Genotyping of microorganisms has become a key tool in the diagnosis of infectious agents. A variety of techniques to profile genetic material have been developed, and complete genome sequencing is emerging as the tool that might, used in perspective, change many of the basic parameters of infectious disease diagnosis and management. The use of high throughput sequencing (HTS), bioinformatics and computational genomics (BCG) and metagenomics is also increasing in the veterinary field. Sequence information is, therefore, playing an increasing role in the diagnosis and management of microbial infections, in the characterisation of infectious agents and in determining the likely distribution of their spread from place to place and through time.

The increasing reliance on generating and using sequence information and the concurrent ever-increasing trend towards global open information systems will have crucial and far-reaching implications for veterinary laboratories and the traditional notification and management of infectious diseases and food-borne infections.

The OIE has the responsibility of taking a leading and central role in the management, interpretation and use of information in animal health and the development of standards for the generation of data during investigations of animal infections on the farm and at any point along the ‘value chain’ linking animals to consumers.

The OIE considers sequence and sequence analysis data should be an integral and necessary part of the reporting of cases and animal disease outbreaks at the international level. New technological tools, including HTS-BCG and metagenomics, should, therefore, be introduced and used in the context of tried and accepted practices in animal disease diagnostics and control processes, including the laboratory quality assurance system.

Strategies, policies and practices for analysing and managing genomic sequence data are, therefore, a priority on the OIE agenda. This will include the development of standards for the generation, storage, management and interpretation of sequences and related epidemiological data. In particular, the objective is to develop a comprehensive approach and an open access database to collect, store and share sequence information relating to animal diseases and food safety.

The OIE intends to make full use of the competence and expertise of its worldwide Reference Centre network as the key to developing policies and practices for the management and use of sequence information under the remit of its mandate. To this end the OIE has launched a pilot project, in which the OIE Reference Centres will play a key role, to develop standards for the management of HTS-BCG to be included in the Manual of Diagnostic Tests and Vaccines for Terrestrial Animals and to include sequencing data in the OIE World Animal Health Information Database.