

Selected Publications from 2021

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

- Kraemer, M., McCrone, J., Hill, V., Bajaj, S., Evans-Pena, R., Lambert, B., Inward, R., Bhatt, S., Volz, E., Ruis, C. and Dellicour, S., 2021. Context-specific emergence and growth of the SARS-CoV-2 Delta variant.
- Campbell, F.B., Darby, A.C., Hurst, G.D. and Siozios, S., Large-scale comparative genomics unravels great genomic diversity across the Rickettsia and Ca. Megaira genera and 2 identifies Torix group as an evolutionarily distinct clade. 3.
- Kevill, J.L., Pellett, C., Farkas, K., Brown, M.R., Bassano, I., Denise, H., McDonald, J.E., Malham, S.K., Porter, J., Warren, J. and Evens, N.P., 2021. A comparison of precipitation and filtration-based SARS-CoV-2 recovery methods and the influence of temperature, turbidity, and surfactant load in urban wastewater. *Science of The Total Environment*, p.151916.
- Namulondo, J., Mulindwa, J., Nyangiri, O.A., Egesa, M., Noyes, H. and Matovu, E., 2021. Gene expression changes in mammalian hosts during schistosomiasis: a review. *AAS Open Research*, 4(54), p.54.
- Duncan, L.M., Carabelli, A.M., Kenyon, J.C. and Lever, A.M., Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B. 1.1. 7.
- Pesole, G. and Chiara, M., 2021. Review 1:" Generation and transmission of inter-lineage recombinants in the SARS-CoV-2 pandemic." *Rapid Reviews COVID-19*.
- Elliott, P., Haw, D., Wang, H., Eales, O., Walters, C.E., Ainslie, K.E., Atchison, C., Fronterre, C., Diggle, P.J., Page, A.J. and Trotter, A.J., 2021. Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. *Science*, p.eabl9551.
- Papoutsopoulou, S., Pollock, L., Walker, C., Tench, W., Samad, S.S., Bergey, F., Lenzi, L., Sheibani-Tezerji, R., Rosenstiel, P., Alam, M.T. and Martins Dos Santos, V.A., 2021. Impact of Interleukin 10 Deficiency on Intestinal Epithelium Responses to Inflammatory Signals. *Frontiers in Immunology*, 12, p.2242.
- Hall, J.P., Wright, R.C., Harrison, E., Muddiman, K.J., Wood, A.J., Paterson, S. and Brockhurst, M.A., 2021. Plasmid fitness costs are caused by specific genetic conflicts. *bioRxiv*.
- Bell-Sakyi, L., Beliavskaia, A., Hartley, C.S., Jones, L., Luu, L., Haines, L.R., Hamilton, J.G., Darby, A.C. and Makepeace, B.L., 2021. Isolation in Natural Host Cell Lines of Wolbachia Strains wPip from the Mosquito Culex pipiens and wPap from the Sand Fly Phlebotomus papatasi. *Insects*, 12(10), p.871.



