제 4주제 : New Disease Identification(4-01～4-54)

4-01. Identification of *Colletotrichum* spp. associated with pepper anthracnose in Korea (oral)

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Pepper anthracnose is one of the major limiting factors in pepper production. During last over 10 years, *Colletotrichum gloeosporioides* has been known as the most prevalent species among five *Colletotrichum* spp. involved as anthracnose causing agents. Recently, however, the change of major species with pepper anthracnose has been proposed. Identification study was performed on 12 test isolates collected from anthracnose disease symptoms on pepper during 2001-2002 and 25 reference isolates obtained from several other host plants. The identification of the isolates with morphological observation and ITS region sequence comparison resulted that 11 ones from 12 test isolates colleted from pepper anthracnose during 2001-2002 were identified as *C. acutatum*. PCR using species-specific primers designed from ITS region sequence suggested a rapid diagnosis method in identifying *C. acutatum* from *C. gloeosporioides*.

4-02. New Epidemic Rots on Fruit, Stem, and Root of Paprika Caused by *Nectria haematococca*

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Since 2000, severe rots on aerial and underground parts of paprika(*Capsicum annum* L.) has occurred in most cultivation glasshouses throughout the country. Totally 169 isolates of a fungus were consistently isolated from the diseased plant tissues of fruits, stems, branches, and roots collected from 19 farms in six provinces. Anamorph stage of the fungus was identified as *Fusarium solani* based on morphological characteristics. However, the fungus readily produced sexual structure of perithecia on infected plant tissues and on agar medium. Since the fungus formed abundant perithecia by single isolate, it was considered as a homothallic strain of *Nectria haematococca*, the teleomorph of *F. solani*. Irregularly globose perithecia with orange to red color formed sparsely to gregariously on dead tissues of fruits and basal stems at the late infection stage, which is a diagnostic sign for the disease. Abundancy of perithecium varied among isolates and they sized 125-220㎛ in diam. Asci enveloping eight ascospores were cylindrical and measured 60-80×8-12㎛. Ellipsoid to obovate ascospores are two-celled and measured 11-18×4-7㎛. Ascospores are hyaline, slightly constricted at the central septum, and revealed longitudinal striations that is a typical trait of the species. This fungus that has never been reported in Korea previously became a threat to paprika cultivation because of its strong pathogenicity and nationwide distribution.

4-03. Cloning and Characterization of a new tobamovirus infecting *Hibiscus rosa-sinensis*)

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A near full-length sequence of a new tobamovirus infecting *Hibiscus rosa-sinensis* L. was determined. The genome consists of 58 nucleotides (nt) 5' UTR, followed by a 4.9 kb ORF which methyl transferase helicase domain (128 kDa) , readthrough protein RNA dependent RNA polymerase (RdRp) 185 kDa and a 52 kDa protein. The 128 kDa protein had a maximum homology of 51.4 % to TMGMV and amino acids (aa) were 54.3 % identical to TMV- vulgare strain. The 185 kDa RdRp had a maximum homology of 53.5% to TMV-Ob and KGMMV-Y and a 59.6% homology at the aa level to CGMMV-SH. The MP gene encodes 282 aa and its theoretical molecular weight is 30.4 kDa. The nt and aa sequence identities of MP ranged from 38.8% to 43.9% and 30.9% to 37.9%, respectively. The CP gene encodes 163 residues and with a theoretical molecular weight of 18.2 kDa The (nt) and aa sequences of the CP were 46.9 % to 51.6% and 45.3% to 57.1% identical to other tobamoviruses, respectively. The predicted virion origin of assembly (OAS) was located in the CP gene. Phylogenetic trees generated based on the nt and aa sequences of RdRp, MP and CP genes indicated that this new virus clustered with subgroup II tobamoviruses. Although the CP ORF of this virus shared a high nt and aa sequence identity with *Sunn-hemp mosaic virus* (SHMV), Western analysis showed that it is serologically unrelated to SHMV. We propose the name Hibiscus virus S (HVS) for this Singapore isolate. This is the first report on a near full-length sequence of a *Tobamovirus* that infects hibiscus.

4-04. Occurrence of crown gall of chrysanthemum caused by *Agrobacterium tumefaciens*.

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Incidence of crown gall on lower stem of chrysanthemum, *Chrysanthemum morifolium* Ramat., was first observed at Hwasung, Gyeonggi, Korea in 2001. Tumors on the stem were 1.5-2 ㎝ in size and semi-round with rough surface texture of dark brown color. Four strains of bacteria isolated from the tumor tissues were characterized. Their colonies were convex, glistening, circular with an entire edge, and white to tannish-cream in color on PDA plus $CaCO_3$. They were gram negative, oxidase positive, and growing on D1M agar. The bacterial isolates inducing gall formation in chrysanthemum were identified as *Agrobacterium tumefaciens* based on biochemical and physiological characteristics, fatty acid profile using Sherlock Microbial Identification System, and substrate utilization patterns using Biolog Identification System. Young chrysanthemum plants inoculated with the bacteria developed typical galls within two to three weeks. Seedlings of tomato and slices of carrot roots also produced typical galls two to three weeks after inoculation. This is the first report on crown gall of chrysanthemum in Korea.