Adam M Blanchard BSc PhD AFHEA   **email:** adam.blanchard@nottingham.ac.uk

Career History

(2019 – Present) Assistant Professor in Computational Biology, *School of Veterinary Medicine and Science, University of Nottingham.*

Course coordinator for MRes Apprenticeship in Bioinformatics. Lecturing MRes Bioinformatics methods, MRes project supervisor.

(2018 – 2019) Senior Lecturer in Genetics, *School of Animal, Rural and Environmental Sciences, Nottingham Trent University.*

Courses Leader for the MSc/MRes/PGDip in Animal Health and Welfare and MSc/MRes in Anthrozoology. Module leader for Animal Health and Disease Surveillance (level 7), Animal and Equine Genetics, and Zoo Conservation Genetics (level 6), Animal Reproduction and Breeding, and Management of Reproduction in Zoo Animals (level 5). Module tutor for Dissertation projects (level 6) and Research Projects (level 7). Personal tutor for level 7 MRes and MSc students and level 4 BSc Hons Animal Biology and BSc Hons Zoo Biology students.

(2018 – Present) Review Editor *Frontiers in Cellular and Infection Microbiology.*

Member of the editorial board and peer review of articles submitted to the journal *Molecular Bacterial Pathogenesis.* Ad-Hoc reviewer for Nature Scientific Reports, BMC Veterinary Research, Frontiers in Microbiology and Plos One

(2015 – 2018) Post-Doctoral Research Fellow - BBSRC Animal Health Research Club *School of Veterinary Medicine and Science, The University of Nottingham*.

Understanding inflammatory processes in ovine footrot to inform rational vaccine design (BB/M012085/1). Development of a multi-tiered MLST schema for the assessment of *Dichelobacter nodosus* (D. nodosus) isolate global diversity. Development of a 3D tissue culture infection model to investigate the host immune response to footrot by recognition of *D nodosus*. Production of ovine recombinant cytokines (IL1-β). Development of transfection studies to monitor activation of TLRs due to infection with *D. nodosus*.

(2009 – 2012) Research Assistant *School of Veterinary Medicine and Science, The University of Nottingham*.

Management of the microbiology laboratories and facilites. Day to day management of the laboratories. Training of staff to use scientific equipment. Supervision of postgraduates and undergraduates in the laboratories. Carrying out generation of preliminary data on projects in multiple disciplines.

(2007 – 2009) Senior Technician *Harlan Laboratories, Shardlow, Derbyshire*.

Management of necropsy technical team. Day to day management of the laboratories. Training of staff to use scientific equipment. Maintaining QA level data.

Higher Education

(2012 – 2015) PhD Demonstratorship *School of Veterinary Medicine and Science, The University of Nottingham*.

Functional annotation of the *Streptococcus uberis* genome sponsored by Zoetis. Development of a laboratory and bioinformatic workflow to determine the essential genome of Streptococci of veterinary and human importance. Additional responsibilities of undergraduate teaching (200 hours a year) and completion of the Associates Teaching Program (ATP) at the University of Nottingham.

(2003 – 2006) BSc Hons Animal Science (Overall 2:1) *School of Animal, Rural and Environmental Sciences, Nottingham Trent University*.

Scholarships

Cold Spring Harbour Helmsley Scholarship: Programming for Biology, Cold Spring Harbour, New York, October 2017

A 4-week intensive course which was as an introduction to using Python 3 for data analysis in a biology setting. This covered the manipulation of data outputs and integrating multiple bioinformatic packages to create a pipeline for data analysis.

Financial Awards

BBSRC (COI): Prediction of phenotype from genotype with respect to bacterial infection, (Co-funded by Dechra) 2019, **£713,000**

Investigating host pathogen interactions by utilising bacterial genome wide association, essential gene determination and molecular typing strategies to identify functionally important coding sequences. This will identify specific and combinatory alleles that underpin the ability of bacterial strains to cause infection, whilst developing a predictive diagnostic workflow.

International Development Research Centre (IRDC/CDRI) InnoVet AMR (COI):
Disease intervention targets for porcine *Streptococcus suis* infections in Vietnam (co-funded by the Canadian Government and the UK Department of Health and Social Care) 2019, **£674,000**

Our aim is to focus on virulence determinants of *S. suis* that circumvent the innate immune response by identifying bacterial components essential for survival or proliferation in whole blood and those responsible for resistance to innate anti-microbial peptides (AMPs). Vaccines aimed at inhibition of such activities through neutralising antibody delivered via maternal colostrum will provide protection during weaning. Given the importance of antimicrobial resistance (AMR) and antibiotic usage for the treatment of these diseases in the porcine, poultry, ruminant and aquaculture industries, our approach provides a high probability of identifying vaccine targets for recombinant vaccine development and feasible, cost-effective vaccination strategy to encourage widespread uptake within LMIC.

