Identification and characterization of four new plant pararetroviruses (genus: *Badnavirus*) infecting ornamental crops

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Abstract

Floriculture crops include foliage plants, patio, and potted ornamentals. In the USA this industry was valuated at 4.80 billion for 2020, and despite the COVID-19 global pandemic is up 9% from the last year (USDA, NASS 2021). Plant viruses affecting ornamental crops can be detrimental reducing the plant vigor and visual appearance. Some viral diseases are transmitted during vegetative propagation and others are transmitted by vectors. Disease detection is vital for the management of viral diseases, and without accurate detection the disease control is limited. The detection of infectious (episomal) forms of plant pararetroviruses in the genus *Badnavirus* is difficult due to the common presence of endogenous virus sequences integrated into the plant genome and their potential for disease activation. The objectives of this research were the identification and characterization of four new badnaviruses present in the ornamental crops Ming aralia (*Polyscias fruticosa*), Aglaonema ‘Chinese evergreen’ (*Aglaonema modestum*), cycads (*Zamia fischeri*), and *Spiraea x bumalda* ‘Anthony Waterer’. This resulted in the complete genome sequence for Polyscias mosaic virus (PoMV), *Aglaonema bacilliform virus* (ABV), Cycad leaf necrosis virus (CLNV), and *Spiraea yellow leafspot virus* (SYLSV). Additionally, detection primers were designed, and some protocols are suggested for routinary virus detection of these badnaviruses. These results are useful for both plant pathologists and plant breeders.