



First reports of *Lettuce big-vein associated virus* and *Mirafiori lettuce big-vein virus* infecting lettuce in Saudi Arabia

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Lettuce (*Lactuca sativa*) is a common vegetable in Saudi Arabia, being cultivated on more than 4000 ha either in open fields or in greenhouses. In March 2014, field lettuce crops were surveyed in the Riyadh region and around 40% of plants were observed to have virus-like symptoms including vein clearing, stunting, deformed leaves and thickening of the main veins (Fig. 1). These symptoms resemble those caused by Lettuce big-vein disease (LBVD), an important disease of lettuce worldwide. Two viruses are associated with LBVD, *Lettuce big-vein associated virus* (LBVaV, *Varicosavirus*) and *Mirafiori lettuce big-vein virus* (MiLBVV, *Ophiiovirus*) which are transmitted by the soil fungus *Oplidium brassicae* (Verbeek *et al.*, 2013). Nineteen samples (17 symptom-bearing and two symptomless) were collected from four fields and total RNA was extracted (Chatzinasiou *et al.*, 2010). The extracted RNA was subjected to a multiplex reverse transcription (RT) PCR for the simultaneous detection of LBVaV and MiLBVV, using specific primers amplifying 296 and 469 bp fragments of their CP genes, respectively (Navarro *et al.*, 2004). The presence of *O. brassicae* was confirmed in the rootlets of all the symptomatic lettuce plants using light microscopy (Rochon, 2009). The results showed that 16 of the 17 lettuce samples showing symptoms were infected with LBVaV, nine with MiLBVV and eight with both LBVaV and MiLBVV. The two symptomless samples were found to be negative for both viruses. Two PCR products from each virus extracted from different plants were randomly selected for direct sequencing. The sequences were submitted to GenBank (Accession Nos.KJ701037, KJ701038, KJ701039 and KJ701040) and analysed using BLAST. Both sequences of LBVaV had 98% nucleotide (100% amino acid) identity with a sequence from Spain (AY366413) and 99% nucleotide (100% aa) identity with sequence from Japan (AB190528).

The two MiLBVV sequences showed 98% (99% aa) and 99% nucleotide identity (99% aa) with an isolate from Spain (AY366418). To our knowledge, this is the first report of the occurrence of LBVD-associated viruses LBVaV and MiLBVV in Saudi Arabia. Further surveys for monitoring the incidence and distribution of both LBVaV and MiLBVV in Saudi Arabia are in progress.

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Figure 1

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