- Marr, N., Meeson, R., Kelly, E.F., Fang, Y., Peffers, M.J., Pitsillides, A.A., Dudhia, J. and Thorpe, C.T., 2021. CD146 Delineates an Interfascicular Cell Sub-Population in Tendon That Is Recruited during Injury through Its Ligand Laminin- α 4. *International journal of molecular sciences*, 22(18), p.9729.
- Castanheira, C.I., Anderson, J.R., Fang, Y., Milner, P.I., Goljanek-Whysall, K., House, L., Clegg, P.D. and Peffers, M.J., 2021. Mouse microRNA signatures in joint ageing and post-traumatic osteoarthritis. *Osteoarthritis and Cartilage Open*, p.100186.
- Hillary, L.S., Farkas, K., Maher, K.H., Lucaci, A., Thorpe, J., Distaso, M.A., Gaze, W.H., Paterson, S., Burke, T., Connor, T.R. and McDonald, J.E., 2021. Monitoring SARS-CoV-2 in municipal wastewater to evaluate the success of lockdown measures for controlling COVID-19 in the UK. *Water Research*, p.117214.
- Staton, G.J., Clegg, S.R., Ainsworth, S., Armstrong, S., Carter, S.D., Radford, A.D., Darby, A., Wastling, J., Hall, N. and Evans, N.J., 2021. Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. *PLoS pathogens*, 17(3), p.e1009464.
- Anna May, M.A., Jonathan Wolf, M.A. and Claire, J., Changes in symptomatology, re-infection and transmissibility associated with SARS-CoV-2 variant B. 1.1. 7: 2 an ecological study 3.
- Darby, A.C. and Hiscox, J.A., 2021. Covid-19: variants and vaccination.
- Fothergill, J., Moore, M.P., Lamont, I.L., Williams, D., Paterson, S., Kukavica-Ibrulj, I., Tucker, N., Kenna, D., Turton, J., Jeukens, J. and Freschi, L., 2020. Transmission, adaptation and geographical spread of the Pseudomonas aeruginosa Liverpool Epidemic Strain. *Microbial Genomics*.
- Royden, A., Christley, R., Jones, T., Williams, A., Awad, F., Haldenby, S., Wigley, P., Rushton, S. and Williams, N.J., Campylobacter Contamination of UK-Produced Halal Chicken at RetailCampylobacter Contamination of UK-Produced Halal Chicken at Retail. *Journal of Food Protection*.
- Penrice-Randal, R., Goldswain, H., Prince, T., Randle, N., Salguero, J., Tree, J., Vamos, E., Nelson, C., Stewart, J.P., Matthews, D.A. and Carroll, M., 2021. Identification and quantification of SARS-CoV-2 leader subgenomic mRNA gene junctions in nasopharyngeal samples shows phasic transcription in animal models of COVID-19 and aberrant patterns in humans. *bioRxiv*.
- Mewamba, E.M., Nyangiri, O.A., Noyes, H.A., Egesa, M., Matovu, E. and Simo, G., 2021. The Genetics of Human Schistosomiasis Infection Intensity and Liver Disease: A Review. *Frontiers in Immunology*, 12.
- Huson, K.M., Atcheson, E., Oliver, N.A., Best, P., Barley, J.P., Hanna, R.E., McNeilly, T.N., Fang, Y., Haldenby, S., Paterson, S. and Robinson, M.W., 2021. Transcriptome and Secretome Analysis of Intra-Mammalian Life-Stages of Calicophoron daubneyi Reveals



Adaptation to a Unique Host Environment. *Molecular & Cellular Proteomics*, 20, p.100055.

- Mashe, T., Takawira, F.T., de Oliveira Martins, L., Gudza-Mugabe, M., Chirenda, J., Munyanyi, M., Chaibva, B.V., Tarupiwa, A., Gumbo, H., Juru, A. and Nyagupe, C., 2021. Genomic epidemiology of the SARS-CoV-2 epidemic in Zimbabwe: Role of international travel and regional migration in spread. *medRxiv*.
- Goodfellow, L., Verwijs, M., Care, A., Sharp, A., Ivandic, J., Poljak, B., Roberts, D., Bronowski, C., Gill, A.C., Darby, A. and Alfirevic, A., 2021. Vaginal bacterial load in the second trimester is associated with early preterm birth recurrence: a nested case-control study. *medRxiv*.
- Golubchik, T., Lythgoe, K.A., Hall, M.D., Ferretti, L., Fryer, H.R., MacInyre-Cockett, G., de Cesare, M., Trebes, A., Piazza, P., Buck, D. and Todd, J.A., 2021. Early Analysis of a potential link between viral load and the N501Y mutation in the SARS-COV-2 spike protein. *medRxiv*.
- Ward, C.M., Aumann, R.A., Whitehead, M.A., Nikolouli, K., Leveque, G., Gouvi, G., Fung, E., Reiling, S.J., Djambazian, H., Hughes, M.A. and Whiteford, S., 2021. White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. *Nature communications*, 12(1), pp.1-12.
- Thomson, E.C., Rosen, L.E., Shepherd, J.G., Spreafico, R., da Silva Filipe, A., Wojcechowskyj, J.A., Davis, C., Piccoli, L., Pascall, D.J., Dillen, J. and Lytras, S., 2021. Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. *Cell*
- Ball, A.L., Bloch, K.M., Rainbow, L., Liu, X., Kenny, J., Lyon, J.J., Gregory, R., Alfirevic, A. and Chadwick, A.E., 2021. Assessment of the impact of mitochondrial genotype upon drug-induced mitochondrial dysfunction in platelets derived from healthy volunteers. *Archives of Toxicology*, pp.1-13.
- Duncan, J.S., Angell, J.W., Richards, P., Lenzi, L., Staton, G.J., Grove-White, D., Clegg, S., Oikonomou, G., Carter, S.D. and Evans, N.J., 2021. The dysbiosis of ovine foot microbiome during the development and treatment of contagious ovine digital dermatitis. *Animal microbiome*, 3(1), pp.1-21.
- Salguero, F.J., White, A.D., Slack, G.S., Fotheringham, S.A., Bewley, K.R., Gooch, K.E., Longet, S., Humphries, H.E., Watson, R.J., Hunter, L. and Ryan, K.A., 2021. Comparison of rhesus and cynomolgus macaques as an infection model for COVID-19. *Nature Communications*, 12(1), pp.1-14.

