



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

Deliverable 2.2 Sample collection

Due Date:	30 th November 2022
Submission Date:	30 th November 2022
Dissemination Level:	CONFIDENTIAL (CO)
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Project acronym: VIRTIGATION	Project Number: 101000570
Start date of project: 1 st June 2021	Project duration: 48 months, until 31 st May 2025



... received funding from the European Union's Horizon 2020 research and innovation
... der grant agreement No 101000570. This output reflects only the author's view and the
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1 PUBLISHABLE SUMMARY

The deliverable 2.2 (D2.2) includes a list of virus infected plant samples collected in participating countries that will be used to develop protocols for full length viral genome sequencing, study virus populations, their diversity, geographical distribution and evolution.

In order to develop protocols for full genome virus sequencing infected plant samples of *Solanaceae* (*Nicotiana benthamiana*, *Solanum lycopersicum*) and *Cucurbitaceae* (*Cucurbita pepo*) were collected and provided by **CSIC**, **JKI** partners, **KUL** and Belgian local tomato growers, while to study virus populations, diversity and evolution the infected plant samples of *Cucurbitaceae* (*Cucumis sativus*, *Luffa aegyptiaca* and *Momordica charantia*) and several weed varieties were collected in India and provided by **NRI** partner.

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 provided by **KUL**, **CSIC**, **JKI partners** and will be used for Nanopore sequencing followed by the bioinformatics analysis of all full-length genomic virus sequences. Meanwhile, the metagenomic analysis will be performed for ToLCNDV infected plant samples provided by **NRI** in collaboration with India. The Nanopore-based sequencing approach will be used to profile virus genomic sequences in cucurbit and weed host samples to study potential reservoirs for ToLCNDV virus evolution and spread. Collection of samples in Europe remains constrained by national regulations for quarantine viruses and those limitations will have to be addressed.