balance of targets and TCGA survival data into a unified score that ranks downregulated miRNAs as therapeutic candidates, with KEGG/GO enrichment to flag off-target effects. In colorectal cancer (149 miRNAs), known tumour-suppressive miRNAs hsa-miR-145-5p, -375 and -139-5p all ranked in the top 10%. Unified rankings correlated only weakly with differential expression ranks (Spearman $\rho = 0.19$), highlighting the value of functional scoring. In ovarian cancer (70 miRNAs), the top candidates hsa-miR-204-5p, -34a-5p, -146a-5p and -29b-3p were all enriched for resisting cell death and replicative immortality, and had largely non-overlapping targets, suggesting combination potential. Pathway analysis linked each to plausible anti-cancer mechanisms, including Hippo, PI3K-Akt and Toll-like receptor signalling, while flagging conflicting effects, such as miR-34a-5p targeting both pro- and anti-apoptotic genes. This pipeline offers a systematic, mechanism-informed approach to prioritising miRNA therapeutics for peritoneal-metastasising cancers.

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Advanced Therapy Medicinal Products (ATMPs): Horizon Scanning to Support Strategic Planning and Future Service Readiness in Wales

Advanced Therapies Wales, North Wales Joint Commissioning Committee, All Wales Therapeutics and Toxicology Centre

Background: Advanced Therapy Medicinal Products (ATMPs), including gene and cell therapies, are transforming treatment options for rare diseases, cancer and other conditions with high unmet need. However, their adoption presents challenges for healthcare systems due to complex commissioning and delivery requirements.
Aim: To develop a horizon-scanning approach that provides stakeholders with an accessible overview of the ATMP pipeline to support service planning and preparedness across Wales.
Methods: Advanced Therapies Wales worked with AWTTC and the NHS Wales Joint Commissioning Committee to produce an ATMP Horizon Scanning Snapshot. Data were sourced from publicly available resources, including NICE, MHRA, EMA and EMC. Therapies were categorised by appraisal status, therapeutic area and treatment type.
Results: The September 2026 snapshot identified 15 ATMPs across 20 indications in the NICE appraisal pipeline. While rare diseases and CAR-T therapies remain the main focus, emerging treatments are expanding into areas such as solid tumours, neurology, ophthalmology and metabolic disorders. The findings highlight both rapid innovation and uncertainty within the pipeline.
Conclusions: Horizon scanning supports workforce and infrastructure planning, commissioning decisions and equitable patient access. As the ATMP pipeline grows, ongoing monitoring will be essential to ensure NHS Wales is prepared to adopt these therapies safely and effectively.

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Defining the transcriptomic regulation of the NLRP3 inflammasome in renal ischaemia reperfusion injury and ischaemic pre-conditioning

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Introduction: Ischaemia Reperfusion Injury (IRI) drives Acute Kidney Injury (AKI) in 15-30% of all patients who undergo abdominal surgery. Ischaemic pre-conditioning (IPC) is a brief period of ischaemia that reduces IRI by unknown mechanisms. Inflammasomes are increasingly being recognised as key players in the pathophysiology of IRI. We used a rat model of IRI-induced AKI and IPC to characterise genes related to inflammasome activation that drive IPC versus IRI.
Methods: Adult, male Lewis rats underwent bilateral kidney IRI, IPC and sham surgery. In IRI, both renal pedicles were clamped for 45 minutes. The IPC group underwent pulsatile-IPC prior to IRI. Kidneys were retrieved at 48 hours and assessed by RNA sequencing.
Results: IRI leads to marked increase in expression of NLRP3 in kidneys. IPC led to renoprotection with attenuated inflammation. Transcriptomic analysis demonstrated a differential expression of genes in injured and pre-conditioned kidneys, particularly NLRP3 (a key inflammasome) and its associated genes. RT-qPCR confirmed the heightened expression of NLRP3 and its associated genes in IRI kidneys, when compared with sham and IPC kidneys.
Conclusions: Renoprotection is associated with attenuation of the NLRP3 inflammasome. Identifying novel therapeutics targeting the NLRP3 inflammasome may have huge potential in limiting IRI-associated AKI in many clinical settings including patients undergoing major abdominal surgery.

