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**First Report of *Onion yellow dwarf virus*, *Leek yellow stripe virus*, and *Garlic common latent virus* in Garlic in Washington State.** H. R. Pappu, Department of Plant Pathology, Washington State University, Pullman 99164; B. C. Hellier and F. M. Dugan, USDA-ARS, Western Regional Plant Introduction Station, Washington State University, Pullman 99164. *Plant Dis.* 89:205, 2005; published on-line as DOI: 10.1094/PD-89-0205C. Accepted for publication 23 November 2004.

Washington State ranks fourth in the country in garlic (*Allium sativum*) production (2). The impact of viruses on garlic production may be significant in Washington State, but little is known about the occurrence or identity of specific viruses (2). The USDA-ARS Western Regional Plant Introduction Station (WRPIS) collects, maintains, and distributes garlic accessions. As part of the regeneration process, accessions are grown in field conditions at the WRPIS farm in Pullman, WA. In June 2004, several WRPIS accessions developed symptoms indicative of viral infection, primarily chlorotic spots and yellow stripes on leaves and scapes. Cultivars Georgia Fire and Georgia Crystal showed more than 90% incidence of symptomatic plants. Some chlorotic spots appeared similar to those caused by *Iris yellow spot virus* on other *Allium* spp. such as *A. cepa*. However, enzyme-linked immunosorbent assay (ELISA), as well as polymerase chain reaction (PCR) with IYSV-specific primers (1) did not reveal the presence of IYSV. Degenerate, group-specific primers to potyviruses (3) and carlaviruses (courtesy of S. D. Wyatt) were used on total nucleic acids extracted from each symptomatic plant with reverse transcription (RT)-PCR. The samples ( $n = 26$ ) gave an RT-PCR product of the expected size with the group-specific potyvirus RT-PCR test. One sample was positive with the carlavirus group RT-PCR test. RT-PCR products from both tests were cloned and sequenced. Comparisons with sequences in GenBank showed that all but one had *Onion yellow dwarf virus* (OYDV), whereas one sample had a mixed infection of OYDV and *Leek yellow stripe virus*. Sequence analysis showed that the carlavirus was *Garlic common latent virus*. Sequence identities ranged from 95 to 99% for each of the viruses when compared with those available in GenBank. All samples were then tested for each of these viruses with commercially available antisera. Results of ELISA confirmed the findings of RT-PCR. To our knowledge, this is the first report for each of these garlic viruses from Washington State. This finding prompts the need for evaluating all garlic accessions for the potential impact of these viruses on garlic germ plasm conservation and distribution.

*References:* (1) L. J. du Toit et al. *Plant Dis.* 88:222, 2004. (2) R. M. Hannan

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