

Update on Potato Mop-Top

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Mop-top, caused by Potato mop top virus (PMTV), is spread by soil-inhabiting powdery scab 'fungus', *Spongospra subterranean* and the virus is becoming increasingly important in the Columbia basin of Washington over the last few years. Tobacco rattle virus, the causal agent of corky ring spot disease is spread by several species of nematodes. Both viruses cause necrosis in tubers. PMTV occurs in the Andean region of South America, Northern and Central Europe and Asia. PMTV was first reported in the US from Maine. Subsequent surveys followed by testing of potato tubers produced in the USA and Canada confirmed its presence in both countries including Idaho and Washington in PNW. PMTV is now well-established in several potato-growing regions of the country but the genetic diversity of the virus is not known. Information on the genetic variability would be useful in devising more effective virus detection tools that would enhance the virus detection and elimination.

Supported by a Coordinated Agricultural Project grant from USDA National Institute of Food and Agriculture, a study was initiated to characterize various PMTV isolates at the molecular level and build a database of genetic fingerprints of the virus populations that exist in the country. As a first step, the complete genome of an isolate from Washington State was characterized. Sequence comparisons of the WA isolate with other known sequences revealed that the RNA Rep-encoded RdRp protein and the RNA CP-encoded coat protein displayed >99% amino acid identity with those of two Nordic (RdRp) and several European and North American isolates (CP) respectively. The RNA TGB-encoded TGB 1 and TGB 3 protein sequences had >99% amino acid identity with the corresponding proteins of the Czech and Danish isolates, whereas the TGB 2 protein is identical to the Colombian isolates. Phylogenetic analysis of the viral genes of the WA isolate reflected the close relationship among the WA and European isolates. We carried out restriction mapping (RFLP) of the viral genome of corresponding DNA of RNA TGB and RNA CP showed that the WA isolate is considered RNA TGB-II and RNA CP-B types, which are prevalent in Europe and other parts of world. Two distinguishable restrictotypes of RNA CP and RNA TGB were found to occur in tubers as mixed infections. Similar analysis of restriction digestion pattern of partial RNA CP and partial RNA TGB revealed that the WA isolate is of restrictotypes RNA TGB-II and RNA CP-B. Based on the RFLP, the WA isolate could be considered as a severe isolate, however, biological characteristics attributed to the severe isolate require to be confirmed. In summary, the complete genome characterization of PMTV from the US is a step toward developing sensitive and rapid diagnostics and could be useful in designing RNAi based approaches for virus resistance.