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Combining Clinical assessment and Lived Experience to Map the Phenotypic Spectrum in an ultra-rare SCAMP5 variant

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Background: An ultra-rare variant within the SCAMP5 gene has been associated with a neurodevelopmental disorder featuring developmental delay, seizures, and neurological abnormalities. With six previously identified cases globally, we present a seventh case of the same variant in a fourteen-year-old female from South Wales which has broadened the known phenotypic spectrum. This poster aims to demonstrate how integrating a family's lived experience with clinical assessment can help establish the phenotype in ultra-rare genetic variants.
Methods: A mixed-methods approach was used. A retrospective review of patient records with an up-to-date clinical assessment (August 2026) was used to construct a "clinical timeline". Concurrently, a "lived experience timeline" is being captured through semi-structured interviews with the patient's family.
Results: The dual timeline identified key crossover events where family insights and the clinical management directly informed one another. Notably, combining parental observations of excessive sleepiness with the existing literature guided investigations to exclude organic causes such as seizures.
Conclusion: Managing ultra-rare conditions, which commonly lack a clinical consensus, requires a dual approach, pairing clinician assessment with patient and family experience.

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Don't forget the researchers: The importance of user experience in genomic data environments

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Background: While substantial investment in secure data environments has increased data volume and availability, data alone does not drive genomic discovery. This study asks: how can genomic data environments better support researchers to find, navigate and use data to generate accurate, reproducible and innovative insights?
Methods: Qualitative user research with 36 researcher participants delivered for Genomics England between October 2025 and September 2026.
Results: Across three projects within the National Genomics Research Library owned by Genomics England, we consistently found that: 1) researchers need routes into the data that match how they think and work; 2) they need meta data to understand what the data means, provenance and utility; and 3) providing high-quality documentation helps but a lasting improvement to the user experience is also contingent on the underlying data and operating models.
Conclusion and recommendations: The provision of genomic and clinical data in secure data environments needs to be designed as an experience, not just documented by organisations who own these datasets.

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Norovirus risk assessment in recreational waters

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Recreational exposure to freshwater and coastal environments contaminated with sewage poses a risk to human health. Viruses such as norovirus (NoV) can cause acute gastroenteritis if ingested during recreational exposure. NoV is frequently detected in receiving waters, highlighting ongoing risks to public health. However, the risk associated with NoV in waterbodies at any one time is often unknown. This research aims to quantify the risk of contracting NoV from contaminated water. We measured norovirus GI and GII concentrations at 10 separate sites within Cardiff Bay over 12 months using PMAxx-based capsid integrity RT-qPCR. The data was used to drive a Quantitative Microbial Risk Assessment (QMRA) which predicted infection risk. We found that risk varied markedly across both space and time, with the higher risks occurring during the autumn and winter months and within the river sites feeding into the bay. Genogroup variability was also observed. These findings have important implications, as they allow users to make informed decisions on water safety, contributing to protecting public health. This case study could be used to further enhance the understanding of risk that NoV poses to public health by recreational contact to contaminated waters.

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Lynch syndrome in Wales: insights from routine health data adapted for surveillance and screening

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Background. Lynch syndrome (LS) is an inherited condition caused by pathogenic variants in MLH1, MSH2, MSH6 and PMS2. LS increases the risk of developing colorectal cancer (CRC), making regular screening key for early diagnosis. Effective patient registration to support such screening is currently lacking in Wales. Aims. To develop a Welsh LS registry (WLSR) for surveillance and screening purposes.
Methods. Genetic test reports from the All-Wales Medical Genomics Service (AWMGS) were adapted to identify patients with LS. Linkage to cancer records from the Welsh Cancer Intelligence Surveillance Unit (WCISU) enabled descriptive and genetic epidemiology.
Results. The WLSR covered 746 pwLS. MSH2 occurred at frequency of 33.6% (n=250), MSH6 at 25.8% (n=192), MLH1 at 23.8% (n=177), PMS2 at 16.4% (n=122) and EPCAM at 0.4% (n=3). Patients tended to receive predictive testing at a significantly younger age (40.7 ± 15.3) than those receiving diagnostic testing (58.7 ± 13.4, p<0.001). Predictive testing was associated with more penetrant variants. First CRC occurred earlier in LS patients than controls (53.9 ± 13.2, 70.7 ± 11.8, p=<0.001). The conditional risk of a pwLS CRC-free at age 25 developing CRC by age 50 was 20% ± 9.6%. This risk varied by gene: MLH1 32%, MSH2 21%, MSH6 12% and PMS2 12%.
Conclusion. This work demonstrates the utility of linked routinely collected genetic data for rare disease surveillance and potential planning of interventions to support cancer prevention.