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

- Carrieri, A.P., Haiminen, N., Maudsley-Barton, S., Gardiner, L.J., Murphy, B., Mayes, A.E., Paterson, S., Grimshaw, S., Winn, M., Shand, C. and Hadjidoukas, P., 2021. Explainable AI

reveals changes in skin microbiome composition linked to phenotypic differences. *Scientific reports*, 11(1), pp.1-18.

- Jayasena Kaluarachchi, T.D., Campbell, P.M., Wickremasinghe, R., Ranasinghe, S., Wickremasinghe, R., Yasawardene, S., De Silva, H., Menike, C., Jayarathne, M.C.K., Jayathilake, S. and Dilhari, A., 2021. Distinct microbiome profiles and biofilms in Leishmania donovani-driven cutaneous leishmaniasis wounds. *Scientific reports*, 11(1), pp.1-14.
- Cao, Y., Dever, K., Sivasankaran, S.K., Nguyen, S.V., Macori, G., Naithani, A., Gopinath, G.R., Tall, B., Lehner, A., Stephan, R. and Srikumar, S., 2021. Alterations in the transcriptional landscape allows differential desiccation tolerance in different strains of Cronobacter sakazakii. *Applied and Environmental Microbiology*, pp.AEM-00830.
- Wondji, C.S., Hearn, J., Irving, H., Wondji, M.J. and Weedall, G., 2021. RNAseq-based gene expression profiling of the Anopheles funestus pyrethroid resistant strain FUMOZ highlights the predominant role of the duplicated CYP6P9a/b cytochrome P450s. *G3 Genes/ Genomes/ Genetics*.
- Worsley, S.F., Davies, C.S., Mannarelli, M.E., Hutchings, M.I., Komdeur, J., Burke, T., Dugdale, H.L. and Richardson, D.S., 2021. Gut microbiome composition, not alpha diversity, is associated with survival in a natural vertebrate population.
- Hooton, S.P., Pritchard, A.C., Asiani, K., Gray-Hammerton, C.J., Stekel, D.J., Crossman, L.C., Millard, A.D. and Hobman, J.L., 2021. Laboratory Stock Variants of the Archetype Silver Resistance Plasmid pMG101 Demonstrate Plasmid Fusion, Loss of Transmissibility, and Transposition of Tn7/pco/sil Into the Host Chromosome. *Frontiers in Microbiology*, 12.
- Smith, S.L., Afonso, M.M., Roberts, L., Noble, P.J.M., Pinchbeck, G.L. and Radford, A.D., 2021. A virtual biobank for companion animals: A parvovirus pilot study. *Veterinary Record*, p.e556.
- Chan, B.K., Elmasry, M., Forootan, S.S., Russomanno, G., Bunday, T.M., Zhang, F., Brilliant, N., Starkey Lewis, P.J., Aird, R., Ricci, E. and Andrews, T.D., 2021. Pharmacological Activation of Nrf2 Enhances Functional Liver Regeneration. *Hepatology*.
- Bushell, F., Herbert, J.M., Sannasiddappa, T.H., Warren, D., Turner, A.K., Falciani, F. and Lund, P.A., 2021. Mapping the Transcriptional and Fitness Landscapes of a Pathogenic E. coli Strain: The Effects of Organic Acid Stress under Aerobic and Anaerobic Conditions. *Genes*, 12(1), p.53.
- Yebra, G., Haag, A.F., Neamah, M.M., Wee, B.A., Richardson, E.J., Horcajo, P., Granneman, S., Tormo-Más, M.Á., de la Fuente, R., Fitzgerald, J.R. and Penadés, J.R., 2021. Radical genome remodelling accompanied the emergence of a novel host-restricted bacterial pathogen. *PLoS Pathogens*, 17(5), p.e1009606.

