

Selected Publications from 2018

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

- Copple, I.M., den Hollander, W., Callegaro, G., Mutter, F.E., Maggs, J.L., Schofield, A.L., Rainbow, L., Fang, Y., Sutherland, J.J., Ellis, E.C., Ingelman-Sundberg, M., Fenwick, S.W., Goldring, S.E., van de Water, B., Stevens, J.L., Park, B.K. Characterisation of the NRF2 transcriptional network and its response to chemical insult in primary human hepatocytes: implications for prediction of drug-induced liver injury. *Springer* (2018).
- Matthews, B.J., Dudchenko, O., et al. Improved reference genome of *Aedes aegypti* informs arbovirus vector control. *Nature* (2018)
- Hall, R.J., Flanagan, L.A., Bottery, M.J., Springthorpe, V.J., Thorpe, S., Darby, A.C., Wood, A.J., Thomas, G.H. A Tale of Three Species: Adaptation of *Sodalis glassinidius* to tsetse biology, *Wiggleworthia* metabolism and host diet. *White Rose Research Online* (2018).
- Daly, K., Kelly, J., Moran, A.W., Bristow, R., Young, I.S., Cossins, A.R., Bravo, D., Shirazi-Beechey, S.P. Host selectively contributes to shaping intestinal microbiota of carnivorous and omnivorous fish. *J. Gen. Appl. Microbiol.* Advance Publication (2018).
- Burgess, S.T.G., Bartley, K., Nunn, F., Wright, H.W., Hughes, M.A., Gemmell, M., Haldenby, S., Paterson, S.J., Rombauts, S., Tomley, F.M., Blake, D.P., Pritchard, J., Schicht, S., Strube, C., Oines, O., Van Leeuwen, T., Van de Peer, Y., Nisbet, A.J. Draft Genome Assembly of the Poultry Red Mite, *Dermanyssus gallinae*. *American Society for Microbiology* (2018).
- Bay, V., Griffiths, B., Carter, S., Evans, N.J., Lenzi, L., Bicalho, R.C., Oikonomou, G. 16S rRNA amplicon sequencing reveals a polymicrobial nature of complicated claw horn disruption lesions and interdigital phlegmon in dairy cattle. *Europe PMC* (2018).
- Thornton, S., Kalirai, H., Sibbring, J., Olohan, L., Kenny, J., Lui, X., Haldenby, S., Hertz-Fowler, C., Coupland, S.E. Developing Next Generation Sequencing (NGS) Panels for Uveal Melanoma to Detect Copy Number and Single Nucleotide Variants; comparing PCR and Hybrid Capture Target Enrichment. *ARVO Annual Meeting Abstract* (2018).
- Lum, F.M., Lee, D., Chua, T.K., Tan, J.J.L., Lee, C.Y.P., Liu, X., Fang, Y., Lee, B., Yee, W.X., Rickett, N.Y., Chia, P.Y., Lim, V., Leo, Y.S., Matthews, D.A., Hiscox, J.A., Ng, L.F.P. Zika Virus Infection Preferentially Counterbalances Human Peripheral Monocyte and/or NK Cell Activity. *mSphere* (2018) Mar 28;3(2).
- Gardiner, L-J., Joynson, R., Omony, J., Rusholme-Pilcher, R., Olohan, L., Lang, D., Bai, C., Hawkesford, M., Salt, D., Spannagl, M., Mayer, K.F.X., Kenny, J., Bevan, M., Hall, N., Hall,



