dwarf virus (SDV, *Sadwavirus*) and Citrus mosaic virus (CiMV) which is reclassified as an isolate of SDV (SDV-CiMV, *Sadwavirus*). RT-PCR methods could detect SDV-CiMV and CTV from leaf samples of unshui citrus. CTV was the prevalent and SDV-CiMV was not common in Jeju island. RT-PCR product of SDV-CiMV-JJ12 were cloned and sequenced. Sequence of the isolate revealed that it was 96.9 % identical to SDV-CiMV-Jp isolate at the nucleotide level. SDV-CiMV-JJ12 was propagated on *Physalis floridana* and sequencing of entire sequences of genome is in progress. Variability of SDV in Jeju island was confirmed by sequence comparisons and restriction mapping analysis.

4-45. Virus-resistant and susceptible transgenic *Nicotiana benthamiana* plants expressing coat protein gene of *Zucchini green mottle mosaic virus* for LMO safety assessment

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Transgenic *Nicotiana benthamiana* plants harboring and expressing coat protein (CP) gene of *Zucchini green mottle mosaic virus* (ZGMMV) were generated for both virus-resistant screening and complementation analysis of related viruses and environmental safety assessment (SA) of living modified organism (LMO) purposes. Transformation of leaf disc of *N. benthamiana* was performed using *Agrobacterium*-mediated method and the pZGCPPGA748 containing the ZGMMV CP and NPTII genes. Two kinds of transgenic homozygous groups, virus-resistant and -susceptible lines, were obtained by screening of challenging homologous virus for T1 generations. Complementation of CP-deficient related virus was analyzed using the susceptible line of ZGMMV. These two pathologically different lines can be useful for host-virus interactions and LMO environmental SA.

4-46 Pathogenicity of infectious *in vitro* transcripts and comparison of RNA3 of *Alfalfa mosaic virus* Korean isolates

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Two Korean isolates of *Alfalfa mosaic virus* (AMV-AZ, AMV-KR) were isolated from azuki bean and potato plants, respectively, and their pathologies were confirmed on some susceptible host plants including pepper, tobacco and red bean plants. Full length cDNAs to RNA1, RNA2 and RNA3 of the two Korean strains were amplified using the long-template reverse transcription (RT)-polymerase chain reaction (PCR) method. RT-PCR products covering entire regions for the three AMV genome RNAs were cloned. RNA transcripts were synthesized in vitro from each clones using T7 RNA polymerase and infectivity test was performed in 9 reassortment sets of transcripts. All the combinations of reassorted transcripts were found to be infectious when inoculated onto *Nicotiana benthamiana* plants, and were not distinguishable to those of wild types. The full-length