

## Detection of sweet potato virus C, sweet potato virus 2 and sweet potato feathery mottle virus in Portugal

CARLA M.R. VARANDA, SUSANA J. SANTOS, MÔNICA D.M. OLIVEIRA, MARIA IVONE E. CLARA,  
MARIA ROSÁRIO F. FÉLIX

Laboratório de Virologia Vegetal, Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Apartado 94,  
7002-554 Évora, Portugal

Received September 10, 2014; accepted May 12, 2015

**Summary.** – Field sweet potato plants showing virus-like symptoms, as stunting, leaf distortion, mosaic and chlorosis, were collected in southwest Portugal and tested for the presence of four potyviruses, sweet potato virus C (SPVC), sweet potato virus 2 (SPV2), sweet potato feathery mottle virus (SPFMV), sweet potato virus G (SPVG), and the crinivirus sweet potato chlorotic stunt virus (SPCSV). DsRNA fractions were extracted from symptomatic leaves and used as templates in single and multiplex RT-PCR assays using previously described specific primers for each analyzed virus. The amplified reaction products for SPVC, SPV2 and SPFMV were of expected size, and direct sequencing of PCR products revealed that they correspond to the coat protein gene (CP) and showed 98%, 99% and 99% identity, respectively, to those viruses. Comparison of the CP genomic and amino acid sequences of the Portuguese viral isolates recovered here with those of ten other sequences of isolates obtained in different countries retrieved from the GenBank showed very few differences. The application of the RT-PCR assays revealed for the first time the presence of SPVC and SPFMV in the sweet potato crop in Portugal, the absence of SPVG and SPCSV in tested plants, as well as the occurrence of triple virus infections under field conditions.

**Keywords:** sweet potato; viruses; Portugal

Sweet potato (*Ipomoea batatas* Lam.), a member of the *Convolvulaceae* family, is an important crop for food security and ranks among the 10 most important food crops worldwide (Clark *et al.*, 2012). It is produced by vegetative propagation, which contributes to the rapid spread of pathogens, particularly viruses (Valverde *et al.*, 2007). The host range of sweet potato feathery mottle virus (SPFMV), sweet potato virus C (SPVC), sweet potato virus G (SPVG), sweet potato virus 2 (SPV2) and sweet potato chlorotic stunt

virus (SPCSV) is limited, with few exceptions, to plants in the *Convolvulaceae* family (Loebenstein *et al.*, 2003). SPFMV, SPVG, SPV2 and SPVC, previously considered a strain of SPFMV (Untiveros *et al.*, 2010), belong to the genus *Potyvirus*, and SPCSV to the genus *Crinivirus*. They form ca. 850 nm long flexuous particles, which embody single-stranded positive-sense RNA genome. Potyviruses are transmitted in a non-persistent manner by aphids, and the crinivirus SPCSV in a semi-persistent manner by whiteflies (King *et al.*, 2012).

SPVG, SPVC, SPV2 and SPFMV are disseminated in several countries (Valverde *et al.*, 2007; Li *et al.*, 2012), however, to our knowledge, only SPV2 was detected in sweet potato plants growing in Portugal (Ateka *et al.*, 2007). SPCSV has been detected in Africa, Israel, Indonesia, Spain, United States and in south and central America (Tairo *et al.*, 2005; Valverde *et al.*, 2007). SPCSV acts synergistically with several

---

E-mail: carlavaranda@uevora.pt; phone: +351 266760851.

**Abbreviations:** CP = coat protein; M-MLV = moloney murine leukemia virus; NJ = neighbor-joining; SPCSV = sweet potato chlorotic stunt virus; SPFMV = sweet potato feathery mottle virus; SPV2 = sweet potato virus 2; SPVD = sweet potato virus disease; SPVC = sweet potato virus C; SPVG = sweet potato virus G; U = units