- A. Hidden variation in polyploid wheat drives local adaptation. *Genome Research* (2018). 28:1–14.
- Foulkes, A.C., Watson, D.S., Carr, D.F., Kenny, J.G., Slidel, T., Parslew, R., Pirmohamed, M., PSORT Consortium, Anders, S., Reynolds, N.J., Griffiths, C.E.M., Warren, R.B., Barnes, M.R. A framework for multi-omic prediction of treatment response to biologic therapy for psoriasis. *Journal of Investigative Dermatology* (2018) Jul 17. pii: S0022-202X(18)32355-8.
 - Siozios, S., Pilgrim, J., Darby, A.C., Baylis, M., Hurst, G.D.D. The draft genome of straining cCpun from biting midges establishes *Cardinium* as a paraphyletic group and reveals a novel gene family expansion in a symbiont. *PeerJ Preprints* (2018).
 - Al-Khafaji, A.M., Clegg, S.R., Pinder, A.C., Luu, L., Hansford, K.M., Seelig, F., Dinnis, R.E., Margos, G., Medlock, J.M., Feil, E.J., Darby, A.C., McGarry, J.W., Gilbert, L., Plantard, O., Sasser, D., Makepeace, B.L. Multi-locus sequence typing of *Ixodes ricinus* and its symbiont *Candidatus* Midichloria mitochondrii across Europe reveals evidence of local co-cladogenesis in Scotland. *Science Direct* (2018)
 - Abbas, A.H., Pereira, S.S., D'Archivio, S., Wickstead, B., Morrison, L., Hall, N., Hertz-Fowler, C., Darby, A.C., Jackson, A.P. The structure of a conserved telomeric region associated with variant antigen loci in the blood parasite *Trypanosoma congolense*. *Genome Biology and Evolution* (2018).
 - Timpon, A.J., de Mestre, A.M., Elliott, J., Haris, P.A., Cheng, Z., Mirczuk, S.A., Callan, L., Rainbow, L., Menzies-Gow, N.J. Seasonal and Dietary Influences on Adipose Tissue and Systemic Gene Expression in Control and Previously Laminitic Ponies. *Science Direct* (2018).
 - Hicks, N., Liu, X., Gregory, R., Kenny, J., Lucaci, A., Lenzi, L., Paterson, D.M., Duncan, K.R. Temperature driven changes in benthic microbial diversity influences biogeochemical cycling in coastal sediments. *Frontiers in Microbiology* (2018).
 - Gemmell, M.R., Berry, S., Mukhopadhyay, I., Hansen, R., Nielsen, H.L., Bajaj-Elliott, M., Nielsen, H. and Hold, G.L., 2018. Comparative genomics of *Campylobacter concisus*: Analysis of clinical strains reveals genome diversity and pathogenic potential. *Emerging microbes & infections*, 7(1), pp.1-17.
 - Timpon, A.J., de Mestre, A.M., Elliott, J., Harris, P.A., Cheng, Z., Mirczuk, S.M., Callan, L., Rainbow, L., Menzies-Gow, N.J. Seasonal and dietary influences on adipose tissue and systemic gene expression in control and previously laminitic ponies. *Journal of Equine Veterinary Science* (2018).
 - Frau, A., Ijaz, U.Z., Campbell, B., Darby, A.C., Kenny, J.G., Hall, N., Probert, C. OWE-010 Bacterial and fungal communities in faeces and biopsies in IBD. *BMJ Journals* (2018).