Research for Clinical Benefit, University of Nottingham (COI)
Neonatal Group B Streptococcus characterisation of invasive and carriage of strains, 2019, **£12,840**

The aim of this proposal is to perform comprehensive analyses of GBS strains associated with clinical disease in neonates and those associated with carriage, to determine genetic relationships and identify key genes/proteins for future control and diagnostic strategies.

Global Challenges Research Funds (GCRF) UKRI (COI):
Investigation of reproductive failure in Ethiopian dairy cattle to improve dairy-based food security, 2019, **£49,536**

The overarching aim of this pilot study proposal is to identify the pathogens responsible for reproductive failure in dairy cattle in Ethiopia and identify mechanisms for implementation of improved treatment strategies that support, animal welfare, human wellbeing and the reduction of antibiotic use. This will focus on comparative analysis of the bacterial causes of (endo)metritis and stillbirth/abortion in Ethiopia through culture and sequence based analysis. This has important implications for the UK dairy industry, given that common metritis bacterial pathogens have been identified in both countries. Our hypothesis is that identification and management of the main causative pathogens for reproductive failure will allow targeted therapeutics and improved management enabling increased production capacity of the dairy sector in Ethiopia. This will be addressed through the following objectives.

Capital Investment, Nottingham Trent University (PI):
Funding secured for new laboratory equipment for the "Microbial Communities Research Centre", 2018, **£110,000**

EPSRC/Bridging the Gap (COI):
The role of sheep in the transmission of AMR between farms and between environments – recolonisation of sheep feet post-footbath treatment, 2017, **£27,133**

Monaghan, T., Sloan, T., Stockdale, S., **Blanchard, A.M**., Emes, R., Wilcox, M., Biswas, R., Nashine, R., Manke, S., Gandhi, J., Jain, P., Bhotmange, S., Ambalkar, S., Satav, A., Draper, L., Hill, C., Kashyap, R., (2020). Metagenomics Reveals Impact of Geography and Acute Diarrhoeal Disease on the Central Indian Human Gut Microbiome. Gut Microbes.

Davies, P.L., **Blanchard, A.M.,** Staley, C.E., Bollard, N.J., Coffey, T.J., Totemeyer, S., (2020). Genomic heterogeneity of Dichelobacter nodosus within and between UK sheep flocks and between age groups within a flock. BMC Microbiol.

Sarker, N., Fabijan, J., Seddon, J., Tarlinton, R., Owen, H., Simmons, G., Thia, J., **Blanchard, A.M.,** Speight, N., Kaler, J., Emes, R.D., Woolford, L., Trott, D., Hemmatzadeh, F., Meers, J., (2019). Genetic diversity of Koala retrovirus env gene subtypes: insights into northern and southern koala populations. J. Gen. Virol.

Reyes, J., Rodriguez-Lecompte, J.C., **Blanchard, A.M**., McClure, J.T., Sánchez, J., (2019). Molecular variability of Streptococcus uberis isolates from intramammary infections in Canadian dairy farms from the Maritime region, Canadian Journal of Veterinary Research.

Shaw, L.M., **Blanchard, A.M**., Chen, Q., An, X., Davies, P., Tötemeyer, S., Zhu, Y.-G., Stekel, D.J., (2019). DirtyGenes: testing for significant changes in gene or bacterial population compositions from a small number of samples. Sci. Rep.

Blanchard, A.M., Jolley, K.A., Maiden, M.C.J., Coffey, T.J., Maboni, G., Staley, C.E., Bollard, N.J., Warry, A., Emes, R.D., Davies, P.L., Tötemeyer, S., (2018). The Applied Development of a Tiered Multilocus Sequence Typing (MLST) Scheme for Dichelobacter nodosus. Front. Microbiol.

Agbaje, M., Rutland, C.S., Maboni, G., **Blanchard, A.M**., Bexon, M., Stewart, C., Jones, M.A., Totemeyer, S., (2018). Novel inflammatory cell infiltration scoring system to investigate healthy and footrot affected ovine interdigital skin. PeerJ.

Maboni, G., **Blanchard, A.M**., Frosth, S., Stewart, C., Emes, R., Tötemeyer, S., (2017). A distinct bacterial dysbiosis associated skin inflammation in ovine footrot. Sci. Rep.

Maboni, G., Davenport, R., Sessford, K., Baiker, K., Jensen, T.K., **Blanchard, A.M**., Wattegedera, S., Entrican, G., Tötemeyer, S., (2017). A Novel 3D Skin Explant Model to Study Anaerobic Bacterial Infection. Front. Cell. Infect. Microbiol.

Blanchard, A.M., Egan, S.A., Emes, R.D., Warry, A., Leigh, J.A., (2016). PIMMS (Pragmatic Insertional Mutation Mapping System) Laboratory Methodology a Readily Accessible Tool for Identification of Essential Genes in Streptococcus. Front. Microbiol.

Blanchard, A.M., Leigh, J.A., Egan, S.A., Emes, R.D., (2015). Transposon insertion mapping with PIMMS – Pragmatic Insertional Mutation Mapping System. Front. Genet.