

## **Selected Publications from 2022**

**The Centre for Genomics Research has contributed to project design, method development/optimisation, data generation or analysis for the following publications:**

- Veltsos, P., Porcelli, D., Fang, Y., Cossins, A.R., Ritchie, M.G. and Snook, R.R., 2022. Experimental sexual selection reveals rapid evolutionary divergence in sex specific transcriptomes and their interactions following mating. *Molecular Ecology* 31 (12), pp.3374-3388.
- Charras, A., Haldenby, S., Smith, E., Egbivwie, N., Olohan, L., Kenny, J.G., Schwarz, K., Roberts, C., Al Abadi, E., Armon, K. and Bailey, K., 2022. Panel sequencing links rare, likely damaging gene variants with distinct clinical phenotypes and outcomes in juvenile onset SLE. *Rheumatology*.
- Murphy, B., Grimshaw, S., Hoptroff, M., Paterson, S., Arnold, D., Cawley, A., Adams, S.E., Falciani, F., Dadd, T., Eccles, R. and Mitchell, A., 2022. Alteration of barrier properties, stratum corneum ceramides and microbiome composition in response to lotion application on cosmetic dry skin. *Scientific Reports* 12 (1), pp.1 11.
- Gómez, P., Hall, A.R., Paterson, S. and Buckling, A., 2022. Rapid decline of adaptation of *Pseudomonas fluorescens* to soil biotic environment. *Biology Letters* 18 (3). P.20210593.
- Wilkinson, S.A., Richter, A., Casey, A., Osman, H., Mirza, J.D., Stockton, J., Quick, J., Ratcliffe, L., Sparks, N., Cumley, N. and Poplawski, R., 2022. Recurrent SARS CoV 2 Mutations in Immunodeficient Patients. *medRxiv*.
- Stirrup, O., Blackstone, J., Mapp, F., MacNeil, A., Panca, M., Holmes, A., Machin, N., Shin, G.Y., Mahungu, T., Saeed, K. and Saluja, T., 2022. Evaluating the effectiveness of rapid SARS CoV 2 genome sequencing in supporting infection control teams: the COG UK hospital onset COVID 19 infection study. *medRxiv*.
- Brunner, F.S., Brown, M.R., Bassano, I., Denise, H., Khalifa, M.S., Wade, M., Kevill, J.L., Jones, D.L., Farkas, K., Jeffries, A.R. and Cairns, E., 2022. City wide wastewater genomic surveillance through the successive emergence of SARS CoV 2 Alpha and Delta variants. *medRxiv*.
- Smallman-Raynor, M.R. and Cliff, A.D., 2022. Spatial Growth Rate of Emerging SARS CoV 2 Lineages in England, September 2020-December 2021. *medRxiv*.
- Harney, E., Paterson, S., Collin, H., Chan, B.H., Bennett, D. and Plaistow, S.J., 2022. Pollution induces epigenetic effects that are stably transmitted across multiple generations. *Evolution Letters*.
- Lythgoe, K.A., Golubchik, T., Hall, M., House, T., MacIntyre Cockett, G., Fryer, H., Thomson, L., Nurtay, A., Buck, D., Green, A. and Trebes, A., 2022. Lineage replacement and evolution captured by the United Kingdom Covid Infection Survey. *medRxiv*.
- Willett, B.J., Grove, J., MacLean, O., Wilkie, C., Logan, N., De Lorenzo, G., Furnon, W., Scott, S., Manali, M., Szemiel, A. and Ashraf, S., 2022. The hyper transmissible SARS CoV 2 Omicron variant exhibits significant antigenic change, vaccine escape and a switch in cell entry mechanism. *medRxiv*.