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Healthcare utilisation of people living with lysosomal storage disorders in Wales

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Background. Lysosomal storage disorders (LSD) are rare metabolic conditions. Barriers to therapies in rare diseases mean families must travel to seek appropriate healthcare services. Little is known of how this applies to LSD patients in Wales. Aim. To use using registries operated by Congenital Anomaly Register and Information Service (CARIS) to understand how people living with LSDs (plwLSDs) access healthcare geographically.
Methods. CARIS registries were queried for LSD ICD-10 and Orphanet codes. Inpatient records were linked and used to compare the frequency of health events by geography across health boards and LSDs.
Results. Across both registries, 124 cases of LSDs were identified making the estimated population prevalence 1 in 25,000. Overall, 63% of care was provisioned in Wales: 41% in the patient's LHB, and 22% elsewhere. Utilisation varies by both LHB and LSD, with most England care sought from North and Mid-Wales, and from patients with mucopolysaccharidosis (MPS). Disproportionately high travel to England was associated with the rarest MPS subtype.
Conclusion. Most of the inpatient healthcare for plwLSDs is provisioned in Wales (63%). Where it is not provisioned in their home LHB, it is predominantly provisioned in South Wales (89%). In England, Manchester is highlighted as a significant care provider for LSDs. Travel burden is likely most significant for patients living farthest from South Wales and the border with England.

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Reanalysis of genomic data doubles the diagnostic yield for Welsh patients recruited to the UK 100,000 Genomes Project

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The 100,000 Genomes Project (100KGP) undertook genome sequencing of patients with rare diseases and cancer to study the role that genes play in disease, and to integrate genomics into UK healthcare. To contribute to 100KGP, the Wales Genomic Medicine Centre (a partnership between the NHS All Wales Medical Genomics Service (AWMGS), Cardiff University and Genomics England) recruited 438 individuals from 154 families that had been subject to pre-genomic genetic testing without reaching a diagnosis. The majority of probands (64%, 98/154) had neurological or neurodevelopmental phenotypes. Genome sequencing, variant calling, gene-based filtering and variant prioritisation were performed by Genomics England. AWMGS undertook clinical interpretation, validation and reporting of variants. Initial diagnostic yield was 20.8% (32/154) with variants of uncertain significance (VUS) reported for 11 more families. Most of the initial findings (81.4%, 35/43) could have been detected by clinical exome sequencing which was standard of care in Wales at the time. Reanalysis of the 100KGP Wales data using updated variant prioritisation tools, expanded gene lists, re-phenotyping and segregation studies, has increased diagnostic yield to 42.2% (65/154). RNA analysis was used to clarify the clinical significance of VUS in COQ4, ENPP, GATAD2B, NCAPD2, and THOC2. These findings demonstrate the clinical utility of genome sequencing, RNA analysis, and periodic reanalysis of genomic data.

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A Programmable Digital Microfluidics Platform for Automated Molecular Workflows Towards Rapid Genomic Testing

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Rapid genomic testing requires integrated and flexible technologies capable of transforming biological samples into analysis-ready material with minimal manual intervention. An electrowetting-on-dielectric active-matrix digital microfluidics (DMF) platform was developed to automate and miniaturise key molecular workflows within a programmable lab-on-a-chip architecture. Fully automated, script-driven DNA extraction and PCR were successfully performed on-chip, demonstrating DNA recovery comparable to conventional manual extraction and reproducible amplification of target regions. Miniaturised processing reduces reagent requirements and hands-on manipulation, supporting cost-efficient and standardised molecular analysis. The reconfigurable architecture supports on-demand processing of individual samples and is capable of multiple independent and multiplex PCR workflows on the same platform, enabling flexible interrogation of genomic targets. This establishes a foundation for targeted genomic analysis and future integration of sequencing and multiomic workflows, with the potential to support rapid, decentralised molecular diagnostics and bring genomic testing closer to the point of need.