

## Research program IZS VE 08/16

**Developing a metagenomic approach to reveal viral etiological agents in unexplained mortality events in freshwater finfish**

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Over the last 10 years, aquaculture has steadily grown worldwide fueled by the increasing demand of the market for seafood and the concurrent depletion of wild stocks. However, its outlook is threatened by diverse challenges, among which the more and more frequent viral disease outbreaks exacerbated by the adoption of intensive farming methods and operational techniques. In addition, emerging viruses have often been difficult to reveal either because unrecognized or unknown. Nowadays, the knowledge of fish viruses is still rather limited and this hampers the implementation of adequate health management tools in aquaculture.

Next-Generation Sequencing (NGS) technologies allow the sequencing of the whole nucleotide content of biological samples, thus permitting the study of complex microbial/viral communities independently of in vitro isolation procedures. However, these approaches have been marginally applied to the study of finfish viruses and in particular to investigate the etiology of mass mortalities in aquaculture.

In light of this, this study aims to:

1. develop, optimize and streamline an NGS approach for the detection of viral diseases in freshwater fish;
2. apply these methodologies both to archived and newly collected biological samples, in order to investigate the etiology of unexplained mortalities and eventually identify emerging viruses.