

## VIRAL DISCOVERY THROUGH VIRAL METAGENOMICS

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The last decade has seen a rapid increase in identification of known and novel viruses. This has primarily been facilitated by new molecular tools and with the advent of high throughput sequencing technologies. Within the context of plant virology, viral metagenomics approaches are becoming more and more attractive to identify viruses circulating in 1) insect vectors, 2) agricultural plants (symptomatic and non-symptomatic), 3) non-cultivated plants that act as reservoir species. Using viral metagenomics approaches, our research group have identified numerous plant-infecting single stranded (ss) DNA viruses in the families *Geminiviridae* and *Nanoviridae* in both cultivated and non-cultivated plants around the world. In addition of this, a large number of novel viruses have also been identified from plants remain to be assigned to new taxons. Nonetheless, data from these studies clearly shows that we have largely underestimated the diversity plant-infecting ssDNA viruses and some of the many of identified viruses are challenging the current viral taxonomy and certain previously held hypothesis of the distribution, host range and origin ssDNA plant viruses.