Research project IZSVe 05/14

Development and application of high-throughput sequencing strategies to identify known and unknown viruses in biological samples from domestic rabbit and avian species with unexplained illnesses

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Viral infectious diseases cause huge economical losses to poultry and commercial rabbit productions due to poor feed conversion efficiency, cost of therapy, increased mortality and in some cases to culling strategies for disease control. Furthermore, a major impact of virus infection, in particular in avian species, is also seen on human health. Some of the recent emerging infectious diseases in humans have been caused by viruses that had their origin in the avian species and the rising number of household pet birds has increased the risk of acquiring zoonotic diseases from these companion animals. The diagnosis of viral infections in domestic rabbit and avian species is complex, due to the wide range of potential pathogens that can present with the same clinical signs. In addition to the many known causes of these infections, it has been suggested that unrecognized infectious agents, including viruses, remain to be discovered.

Recent advances in the Next-Generation Sequencing (NGS) technologies have offered the potential of unbiased sequencing of the nucleic acid content of biological samples. However, these approaches have been rarely used in the veterinary environment and in particular for the characterization of viral diversity in rabbits and birds.

In this light, the aims of this study are to develop, optimize and streamline an NGS approach for culture-independent detection of viral diseases and to apply these methodologies both to archived and newly collected biological samples from poultry, commercial rabbits and most common pet birds in order to investigate the aetiology of unexplained illnesses and for eventually identifying emerging viruses.