

Shifting from pathogen to pathobiome paradigm raises questions on infectious disease management strategies. Disease-based strategies can be antagonist to reach a level of animal health in animal farming systems. According to our results in Corsica, bovine tuberculosis, echinococcosis, trichinosis, hepatitis E virus and Aujeszky virus are pathogens found together in the same pig herds but these pathogens fall under various modes of regulations, based on the use of different tools.

For example, we show co-infection between Aujeszky and hepatitis E virus as an indicator of animal infectious interaction between domestic pigs and wild boars, which pattern is different according to herd management practices. Whereas Aujeszky virus is supposed to be the object of drastic management measures, HEV management does not exist. Else, whereas bovine tuberculosis and trichinosis are detected through systemic controls in slaughterhouses, bovine tuberculosis is subject to specific epidemiological surveys and prophylaxis on cattle but not on pigs. *Echinococcosis* and *trichinosis* raise questions on slaughterhouse geographical control at the scale of the territory, and the identification of various HEV strains highlight different infectious pathways.

Moreover, implementing a pathogen management measure can affect an equilibrium at the levels of the animal and the herds as well as at the level of the territory. The notion of socio-pathosystem provides a framework to capture multi-pathogen infection dynamics under various human management practices. This communication aims at presenting results from different studies carried out by INRA and its partners in Corsica, raising questions on how to implement relevant disease strategies that take into account complex microbial communities and the presence of diverse pathogens under diverse management devices within an animal territory.

P29. Development of MetaXplor: a viral metagenomics database.

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Recent metagenomics-based studies have identified hundreds of unknown viruses living in environmental and ornamental hosts. While genomic, transcriptomic and metagenomic next generation sequencing (NGS) datasets are exponentially increasing, a large part of the virus-related sequences is probably still missed because (i) bioinformatics tools are still under-developed and (ii) our scientific community does not always share datasets. It is therefore crucial to better share, clean, store and analyze these datasets in order to better describe and characterize the virus diversity. In order to fulfill this objective, we have developed a novel Web-accessible NoSQL database – called MetaXplor – that archives reads and contigs obtained from viral metagenomics studies. This database also displays modules of (i) geolocalization of the samples, (ii) searches using similarity-based method (BLAST approaches), (iii) searches using Keywords:, and (iv) phylogenetic placements of the reads on reference phylogenetic trees.

Keywords: Viral metagenomics, bioinformatic tools, database

P30. Air microbiota in animal slaughterhouse: how metagenomic detection can help epidemiological studies?



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