- Bell-Sakyi, L., Darby, A.C., Baylis, M., Makepeace, B.L., The Tick Cell Biobank: A global resource for *in vitro* research on ticks, other arthropods and the pathogens they transmit. *Science Direct* (2018).
- Olohan, L., Gardiner, L-J., Lucaci, A., Steuernagel, B., Wulff, B., Kenny, J., Nall, N., Hall, A. A modified sequence capture approach allowing standard and methylation analyses of the same enriched genomic DNA sample. *BMC Genomics* (2018).
- Warrenfeltz, S., Basenko, E.Y., Crouch, K., Harb, O.S., Kissinger, J.C., Roos, D.S., Shanmugasundram, A., Silva-Franco, F. EuPathDB: The Eukaryotic Pathogen Genomics Database Resource. *Eukaryotic Genomic Databases* (2018).
- Burgess, S.T.G., Barley, K., Marr, E.J., Wright, H.W., Weaver, R.J., Prickett, J.C., Hughes, M.A., Haldenby, S., Le, P.T., Rombauts, S., Van Leeuwen, T., Van de Peer, Y., Nisbet, A.J. Draft Genome Assembly of the Sheep Scab Mite, *Psoroptes ovis*. *Genome Announcements* (2018).
- Heys, C., Lize, A., Blow, F., White, L., Darby, A.C., Lewis, Z.J. The effect of gut microbiota elimination in *Drosophila melanogaster*: A how-to guide for host-microbiota studies. *Wiley Ecology and Evolution* (2018). DOI: 10.1002/ece3.3991.
- Basenko, E.Y., Pulman, J.A. Shanmugasundram, A., Harb, O.S., Crouch, K., Starns, D., Warrenfeltz, S., Aurrecochea, C., Stoeckert Jr., C.J., Kissinger, J.C., Roos, D., Hertz-Fowler, C. FungiDB: an integrated bioinformatic resource for fungi and oomycetes. *Journal of Fungi* (2018).
- Williams, D., Fothergill, J.L., Evans, B., CAples, J., Haldenby, S., Walshaw, M.J., Brockhurst, M.J., Winstanley, C., Peterson, S. Transmission and lineage displacement drive rapid population genomic flux in cystic fibrosis airway infections of a *Pseudomonas aeruginosa* epidemic strain. *Microbiology Society* (2018). doi:10.1099/mgen.0.000167
- Coates-Brown, R., Moran, J., Pongchaikul, P., Darby, A.C., Horsburgh, M.J. Comparative Genomics of *Staphylococcus* Reveals Determinants of Speciation and Diversification of Antimicrobial Defense. *bioRxiv* (2018).
- Gaither, M.R., Gkafas, G.A., de Jong, M., Sarigol, F., Neat, F., Regnier, T., Moore, D., Grocke, D.R., Hall, N., Liu, X., Kenny, J.G., Lucaci, A., Hughes, M.A., Haldenby S., Hoelzel, A.R. Genomics of habitat choice and adaptive evolution in a deep-sea fish. *Nature Ecology & Evolution* (2018) doi:10.1038/s41559-018-0482-x.
- Kimuda, M.P., Noyes, H., Mulindwa, J., Enyaru, J., Alibu, V.P., Sidibe, I., Mumba Ngoyi, D., Hertz-Fowler, C., MacLeod, A., Tastan Bishop, O., Matovu, E., TrypanoGEN Research Group as members of The H3Africa Consortium. No evidence for association between APOL1 kidney disease risk alleles and Human African Trypanosomiasis in two Ugandan populations. *PLoS Negl Trop Dis.* (2018) Feb 22;12(2):e0006300. doi: 10.1371/journal.pntd.0006300.

- Pascoal, S., Liu, X., Fang, Y., Paterson, S., Ritchie, M., Rockliffe, N., Zuk, M., Bailey, N. Increased socially mediated plasticity in gene expression accompanies rapid adaptive evolution. *Ecology Letters* (2018) DOI: 10.1111/ele.12920.
- Leng, J., Proudman, C., Darby, A.C., Blow, F., Townsend, N., Miller, A., Swann, J. Exploration of the faecal microbiota and biomarker discovery in equine grass sickness. *Journal of Proteome Research* (2018).
- Dong, X., Chaisiri, K., Xia, D., Armstrong, S.D., Fang, Y., Donnelly, M.J., Kadowaki, T., McGarry, J.W., Darby, A.C., Makepeace, B.L. Genomes of trombidid mites reveal novel predicted allergens and laterally-transferred genes associated with secondary metabolism. *bioRxiv* (2018) doi: <https://doi.org/10.1101/259044>.

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

- Costeira, R., Dohert, R., Allen, C.C.R., Larkin, M.J., Kulakov, L.A. Analysis of viral and bacterial communities in groundwater associated with contaminated land. *Science Direct* (2018).
- Davies, H.S., Rosas-Moreno, J., Cox, F., Lythgoe, P., Bewsher, A., Livens, F.R., Robinson, C. H., Pittman, J.K. Multiple environmental factors influence ²³⁸U, ²³²Th and ²²⁶Ra bioaccumulation in arbuscular mycorrhizal-associated plants. *Science Direct* (2018).
- Padfield, D., Buckling, A., Warfield, R., Lowe, C., Yvon-Durocher, G. Linking phytoplankton community metabolism to the individual size distribution. *Ecology Letters* (2018).
- Wilding, C.S., Weedall, G.D. Morphotypes of the common beadlet anemone *Actinia equina* (L.) are genetically distinct. *Science Direct* (2018).
- Newham, K.K., Garnett, M.H., Robinson, C.H., Cox, F. Discrete taxa of saprotrophic fungi respire different ages of carbon from Antarctic soils. *Scientific Reports* 8 Article number: 7866 (2018).
- Jones, J.C., Fruciano, C., Marchant, J., Hildebrand, F., Forslund, S., Bork, P., Engel, P., Hughes, W.O.H. The gut microbiome is associated with behavioural task in honey bees. *Insectes Sociaux* (2018).
- Diaz, M., Wegmann, U., Akinyemi, N., Oguntoyinbo, F.A., Sayavedra, L., Mayer, M.J., Narbad, A. Complete Genome Sequence of *Ochrobactrum haematophilum* F11154, Isolated from Kanu-Zaki, a Nigerian Millet-Based Fermented Food. *American Society for Microbiology* (2018).

