

Genome diversity of members of the genus *Tobamovirus* and its implications

Ki Hyun Ryu

**Plant Virus GenBank, Division of Environmental
and Life Sciences, Seoul Women's University**

The genus *Tobamovirus* is one of the best-characterized plant virus groups, viruses in this genus infect plants in a wide range of species throughout the world and cause substantial crop losses. Various species of the genus cause diseases in tobacco, tomato, pepper, orchid, cucumber, melon, bean, cactus, or crucifer plants. There are 22 members (species) and 1 tentative species in the genus *Tobamovirus*. These viruses are easily transmitted mechanically, and are very stable both physically and chemically. Tobamoviruses infect almost all cells within the systemic host plant, reaching high titers. Tobamoviruses usually cause disease by preventing proper chloroplast development, resulting in leaves and fruit with a mottle and mosaic pattern of light and dark green on stunted plants. Tobamoviruses can be grouped based on host range and genome structure and sequence identities. Fully sequenced tobamoviral genomes share 43 - 83 % identity. There are at least 4 different tobamoviruses described in cucurbit crops in the world thus far: *Cucumber green mottle mosaic virus* (CGMMV), *Cucumber fruit mottle mosaic virus* (CFMMV), *Kyuri green mottle mosaic virus* (KGMMV), and *Zucchini green mottle mosaic virus* (ZGMMV). Their full genome sequence information and comparative analysis have been described. They can be divided into two subgroups based on comparisons of sequences and phylogenetic analysis: subgroup I comprising the strains and isolates of CGMMV and subgroup II including CFMMV, KGMMV (formerly referred to as CGMMV-C), the Yodo strain of KGMMV (KGMMV-Y; formerly referred to as CGMMV-Y) and ZGMMV. Very recently, we have named a new tobamovirus, we call as *Cactus mild mottle virus* (CMMoV), from infected cactus crop. Phylogenetic analysis of the known tobamoviruses including this cactus-infecting tobamoviruses revealed that they can be categorized into at least 5 different subgroups in all coding regions which is quite matched to host ranges suggesting tobamovirus-host coevolution is occurred during the long periods. Some studies on tobamovirus populations have noted either RNA sequence stability or viral evolution, depending on

the evolutionary conditions placed on the virus and methods of detection of mutants and haplotypes. An examination of 53 isolates of *Tobacco mild green mosaic virus* (TMGMV), a species of the genus *Tobamovirus*, from different parts of the world was noted for the relatively small sequence diversity values obtained. In a greenhouse experiment, a field population of TMGMV from *Nicotiana glauca* was serially passaged through *N. tabacum* cv. Samsun and found to have maintained the original sequence even after 23 passages. Populations of the type species of the genus, *Tobacco mosaic virus* (TMV) directly derived from local lesions have been shown to harbor a great variety of variants, some of which are thought have arisen from mutation. Studies on a necrotic lesion mutant of TMV found that certain physiological changes in the host induced the rapid domination of this mutant in the TMV population. These experimental studies indicate that TMV is capable of rapid evolution if sufficient selective pressure were provided, a trait of viruses of both plants and animals. In this study, the population diversity of progeny viruses of KGMMV in consecutive serial passages of two systemic hosts, zucchini squash and cucumber plants, established from genetically identical viral RNA, were investigated and were discussed.