

Next generation sequencing platforms for potato virus hunting, surveillance and discovery

Abstract.

Potato (*Solanum tuberosum* L.) is a key alternative to maize crop in Kenya. However, pests and diseases affect the yields. Information on Irish potato virology is continually patchy. Viral disease dynamics require constant updating to track new and novel agents. Efforts to mitigate viruses and crop breeding for tolerance can be determined this way. In Kenya, key potato viruses include: Potato Leaf Roll Virus (PLRV), Potato Virus X (PVX), Potato Virus S (PVS) and Potato Virus Y (PVY). Detection of these viruses has been through symptomatology, serology and nucleic-acid approaches. Molecular biology has revolutionary developments in sequencing technologies influencing diagnosis of plant viruses. Massive parallel sequencing has promoted detection, identification and discovery of novel viruses in plants without use of antibodies or prior virus knowledge. Complete viral genomes can be sequenced from asymptomatic and symptomatic samples. Viral metagenomics, diversity and genome variability can be deduced this way. Next generation sequencing platforms bring robustness, timeliness and affordability to virus detection. However, few studies have attempted to utilize it in unravelling potato virology beyond the routine detectable agents in the country. The current study reviews diagnosis of Irish potato viruses in Kenya against the techniques used, comparing them to next generation sequencing.

Authors:

Alfred Alinda, Rose Onamu, David Read, Genevieve Thompsons, John Muoma