

Complete Genome Sequence and Analysis of Carnation Italian Ringspot Virus from *Erigeron annuus* (L.) Pers. in Korea

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In this study, we aimed to study carnation italian ringspot virus (CIRV) in *Erigeron annuus* (L.) Pers. in Bonghwa County, Korea. The collected samples showed mosaic and malformation symptoms. To identify the virus species, we performed high-throughput sequencing, reverse transcription polymerase chain reaction, and cloning. The virus was confirmed to be an unreported species, and therefore we performed genome sequencing of the samples. The complete genome was 4,746 nucleotides in length. The CIRV contained five open reading frames (ORFs), and it showed the typical features of members of the genus *Tombusvirus*. Phylogenetic analyses revealed that CIRV isolates had the highest nucleotide identities with the CZ isolate (95.89%) from Korea. In recent years, these viruses have sporadically been reported in floral scent and medicinal plants. This research found the first natural host infected with CIRV, and provides baseline information to determine the correlation between weeds and crops.

Key words: Carnation Italian ringspot virus, *Erigeron annuus* (L.) Pers., Tombusvirus

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