DISEASE NOTES

First Report of *Garlic common latent virus* Infecting Garlic in Serbia

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Garlic common latent virus (GarCLV; genus *Carlavirus*, family *Betaflexiviridae*) is one of the most common viruses in garlic (*Allium sativum* L.) crops in the Mediterranean area (Katis et al. 2012). In June 2011, garlic plants showing virus-like symptoms including mild mosaic and yellow streaks on leaves followed by growth reduction were observed in one bulb crop in the Ljutovo locality (North Bačka District) in Serbia. Affected plants occurred throughout the field and disease incidence was estimated at 30%. A total of 25 symptomatic plants were collected and tested using commercial double-antibody sandwich (DAS)-ELISA diagnostic kits (Bioreba AG, Reinach, Switzerland) for the presence of several *Allium* viruses including GarCLV, *Onion yellow dwarf virus*, *Leek yellow stripe virus*, and *Iris yellow spot virus* (Pappu et al. 2005). Commercial positive and negative controls were included in each assay. GarCLV was detected serologically in 22 out of 25 garlic samples, but no other tested viruses were found. The virus was mechanically transmitted

from an ELISA-positive sample (553-11) to five plants of each *Chenopodium quinoa* and *A. sativum* 'Bosut' using 0.01 M phosphate buffer (pH 7). All inoculated *C. quinoa* showed local chlorotic lesions, while *A. sativum* 'Bosut' developed mild mosaic, 4 and 14 days postinoculation, respectively. For further confirmation of the virus identity, total RNA from all naturally and mechanically infected garlic plants was extracted with the RN Plant Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructio subjected to reverse transcription (RT)-PCR. RT-PCR was carried out with One-Step PCR Kit (Qiagen) using GarCLV-specific primer pair, 1-GCLV and 2-GCLV (Parrano et al. 2012), designed to amplify a 960-bp fragment covering the entire coat protein (CP) gene. Total RNA extracted from healthy garlic leaves, as well as molecular-grade water, were included as negative controls in the RT-PCR analysis. A product of the expected size was obtained from all naturally and mechanically infected garlic plants, but not from healthy controls. The amplified product derived from isolate 553-11 was purified (QIAquick PCR Purification Kit, Qiagen) and sequenced directly in both directions using the same primer pair as in RT-PCR (GenBank Accession No. KP208802). Multiple sequence alignment of the 553-11 isolate CP sequence with those available in GenBank, conducted with MEGA 5 software (Tamura et al. 2011), revealed that Serbian garlic isolate showed the highest nucleotide identity (97.9%; 100% amino acid identity) with GarCLV isolate from South Korea (AF538951). Garlic is widely and traditionally grown in Serbia and the impact of viruses on garlic production may be significant, but so far little is known about the identity and the occurrence of specific viruses. To our knowledge, this is the first report of GarCLV on garlic in Serbia. Although the distribution and economic impact of GarCLV on garlic crops in Serbia still needs to be investigated, the presence of this pathogen is of great importance regarding its demonstrated ability to compromise garlic production.

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