First report of the detection of *Bean yellow mosaic virus* (BYMV) on *Tropaeolum majus*; *Hippeastrum spp.* and *Liatris spp.* in South Africa

A. Schulze[1], R. Roberts[1,2] and G. Pietersen[1,2]

[1]FABI, Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria, 0002 South Africa.

[2]Agricultural Research Council-Plant Protection Research Institute, Pretoria, South Africa.

The potyvirus, *Bean yellow mosaic virus* (BYMV) is an economically important plant virus which infects many leguminous crops (family *Fabaceae*) as well as members of the *Liliaceae*. BYMV has been detected in South Africa on *Freesia* spp., *Gladiolus hortulanus, Lathyrus odoratus, Lupinus albus, Viola odoratus* (Gorter, 1977) and *Pisum sativum* (Jooste et al., 2001), but few further studies have been conducted on this virus locally. During the current study, a RT-PCR capable of generic detection of potyviruses (Zheng *et al*., 2010) was utilised to detect these viruses from plant samples submitted by growers and previously shown to contain potyvirus-like flexuous rod-shaped particles by electron microscopy. Plant material of these were deposited in a local virus repository (National Plant Virus and Antiserum Collection, Agriculture Research Council- Plant Protection Research Institute, Pretoria). The RT-PCR is directed at a 350 bp region of the nuclear inclusion body gene and the primer pair were the published NIb2F and NIb3R pair (5'-GTITGYGTIGAYGAYTTYAAYAA-3'; 5'-TCIACIACIGTIGAIGGYTGNCC-3'). All samples yielding amplicons of the expected size from the RT-PCR reaction were subjected to Sanger sequencing. Five samples (Accessions 91/0266, 92/0259, 94/1815, 95/0987, 95/0971) had nucleotide sequences indicative of BYMV infection when aligned to the cognate region of 48 potyvirus sequences previously deposited in GenBank and occurred in the same clade as BYMV in Maximum Likelihood derived dendrograms derived from these alignments. The sources had, respectively, 90%, 94%, 94%, 97% and 99% nucleotide identity with various BYMV strains. The presence of BYMV in these samples was confirmed by $F(ab')_2$ ELISA using antiserum specific to BYMV-Scott (Barnett et al., 1984) with BYMV-Scott itself used as positive control (Average $OD_{405nm} = 2.33$). All five samples yielded absorbance values (Average OD_{405nm} between 1.044 and 1.893) which were higher than at least two standard deviations above the mean of the healthy control ($OD_{405nm} > 0.517$), thereby confirming the presence of BYMV. This identification is therefore based on the initial presence of potyvirus like particles, amplification with generic potyvirus PCR primers, nucleotide sequence of the amplicons obtained and also by a positive reaction in ELISA. This confirms the previous finding in South Africa of BYMV from *L. albus* (sample 94/1815 collected April, 1994 from Pietermaritzburg; GenBank accession KX907126), infection of BYMV on *Freesia* spp. (sample 95/0971; collected July, 1995 from the Quarantine Station, Marikana, GenBank accession: KX907125), but also reports the infection of BYMV on *Liatrus spp.* (sample 95/0987 collected July, 1995 from Pretoria; GenBank accession: KX757143) and *Hippeastrum spp.* (sample 91/0259 collected July, 1991 from Brits; GenBank accession KX907124), and for the first time in this country and internationally on *Tropaeolum majus*

(sample 91/0266 collected July, 1991 from Pietermaritzburg; GenBank accession: KX757144).

References

OW Barnett et al. VI International Symposium on Virus Diseases of Ornamental Plants 164. pp209. 1984.

GJMA Gorter, Index of Plant Pathogens and the diseases they cause in cultivated plants in South Africa. Science Bulletin 392 Department of Agricultureal Technical services, South Africa. 1977

AEC Jooste et al. African Plant Protection 7. pp59, 2001.

L Zheng *et al*. *Plant Pathology 59*. pp211. 2010.