# Additional Table and Figures

**Table S1.** *Primer sequences for RT-qPCR to detect viral accumulation and assess photosynthesis and the Calvin cycle pathway*

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| **Name** | **Sequence (5' to 3')** | **Size (bp)** |
| *Viral Primers* | |  |
| FCP-F | ATCAAAGGGTGCGAGGGATA | 226 |
| FCP-R | GTCCCCTTTCACTCCCTCAT |
| CCP-F | TGTGAGGCAAATTTCAGGGG | 210 |
| CCP-R | ACGTCGGGCATATTGGATTG |
| CR3-F | TGCTGAATCTCTGTCGTTGC | 223 |
| CR3-R | ATGCACAACCAACCAACCAA |
| *Photosynthesis Pathway Primers* | |  |
| spPsbN-F | CAGCGACCCTAGTTACCATCTTTC | 119 |
| spPsbN-R | TCCATGTTCTTCGAATGGATCTCT |
| spPsbA-F | AGCCTATGGGGTCGTTTCTG | 236 |
| spPsbA-R | CCTATAGCTGCAGAAGTCGGA |
| spPsbC-F | CGCGCATTTGTATGGTCTGG | 227 |
| spPsbC-R | AAACCAGTAGGGCCTTGAGC |
| spPsaA-F | TGGATCACTTAGCCACGCTT | 201 |
| spPsaA-R | GGCCCCGATACTACCACTTG |
| *Calvin Cycle Pathway Primers* | |  |
| spRbcL-F | ACCGATGGACTTACCAGCCT | 181 |
| spRbcL-R | GCAGTGCTTTGAACCCAAATACA |
| spRbcS1-F | GTCCGCCGACTTTACTTCCATCT | 265 |
| spRbcS1-R | CAGCTTCCACATGGTCCAGTAT |
| spRca-F | GAGAAGGTGAACGAGAGGCTT | 193 |
| spRca-R | TAATGGCATCTGCGTTAGCGT |
| spFBA5-F | ATGACATCAAGAAATGCGCCG | 150 |
| spFBA5-R | CTTCTGCTGCAACCTTTGGGC |
| *Housekeeping Gene Primers* | |  |
| spACT\_F | GTTATGGTTGGGATGGGACA | 199 |
| spACT\_R | GTGCCTCGGTAAGAAGGACA |

**Fig. S1** Representative photographs of plants from the six treatment groups under both growth conditions. Side-view photographs of wild-type sweetpotato plants that were either healthy (Wt-H) or infected with SPFMV (Wt-F), SPCSV (Wt-C), or both viruses (Wt-FC), as well as transgenic sweetpotato plants expressing RNase3 of SPCSV that were either healthy (R3-H) or infected with SPFMV (R3-F). Plants were grown in the growth chamber (GC) or at the NaPPI facility (NaPPI) and were photographed at 31 dpt.

**Fig. S2** Effects of viral infection on PSII of sweetpotato plants as characterized by ChlF imaging.Measurements of PSII parameters were carried out over 29 dpt in wild-type and transgenic sweetpotato plants. Data are shown as the mean ± SE (n = 7−10). Tables on the right display data-fitted model mean values of the six groups clustered in different subsets (Subs.) by Tukey’s HSD test according to their significance (Sig.). (A−D), The response of photosystem II (PSII) was assessed by minimum fluorescence in the dark-adapted state (F0) (A), maximum fluorescence in the dark-adapted state (Fm) (B), variable fluorescence in the dark-adapted state (Fv) (C), and variable fluorescence in the light-adapted state (Fv’) (D).

**Fig. S3** Analyzed top-view images of sweetpotato plants from the NaPPI plant phenotyping platform. Top-view images of wild-type sweetpotato plants that were either healthy (Wt-H) or co-infected with SPFMV and SPCSV (Wt-FC) from 3 to 17 dpt. Photographs were obtained using the three imaging systems from the NaPPI facilities: visible-light image (RGB); ChlF represented by variable fluorescence in the dark-adapted state (Fv), photochemical quenching (qP), and effective quantum yield of PSII (ФPSII); and TIR imaging. False-color images of ChlF parameters display a heat map color scale from dark blue to red ranging from 0 to 700 for Fv and from 0 to 1 for qP and ФPSII, whereas the TIR parameter is represented by a heat map color scale from blue to red ranging from the lowest to the highest temperature.



**Fig. S1**

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**Fig. S2**



**Fig. S3**