

HIGH THROUGHPUT SEQUENCING, BIOINFORMATICS AND COMPUTATIONAL GENOMICS (HTS-BCG): EVOLUTION OR REVOLUTION?

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Over the past few decades, the development and application of novel molecular techniques have resulted in rapid advancements in animal disease diagnostics. The possibility of detecting and identifying infectious agents based on the presence of their nucleic acid molecules has been exploited by various molecular diagnostic methods. The OIE has actively supported the early adoption and use of these techniques. Recent advancements in high-throughput sequencing (HTS) and sequence data analysis have revolutionised research in many areas of biology and medicine. More specifically, HTS has dramatically increased the amount of sequence information that can be generated and allows unbiased sequencing without prior knowledge of the nucleotide content in a sample. Culture-independent HTS-based approaches to pathogen discovery have already demonstrated their ability to detect both known and novel microorganisms (1, 2). The field has evolved rapidly, making HTS technologies less costly and more accessible, and has reached a stage where HTS can be used as a resource-intensive but powerful tool for better diagnosis and disease control.

Our OIE Collaborating Centre has established skills and facilities for HTS-based detection and characterisation of viruses. The use of the latest HTS technologies and bioinformatics tools have improved our ability to detect even low-copy-number pathogens. However, the limit of detection is still determined by the abundance of the pathogens in relation to the host background. It is therefore important to consider sample preparation and enrichment protocols as integrated steps in the overall methodology. In collaboration with veterinary practitioners and partner institutes in the OIE global network, we have collected samples from a wide range of domestic and wild animals with various clinical syndromes of unknown aetiology. HTS-based investigations of these samples have resulted in the identification of a novel bocavirus, Torque Teno viruses, astroviruses, kobuviruses, new variants of honeybee and dolphin viruses, as well as other infectious agents (2).

1. HOFFMANN B., *et al.* (2012). Novel orthobunyavirus in cattle, Europe, 2011. *Emerg. Infect. Dis.*, **18** (3), 469–472.
2. BELÁK S., *et al.* (2013). New viruses in veterinary medicine, detected by metagenomic approaches. *Vet. Microbiol.*, **165** (1–2), 95–101.