- Kirse, A., Bourlat, S.J., Langen, K. and Fonseca, V.G., 2021. Metabarcoding Malaise traps and soil eDNA reveals seasonal and local arthropod diversity shifts. *Scientific reports*, 11(1), pp.1-12.
- Radapong, S.A.R.A.Y.U.T., 2021. Investigation of oxyresveratrol cytotoxicity (Doctoral dissertation, Liverpool John Moores University).
- Buttimer, C., Lynch, C., Hendrix, H., Neve, H., Noben, J.P., Lavigne, R. and Coffey, A., 2020. Isolation and characterization of Pectobacterium phage vB PatM CB7: New insights into the genus Certrevirus. *Antibiotics*, 9(6), p.352.
- Kanakis, I., Alameddine, M., Folkes, L., Moxon, S., Myrtziou, I., Ozanne, S.E., Peffers, M.J., Goljanek-Whysall, K. and Vasilaki, A., 2021. Small-RNA sequencing reveals altered skeletal muscle microRNAs and snoRNAs signatures in weanling male offspring from mouse dams fed a low protein diet during lactation. *Cells*, 10(5), p.1166.
- Ferdousi, A., Chang, X. and Jones, M., 2021. Transcriptomic analysis for differential expression of genes involved in secondary metabolite production in Narcissus pseudonarcissus field derived bulb and in vitro callus. *Industrial Crops and Products*, 168, p.113615.
- Mahalhal, A., Burkitt, M.D., Duckworth, C.A., Hold, G.L., Campbell, B.J., Pritchard, D.M. and Probert, C.S., 2021. Long-Term Iron Deficiency and Dietary Iron Excess Exacerbate Acute Dextran Sodium Sulphate-Induced Colitis and Are Associated with Significant Dysbiosis. *International journal of molecular sciences*, 22(7), p.3646.
- Perez-Sepulveda, B.M., Predeus, A.V., Fong, W.Y., Parry, C.M., Cheesbrough, J., Wigley, P., Feasey, N.A. and Hinton, J.C., 2021. Complete Genome Sequences of African Salmonella enterica Serovar Enteritidis Clinical Isolates Associated with Bloodstream Infection. *Microbiology resource announcements*, 10(12).
- Slater, R., Frau, A., Hodgkinson, J., Archer, D. and Probert, C.A., 2021. Comparison of the Colonic Microbiome and Volatile Organic Compound Metabolome of Anoplocephala perfoliata Infected and Non-Infected Horses: A Pilot Study. *Animals* 2021, 11, 755.
- Olofsson, J.K., Curran, E.V., Nyirenda, F., Bianconi, M.E., Dunning, L.T., Milenkovic, V., Sotelo, G., Hidalgo, O., Powell, R.F., Lundgren, M.R. and Leitch, I.J., 2021. Low dispersal and ploidy differences in a grass maintain photosynthetic diversity despite gene flow and habitat overlap. *Molecular Ecology*, 30(9), pp.2116-2130.
- Richards-Rios, P., Wigley, P., López, J., Wormell, D. and Barbón, A., 2021. Changes in the faecal microbiome of pied tamarins (Saguinus bicolor) associated with chronic, recurrent diarrhoea and weight loss. *Animal Microbiome*, 3(1), pp.1-15.



- Hearn, J., Plenderleith, F. and Little, T.J., 2021. DNA methylation differs extensively between strains of the same geographical origin and changes with age in *Daphnia magna*. *Epigenetics & Chromatin*, 14(1), pp.1-14.
- Cicconardi, F., Lewis, J.J., Martin, S.H., Reed, R.D., Danko, C.G. and Montgomery, S.H., 2021. The effects of chromosome fusions on genetic diversity and evolutionary turnover of functional loci consistently depends on chromosome size. *bioRxiv*.
- Orkin, J.D., Montague, M.J., Tejada-Martinez, D., de Manuel, M., Del Campo, J., Hernandez, S.C., Di Fiore, A., Fontseré, C., Hodgson, J.A., Janiak, M.C. and Kuderna, L.F., 2021. The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. *Proceedings of the National Academy of Sciences*, 118(7).
- Andreassi, C., Luisier, R., Crerar, H., Darsinou, M., Blokzijl-Franke, S., Lenn, T., Luscombe, N.M., Cuda, G., Gaspari, M., Saiardi, A. and Riccio, A., 2021. Cytoplasmic cleavage of IMPA1 3' UTR is necessary for maintaining axon integrity. *Cell Reports*, 34(8), p.108778.
- Bouyer, J., Culbert, N.J., Dicko, A.H., Pacheco, M.G., Virginio, J., Pedrosa, M.C., Garziera, L., Pinto, A.M., Klaptocz, A., Germann, J. and Wallner, T., 2020. Field performance of sterile male mosquitoes released from an uncrewed aerial vehicle. *Science Robotics*, 5(43).