



VIRTIGATION – Emerging viral diseases in tomatoes and cucurbits: Implementation of mitigation strategies for durable disease management

Deliverable 2.3 Protocols for full genome sequencing

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1 PUBLISHABLE SUMMARY

The deliverable 2.3 (D2.3) compiles the protocols for full length genome sequencing of circular DNA and linear RNA viruses designed to study virus populations, their diversity, geographical distribution and evolution.

In order to develop protocols for full genome virus sequencing *Cucurbitaceae* (*Cucurbita pepo*) and *Solanaceae* (*Solanum lycopersicum*) plant samples infected with Tomato leaf curl New Delhi virus (ToLCNDV), Tomato yellow leaf curl Sardinia virus (TYLCSV) and Tomato brown rugose fruit virus (ToBRFV) were collected by **CSIC** and **KUL**.

The protocols allow for the in-depth profiling of DNA and RNA virus populations in infected plant samples in 3 steps: 1) Enrichment of viral RNA and DNA, 2) Virus sequencing using Oxford Nanopore technology, 3) Sequencing data analysis with the Genome Detective online analysis tool designed by EW (D2.4).