



Association of Veterinary Consultants

***The role of metagenomics in the identification of new pathogens***

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# AVC – role and activities

- Qualified veterinarians, international in geography and scope – Europe, Asia-Pacific, Africa, the Americas
- All working in small independent consultancies or SMEs
- Providing advice, practical assistance and support to enterprises such as feed additive, pharmaceutical, vaccines, food production companies & governments
- Organising laboratory, pre-clinical and clinical studies for new animal health and nutrition products
- Experienced with all types of animals including pets, farm, aquaculture and bees, epidemiology, disease management
- Some also involved in other aspects of applied biosciences eg human biotechnology, biomaterials, investment, market strategy, communication and education
- AVC is an Interested Party at EFSA, EMA and HMA and provides responses to consultations

# AVC and Emerging Risks - Topics

## Metagenomics

➔ **Definition & History**

➔ **Fields of use**

➔ **Application to detection of emerging pathogens**



# Metagenomics: Definition & History 1

- **The analysis of a collection of genetic material (genomes) from a mixed community of organisms (microbiome)**
- **“Metagenomics” first used in 1998 (Handelsman *et al.*) - soil microbiome analysis for Natural Product discovery**
- **Global Ocean Sampling 2003-2007**
- **Cultivation-independent**
- **Dependent on Polymerase Chain Reaction and other snipping, amplification, matching techniques**
- **Very much dependent on quality of existing sequence libraries**

# **Metagenomics: Definition & History 2**

- **Sequences can be cloned into industrial organisms and products of gene expression screened, even if organisms are unknown**
- **Sequences can be scanned against libraries to determine similarities or if are completely unknown**
- **Development of High-Throughput next-generation Sequencing technologies have accelerated use**
- **Development of Big Data management methods has significantly enhanced accuracy and impacts**
- **Shift from metagenome mining for new molecules to microbiome analysis for environmental, biodiversity, disease, physiology understanding**

# Metagenomics – Fields of Use 1

**Understanding and making use of metagenomics has applications in all “colours” of biotechnology**

- **red** – health-related, for humans and animals
- **green** – agriculture and crops
- **blue** – aquatic bioresources
- **white** – industrial
- **grey** – environmental
- **yellow** – food



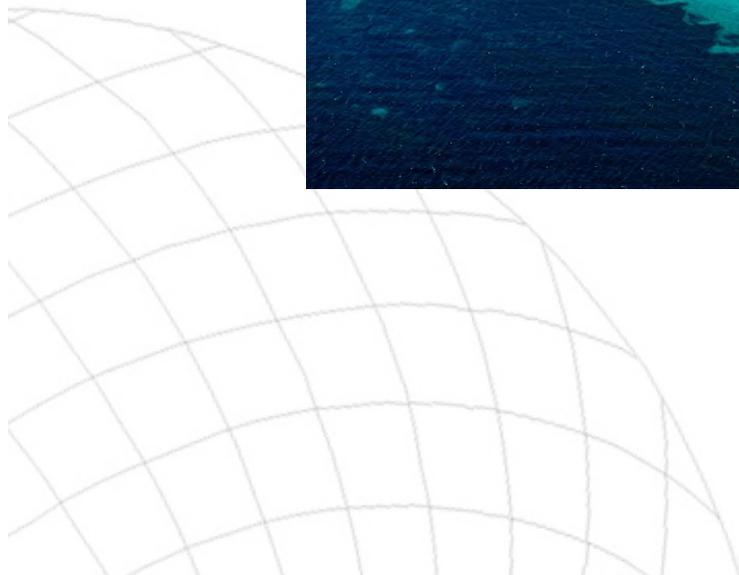
# Recent application – Lake Hillier Australia



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*Assumed to  
be Dunaliella  
– but primarily  
Purple  
Sulphur-  
Producing  
bacteria and  
Salinibacter*



## Metagenomics – Fields of Use 2

**Metagenomic profiling maps the genes of known organisms and picks up the presence of unknown organisms**

- Deep-sea microbiomes
- Gut, respiratory and skin microbiomes
- Microbial pathogens analysis
- Environmental remediation microbes
- Soil microbiome
- Rhizosphere organisms
- Viral metagenomics



# Metagenomics & Pathogens 1

Profiling of emerging pathogens or complexes requires sequence-independent amplification – eg displacement polymerase – and HTS systems eg Illumina

- Bocavirus, torque teno virus, circoviruses 2 & 3 in pigs
- Bee viruses
- Bat coronaviruses
- Bovine mixed pathogens
- Screening for arthropod vectors and pathogens

Use in diagnostics aided by Functional Metagenomics in addition to structural metagenomics

# Metagenomics & Pathogens 2

Sampling, sample preparation, nucleic acid release, removal of debris & interference etc., capture of sequence information, matching against libraries, assessment of degrees of similarity/homology, alignment with known pathogens, assignment to new/previously-unknown pathogens.

- Bovine respiratory viruses – adeno, influenza D, rhinitis A, plus new astrovirus, picobirnaviruses
- Bovine mastitis - deep Whole Metagenome Sequencing - specific bacterial genera, viruses and, surprisingly, Archaea
- Bovine reproductive disorders – strongest association with Bacteroidetes, Fusobacteria

# Metagenomics Refs

Handelsman J, Rondon MR *et al.* (1998) doi: 10.1016/s1074-5521(98)90108-9

Simon C and Daniel R (2009) doi: 10.1007/s00253-009-2233-z

Blomström A-L (2011) doi: 10.1080/01652176.2011.604971

Ng TFF, Kondov NO *et al.* (2015) doi: 10.1128/JVI.00064-15

Cuervo-Soto LI, López-Pazos SA and Batista-García RA (2018) doi: 10.5772/intechopen.72634

Hoque MN, Istiaq A *et al.* (2019) doi: 10.1038/s41598-019-49468-4

Kaszab E, Doszpoly A *et al.* (2020) doi: 10.1016/B978-0-12-816352-8.00002-3

Mohsin H, Asif A *etal.* (2020) doi: 10/1007/s00203-020-02105-5

Ong CT, Turni C *et al* (2021) doi: 10.1186/s42523-021-00106-3