K-21 Detection of cymbidium mosaic virus and odontoglossum ringspot virus by RT-PCR from Doritaenopsis orchid plants in Korea
Su Min Kim and Sun-Hee Choi. Department of Horticulture, Biotechnology and Landscape Architecture, Seoul Women’s University 621 Hwarango, Nowon, Seoul 139-774, Korea
Cymbidium mosaic virus (CymMV) and Odontoglossum ringspot virus (ORSV) were detected from Doritaenopsis orchid plants (Doritis × Phalaenopsis) showing bad growth condition by reverse transcription- polymerase chain reaction (RT-PCR). Total RNAs were isolated from Doritaenopsis leaves using SDS- proteinase K/phenol extraction, and RT-PCR was conducted with virus-specific primers in order to amplify the CymMV and ORSV coat protein region. As a result, out of a total of 30 samples, 18 samples were detected with CymMV CP fragments (60%), 14 samples were detected with ORSV CP fragments (46.7%). Twelve samples (40%) were revealed to be infected with both viruses. Sequence analysis showed that the CymMV CP nucleotide sequence of Doritaenopsis ‘Mantefon’ shared 98% homology with the Chinese SMi2 strain and Doritaenopsis ‘Superstar’ shared 99% homology with the DEK28 strain. The ORSV CP nucleotide sequence of Doritaenopsis ‘Mantefon’ shared 100% homology with the Chinese FS4 strain and Doritaenopsis ‘Greenbear’ shared 99% homology with the Hangzhou strain.

K-22 A simple and rapid diagnostic method for Tomato yellow leaf curl virus without DNA extraction
Tomato production is clearly affected by many bacterial, fungal and viral diseases. Of them, Tomato yellow leaf curl virus (TYLCV) causes severe damage to economical losses of tomato production in Korea since 2008. So, it is highly required that a rapid and simple diagnostic method for TYLCV is developed. In convention methods, the DNA extraction procedure from suspicious tomato tissues is indispensable for TYLCV detection using gene-based detection systems, such as PCR. We newly designed a primer set specific to TYLCV genomic DNA and a pair of primers specific to tomato β-tubulin gene as an internal control were synthesized for direct detection of TYLCV in tomato tissues without DNA extraction procedure. The primer set using direct PCR showed clear detection of TYLCV infection in one tube from tomato leaf tissues collected from farms, suggesting that the primer set allows a simple, economical and rapid diagnosis of TYLCV from tomato plants for practical use.

K-23 Epidemiological identification and molecular genetic characterization of Tomato chlorosis virus population in Korea
Ye-Ji Lee1,2, Eui-Jun KI, Hae-Ryun Kwak1, Mi-Kyeong Kim1, Jung-Kyun Seo1, Chang-Seok Kim1, Suk-Chan Lee2* and Hong-Soo Choi2. Crop Protection Division, National Academy of Agricultural Science, Rural Development Administration, Suwon 441-707, Korea; 1Department of Genetic Engineering, Sungkyunkwan University, Suwon 440-746, Korea
Tomato chlorosis virus (ToCV) is a whitefly-transmitted, phloem-limited, bipartite Crinivirus. In 2013, severe interveinal yellowing and chlorosis symptoms characteristics of ToCV infections were observed in tomato greenhouses in Korea. High population densities of whitefly, which could transmit ToCV, were also observed on tomato crops in all the greenhouses investigated. The presence of ToCV was confirmed by a specific RT-PCR in the collected tomato samples. Interestingly, most samples infected with ToCV were co-infected with TYLCV in Korea. The complete genomic sequences of 10 isolates from different areas in Korea were characterized. This study is the first to report ToCV infection and analysis of the complete genome sequences of ToCV isolates obtained in Korea. In addition, I might provide important insights into the molecular variation and genomic structure of ToCV isolates in Korea as well as genetic relationships with the isolates from other countries. Comparisons of nucleotide identity and genome structures between the ToCV Korean isolates and the previously reported isolates showed that the length of RNA1 was mainly 8594 nt except for the Jeju isolate from Korea and full-length nucleotide size of RNA2 was in range of 8242-8247 nt. Analysis of the complete nucleotide sequences of the ToCV Korean isolates with all other ToCV isolates showed that the overall sequence identities were ranged from 97.4 to 99.7% for RNA1 and from 97.5 to 99.7% for RNA2. The phylogenetic trees constructed using the full length nucleotide sequences of ToCV RNA1 and RNA2 revealed that the ToCV isolates could be clustered into three groups. It suggested that ToCV Korean isolates have three independent origins.

K-24 Molecular characterization of the Cucurbit aphid-borne yellows virus isolates based on analyses of complete genome sequences
Hae-Ryun Kwak1, Mi-Kyeong Kim1, Eun-A Kim1, Hee-Ju Lee2, Jun-Chul Shin2, Ye-Ji Lee1, Jung-Kyun Seo1, Chang-Seok Kim1, Jeong-Soo Kim1 and Hong-Soo Choi2. Crop Protection Division, National Academy of Agricultural Science, Wanju 565-851, Korea; 1Vegetable Research Division, National Institute of Horticultural and Herbal Science, Wanju 565-852; 2Department of Plant Medicine, Andong National University, Andong 760-749, Korea
The complete genome sequences of twenty-two isolates of Cucurbit aphid-borne yellows virus (CABYV), collected from melon showing yellowing symptom in Korea during the years 2013-2014, were determined and analyzed comparatively along with previously reported CABYV genome sequences. The complete genomes were found to be 5680-5684 nucleotides in length and encode six open reading frames (ORFs) which are separated into two regions by a non-coding internal region (IR) of 199 nucleotides. Their genomic organizations are typical for a member of the genus Polerovirus. Based on phylogenetic analyses of complete nucleotide (nt) sequences, CABYV isolates were divided into four groups; the Asian, Mediterranean, Taiwanese, and R groups. The CABYV Korean isolates were clustered with the Asian group over 94% nt sequence identity. On the other hand, nt sequence identities of the CABYV Korean isolates were 87-89% to the Mediterranean group, 88% to the Taiwanese group, 81-84% to the CABYV-R group, and 72% to another Polerovirus, Melon aphid-borne yellows virus (MABYV). Recombination an important evolutionary force in the genetic diversification of CABYV population in Kor.