- McGee, C.F., Storey, S., Clipson, N., Doyle, E. Concentration-dependent responses of soil bacterial, fungal and nitrifying communities to silver nano and micron particles. *Environmental Science and Pollution Research* (2018).
- Piwosc, K., Calkiewicz, J., Golebiewski, M., Creer, S. Diversity and community composition of pico- and nanoplanktonic protists in the Vistula River estuary (Gulf of Gdansk, Baltic Sea). Science Direct (2018) doi.org/10.1016/j.ecss.2018.04.013.
- Lyons, T., Bielak, A., Doyl, E., Kuhla, B. Variations in methane yield and microbial community profiles in the rumen of dairy cows as they pass through stages of first lactation. *Journal of Dairy Science* (2018).
- Broberg, M., Doonan, J., Mundt, F., Denman, S., McDonald, J.E. Integrated multi-omic analysis of host microbiota interactions in acute oak decline. *BMC* (2018) 6:21 <https://doi.org/10.1186/s40168-018-0408-5>.
- Wang, K., Yin, X., Mao, H., Chu, C., Tian, Y. Changes in structure and function of fungal community in cow manure composting. *Bioresource Technology* (2018) <https://doi.org/10.1016/j.biortech.2018.01.064>
- Sharp, C., Golubchik, T., Gregory, W.F., McNaughton, A.L., Gow, N., Selvaratnam, M., Miream A., Foster, D., Andersson, M., Klenerman, P., Jeffery, K., Matthews, P.C. Oxford Screening CSF and Respiratory samples ('OSCAR'): results of a pilot study to screen clinical samples from a diagnostic microbiology laboratory for viruses using Illumina next generation sequencing. *BMC Research Notes* (2018) 11:120. <https://doi.org/10.1186/s13104-018-3234-8>.
- Grébert, T., Doré, H., Partensky, F., Farrant, G.K., Boss, E.S., Picheral, M., Guidi, L., Pesant, S., Scanlan, D.J., Wincker, P., Acinas, S.G., Kehoe, D.M., Garczarek, L. Light color acclimation is a key process in the global ocean distribution of *Synechococcus cyanobacteria*. *PNAS* (2018) <https://doi.org/10.1073/pnas.1717069115>.
- Almeida, E.L., Margassery, L.M., Kennedy, J., Dobson, A. Draft Genome Sequence of the Antimycin-Producing Bacterium *Streptomyces* sp. Strain SM8, Isolated from the Marine Sponge *Haliclona simulans*. *Genome Announcements* 6, no. 4 (2018): e01535-17
- Hesse, E., O'Brien, S., Tromas, N., Bayer, F., Luján, A.M., Veen, E.M., Hodgson, D.J., Buckling, A. Ecological selection of siderophore-producing microbial taxa in response to heavy metal contamination. *Ecology Letters* 21, no. 1 (2018): 117-127.
- Heidrich, E.S., Dolfig, J., Wade, M.J., Sloan, W.T., Quince, C., Curtis, T.P. Temperature, inocula and substrate: Contrasting electroactive consortia, diversity and performance in microbial fuel cells. *Bioelectrochemistry* 119 (2018): 43-50

- Ainsworth, S., Petras, D., Engmark, M., Süßmuth, R.D., Whiteley, G., Albulescu, L-O., Kazandjian, T.D., et al. The medical threat of mamba envenoming in sub-Saharan Africa revealed by genus-wide analysis of venom composition, toxicity and antivenomics profiling of available antivenoms. *Journal of proteomics* 172 (2018): 173-189.