**The Centre for Genomics Research has generated data and/or analysis for the following publications:**

- Stirrup, O., Blackstone, J., Mapp, F., MacNeil, A., Panca, M., Holmes, A., Machin, N., Shin, G.Y., Mahungu, T., Saeed, K. and Saluja, T., 2022. Effectiveness of rapid SARS-CoV-2 genome sequencing in supporting infection control for hospital-onset COVID-19 infection: Multicentre, prospective study. *Elife*, 11, p.e78427.
- Chechet, G.D., Kwaga, J.K., Yahaya, J., Noyes, H., MacLeod, A. and Adamson, W.E., 2022. SARS-CoV-2 seroprevalence at urban and rural sites in Kaduna State, Nigeria, during October/November 2021, immediately prior to detection of the Omicron variant. *International journal of epidemiology*.
- Mulindwa, J., Namulondo, J., Kitibwa, A., Nassuuna, J., Nyangiri, O.A., Kimuda, M.P., Boobo, A., Nerima, B., Busingye, F., Candia, R. and Namukuta, A., 2022. High prevalence of Schistosoma mansoni infection and stunting among school age children in communities along the Albert-Nile, Northern Uganda: A cross sectional study. *PLOS Neglected Tropical Diseases*, 16(7), p.e0010570.
- Kozjek, K., Manoharan, L., Ahrén, D. and Hedlund, K., 2022. Microbial functional genes influenced by short-term experimental drought across European agricultural fields. *Soil Biology and Biochemistry*, p.108650.
- Davies, C., 2021. Pathogens and the maintenance of genetic variation in an island population of the Seychelles warbler (Acrocephalus sechellensis) (Doctoral dissertation, University of East Anglia).
- Takebayashi, Y., Dulyayangkul, P., Satapoomin, N., Ismah, W.A.K.W.N., Williams, O.M., Macgowan, A.P., Heesom, K.J., Williams, P.B. and Avison, M.B., 2022. Identification and characterisation of Klebsiella pneumoniae and Pseudomonas aeruginosa clinical isolates with atypical  $\beta$ -lactam susceptibility profiles using Orbitrap liquid chromatography-tandem mass spectrometry. *bioRxiv*.
- Nolan, S., Hayes, N., O Flaherty, V., Burgess, C., Brennan, F. and Walsh, F., 2022. Data based slurry treatment decision tree to minimise antibiotic resistance and pathogen transfer while maximising nutrient recycling.
- Baker, M., Williams, A.D., Hooton, S.P., Helliwell, R., King, E., Dodsworth, T., Baena-Nogueras, R.M., Warry, A., Ortori, C.A., Todman, H. and Gray-Hammerton, C.J., 2022. Antimicrobial resistance in dairy slurry tanks: a critical point for measurement and control. *bioRxiv*.
- Bengtsson, R.J., Simpkin, A.J., Pulford, C.V., Low, R., Rasko, D.A., Rigden, D.J., Hall, N., Barry, E.M., Tennant, S.M. and Baker, K.S., 2022. Pathogenomic analyses of Shigella isolates inform factors limiting shigellosis prevention and control across LMICs. *Nature microbiology*, pp.1-11.



- Y., Msefula, C., Nyirenda, T.S., Olgemoeller, F., Perez-Sepulveda, B., Hinton, J.C., Owen, S.V., Feasey, N.A. and Ashton, P.M., 2022. Case-control investigation of invasive Salmonella disease in Africa-comparison of human, animal and household environmental isolates find no evidence of environmental or animal reservoirs of invasive clades/strains. *medRxiv*.
- Staunton, C.A., Owen, E.D., Hemmings, K., Vasilaki, A., McArdle, A., Barrett-Jolley, R. and Jackson, M.J., 2022. Skeletal muscle transcriptomics identifies common pathways in nerve crush injury and ageing. *Skeletal muscle*, 12(1), pp.1-20.
- Larcombe, S.D., Capewell, P., Jensen, K., Weir, W., Kinnaird, J., Glass, E.J. and Shiels, B.R., 2022. Susceptibility to disease (tropical theileriosis) is associated with differential expression of host genes that possess motifs recognised by a pathogen DNA binding protein. *Plos one*, 17(1), p.e0262051.
- Gupta, J.K., Care, A., Goodfellow, L., Alfirevic, Z., Müller-Myhsok, B. and Alfirevic, A., 2022. Genome and transcriptome profiling of spontaneous preterm birth phenotypes. *Scientific reports*, 12(1), pp.1-10.
- Batie, M., Frost, J., Shakir, D. and Rocha, S., 2022. Regulation of Chromatin Accessibility by hypoxia and HIF. *bioRxiv*.