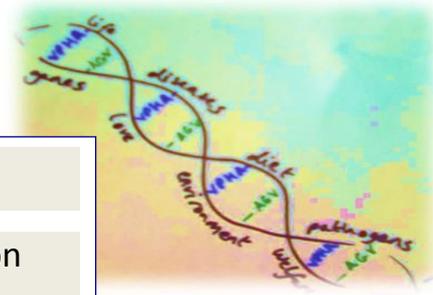


SEQUENCES & CONSEQUENCES

Bringing together the strands of life



PROVISIONAL PROGRAMME

Different from previous conferences: **Official dinner on Friday evening, 11 October 2019 with the conference finishing on Saturday** afternoon. It costs **£100 less** than previous autumn conferences.

Registration starts on Saturday at 8.00 am, Conference starts at 9.30 Finishes 16.30 – 17.00



DR ALEX CAGAN

How can whales exist? Somatic mutations across the animal kingdom!

Organisms accumulate mutations in the DNA in their cells throughout their lifetime. This process can lead to cancer and may contribute to aging. Recent advances in genome sequencing have enabled us to study how these somatic mutations accumulate in normal human tissues. However, we know almost nothing about how somatic mutations accumulate in non-human species. A better understanding of how mutations occur in non-human species may have major implications for our understanding of cancer and ageing, including improved monitoring and possibly novel preventative therapeutic strategies.

Alex studied anthropology and primate behaviour at the University of Cambridge. He then moved to Germany to obtain his PhD at the Max Planck Institute of evolutionary anthropology in Leipzig. His PhD research was on the genetic basis of tameness in domestic animals, which involved studying silver fox, mink and rat populations that were experimentally domesticated in Novosibirsk, Siberia in the world's longest running animal breeding experiment. Alex now works as a post-doctoral researcher at the Wellcome Sanger Institute. His current work is focused on investigating somatic mutations in non-human species and their implications for ageing, cancer and other diseases.



DR LESLEY LARKIN

Surveillance Lead, Gastrointestinal Infections, Public Health England

Whole genome sequencing – sink or swim...

The replacement of traditional typing methods for Salmonella and other zoonotic pathogens with whole genome sequencing technology is revolutionising our ability to apply 'high definition' case ascertainment criteria, identify foodborne pathogen sources and transmission pathways and assess efficacy of control interventions. With these

opportunities come challenges too and the role of veterinarians in public health protection is now more vital than ever before.

Lesley qualified as a veterinarian from Onderstepoort, South Africa and then moved to the UK for what was intended to be a short stay to ‘explore Europe’. Nine years later, spent mostly in production animal practice, she was still working in the UK. After moving to Defra at the end of 2006, she worked as a Veterinary Advisor on zoonoses, primarily focussed on control of foodborne zoonoses and the implementation of the Salmonella National Control Programmes. In 2015 she moved to a new role as an epidemiologist at Public Health England working on infectious gastrointestinal disease surveillance and outbreak response.



ELEANOR BROWN

Veterinary Head of TB Policy Advice, APHA

Bovine TB genetic analysis – understanding and using the bovine TB “fingerprint”

In England, bovine TB is geographically clustered, as indicated by different genetic types. Recent advances in Whole Genome Sequencing gives us a bTB genetic fingerprint that opens up the possibility to better understand and even quantify transmission pathways. This presentation will give an overview of this new tool, from research to policy use.

Ele graduated from the University of Cambridge in 2005. She worked in mixed practice before undertaking an MSc in the control of infectious disease in animals. She currently works for APHA, as the head veterinary adviser to Defra’s TB Programme.



CHARLIE MASON Humane Slaughter Association ***Technical Director, Humane Slaughter Association***

Consequences of Surveying livestock markets in England and Wales

The results of an independent survey of a representative sample markets across England and Wales, carried out by the Humane Slaughter Association (HSA) in 2017 /2018 compared to the results of a similar study, carried out by the HSA and the Royal Veterinary College in 2006/07. In terms of facilities some improvements were recorded in different areas in a number of markets. By disseminating the results of this survey, it is hoped that plans for any new livestock markets, including improvements to existing premises, and other livestock handling facilities such as collection centres and abattoir lairages, will include the improved features highlighted in the HSA report.



DR JOANNE CONINGTON SRUC

Breeding for host resistance to disease in sheep and goats – using genomic selection in practice

Livestock breeding methods have traditionally used breeding values to identify superior livestock. The use of genomic information to improve health and welfare is now routinely being used in some livestock sectors. The challenges and opportunities that genomic selection brings to the sheep and goats, and what needs to be in place for it to work effectively will be discussed.

Joanne is Head of the Agriculture Department at SRUC's Central Faculty (Edinburgh, Oatridge and Roslin). She is an applied livestock geneticist and has worked mainly on genetic and genomic technologies for sheep and goats. Her key area of interest is in the development of new phenotypes for their application into breeding programmes including disease resistance such as breeding for resistance to footrot, mastitis and internal parasites, lamb survival and adult longevity.