

DISEASE NOTE

PREVALENCE OF SAFFRON LATENT VIRUS (SaLV), A NEW POTYVIRUS SPECIES, IN SAFFRON FIELDS OF IRAN

S. Parizad¹, A. Dizadji¹, M. Koochi Habibi¹, S. Winter², S. Kalantari³, F. Garcia-Arenal⁴ and M.A. Ayllón⁴¹Department of Plant Protection, College of Agriculture and Natural Resources, University of Tebran, Karaj, Iran²German Collection of Microorganisms and Cell Cultures, DSMZ, Braunschweig, Germany³Department of Horticultural Science, College of Agriculture and Natural Resources, University of Tebran, Karaj, Iran⁴Centro de Biotecnología y Genómica de Plantas. Universidad Politécnica de Madrid (UPM)-Instituto Nacional de Investigación Agraria y Alimentaria (INIA), Campus de Montegancedo, Pozuelo de Alarcón 28223, Madrid, Spain; Departamento Biotecnología-Biología Vegetal, E.T.S.I. Agronómica, Alimentaria y de Biosistemas, UPM, 28040 Madrid, Spain

Saffron (*Crocus sativus*, Iridaceae), a crop widely grown in Iran, was checked in 2011-2015 for the presence of potyviruses collecting a total of 890 leaf tissue samples. DAS- or ACP-ELISA were performed using a *Potyvirus* genus-specific and other commercial kits (DSMZ, Germany) against 16 different viruses, including three potyviruses, i.e. bean yellow mosaic virus (BYMV), turnip mosaic virus (TuMV) and soybean mosaic virus (SMV), previously reported from *C. sativus* (Grilli Caiola and Faoro, 2011). The results showed that 641 samples (>70%) reacted positively only with *Potyvirus* genus-specific and bean common mosaic virus (BCMV)-specific antibodies. The coat protein (CP) gene and 3'-terminal sequence of the saffron potyvirus was amplified using generic potyvirus primers PV21/T7 and PV1/SP6 (Mackenzie *et al.*, 1998). The deduced CP sequence shared only 69% amino acid identity to BCMV. The complete 9693 nt genome sequence [excluding poly(A)tail] of isolate Ir-Kh1 was obtained by primer walking and deposited in GenBank (accession No. KY562565). Whole genome nucleotide sequence analysis showed highest identity value of 69% with East Asian passiflora virus (EAPV, KP114137) and 68% with SMV (AJ310200), bean common mosaic necrosis virus (BCMN, HG792063) and wisteria vein mosaic virus (WVMV, AY656816). Based on the current species demarcation criteria for *Potyviridae* (Adams *et al.*, 2005), the saffron-infecting virus is a new species in the *Potyvirus* genus tentatively named saffron latent virus (SaLV), grouping into the BCMV subgroup of the genus. The presence of SaLV was verified in all 70 ELISA-positive samples by RT-PCR using SaLV-specific primer pair For/Rev (5'-ACCATACATTG-CAGAGACAGC-3'/ 5'-CGAAAGGTGGTAGAACCACTC-3'), designed on the CP gene. The high prevalence of SaLV may be due to vegetative propagation of saffron, which cannot undergo an effective selection because of the latency of infections.

Adams M.J., Antoniw J.F., Fauquet C.M., 2005. Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Archives of Virology* **150**: 459-479.

Grilli Caiola M., Faoro F., 2011. Latent virus infections in *Crocus sativus* and *Crocus cartwrightianus*. *Phytopathologia Mediterranea* **50**: 175-182.

Mackenzie A.M., Nolan M., Wei K-J., Clements M.A., Gowanlock D., Wallace B.J., Gibbs A.J., 1998. Ceratobium mosaic potyvirus: another virus from orchids. *Archives of Virology* **143**: 903-914.

Corresponding author: A.Dizadji
E-mail: adizaji@ut.ac.ir

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FIRST REPORT OF THE UREDINIAL AND TELIAL STATES OF *PUCCINIA HERACLEI* IN PAKISTANA. Ishaq¹, N.S. Afshan², A.R. Niazi¹ and A.N. Khalid¹¹Department of Botany, Faculty of Life Sciences, Quaid-e-Azam Campus, University of the Punjab, Lahore, Pakistan²Centre for Undergraduate Studies, Faculty of Science, Quaid-e-Azam Campus, University of the Punjab, Lahore, Pakistan

During a uredinological survey carried out in September 2011 in Deosai Plains, Pakistan, leaves of the medicinally important herb *Heracleum candicans* Wall. were found to be infected with a rust fungus. Uredinia were amphigenous, scattered, minute. Urediniospores were globose to subglobose, hyaline to light brown, (21-) 24-33 × (24-) 31-34 (-39) μm; wall hyaline, (2.1-) 2.8-4 (-4.4) μm thick, echinulate; germ pores 1-2, tending to be equatorial. Telia were small, scattered, pulverulent. Teliospores were 1-2 celled, 1-celled spores globose to subglobose, hyaline, 23-30 × 27-36 μm; wall 2.8-4.2 μm thick, 3-5 (-7) μm thick at apex, pedicel up to 12 μm long. 2-celled spores ovate, hyaline to light brown, 23-28 × 32-44 (-47) μm; wall 3-5 μm thick, reticulate, 3-5 μm thick at apex, pedicel broken mostly, up to 7 μm long. Based on these morphological traits and spore dimensions, the rust was identified as *Puccinia heraclei* Grev., a sample of which was deposited in LAH Herbarium (LAH Herbarium No. 1204) of the University of the Punjab, Lahore. It has previously been reported on *Heracleum sphondylium* Bourq. ex Reut. in Britain (Wilson and Henderson, 1966). The aecial stage of this taxon has previously been reported from Murree hills of Pakistan on same host by Arthur and Cummins (1933). To the best of our knowledge it is first record of uredinial and telial states of *P. heraclei* in Pakistan.

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Arthur J.C., Cummins G.B., 1933. Rusts of Northwest Himalayas. *Mycologia* **25**: 397-406.

Wilson M., Henderson D.M., 1966. British rust fungi, Cambridge University Press, Cambridge.

Corresponding author: A. Ishaq
E-mail: aamna_ishaq@yahoo.com

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