



Natural occurrence of *Ornithogalum mosaic virus* newly reported on gladiolus in India

Charanjeet Kaur¹, S.K. Raj^{1*}, S.K. Snehi¹, A.K. Goel² and R.K. Roy²

¹ Molecular Plant Virology, CSIR- National Botanical research Institute, Rana Pratap Marg, Lucknow-226001, Uttar Pradesh, India; ² Botanic Garden, CSIR-National Botanical Research Institute, Rana Pratap Marg, Lucknow-226001, Uttar Pradesh, India

*E-mail: skraj2@rediffmail.com

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Gladiolus is an important ornamental plant, grown for the floriculture industry in India. More than 110 cultivars are being maintained at the National Botanical Research Institute (NBRI), Lucknow. However, the quality and quantity of gladiolus flowers have been greatly reduced in the last two to three years due to virus infections of commercial importance. During December 2010 symptoms of mosaic, chlorotic spots on leaves and floral deformations were observed in 27 gladiolus plants growing at gardens of NBRI, Lucknow, India. Cucumber mosaic virus (CMV) and potyvirus infections have been recorded on gladiolus (Katoch *et al.*, 2003); therefore the infection of these viruses was suspected. Plants with appropriate symptoms were tested for the presence of CMV and potyviruses by Western blot immunoassays. Three out of five samples were found positive with the antiserum for a potyvirus isolated from *Narcissus sp.* (Aminuddin *et al.*, 1999) but none reacted positively to CMV antiserum (PVAS 242a, ATCC, USA).

To confirm the identity of these viruses, RT-PCR was performed using CMV and potyvirus specific primers, and the total RNA of symptom-bearing and symptomless leaf samples of gladiolus isolated using the RaFlex Total RNA isolation kit (GeNei, Bangalore, India). Several attempts failed to amplify any RT-PCR amplicon using the coat protein gene specific primers of CMV (AM180922/AM180923) (Srivastava, 2003). RT-PCR using a pair of degenerate oligonucleotide primers (Pot 1 and Pot 2) designed for Potyviridae (Gibbs & Mackenzie, 1997) resulted in amplicons of expected size (~1.5 Kbp) from leaf samples of symptom-bearing gladiolus (3/5) but not from the healthy ones (Fig. 1). The amplicons obtained from three symptom-bearing samples were bi-directionally sequenced and the resulting consensus sequence was deposited in GenBank (Accession No. JF682235). BLASTn analysis (JF682235) revealed the highest sequence identity (87-88%) with the polyprotein gene sequence of the *Ornithogalum mosaic virus* (OrMV) isolates including those from *Iris tingitana* (AY994107, AF203528, FJ618533); *Narcissus* spp. (AJ493580); *Vanilla fragrans* (AY845013, AY845014) and *Ornithogalum thyrsoides* (AF080587) and a 78% sequence identity with that of the OrMV gladiolus virus isolate GLA-11 from the Netherlands (FJ573184).

Phylogenetic analysis was performed using MEGA 4.0 tool (Tamura *et al.*, 2007). This revealed the closest relationship of the virus isolate (JF682235) with isolates of OrMV from *Narcissus* . (AJ493580), *I. tingitana* (AY994107, FJ618533, AF203528) and *Vanilla* . (AY845013, AY845014) (Fig. 2), which suggests the identification of an OrMV-related isolate in gladiolus in Lucknow, India. The existence of OrMV from India on *I. tingitana* has been previously reported (Chandel *et al.*, 2006) but there is no record of natural occurrence of OrMV in gladiolus except from the Netherlands. The natural occurrence of OrMV on gladiolus is a new report from India that may have a phytosanitary impact on gladiolus export.

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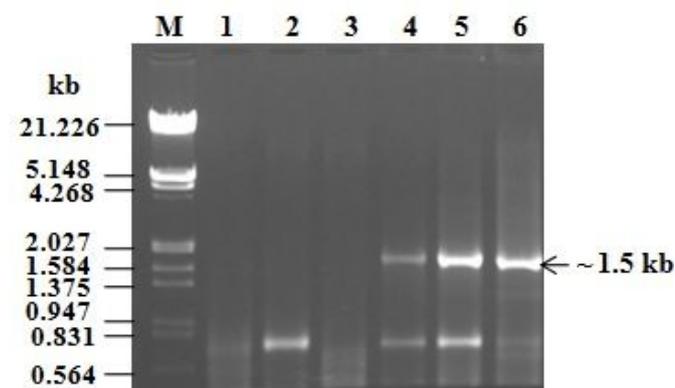


Figure 1

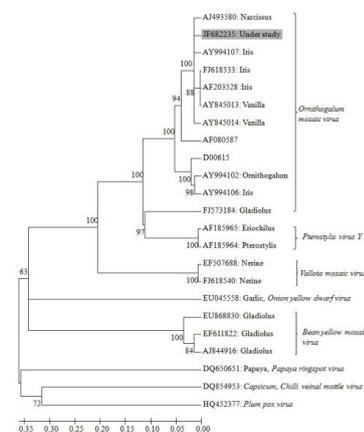


Figure 2

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