

## Pathology and viral metagenomics, a recent history

Bernardo P.<sup>1</sup>, Fernandez E.<sup>1</sup>, Filloux D.<sup>1</sup>, Albina E.<sup>2,3</sup>, Eloit M.<sup>4</sup>, Roumagnac P.<sup>1</sup>

<sup>1</sup> CIRAD-INRA-SupAgro. UMR BGPI, TA A-54/K, Campus International de Baillarguet, F-34398 Montpellier Cedex 5.

<sup>2</sup> CIRAD, UMR CMAEE, F-97170 Petit-Bourg, Guadeloupe, France

<sup>3</sup> INRA, UMR1309 CMAEE, F-34398 Montpellier, France

<sup>4</sup> Institut Pasteur, Laboratoire de Découverte de Pathogènes, Département de Virologie, 28 rue du Docteur Roux, 75015 Paris, France

philippe.roumagnac@cirad.fr

Human, animal and plant viral pathologies have greatly benefited from recent metagenomics development. Viral metagenomics is a culture-independent approach used to investigate the complete viral genetic populations of a sample. The last decade, metagenomics concepts and techniques that were first used by ecologists, progressively spread into the scientific field of viral pathology. The sample, which has been a fraction of ecosystems for ecologists, became for pathologists organisms that host millions of microbes and viruses. This new approach, providing without *a priori* high-resolution qualitative and quantitative data on the viral diversity, is now revolutionizing the way pathologists decipher viral diseases. This review describes the very last improvements of the high throughput next generation sequencing methods and discusses the applications of viral metagenomics in viral pathology, including discovery of novel viruses, viral surveillance and diagnostic, large-scale molecular epidemiology, and viral evolution.